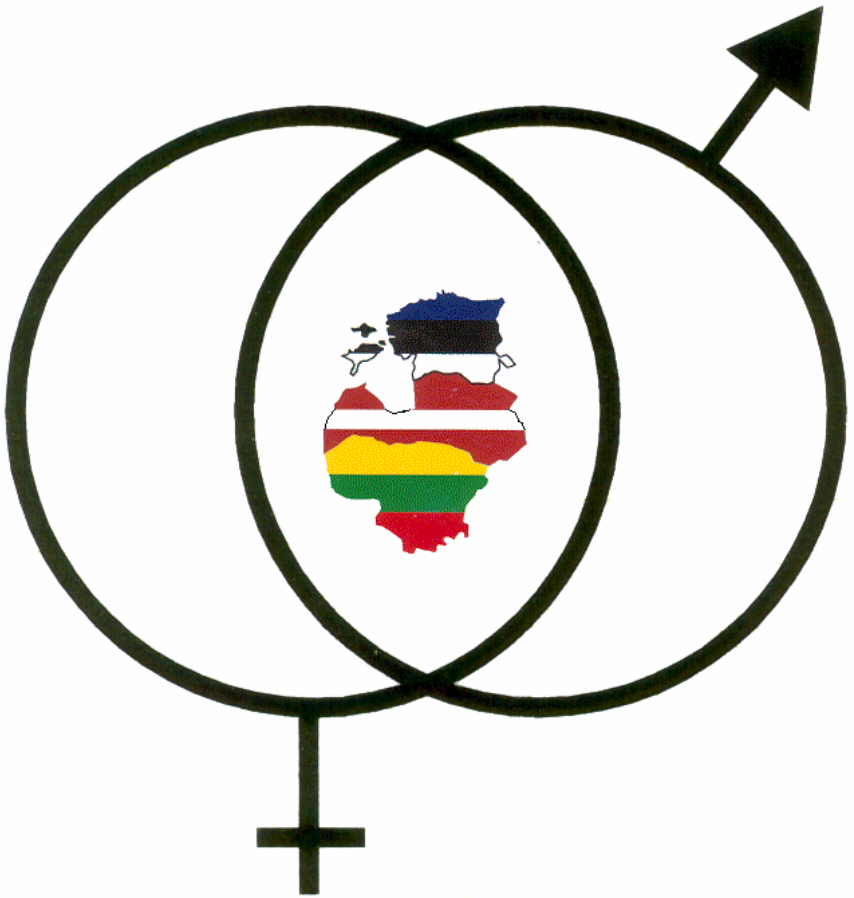
# ANIMAL BREEDING in the BALTICS



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**ORGANIZER:**
Institute of Animal Science of Estonian Agricultural University
Estonian Animal Breeding Association

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Nordic Gene Bank for Farm Animals
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## WELCOME FROM THE CHAIRMAN OF THE ORGANISING COMMITTEE

Ten years ago the leaders of animal breeding departments of Baltic agricultural universities decided to restore scientific contacts with colleagues. As a result of this agreement, in 1995 Estonia started the tradition of Baltic Animal Breeding Conferences. After two tours around three Baltic States, the conference is coming back to Tartu where it began 10 years ago. Welcome to Estonia!

Scientific contacts have been extended through collaboration between the Nordic countries and many EU member states. For the first month we belong to the EU that gives us new opportunities but also adds responsibilities by open competition. The most important result is that junior researchers of the Baltic States have been acquainted with each other and are actively taking part in international research programmes.

In the proceedings of the conference 458 scientific publications have been published in 10 years. Estonia has been more successful in the number of publications (183), compared to Lithuania (137) and Latvia (85) but in recent years competition has increased. In the future the organizers should guarantee that all publications in the proceedings are prereviewed, entered into international databases (CAB International etc.) and that correct scientific English is used.

In the Baltic States cattle breeding (188) is taking priority over pig breeding (95) in research work as in economy as well. It would be difficult to draw a line between breeding and genetics, therefore the number of studies concerning genetics (37) was surely greater. In this field of study the Baltic States have been remarkably successful during recent years due to Nordic–Baltic joint research programmes.

Competition between countries in breeding work as well as in research is stiff. It is very pleasant that researchers from Finland, Germany, Norway etc. are participating in it. This is the key to a successful future.

Prof Dr Olev Saveli

**CONTENTS**

# INVESTIGATIONS ON SOMATIC CELL COUNT IN SWISS DAIRY PRODUCTION SYSTEMS

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## Introduction

After infertility, mastitis is the second most common reason for involuntary culling in Swiss dairy production (Aeberhard et al., 1997), accounting for 13 % of all cullings. Somatic cell count (SCC) is an appropriate parameter to describe mastitis due to its high genetic correlation of about 0.8 to the susceptibility of mastitis (Dopp et al., 1998). The aim of the present study was to analyse the influence of fixed effects on SCC, with special consideration of typical housing systems in Switzerland.

## Material and Methods

Data was provided by the Swiss Brown Cattle Breeders Association. The analysis was based on the results of monthly milk recording (n = 1,866,242). 1,674 farms out of 15 cantons in Eastern and Central Switzerland were randomly selected for the supply of data. Three zone types (valley, middle, and higher mountain) were considered, according to site altitude, local and traffic circumstances, and topography. The recording was defined on the observation period from January, 1994 to May, 2002. Information on housing system was documented within the linear description of exterior in primiparous cows since January, 1998. Tie-stall barns (n = 1,045) and loose housing systems (n = 629) were differentiated. The time interval wherein housing conditions changed from tie-stall barn to loose housing system was termed 'changing period'.

The performance parameters recorded were: milk yield, fat percentage, protein percentage, lactose percentage, milk urea content, and somatic cell count. According to the plausibility criterions stated by Dopp et al. (1998), 1,866,242 records from 82,775 cows remained for the statistical analysis.

Linear somatic cell score (SCS) was computed to achieve a normal distribution of the data, specified by an international standard. Data analysis was performed applying the MIXED procedure in the SAS statistical package (SAS, 2002). An F-test was conducted to obtain an indication about the importance (level of significance, p) of the fixed effects. The animal was treated as random variable, because the monthly milk recording results were repeated measurements of a cow. The farm, combined with year and season, was also treated as random due to the high number of herds involved in the study.



The following mixed model, based on restricted maximum-likelihood techniques, was finally used to evaluate the influence of fixed and random effects on SCS:

$$Y_{ijklmnopq} = \mu + HS_i + Z_j + CA_k + b_0(my_l) + b_1(fe_m) + b_2(pr_n) + b_3(D/c) + b_4(D/c)^2 + b_5\log(c/D) + b_6[\log(c/D)]^2 + hys_o + animal_p + e_{ijklmnopq}$$

| | | |
|---|---|---|
| $Y_{ijklmnopq}$ | = observation value | |
| $\mu$ | = population mean | |
| $HS_i$ | = fixed effect of the housing system | (i = 1, 2, 3) |
| $Z_j$ | = fixed effect of the zone | (j = 1, 2, 3) |
| $CA_k$ | = fixed effect of calving age within lactation number | (k = 1, 2, ..., 9) |
| $my_l$ | = co-variable milk yield per day | |
| $fe_m$ | = co-variable fat percentage | |
| $pr_n$ | = co-variable protein percentage | |
| $b_0$-$b_2$ | = regression coefficients on linear effects $my_l$, $fe_m$, and $pr_n$ | |
| $b_3$-$b_4$ | = regression coefficients on lin. and quadr. effect of the quotient D/c, with D = day in milk and c = 380 (const.) | |
| $b_5$-$b_6$ | = regression coefficients on lin. and quadr. effect of [log(c/D)] | |
| $hys_o$ | = random effect of herd-year-season | (o = 1, ..., 56,916) |
| $animal_p$ | = random effect of the animal | (p = 1, ..., 82,775) |
| $e_{ijklmnopq}$ | = random residual error | |

## Results

During the period of data collection, 517 farms changed their housing system to cubicles. The median herd size in farms with tie-stall barns was 17.4 and 26.8 in farms with cubicles. An overview about the descriptive statistics of the data set is given in table 1.

All effects were significant on SCS at a level of $p < 0.001$. Least-square-means (LSM) for SCS for the fixed effects of zone and housing system are presented in Figure 1. Highest level of SCS was observed in valley situated farms (2.75), whereas in both, mountain zone 1 (2.48) and 2 (2.56), SCS was at a lower level. The differences between housing systems were comparatively low. Best results were recorded in tie-stall barns (2.53), indicated by a SCS 0.08 lower than in the changing period, and 0.12 lower than in loose housing systems. An overview about the LSM for SCS for calving ages within lactation number is demonstrated graphically in Figure 2. The first and the second lactation were subdivided into three age classes each, third lactation was classified in two groups; lactations greater than 3 were no more subdivided. By far, lowest level of SCS was observed in primiparous cows, increasing continuously to the animals

with lactation number greater than 3 (3.31). Between the calving age classes within lactation number, the differences in SCS were not significant. There was only a slight tendency towards higher SCS in each group of older animals.

Table 1. Means (ξ), standard deviations (sd), minima (min), and maxima (max) of the data set. (n = 1,866,242)

| Trait | ξ | sd | min | max |
|---|---|---|---|---|
| Age at first calving (mo.) | 32.3 | 3.5 | 17.0 | 41.0 |
| Lactation number | 2.9 | 1.7 | 1.0 | 7.0 |
| Milk yield (kg) | 19.92 | 6.57 | 1.0 | 78.0 |
| Fat percentage (%) | 4.07 | 0.55 | 1.5 | 8.5 |
| Protein percentage (%) | 3.44 | 0.37 | 1.5 | 7.7 |
| Lactose percentage (%) | 4.97 | 0.23 | 1.4 | 7.7 |
| Milk urea content (mg/dl) | 26.71 | 8.21 | 2.0 | 60.0 |
| SCC (cells/ml in 1,000) | 171.2 | 354.2 | 5.0 | 997.7 |
| SCS[1] | 2.69 | 1.67 | -1.3 | 9.6 |

[1]calculated with the international formula [SCS = log2 (SCC / 100,000) + 3]

The random effect of herd-year-season explained only a small part of the variance, accounting 3.5 % on the total variance, whereas the random animal-effect explained about 10.0 % of the total variance.

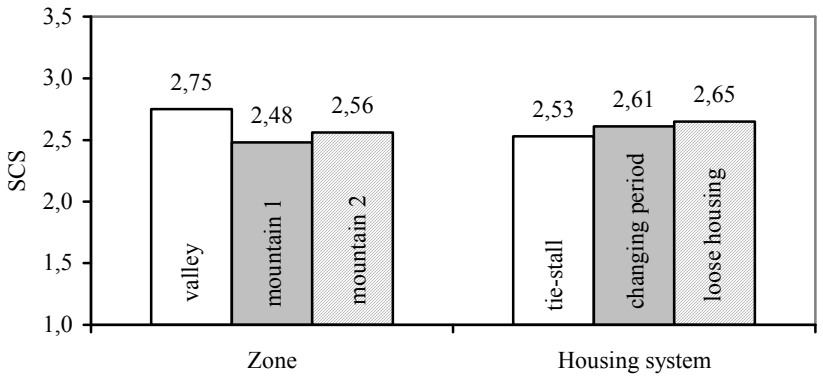


Figure 1. Least-square-means (LSM) for somatic cell score (SCS) of the fixed effects of zone and housing system. Standard errors were at a level of 0.02. (n = 1,866,242)



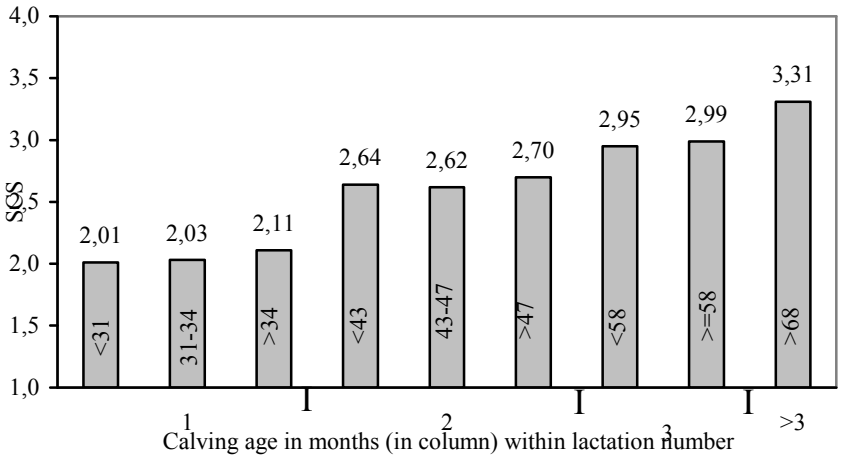


Figure 2. Least-square-means (LSM) for somatic cell score (SCS) for calving age (months) within lactation number. Standard errors were at a level of 0.02. (n = 1,866,242)

**Discussion**

In this study, slightly higher SCS were observed in loose housing systems. Valde et al. (1997) did not find any significant difference in mean SCS between free-stall and tie-stall herds. In the paper of Matzke et al. (1992) less cases of mastitis were identified in loose housing compared to tie-stall barns. Six clusters of risk factors (production indexes, housing, hygiene, health disorders, milking management, and milking machine) to have a potential relationship with the incidence of mastitis were characterised by Elbers et al. (1998). Within the data recording period many farmers changed their housing system from tie-stall barns to loose housing systems. A new housing system means for both, the farmer and the animal, to adapt to a new environment, i.e., new lying, moving, feeding, and milking area. The process of acclimatising may contribute in problems, disorders, and diseases, what means predisposing factors for higher SCS. This fact is confirmed by the increased SCS in the 'changing period'. The highest SCS in loose housing has mainly two reasons: The 'changing period' does not completely contain the real process of adapting to the new environment. That means that problems may have been appeared temporally delayed. Further on, it must be considered that conventional tie-stall barns, in combination with regular outdoor exercise, represent a well adapted environment for producing milk with healthy cows.

According to the present results, Haile-Mariam et al. (2001) also found SCS increasing with parity. The main reason is the greater opportunity for exposure to mastitis-causing pathogens. The calving age within parity also influenced SCS. Mostly, the differences between the classes were not significant, but there was a general tendency towards higher SCS in older animals. This trend was also investigated by Schutz et al. (1990).

Corresponding to the co-variance parameters estimated with the present model, Danuser (1992) found a higher animal variation within herd for SCS, but smaller variation between herds.

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# MICROSATELLITE ANALYSIS FOR MAKING CONSERVATION PRIORITIES AMONG NORTH EUROPEAN CATTLE BREEDS


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**Introduction**

Genetic diversity present in world's domestic animal breeds allows the existence of livestock even in the most extreme environments globally, providing a range of products and functions, needed for livelihood security. Unfortunately, a large number of breeds has been lost and due to limited resources which could be devoted to conservation more breeds are at risk of extinction (Scherf, 2000). Therefore, a decision on a selection of breeds for conservation must be made.

Recently two different approaches utilizing molecular genetic variation to assess conservation priorities have been developed. The Weitzman (1992) approach constructs maximum-likelihood trees based on pair wise genetic distances and suggests that in efficient conservation scheme the total length of the branches on the tree should be maximized. Alternatively, in the Eding et al. (2002) approach the genetic diversity is assessed on estimates of average kinship coefficients between and within populations. The breeds are evaluated for their contributions to a core set of populations, which are constructed such that the kinship within the set is minimal.

Several studies have been made based on one of those approaches in order to evaluate the importance of domestic animal breeds to the conservation of genetic diversity (Thaon d'Arnoldi, 1998; Cañón et al., 2001; Eding et al., 2002; Grigaliunaite et al., 2002; Reist-Marti et al., 2003). The aim of this study was to compare the conservation values these two methods give to the Nordic-Baltic cattle breeds and to investigate relationship between the methods.

**Materials and Methods**

*Cattle breeds:* In the study 35 cattle breeds from Northern Europe and Baltic countries with 11-49 individuals per breed were included. These breeds were: Lithuanian Red (41 individuals analyzed), Lithuanian Black and White (41), Lithuanian White Backed (40), Lithuanian Light Grey (41), Latvian Brown (40), Latvian Blue (40), Danish Red in Latvia (40), Estonian Native (40), Estonian Red

(40), Polish Black and White (30), Ringamåla (20), Fjällnära (15), Väne (18), Bohus Poll (14), Swedish Mountain cattle (41), Swedish Holstein Friesian (44), Swedish Red and White (39), Swedish Red Polled (34), Eastern Finncattle (31), Northern Finncattle (26), Western Finncattle (41), Finnish Ayrshire (46), Finnish Holstein Friesian (43), Icelandic cattle (44), Jutland breed (49), Red Danish (39), Danish Jersey (41), Danish Black Pied (27), Doela cattle (35), Western Fjord cattle (41), Telemark cattle (46), Western Red Polled (36), Eastern Red Polled (11), Blacksided Troender (34), Norwegian cattle (38).

*Genetic loci studied*: In total 1246 individuals were genotyped for 19 microsatellite markers: *INRA005, INRA023, INRA032, INRA035, INRA037, ETH3, ETH10, ETH152, ETH225, HEL1, HEL5, HEL9, HEL13, BM1818, BM1824, BM2113, CSSM66, ILST005* and *ILSTS006* (http://neurocad.lva.lt)

*Statistical analyses*: The quantification of genetic diversity among the breeds was performed using Eding et al. (2002) method and the Weitzman (1992) approach with implementation of Canon et al. (2001) using Chord distance (Cavalli-Sforza and Edwards, 1967).

**Preliminary results and Discussion**

We have analyzed 19 autosomal microsatellites in 35 cattle breeds to quantify the contribution of the breeds on total genetic diversity in the North European area and to determine the effects of breed losses on the diversity. In the quantification of genetic diversity by the method of Eding et al. (2002) the kinships between the breeds were calculated using the weighted log linear model. From the kinship matrix the contributions of the breeds to a core set, which is constructed so that the kinship within the core set of the breeds is minimal, were calculated as described by Eding et al. (2002). Eleven breeds showed contribution values above zero, where Eastern Finncattle was identified as a breed with highest contribution to the genetic diversity in the Nordic-Baltic area (results not shown).

In the set of 35 studied populations there were included old native as well as modern active production breeds. Since the modern cattle breeds normally are not under the risk of extinction, neither need efforts for conservation, a 'safe' set including 11 populations from 8 countries was created. By retaining only the 'safe' set compared to the full set of breeds the genetic diversity presented in the Nordic-Baltic area would be reduced by 1.81 % according to Eding et al. (2002) and by 72 % according to the Weitzman (1992) method. The remaining breeds were one by one included into the 'safe' set and their potential to reduce the loss of genetic variation was evaluated. Results indicated that in addition to the 'safe' set, by preserving one of the non-safe breeds, the loss of genetic diversity would be reduced from 1.81 % to an average of 1.55 % calculated by Eding et al. (2002) and from 72 % to 69 % calculated by Weitzman (1992) method.



The loss of diversity values obtained for single breeds from both methods separately were plotted against each other to study the relationship between the methods. However, no correlation between the values was detected (r = -0.08; Figure 1) indicating that Eding et al. (2002) and Weitzman (1992) approaches give different type of information.

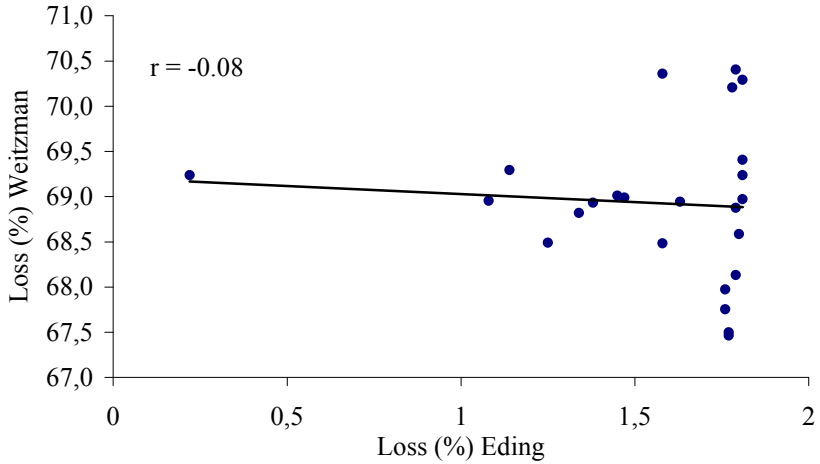


Figure 1. Relative loss (%) of genetic variation when the 'safe' set of breeds plus one particular non-safe breed is retained compared to the full set of breeds.

Weitzman does not take into account within-breed genetic variation and gives higher diversity value for the breeds that have diverged farthest from the root of the tree, while Eding et al. (2002) methods evaluates within- and between-breed diversity and favours populations that are least divergent from the ancient parental populations.

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# FACTORS AFFECTING THE STABILITY OF MILK PRODUCTIVITY TRAITS OF LATVIAN BROWN COWS

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## Introduction

Animal monitoring is an individual control system for animals, which ensures productivity and product quality data for breeding value estimation.

In monitoring rules also monitoring over-surveillance is provided, which in Latvia is done by Pedigree State inspection. All monitored herds are subjects of over-surveillance. According to the instruction of Ministry of Agriculture, monitoring over-surveillance can be done in three days after instant control. Control data are avoided and not used in lactation records if over-surveillance data repeatedly differ from data obtained during cow control (5% in milk yield, 3% in fat content, 2% in protein content).

Temporary fluctuations in milk productivity of cows of different age and physiological condition can be caused by factors of external environment, such as changes in feed ration, lack of drinking water, high air temperatures, changes in milking regime, incomplete milking of cows, animals being in heat, and others (Huth, 1994).

For owners of herds, controllers and pedigree inspectors it is important to know how much milk productivity parameters, subjected to control, can change under the influence of different factors.

Research with Holstein breed animals shows that the repeatability coefficient value equals 42.7%, fat yield = 41.0%, but protein yield = 41.2% (Dematawewa et al., 1998).

Research about repeatability of milk productivity traits shows that the highest value of repeatability coefficient from 0.73 to 0.77 is for milk yield, but the lowest from 0.24 to 0.51 is for fat content in milk (Paura et al., 2003).

The goal of our research is to find out milk productivity traits daily variation and repeatability for animals of different age and physiologic condition.

## Materials and Methods

Research was carried out in the herd of Latvian Brown breed cows at the Training and Research Farm of the Latvia Agriculture University “Vecauce” in 32 days from mid-July till mid-August in 2002. In the trial there were 69 cows in the first and later lactations, reared by one person. The cows were in different phases of lactation at the beginning of the research. On the farm, semi-automatic milking equipment and measuring instruments from the company *De Laval* were used for milking cows, milk yield recording and making samples of milk. 2126 milk samples were analysed for fat,

protein and lactose content in milk laboratory of the Kurzeme Artificial Insemination Station using *Milko-Skan 133B* and *Fossomate-90* in somatic cell counting.

In the summer of 2002 cows were fed on pasture. For fodder, from 4 P.M. till morning, haylage or hay made from the mixture of alfalfa and grass was used. Besides, in evenings cows were also fed with concentrate. There were hot and dry weather conditions during the research, because for 19 days the temperature exceeded 24 °C, reaching the maximum at 31 °C. Also humidity was under 70% for 20 days and reached 95% only on one day.

Statistical processing of the obtained data was used. Repeatabilities of milk productivity traits were estimated from the variance component using intraclass correlation ( $r_w^2 = \frac{\sigma_\alpha^2}{\sigma_\alpha^2 + \sigma_e^2}$ ) and the coefficient of variation (CV %) on the test period.

For variance component estimation the following linear model was used:

$$y_{ijkl} = \mu + \alpha_i + L_j + LF_k + D_l + e_{ijkl}, \text{ where}$$

$y_{ijkl}$ – investigated item; $\mu$ general mean; $a_i$ – cow's effect (random, i = 1…69);
$Lj$ - Lactation (fixed, j = 1...3); $LF_k$ - Lactation phase (fixed, k = 1...3);
$D_l$ – Investigation day (fixed, l = 1…32); $e_{ijkl}$- residual;
Z test was used for comparing coefficient of variation.

**Results**

In the beginning of research, the cows' average milk yield was 17.36 kg and average milk quality parameters were: fat content 4.19%, protein content 3.04%, lactose content 4.79% and logarithm of somatic cells count was (SCC_log) 3.51, corresponding to higher milk class. Changes in milk productivity traits are shown in Figures 1 and 2.

The greatest variation in milk yield for all groups was observed in day 26, when milk yield decreased by 1.75 kg or 10.4%. By evaluating each animal's milk yield fluctuations in research days, we found that the average value of variation coefficient was 9.77%, but the maximum milk yield variation for individual animals exceeded 20%.

The most varying feature was fat content in milk; the average variation coefficient value of each animal was 10.94%. In the research group there were animals whose fat content fluctuation exceeded 30%. We observed drastic fluctuations in fat content during the research. The group's lowest average fat content 3.78% was determined on the second day of the research. But already on the third day it grew to 4.25%, or increased by 12.4%. The fluctuations of protein and lactose content were lower, variation coefficient value - 4.02% and 1.84%, respectively. Changes in the quantity of somatic cells in milk during the days of research were the biggest – 36.94%.



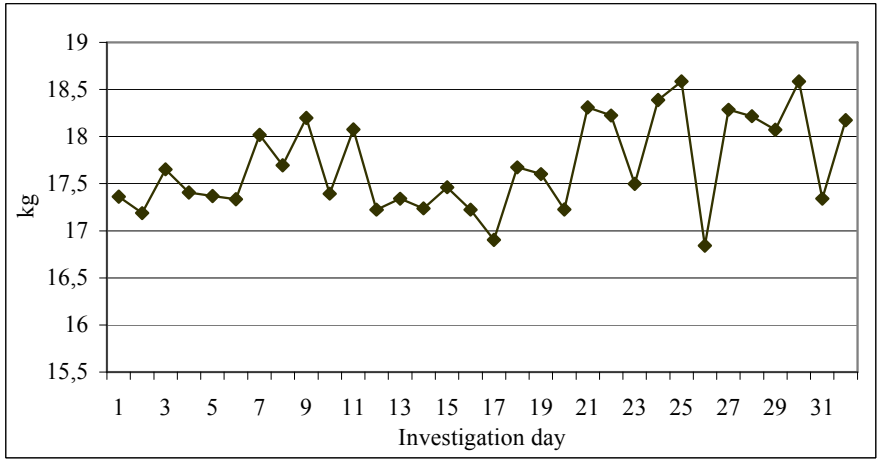


Figure 1. Cows' Average milk yield (kg) on the research days

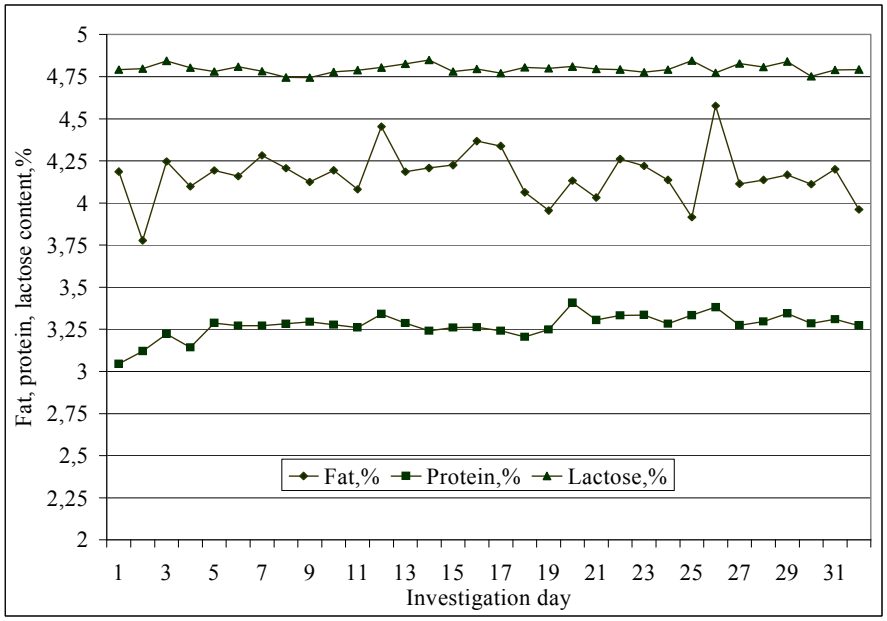


Figure 2. Average fat, protein and lactose content in milk on different research days

Our study revealed that all traits of cow's milk productivity, except only for lactose content in milk, are substantially affected by the age of a cow, lactation phase and day of the research (Table 1).

Table 1. Effect of investigated factor on changes of milk productivity traits

| Factor | *p-value* | | | | |
|---|---|---|---|---|---|
| | Milk yield, kg | Fat content, % | Protein content, % | Lactose content, % | SCC_log |
| Lactation | *** | 0.004** | *** | 0.052 | *** |
| Lactation phase | *** | *** | *** | *** | *** |
| Investigation day | 0.004** | *** | *** | 0.389 | *** |

***p-value* < 0.01; *** *p-value* < 0.001 factor is significant

*SCC_log = log2 (SCC/100 000) + 3 (DA at al.. 1992)*

The variations of milk quantity and content from animals of different age and physiologic status in the days of research were found out by calculating variations and repeatability coefficients (Table 2).

Analysing daily changes in milk productivity traits for cows of different age it can be seen that during the research, the cows in the first lactation showed the lowest fluctuation in all investigated traits, except for somatic cells count in milk. The biggest fluctuation was observed for the cows in the third and later lactations. Their milk yield variation was 10.01% to 11.71% and for fat content 9.49 to 17.01%.

Comparing milk productivity traits, day to day fluctuations for animals of different age and physiologic condition, it can be seen that the second lactation phase is the most stable. It was used to compare if milk productivity traits variation changes are statistically significant. The biggest milk yield variation is in the first lactation phase - 7.76% to 11.11%. For the second lactation animals' milk yield variation substantially exceeded variation coefficient value of the second phase ($p<0.05$). Also for cows being in the third lactation phase the fluctuation of milk yield was high (8.99% to 11.71%). The first lactation animals' fluctuation in the third phase substantially exceeded the second lactation phase fluctuation ($p<0.001$).

The biggest variation in fat content was for animals of the first lactation phase - 8.90% to 17.01%. For cows of later lactation it exceeded fat content in milk, being statistically significant ($p<0.01$) in the second lactation phase. The lowest fat content fluctuation was in the third lactation phase - 5.98% to 9.49%.

Day to day changes for protein and lactose content were between few per cents - from 3.32% to 4.81% and from 1.16% to 2.37%, respectively. For the cows of later lactations, the first and the third lactation phase fluctuation



significantly differed from the second phase fluctuation that was the most stable one ($p<0.05$; $p<0.01$).

During the research, somatic cell count in milk of cows of different age and physiological condition varied within in a wide range from 19.32% to 61.69%.

Table 2. Coefficients of variation (CV, %) and repeatability ($r_w^2$) in different lactation and lactation phases

| Traits | The 1st lactation | | | | | |
|---|---|---|---|---|---|---|
| | The 1st lactation phase n=239 | | The 2nd lactation phase n=64 | | The 3rd lactation phase n=96 | |
| | CV,% | $r_w^2$ | CV,% | $r_w^2$ | CV,% | $r_w^2$ |
| Milk yield, kg | 7.76 | 0.462 | 7.72 | 0.771 | 10.79*** | 0.125 |
| Fat content,% | 8.90 | 0.388 | 8.60 | 0.567 | 6.04 | 0.581 |
| Protein content,% | 3.56 | 0.637 | 3.32 | 0.798 | 3.61 | 0.485 |
| Lactose content,% | 1.36 | 0.768 | 1.16 | 0.696 | 1.46 | 0.437 |
| SCC_log | 56.80 | 0.644 | 61.69 | 0.345 | 26.53** | 0.128 |
| The 2nd lactation | | | | | | |
| | n=335 | | n=192 | | n=128 | |
| Milk yield, kg | 10.43* | 0.629 | 7.72 | 0.743 | 8.99 | 0.125 |
| Fat content,% | 15.74** | 0.161 | 7.28 | 0.600 | 5.98 | 0.581 |
| Protein content,% | 4.81*** | 0.357 | 3.50 | 0.861 | 3.46 | 0.485 |
| Lactose content,% | 2.36** | 0.297 | 1.56 | 0.744 | 1.57 | 0.437 |
| SCC_log | 45.50** | 0.304 | 27.27 | 0.781 | 30.0 | 0.128 |
| The 3rd and > lactations | | | | | | |
| | n=304 | | n=480 | | n=288 | |
| Milk yield, kg | 11.11 | 0.656 | 10.01 | 0.546 | 11.71 | 0.606 |
| Fat content,% | 17.01** | 0.208 | 9.75 | 0.196 | 9.49 | 0.558 |
| Protein content,% | 4.64* | 0.577 | 4.28 | 0.526 | 3.63** | 0.788 |
| Lactose content,% | 2.37* | 0.306 | 1.92 | 0.408 | 1.63 | 0.849 |
| SCC_log | 31.41 | 0.312 | 40.94 | 0.718 | 19.32** | 0.649 |

*p-value* <0.05; ***p-value* < 0.01; *** *p-value* < 0.001 factor is significant

Analysing the repeatability of milk productivity traits, it is seen that fat content in milk is the trait with the lowest repeatability coefficient values (0.161 to 0.558).

Repeatability coefficient values for milk yield were from 0.125 to 0.771.

The amplitude of repeatability coefficient for protein content was from 0.357 to 0.861, and for that of lactose content in milk was from 0.297 to 0.849.

**Conclusions**

1. Cow's age significantly affected the milk productivity traits subjected to the tests. The biggest fluctuation was observed for the cows of the third and later lactations. Their milk yield variation was from 10.01% to 11.71% and fat content variation from 9.49 to 17.01%.
2. The lowest fluctuation of milk productivity traits for cows of different age was observed in the second lactation phase. Milk productivity traits fluctuation for the cows of later lactations in the first phase of lactation exceeded the fluctuation in the second phase statistically significantly ($p<0.05...0.001$).
3. Higher values of repeatability and lower coefficients of variation indicated greater stability of milk productivity traits.

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**EXPERIENCES OF JOINT NORDIC GENETIC EVALUATION**

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**Summary**

The four Nordic countries have agreed to co-operate in semen production of dairy cattle. A joint genetic evaluation is needed to improve the accuracy of across country evaluation of bulls and cows. The need for comparison of cows arises from joint nucleus breeding programmes and bull dam selection.

Combining data from four different countries and integrating the statistical models into one single multiple country model with a unity genetic correlation across countries has not been an easy task. The results show, however, that the joint evaluation is feasible.

The aim of this paper is to give some preliminary results of a joint prediction of breeding values from performance records in Nordic countries. The motivation and the possibilities of the joint Nordic breeding programme are also discussed.

*Keywords: across country evaluation, functional traits, joint breeding programme*

**Introduction**

Accurate comparison and selection of bulls and cows across the Nordic countries will be of great importance in the future since the countries have agreed on joint semen production. To improve the possibilities for such a comparison the breeding organisations have established a new company *Nordic Cattle Genetic Evaluation (NCGE)*, which has a responsibility to develop and run genetic evaluations from joint Nordic data. The company was originally started with four Nordic countries, but recently Norway has withdrawn out from it.

The aim is to run joint genetic evaluation of dairy cattle for milk and fertility traits in 2004 and in full scale for all traits form 2006, when the majority of first crop of jointly owned bulls will have enough daughter information for progeny testing. These Nordic evaluations will then replace the national evaluations. Another advantage in joint evaluation is a possibility for more efficient utilisation of knowledge and resources in the field of genetic evaluation.

In this paper we will discuss the possibilities and difficulties of prediction of breeding values across Nordic countries.

**Data**

Accurate genetic evaluation depends on reliable data on performance, environmental effects and pedigree information. The work until now has shown the pedigree recording as one of the most crucial things in across country evaluation. In the past all Nordic countries gave a new national herd book number to imported animals. In recent years, after joining the Interbull evaluations, the bull ID-number in the country of origin has been linked to this new national herd book number. Hence it was quite easy to identify bulls across Nordic countries. Linking of cows was much difficult. A lot of manual work was needed to build up proper pedigree file for a joint evaluation.

The recording of milk traits is well harmonised across countries. Since the national models were used as a starting point to the Nordic model, the data were edited to fit the national model in each country. This generated some problems during the exercise, since changing the model to fit better with the Nordic data very often required new editing. This is difficult because different coding and numbering of class variables and back transforming are needed. Also comparison of the results across countries has shown to be difficult, when the grouping and renumbering of class variables hides the original management groups.

Characteristic to all Nordic countries is the nation-wide health recording, utilising the information of veterinary treatments, and the use of this information in genetic evaluation and selection. In Finland the veterinarians write down the treatment of a cow on a health card and an AI technician collects the information and sends it forward to the central database. In a recent Nordic study (Valde et al., 2002) some differences were found between countries in disease frequencies. These differences might be due to differences in the true disease incidence, differences in the farmers' attitude to treat the animals, differences in the recording of treatments and differences in calculations of the disease incidence. Although differences in frequencies have an effect on the variance of a trait the results of genetic evaluation with standardised and non-standardized records across countries were very similar.

**Prediction of breeding values**

Genetic evaluation is of fundamental value in animal breeding, since the selection of animals is most accurately carried out by using the estimated breeding values (EBV) or predicted transmitting ability (PTA) of traits in the breeding goal. Good predictions depend upon high-quality data, appropriate models and good estimates of (co)variances.

Good-quality data have been used intensively to study evaluation methods in Finland and other Nordic countries. During the last 20 years much research has been carried out on BLUP methods, which are now the most widely used procedures for predicting breeding values in livestock. Much of the research has



been on milk traits, where sire models have first been replaced by animal models in the early 90'ies and recently by test day models. In Nordic countries other traits have not been neglected, either. In the last decades fertility traits, health traits, conformation traits and calving traits have all been analyzed and used in national evaluation procedures. Predicting the breeding values of functional traits forms the base for the so called "Nordic profile" (Juga, 1998, Juga *et.al.,* 1999), since selection for total merit requires information on all economically important traits.

**Joint Nordic genetic evaluation**

The background for the establishment of NCGE and a development of a joint evaluation system has been described by Juga (2002). Four projects are carried out simultaneously, one in milk traits, one in fertility traits, one in clinical mastitis and one in type traits. The aim is to transfer the national evaluations to a joint Nordic evaluation using performance data of all four Nordic countries.

*Milk traits*

The development of joint Nordic model for milk traits has been carried out as a joint project with Danish and Finnish teams. This work has involved people in Dansk Kvaeg, Danish Institute of Agricultural Sciences, Finnish Animal Breeding Association and MTT Agrifood Research.

The aim is to include test day records from Denmark and Finland and 305 records of three lactations from Sweden using a "Meta model", developed by Mäntysaari (2002). The model will be a single country model with $r_G = 1$ between countries, but a multiple trait model for milk, protein and fat as well as the first, the second and later lactations. The model for environmental effects will follow the current statistical models in respective countries. Additional problems to be solved are correction for heterogeneous variance, accounting for heterosis in breed crosses, blending of foreign information, accuracy of the predicted breeding values and running the Interbull tests for genetic trend.

The combined data on red populations comprises of some 32 million test-day records from Finland, more than six million test-day records and one million 305 day records from Denmark, and more than one million 305 day records from Sweden resulting altogether in more than 40 million observations with approximately five million animals in the joint pedigree file.

Preliminary results show that combining lactation records from one country and TD records from another country with a random regression model is technically feasible even with large nationwide data sets. All the basic elements of the statistical model have already been included and the model runs successfully in the super computer, based in Foulum, Denmark. The results show that the genetic trend for Finnish sires in different lactations (Figure 1) is very similar to the genetic trend of the Finnish national evaluation.

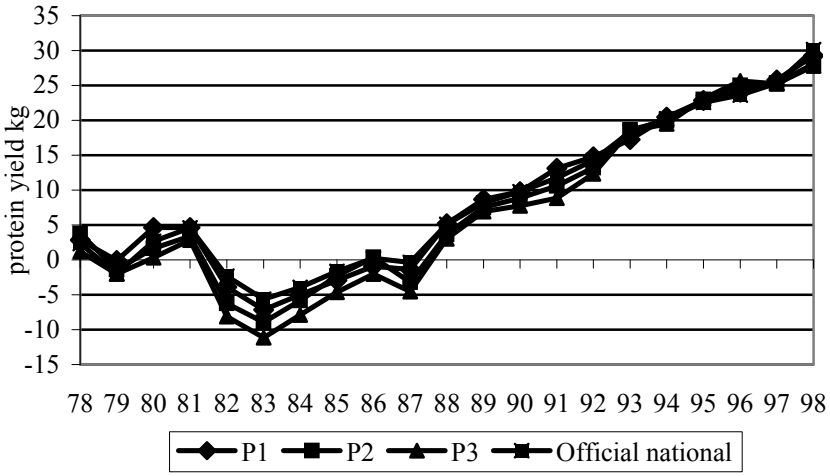


Figure 1. Genetic trend on Finnish sires from the Nordic model on protein yield for the 1st, 2nd and 3rd lactation compared with the official Finnish national evaluation.

Some problems exist, however, in defining a good model for Danish data. Especially the heterosis effects jointly with genetic groups and age x stage of lactation in different breeds have proved to be difficult to model properly.

*Fertility*

The development of Nordic model for fertility traits is carried out in Denmark and Sweden. In fertility traits the heifers will be evaluated for non-return rate, interval from the first to the last insemination, number of inseminations, heat strength and fertility treatments. Cows will additionally be evaluated on interval from calving to the first insemination. The development and testing of models for fertility traits includes testing the traits as single traits or multiple traits, heifers and cows with different parities and single versus multiple country models. Like in the milk traits, the model for environmental effects followed the current statistical models in respective countries, but some changes have been made to better account for e.g. age effects. The preliminary results of joint evaluation of fertility traits have been published by Fogh et al. (2003).

The preliminary results show that the genetic trend for fertility traits is negative due to the high use of Holstein in recent decades. From Figures 2, 3 and 4 can be seen that the so called "holsteinisation" has started first in Denmark, where almost all old Friesian cattle (BW) has been replaced with Holstein breed



(US). The development has been rapid also in Sweden, but in Finland the process is still ongoing. We need to recognise this difference and take account of heterosis if we want to compare the current Holstein populations correctly across Nordic countries.

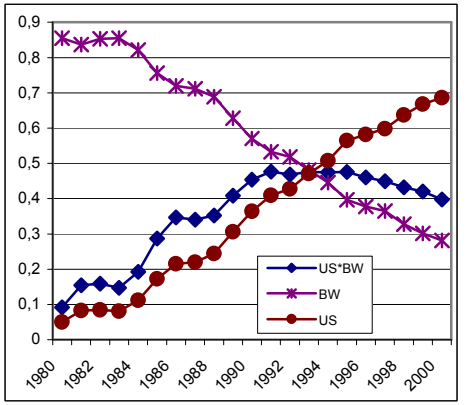


Figure 2. Heterozygosity and breed proportions in Sweden. Friesian cattle (BW), Holstein (US).

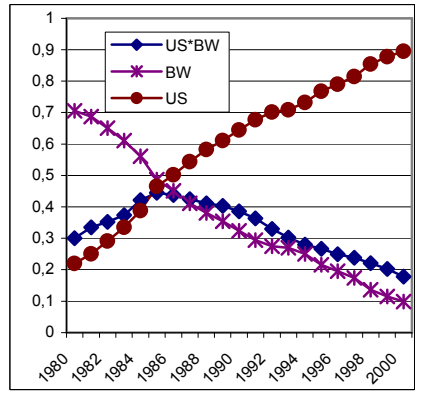


Figure 3. Heterozygosity and breed proportions in Denmark. Friesian cattle (BW), Holstein (US).

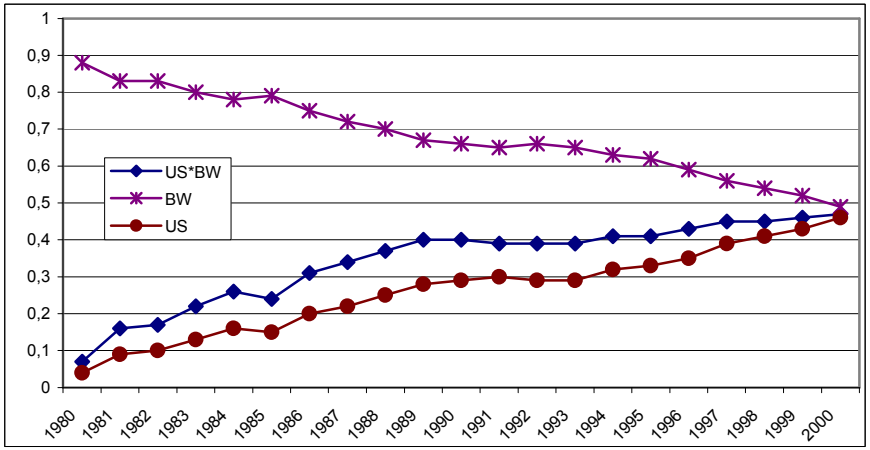


Figure 4. Heterozygosity and breed proportions in Finland. Friesian cattle (BW), Holstein (US).

*Mastitis*

The data for mastitis treatments from all Nordic countries were collected and sent to GENO for analysis. Mastitis were defined as 0 or 1 based on whether or not the cow had at least one recorded veterinary treatment of mastitis at the defined intervals of lactation. Preliminary results from a joint Nordic evaluation for mastitis was presented by Heringstad et al. (2003) in the Interbull meeting in Rome.

We have also studied the effect of different definitions of mastitis. The first lactation was either split into two intervals, namely treatments before 50 days after calving (Ma50) and treatments after that period (Ma51_300.) Other two options for the 1st lactation were defined as one short interval (Ma150) or one full lactation interval (Ma300). For the second and third lactation 150 d (Ma2_150, Ma3_150) or 300 d (Ma3-150, Ma3_300) of lactation were used. In Figure 5 we show some results of this comparison. The four traits (Figure 5) show similar genetic trends, relative flat in the beginning and increasing from 1989 onwards.

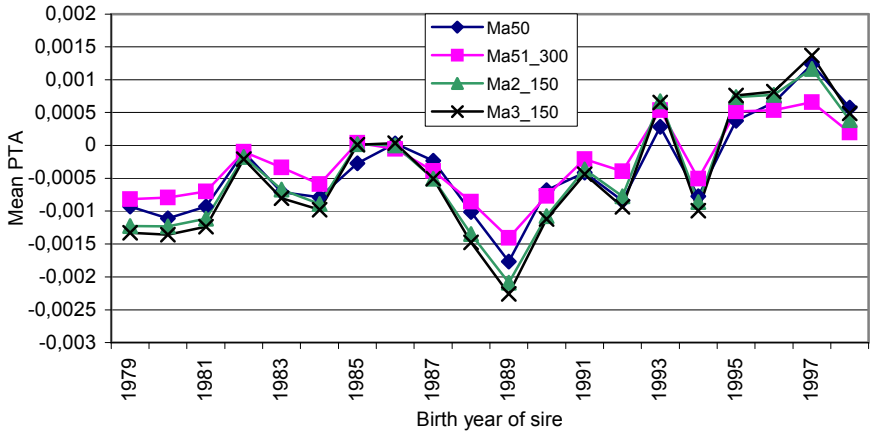


Figure 5. Genetic trends given as mean PTA by birth year of sire, for sires born from 1979 to 1998, for the four mastitis traits in Nordic Holstein.

The research on comparison and validation of different statistical models still continues. After the choice of the best model for clinical mastitis we will include information from correlated traits, e.g. somatic cell count and some udder conformation traits to a multiple trait model to predict the udder health better. It is important to increase the accuracy of prediction of genetic merit for udder health at early stages of lactation, since evaluation of milk traits reach publication limit quite soon after calving due to a fast accumulation of test day records.



**The possibilities of Nordic co-operation to global Ayrshire breeding**

The Nordic Ayrshire progeny testing scheme supported by the MOET scheme is by far the largest breeding programme in the world and hence the genetic response achieved in the programme is of importance to global Ayrshire breeding. The Interbull results have proved the superiority of the Nordic bulls in production traits. Until now the concern in many countries has been the conformation of Nordic Ayrshire cattle. Since Interbull now provides a comparison of conformation traits, it is possible to find good production bulls with adequate conformation.

A good example of successful utilization of Nordic genetics is the New Zealand Ayrshire breeding programme. Both Finnish and Swedish bulls have been heavily used in the programme and the results show the improvement of the production with no loss in conformation. This improvement has been achieved, even the management in New Zealand differs very much from the Nordic countries.

Another group of countries that have found the Nordic genetics valuable are the Baltic countries. In a recent study the Swedish Red was found the most suitable source of genetics for the Latvian brown cattle (Strautmanis, 2003).

The modern Ayrshire breed is a competitive breed to fight against the global "holsteinisation" and it has also a huge potential in commercial crossings in the Holstein herds. We should keep the Ayrshire breeding free of Holstein importation and rely on our own breeding programme. Only this enables the Ayrshire to be a real alternative in the future as well.

**Conclusions**

Moving from MACE methodology to joint evaluation of breeding values from performance records will increase the accuracy of selection across Nordic countries, will enable comparison of cows and bulls between countries, harmonisation of data editing and genetic evaluation systems and will make the comparison of animals easier for farmers in different Nordic countries. Harmonization of health recording between Nordic countries would improve the accuracy of joint evaluation further.

The results so far have shown the joint evaluation to be feasible. The goal is to start the service in joint evaluation in the first traits already during 2004. Completing the evaluation portfolio to include all traits will take couple of more years. The joint evaluation will replace the national evaluations and will also provide the data used in Interbull for international comparison of sires.

More accurate comparison of animals over the borders is necessary for the development of joint breeding programme. Joint testing scheme with an integrated nucleus breeding programme will keep the Nordic breeding programmes competitive on European scale and will enable the selection of animals according

to Nordic profile. A challenge for the future is to avoid the possible negative side effects of effective breeding programme by utilizing modern methods of optimising selection and risk in breeding programme.

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# THE DEPENDENCE OF SOMATIC CELL COUNT IN MILK ON THE MORPHOLOGICAL TRAITS OF BLACK-AND-WHITE COWS' UDDER

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**Introduction**

Resistance to mastitis is included in the breeding objective of many countries [2, 3, 6, 7, and 8].

The choice of a selection criterion to improve mastitis resistance should be based on the following characteristics: the trait must be biologically relevant, i.e. discriminating appropriately healthy and diseased animals; it must be easy and inexpensive to record extensively and must exhibit genetic variation [5, 9].

Milk somatic cell count is a long-established barometer of milk quality [1, 9].

An elevated somatic cell count is an indicator of udder infection (mastitis) [5, 9].

**Materials and methods**

Researches have been carried out at the State Laboratory for Milk Control "Pieno tyrimai", at the Laboratory of Animal Breeding Value Establishment and Biometry of Lithuanian Veterinary Academy and at the Lithuanian Black-and-White Cattle Improvement Association during the period between 01.01.1998...31.12.2002. A total 730 cows were evaluated. Seven of the udder morphological traits, including fore udder attachment (FUA), udder height (UH), central ligament (CL), udder depth (UD), teat placement (TP), teat length (TL) and teat thickness (TT) using the recommendation of international type evaluation of dairy cattle were estimated.

Statistical analyses were carried out using "R" package.

The aim of this study was to estimate the relationships between SCC in milk and morphological traits of udder a cows of Black-and-White breed cows in Lithuania.

**Results and discussion**

The Lithuanian Black-and-White breed comprises 74% of the total the Lithuanian cattle population. The average milk yield of those cows in 2002/2003 milk recording year was 5112 kg with 4.32% fat and 3.35% protein (Table 1).

In the last seven years the average milk production, fat and protein yields of Black-and-White cows has increased (41.7% - 46.1%).

The angular traits for the breeding of the Lithuanian Black-and-White cattle are: the milk yield, the content of milk protein and fat, the count of somatic cells, the fertility of animals and their health, the conformation, the condition of udder, the milking attributes and the general disposition [4].

Table 1. Milk production of Black-and-White cows in Lithuania

| Years | Average no. of cows | Milk kg | Milk fat | | Milk protein | |
|---|---|---|---|---|---|---|
| | | | % | kg | % | kg |
| 1996 - 1997 | 81770 | 3722 | 4.09 | 152 | 3.27 | 122 |
| 1997 - 1998 | 82431 | 4276 | 4.20 | 180 | 3.22 | 138 |
| 1998 - 1999 | 80184 | 4403 | 4.23 | 186 | 3.13 | 138 |
| 1999 - 2000 | 67235 | 4551 | 4.33 | 197 | 3.22 | 146 |
| 2000 - 2001 | 63717 | 5000 | 4.28 | 214 | 3.26 | 163 |
| 2001 - 2002 | 84237 | 5136 | 4.20 | 216 | 3.29 | 169 |
| 2002 - 2003 | 113520 | 5112 | 4.32 | 220 | 3.35 | 171 |

The delivery control of milk with high somatic cells counts (SCC), established by an EU directive (92/46) for dairy cattle.

Collection of SCC in test-day samples was started in Lithuania nine years ago and recorded on a monthly.

A high number of somatic cells decreases milk quality and also reduces milk productivity. The results are shown in Table 2. The increase of SCC from 200 thousand/ml have decreased the milk yield of Black-and-White cows from 15.7% to 19.6%, milk fat production in kg - from 12.0 to 14.9%, milk protein production in kg - from 11.6% to 18.0%.

Table2. The production of Black-and-White cows in I– III lactations depending on SCC

| Class of the SCC, thousand/ml | Milk, kg | | | Milk fat, kg | | | Milk protein, kg | | |
|---|---|---|---|---|---|---|---|---|---|
| | Lactation | | | | | | | | |
| | I | II | III | I | II | III | I | II | III |
| >200 | 4179 | 4608 | 4953 | 180 | 198 | 212 | 129 | 149 | 160 |
| 201 – 400 | 3775 | 4016 | 4424 | 166 | 178 | 197 | 122 | 138 | 148 |
| 401 – 800 | 3712 | 4030 | 4400 | 164 | 181 | 196 | 122 | 138 | 149 |
| 801> | 3641 | 4019 | 4106 | 165 | 183 | 184 | 120 | 140 | 142 |

Type classification is an important tool in the management of a profitable dairy herd.

Assuming the observed traits of udder the Lithuanian Black-and-White cows were estimated on the count of somatic cells in milk.

According to the selection program of this breed [4] the optimal udders estimations of the Lithuanian Black-and-White cows must be 9 points for all traits of udder but for teat thickness, placement and length must be 5-6 points.



The results shown in Table 3 demonstrating the optimal estimation of udder traits have positive influence on SCC in milk.

Table 3. The dependence of SCC in milk on the morphological traits of udder

| The udder est., points | FUA | | UH | | CL | | UD | | TP | | TL | | TT | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | SCC, thousand/ml | | | | | | | | | | | | | |
| | $\bar{x}$ | δ | $\bar{x}$ | δ | $\bar{x}$ | δ | $\bar{x}$ | δ | $\bar{x}$ | δ | $\bar{x}$ | δ | $\bar{x}$ | δ |
| 1 | 1012 | 1419 | 251 | - | 2093 | 2903 | - | - | 429 | 251 | 626 | 1125 | 281 | 250 |
| 2 | 674 | 667 | 319 | 318 | 753 | 1194 | 652 | 502 | 612 | 1268 | 485 | 809 | 640 | 1188 |
| 3 | 1103 | 1707 | 999 | 1372 | 468 | 651 | 1088 | 1907 | 658 | 1003 | 539 | 1090 | 513 | 982 |
| 4 | 576 | 853 | 594 | 938 | 394 | 381 | 1962 | 1997 | 650 | 1297 | 454 | 697 | 526 | 797 |
| 5 | 443 | 780 | 327 | 675 | 579 | 980 | 559 | 1004 | 368 | 641 | 526 | 733 | 535 | 892 |
| 6 | 375 | 646 | 456 | 848 | 489 | 865 | 502 | 831 | 361 | 515 | 300 | 220 | 515 | 983 |
| 7 | 585 | 1132 | 282 | 275 | 568 | 1059 | 425 | 782 | 577 | 1016 | 265 | 184 | 407 | 397 |
| 8 | 277 | 317 | 101 | - | 409 | 884 | 238 | 334 | 611 | 982 | 48 | - | 123 | 40 |
| 9 | 243 | 168 | - | - | 200 | 266 | 155 | 88 | 554 | 886 | 405 | - | 270 | 231 |

We found that each of the measured traits of udder had a different effect on the count of somatic cells in milk.

Slight phenotypic correlations with morphological traits of udder such as the length of teats (-0.07) and the thickness of teats (-0.04) were calculated.

The length and thickness of teats have had a little impact on the count of somatic cells in milk (0.81-0.82%; $P<0.001$), whereas the impact of the udder depth, the udder height, fore udder attachment and central ligament was determined as 6.14%, 5.84%, 5,01% and 2.95% respectively ($P<0.001$). However all features taken together resulted a great impact on the count of somatic cells in milk, presenting 18.9% ($P<0.001$).

**Conclusions**

In the last seven years the average milk production, fat and protein yields of Black-and-White cows has increased. The milk yield has increased by 37.4%, fat yield by 44.7%, protein yield by 40.2%.

The analysis of somatic cell count in milk of Black-and-White cows in different lactations shows that the increase of SCC have decreased the milk yield from 15.7% to 19.6%, milk fat - from 12.0 to 14.9% and milk protein production - from 11.6% to 18.0%.

The analysis indicated significant influence ($P<0.001$) of the morphological traits of udder on the SCC in milk.

On the basis of the research results we can assume that cow's selection according to the morphological traits of udders would allow reducing the count of somatic cells in milk.

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## ON SOMATIC CELL COUNT IN MILK

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**Introduction**

Increasing awareness of public health and food safety issues have led to a greater interest in milk quality in recent years. The key milk quality element being regulated is somatic cell count (SCC). High SCC levels are not only known to pose a directly public health, but also reflect mammary infection and overall quality of management. Moreover, lower SCC levels have been shown to be related to higher milk yield and better dairy product quality, and are, therefore, of economic value. The types of cells present in milk must be known because uninfected milk consists mainly of macrophages (60%) and lymphocytes (28%), with few (5 to 12%) polymorphonuclear leukocytes PMN (Kelly et al., 2000). In mastitic milk, the percentage of PMN has been shown to increase considerably up to 90%. Therefore, it is suggested that PMNC (polymorphonuclear leukocytes count) may be used as a good marker for the presence of bacterial infection in bovine quarters (Pillai et al., 2001). A SCC level of 200,000 cells/ml or less is considered physiologically typical. Somatic cells in milk increase primarily due to the presence of mastitis organisms in the udder (Nash et al., 2003). The European Union requires that milk used for dairy products sold in its territory has SCC levels below 400,000 cells/ml. New Zealand and Australia require similar levels, and Canada requires milk to have below 500,000 cells/ml (Sargeant et al., 1998; Norman et al., 2000). In the United States, the current national penalty level is 750,000 cells/ml and over. Research has shown that milk losses start at about 100,000 SCC. Many US (organic) dairy cooperatives also require SCC to be less than 400,000 cells/ml (van Schaik et al., 2002). Milking procedures vary a great deal from one farm to another. A good milking procedure increases milk production and labour efficiency and decreases the number of new infections in the herd. This is the factor that has the greatest impact on udder health.

**Materials and Methods**

Data were collected from Põlula experimental farm. Estonian Red (ER), Red Holstein (RHF), Estonian Holstein (EHF, $EHF_t$), Estonian Native (EN) dairy cows' 305-day milk components and milk somatic cell count were analysed. At the end of 2000, when this trial was started, the Estonian Holstein heifers were divided into two groups: heifers of average (RBV<112; EHF) and above average relative breeding value for milk production index (RBV>112; $EHF_{t)}$. RHF group was formed from the offspring of the Estonian Red cows and the Red Holstein bulls (HF 75%). The first heifers of the Estonian Red breed calved in September 2000, and those of the Estonian Native Breed in summer 2001. The length of the

investigation was from October 2000 to December 2003. The dairy cows of all the experimental groups were kept under similar conditions and fed total mixed ration *ad libitum*. The data on 305-day milk yield, fat and protein content, fat and protein yield and somatic cell count were collected in first and second lactation and in the Estonian Red trial group in third lactation as well. Cows' sire, breed, calving month, lactation, and milking operator were fixed in a database. Cows were milked using a standard milking routine, including pre-stripping and cleaning with individual cotton towels. Teats were post-dipped with 0.5% iodine. Monitoring of the working operations of the milking operators, milking the cows selected for our trials was carried out. The duration of each element of the working process was recorded. All statistical analysis were performed with SAS system. Before analysis for positively skewed milk somatic cell count the logarithm transformation was applied. To study the relation between milk somatic cell count and milk components the correlation analysis on 305- day traits was implemented. The effects of different factors on somatic cell count in milk were determined using the repeated measures general linear models analysis with SAS system MIXED procedure. The fixed effects of breed, lactation, year of birth and calving month, and the random effect of sire were studied based on 305 - day somatic cell count in milk. The fixed classification effects of breed, lactation, lactation month and milking operator, the fixed continues effects of milking operations (cow preparation for milking, delay in applying the milking unit to the cow, machine stripping and over-milking) and the random effect of the sire were studied based on test day records.

**Results**

Table 1 demonstrates a higher somatic cell count in milk in both experimental groups of the Estonian Holstein breed (EHF; $EHF_t$), primarily in Estonian Holstein ($EHF_t$) in second lactation (631,000 cells/ml). In first lactation the lowest somatic cell count (207,000 cells/ml) was detected in Estonian Red breed trial group. Remarkably higher milk somatic cell count was observed in Estonian Holstein breed ($EHF_t$) in first lactation (381,000 cells/ml). Five cows from the Estonian Red breed trial group finished the third lactation with milk somatic cell count of 282,000 cells/ml (Table 1).

The phenotypic correlations between milk somatic cell count and milk yield were on a low level in Estonian Holstein, Red Holstein as well as in all investigated breeds together. The highest negative correlations were shown by the Estonian Red breed in first and third lactation (-0.417*/-0.649), and the Estonian Native breed in first lactation (-0.892*). The highest negative correlations were observed between milk somatic cell count and protein yield in the Estonian Red breed in first lactation (-0.334*) and in third lactation (-0.648), and in the Estonian Native breed in first lactation (-0.974**).



Table 1. Milk yield, somatic cell count (SCC) and SCC log in the 1st, 2nd and 3rd lactation by different breeds

| Item | Breed | Lactation | No | Mean | Std deviation | Min | Max |
|---|---|---|---|---|---|---|---|
| Milk, kg | ER | I | 27 | 7822 | 1129 | 5607 | 9971 |
| | RHF | | 17 | 8520 | 1373 | 5796 | 10859 |
| | EHF | | 21 | 9257 | 999 | 6772 | 10890 |
| | $EHF_t$ | | 23 | 9077 | 1598 | 5778 | 12196 |
| | EN | | 6 | 6514 | 1253 | 4835 | 8483 |
| | ER | II | 21 | 9060 | 1193 | 6940 | 11555 |
| | RHF | | 12 | 9605 | 965 | 7079 | 10533 |
| | EHF | | 12 | 11109 | 1235 | 9728 | 13319 |
| | $EHF_t$ | | 10 | 10430 | 1622 | 8719 | 13480 |
| | EN | | 2 | 8447 | 1327 | 7508 | 9385 |
| | ER | III | 5 | 8989 | 778 | 7995 | 9756 |
| SCC | ER | I | 27 | 207 000 | 234 000 | 20 000 | 803 000 |
| | RHF | | 17 | 272 000 | 306 000 | 32 000 | 1 146 000 |
| | EHF | | 21 | 326 000 | 393 000 | 39 000 | 1 589 000 |
| | $EHF_t$ | | 23 | 381 000 | 374 000 | 30 000 | 1 349 000 |
| | EN | | 6 | 243 000 | 164 000 | 42 000 | 539 000 |
| | ER | II | 21 | 458 000 | 459 000 | 40 000 | 1 517 000 |
| | RHF | | 12 | 371 000 | 379 000 | 49 000 | 1 332 000 |
| | EHF | | 12 | 375 000 | 414 000 | 35 000 | 1 387 000 |
| | $EHF_t$ | | 10 | 631 000 | 614 000 | 28 000 | 2 004 000 |
| | EN | | 2 | 141 000 | 82 000 | 83 000 | 199 000 |
| | ER | III | 5 | 282 000 | 136 000 | 93 000 | 420 000 |
| SCC, log | ER | I | 27 | 4.75 | 1.13 | 2.99 | 6.69 |
| | RHF | | 17 | 5.06 | 1.11 | 3.47 | 7.04 |
| | EHF | | 21 | 5.24 | 1.05 | 3.67 | 7.37 |
| | $EHF_t$ | | 23 | 5.46 | 1.05 | 3.41 | 7.21 |
| | EN | | 6 | 5.25 | 0.84 | 3.73 | 6.29 |
| | ER | II | 21 | 5.63 | 1.07 | 3.70 | 7.32 |
| | RHF | | 12 | 5.50 | 0.94 | 3.89 | 7.19 |
| | EHF | | 12 | 5.17 | 1.29 | 3.55 | 7.23 |
| | $EHF_t$ | | 10 | 5.83 | 1.37 | 3.32 | 7.60 |
| | EN | | 2 | 4.86 | 0.62 | 4.42 | 5.29 |
| | ER | III | 5 | 5.51 | 0.62 | 4.52 | 6.04 |

Table 2. Correlations between log milk somatic cell count (SCC log) and milk components in the 1st, 2nd and 3rd lactation by different breeds

| Breed | Lactation | No | Milk, kg | Fat, % | Fat, kg | Protein, % | Protein, kg |
|---|---|---|---|---|---|---|---|
| ER | I | 27 | -0.417* | 0.216 | -0.308 | 0.195 | -0.334* |
| | II | 21 | 0.017 | -0.176 | -0.087 | 0.438* | 0,178 |
| | III | 5 | -0.649 | 0.157 | -0.581 | 0.080 | -0.648 |
| RHF | I | 17 | 0.200 | -0.159 | 0.123 | 0.270 | 0.340 |
| | II | 12 | -0.287 | -0.163 | -0.327 | 0.188 | -0.143 |
| EHF | I | 21 | 0.106 | -0.247 | -0.130 | -0.175 | 0.000 |
| | II | 12 | 0.252 | -0.232 | 0.024 | 0.369 | 0.336 |
| $EHF_t$ | I | 23 | 0.007 | -0.337 | -0.225 | 0.075 | 0.003 |
| | II | 10 | 0.046 | -0.195 | -0.161 | 0.322 | 0.180 |
| EN | I | 6 | -0.892* | -0.247 | -0.944** | 0.034 | -0.974** |
| Total | I | 107 | 0.004 | -0.117 | -0.124 | -0.044 | -0.032 |
| | II | 58 | 0.007 | -0.169 | -0.131 | 0.349 | 0.169 |
| | III | 8 | -0.271 | 0.171 | -0.275 | -0.382 | -0.472 |

The different factors affecting somatic cell count in milk were analyzed. These were bull, lactation, breed, calving month, milking operator. Cows of all test groups were milked three times a day. First of all, the data from all breeds together were analyzed. Based on the results of the analysis, the most essential factors affecting milk somatic cell count appeared to be lactation ($P<0.01$), milking operator and bull ($P<0.05$). Breed had also a small effect, but this was not statistically significant. Differences in milk somatic cell count between different breeds were estimated by least square means. Most essential difference was between the test groups of the Estonian Red (ER) and Estonian Holstein breed (EHF, $EHF_t$). By the end of second lactation there remained 21 Estonian Red cows from 27, only 12 Estonian Holstein (EHF) cows from 21, and 10 Estonian Holstein ($EHF_t$) cows from 23. Estonian Red (ER) test group was more resistant than other test groups. Calving month was not a significant factor affecting the milk somatic cell count ($P>0.05$).

Moreover, the factors affecting milk somatic cell count were analyzed per each breed separately. The milk SCC of the test group of the Estonian Holstein breed ($EHF_t$) was most affected by bull ($P<0.01$) and lactation ($P<0.05$). The milk SCC of the test group of the Estonian Native breed (EN) was influenced by lactation ($P<0.01$) and by bull ($P<0.05$). Similar factors had an impact on the test group of the Red Holstein breed (RHF). Milking operator affected milk somatic cell count in test groups of all breeds, but most essentially ($P<0.01$) in both test groups of the Estonian Holstein breed (EHF, $EHF_t$). The cows of the test groups were milked by 13 different milking operators. The most susceptible to the change



of milking operators were the cows of the Estonian Holstein (EHF; $EHF_t$) test group.

**Conclusions**

On the basis of data analyses, it appeared that major factors influencing the milk somatic cell count were lactation ($P<0.01$), milking operator, and bull ($P<0.05$).

Breed had also a small effect, but it was not statistically significant. Differences in milk somatic cell count between different breeds were estimated by least square means. Most essential difference was observed between the test groups of the Estonian Red (ER) and Estonian Holstein breed (EHF, $EHF_t$).

Calving month was not a significant factor affecting the milk somatic cell count ($P>0.05$).

The milk SCC of the test group of the $EHF_t$ was most affected by bull ($P<0.01$) and lactation ($P<0.05$). The milk SCC of the test groups of the Estonian Native breed (EN) as well as Red Holstein breed (RHF) was affected by lactation ($P<0.01$) and bull ($P<0.05$) .

Milking operator affected milk somatic cell count in test groups of all breeds, but most essentially ($P<0.01$) in both test groups of the Estonian Holstein breed (EHF, $EHF_t$).

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## GENETIC AND ENVIRONMENTAL INFLUENCES ON UREA CONCENTRATION IN DAIRY COWS' MILK

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### Introduction

Many animal recording centres offer testing for urea in milk. Automated fast and inexpensive infrared spectrophotometric methods were introduced in early 1990s (Godden et al., 2001). In Estonia the Animal Recording Centre delivers to producers this data since the 1996. Level of urea is used as an indicator of whether a cow is consuming the proper quantity and proportion of protein and energy in its diet. The concentration of urea is known to vary with the amount of protein in the diet, amount of urine excreted, water intake, dry matter intake, sampling methods, breed, season, herd management, energy intake and parity (Godden et al., 2001; Ferguson, 2002). High-yielding cows in Estonia may have been overfed protein and/or underfed energy, and this leads to the increase in urea level in cows' blood and milk (Sikk, 1997). At high level, urea may cause fertility problems (Larson et al., 1997; Piatkowski et al., 1981). There are a few studies about its heritability, and about the extent of other genetic and environmental factors having influence on it. The objective of this study was to determine the effect of sire, owner, farm, lactation number, sire-owner interaction, and owner-lactation number interaction on urea concentration in milk. The heritability of milk urea concentration (MU) and its genetic correlations with yields of milk, fat, protein, and fat and protein content were also estimated.

### Material and Methods

This study was based on the data of the Estonian Red (ER), Estonian Holstein (EHF) and Estonian Native (EN) cows that started lactating in January, 2002. The data were obtained from the database of the Animal Recording Centre (Table 1).

To guarantee the accuracy in studying the effect of genotype and environment as well as the genotype-environment interaction on urea concentration in milk, the sires with 1 - 2 descendants and the farms with 1 - 2 cows were not included. Due to a very small number of cows, the EN - group was not taken into consideration either. The analysis involved 3,734 cows of the Estonian Holstein breed with the recorded data on their sire, owner, farm and lactation, and 1,431 cows of the Estonian Red breed. The number of sires was 170 and 126, and that of farms 238 and 136, respectively.

Table 1.Essential parameters for milk, milk fat and protein yield, milk fat and protein percentage and urea concentration

| | Milk, kg | Fat, kg | Protein, kg | Fat, % | Protein, % | Urea, mg/dl |
|---|---|---|---|---|---|---|
| | EHF (*n*=5175) | | | | | |
| $\bar{x}$ | 6175.7 | 258.95 | 196.41 | 4.203 | 3.173 | 24.81 |
| s | 1508.7 | 67.53 | 51.39 | 0.494 | 0.196 | 5.38 |
| min | 2004.0 | 85.50 | 60.60 | 2.820 | 2.560 | 1.20 |
| max | 12795.0 | 533.70 | 432.00 | 6.420 | 4.060 | 45.90 |
| | ER (*n*=2042) | | | | | |
| $\bar{x}$ | 5339.9 | 234.07 | 175.82 | 4.388 | 3.291 | 25.57 |
| s | 1305.0 | 62.41 | 44.43 | 0.519 | 0.197 | 5.69 |
| min | 2078.0 | 76.70 | 63.00 | 2.700 | 2.760 | 8.40 |
| max | 10587.0 | 520.60 | 371.30 | 6.550 | 4.260 | 51.00 |
| | EN (*n*=28) | | | | | |
| $\bar{x}$ | 4296.5 | 203.86 | 143.85 | 4.770 | 3.365 | 24.81 |
| s | 973.6 | 49.86 | 30.59 | 0.734 | 0.276 | 7.14 |
| min | 2382.0 | 106.90 | 74.70 | 3.860 | 3.080 | 15.90 |
| max | 6827.0 | 304.70 | 218.50 | 6.450 | 4.330 | 37.80 |

To study the importance of the recorded factors affecting total variation in milk urea concentration, the following model was used:

$$y_{ijklm} = \mu + S_i + O_j + SO_{ij} + F_{k(j)} + L_l + OL_{jl} + e_{ijklm}, \qquad (1)$$

where $y$ – milk urea content in a definite cow, $\mu$ – mean urea content, $S_i$ – sire $i$ effect, $O_j$ – owner $j$ effect, $SO_{ij}$ – sire $i$ - owner $j$ interaction, $F_{k(j)}$ – owner $j$ -farm $k$ interaction, $L_l$ – lactation $l$ effect, $OL_{jl}$ – owner $j$ - lactation $l$ interaction, and $e_{ijklm}$ – random error. The urea concentration variance model comprised a sum of similar components:

$$\sigma_y^2 = \sigma_S^2 + \sigma_O^2 + \sigma_{OS}^2 + \sigma_F^2 + \sigma_L^2 + \sigma_{OL}^2 + \sigma_e^2$$

where $\sigma_y^2$ – urea concentration variance, $\sigma_S^2$, $\sigma_O^2$, $\sigma_{OS}^2$, $\sigma_F^2$, $\sigma_L^2$ and $\sigma_{OL}^2$ – variance components characterizing the effect of sire and owner, sire-owner interaction, effect of farm and lactation, and owner-lactation interaction, respectively, $\sigma_e^2$ – random variation.



In the estimation of heritability and genetic correlations, all the factors as the fixed genetic parameters for concentration of milk urea, comprised in the model (1), except for genetic effect of sire, were considered fixed, whereas the sire-owner interaction was excluded from the model as an insignificant factor. Heritabilities were estimated on the basis of sire model according to the formula $h^2 = 4\sigma_s^2 / \sigma_y^2$, and the genetic correlations according to the equation $r_g = \sigma_{S_1S_2} / \sqrt{\sigma_{S_1}^2 \sigma_{S_2}^2}$, where $\sigma_{S_1}^2$ represents the variation of one variable related to the effect of sire, and $\sigma_{S_2}^2$ represents that of another variable, while $\sigma_{S_1S_2}$ describes covariation between sire effects. The phenotypic correlations between urea concentration and other milk productivity data were expressed by Spearman correlation coefficients.

The data was processed by using SAS program, and the variance components were estimated by REML method.

**Results**

Table 2 indicates that the statistically significant factors affecting the milk urea concentration appeared to be owner, farm nested to owner, and sire. The relevant determination coefficients in EHF breed were 0.39, 0.14 and 0.06. The results of ER breed were similar to those of EHF breed – 0.37, 0.15 and 0.03, respectively. As for EHF breed, the interaction between sire and owner was not observed. In ER breed, the interaction was statistically insignificant – 0.005. Neither had the lactation-owner interaction nor the lactation number any effect on urea concentration in milk. The data presented in Table 2 are illustrated in Figure 1.

Table 2. Share and statistical significance of the studied factors on milk urea concentration (based on Model 1)

| Factor | EHF | | EPK | |
|---|---|---|---|---|
| | $\sigma_F^2/\sigma_y^2$ * | p | $\sigma_F^2/\sigma_y^2$ | p |
| Sire | 0.059 | <0.001 | 0.032 | 0.002 |
| Sire *Owner | 0.000 | . | 0.005 | 0.350 |
| Owner | 0.388 | <0.001 | 0.370 | <0.001 |
| Farm (Owner) | 0.135 | <0.001 | 0.153 | 0.003 |
| Lactation No | 0.000 | 0.362 | 0.003 | 0.246 |
| Owner* Lactation No | 0.008 | 0.054 | 0.017 | 0.107 |
| Residual | 0.409 | <0.001 | 0.420 | <0.001 |

* ratio of factor-specific variance components

$\sigma_F^2 \in \{\sigma_S^2, \sigma_O^2, \sigma_{OS}^2, \sigma_F^2, \sigma_L^2, \sigma_{OL}^2, \sigma_e^2\}$ to total variance $\sigma_y^2$

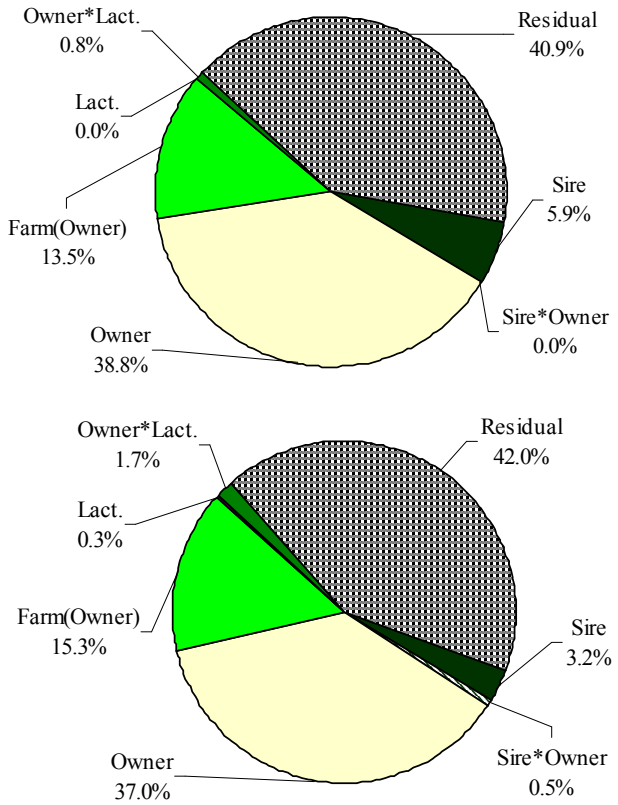


Figure 1. Share of factors affecting milk urea concentration in (a) EHF and (b) ER cows

The heritability of milk urea concentration of the Estonian Red breed cows appeared to be 0.32, and that of the Estonian Holsteins was 0.50 (Table 3).

Phenotypic and environmental correlations between milk urea concentration and milk yield traits were in ER and EHF breeds similar, whereas genetic correlations in ER breed were weakly positive and in EHF breed, on the contrary, weakly negative.

Thus, selection of EHF toward decrease in milk urea content may lead to some increase in lactation milk yield.



Table 3. Heritabilities of milk urea concentration and phenotypic ($r_p$), genetic ($r_g$) and environmental ($r_e$) correlations between milk yield traits

| Correlations | Milk, kg | Fat, kg | Protein, kg | Fat, % | Protein, % |
|---|---|---|---|---|---|
| | ER – $h^2$ = 0.32 | | | | |
| $r_p$ | 0.20 | 0.19 | 0.16 | 0.02 | -0.14 |
| $r_g$ | 0.34 | 0.27 | 0.32 | -0.12 | -0.06 |
| $r_e$ | 0.14 | 0.07 | 0.09 | -0.08 | -0.17 |
| | EHF – $h^2$ = 0.50 | | | | |
| $r_p$ | 0.19 | 0.17 | 0.17 | -0.03 | -0.06 |
| $r_g$ | -0.24 | -0.20 | -0.27 | -0.31 | -0.07 |
| $r_e$ | 0.14 | 0.06 | 0.08 | -0.09 | -0.19 |

**Discussion and Conclusions**

This study involved only a few factors that affect milk urea concentration. As expected, the milk urea concentration was most influenced by owner and farm, as the amount and quality of feed distributed to cows depend on owner and farm-workers. 67% of the statistically significant factors investigated in this study constituted the effect of owner as an environmental factor on both breeds, the effect of farm on ER and EHF cows was 27 and 23%, and the effect of sire as a genetic factor was 6 and 10%, respectively. The study revealed that there were no differences in milk urea concentration of different cattle breeds raised in Estonia, and the lactation number had no effect on the average milk urea concentration of a lactation. The results from Godden et al. (2001) showed that there was a difference in urea concentration of the first and second lactation milk by lactation days. At the beginning of a lactation period, the urea content of the first lactation cows was lower than that of the second lactation cows, and it was quite the contrary at the end of the lactation. But similar results in the heritability of milk urea concentration were obtained in studying Ontario cattle in Canada where the heritability of MU of the first three lactations of the Canadian Holsteins was 0.44, 0.59 and 0.48, respectively (Wood et al., 2003). Genetic correlations between MU and yield traits showed a weak positive relationship in ER breed and a weak negative relationship in EHF breed. Thus, there may be differences between breeds, as Wood *et a.l*, (2003) found a very weak positive genetic correlation between these traits.

Rajala-Schultz et al. (2001) used survival analysis to study the relationship between milk urea nitrogen (MUN) and days to calving and conception. Compared to herdmates with MUN above15.4 mg/dl, cows with MUN levels below 10.0 were 2.4 times more likely to be confirmed pregnant in a subsequent exam. The advantage decreased as MUN increased. Proportion between MU and MUN is 1:0.467. Consequently, 15.4 mg/dl MUN equals to 33 mg/dl MU. The

average of Estonian cattle breeds was 25 mg/dl, and 13% of cows had average lactation MU over 33 mg/dl. If our herds had similar conception results with previous results by Rajala-Schultz et al. (2001) then there is material to be worked on in the future by both owners and breeders of cows.

These results indicate and support results of other autors (Wood et al., 2003), that environmental effects explained the majority of the variance in MU. Therefore management is an important source of variability and has a crucial role in maintaining optimum MU level. At the same time, the heritabilities are moderate and selection could be an effective approach for altering MU.

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## EFFECT OF κ-Cn AND β-Lg GENETIC VARIANTS ON THE MILK RENNETING PROPERTIES ON PÕLULA RESEARCH FARM

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**Introduction**

Since the discovery of genetic polymorphism in β-lactoglobulin by Aschaffenburg and Drewry (1955), genetic variants have been found in all major milk proteins and many researchers from different countries have demonstrated that milk composition, milk yield and technological properties are connected with milk protein genetic variants. Several studies have demonstrated the influence of genetic variants of milk proteins on the contents of protein and casein in milk (Buchberger, Dovč, 2000). These findings have aroused the interest of many research groups around the world because of the potential using of milk protein genes as markers to aid in the selection for milk yield and quality. The majority of the reports are based on comparisons between variants of κ-casein and β-lactoglobulin (Ng-Kwai-Hang, 1998). As the $\alpha_{s1}$-casein locus is especially monomorphic and variant B occurs in most breeds with frequency of 95...<99%, there is practically no report in the literature regarding relationships between genetic variants of the protein and production traits. Due to a large number of alleles occurring at β-casein locus, the reports on association between β-Cn variant and the composition and technological properties of milk are conflicting.

This research is carried out on Polula Research Farm and is preliminary for a larger study, the purpose of which is finding connections between milk renneting properties of dairy breeds in Estonia, and genetic variants of κ-casein and β-lactoglobulin.

**Materials and Methods**

During 2001...2002, the milk samples (n=2161) were collected twice a month from 87 Põlula Research Farm cows of five experimental groups, formed on a basis of dairy breeds raised in Estonia: Estonian Holstein, with higher pedigree index > 112 (EHF-t), Estonian Holstein, with middle pedigree index 95…112 (EHF), Red-and-White Holstein (RHF), Estonian Red (ER), and Estonian Native (EN).

The milk coagulation properties were determined using a Formagraph. Three milk coagulation parameters were measured from the diagrams: milk coagulation time (RCT – time in minutes from the addition of rennet into milk up to the beginning of coagulation), curd-firming time ($K_{20}$ – time in minutes from the beginning of coagulation to the moment the width of the diagram was 20 mm),

and firmness of the curd ($E_{30}$ – width of the diagram in mm 30 min after the addition of rennet) (Kübarsepp et al., 2003). Milk calcium and phosphorus contents were determined by using IDF standard methods (36A:1992, 42B:1990). Daily performance, milk protein and fat contents and somatic cell count (SCC) data were received from Estonian Animal Recording Centre.

Genetic variants of κ-casein and β-lactoglobulin were determined by PCR-RFLP analysis in the Laboratory of Genetics of the Institute of Animal Science. The genomic DNA was extracted from blood.

The cows were fed identically *ad libitum* on a well-balanced totally mixed ration.

**Statistical Analysis**

Results were evaluated statistically using mixed linear model including both discrete and continuous effects and assuming a first-order autoregressive variance structure of the repeated measurements of the individual cow (SAS INST. Inc., 1991). In order to estimate the effects of different factors on milk coagulation parameters the following model (P<0.001) was assumed:

$$Y_{ijklmno} = \mu + group_i + parity_j + month_k + Cn_l + Lg_m + b_1 \cdot protein_{ijklmno} + b_2 \cdot Ca_{ijklmno} + b_3 \cdot pH_{ijklmno} + b_4 \cdot SCC_{ijklmno} + e_{ijklmno},$$

where

$Y_{ijklmno}$ – rennet coagulation parameters (RCT, $K_{20}$, $E_{30}$),

μ – general mean,

$group_i$ – fixed effect of trial group, $i \in \{EHF\text{-}t, EHF, RHF, ER, EN\}$,

$parity_j$ – fixed effect of parity, $j \in \{1, 2\}$,

$month_k$ – fixed effect of month of lactation,

$Cn_l$ – fixed effect of κ-casein genotype class, $l \in \{1, 2, 3\}$,

$Lg_m$ – fixed effect of β-lactoglobulin genotype class, $m \in \{1, 2, 3\}$,

$protein_{ijklmno}$ – milk protein content,

$Ca_{ijklmno}$ – milk calcium content,

$pH_{ijklmno}$ – milk pH,

$SCC_{ijklmno}$ – logarithmically transformed milk SCC,

$b_1$, $b_2$, $b_3$, $b_4$ – linear regression coefficients,

$e_{ijklnmno}$ – random residual effect including effect of repeated measurements of the cows.

**Results and Discussion**

All measured coagulation parameters were significantly better for the κ-casein BB and worse for the κ-casein AA genotype (Table 1). κ-Cn BB exhibited also the lowest percentage of non-coagulated milk samples and samples that did not



reach $K_{20}$ 30 min after enzyme addition. β-Lg genotypes had no significant effect on milk coagulation parameters, only milk coagulation time was the shortest and percentages of non-coagulated milk samples and samples with poor coagulation properties ($NK_{20}$) were lower for the β-Lg AA genotype. Similar results have been obtained by Ikonen and Ojala (1995) at Finnish cattle breeds. Milk coagulation time was the shortest for the β-Lg AA genotype in the FAy, whereas the β-Lg genotypes had no significant effect on any renneting trait in the FFr.

Table 1. Least square means of milk coagulation parameters, and mean milk production traits for different κ-casein and β-lactoglobulin genotypes

| Traits | κ-casein | | | β-lactoglobulin | | |
|---|---|---|---|---|---|---|
| | AA | AB | BB | AA | AB | BB |
| No. of animals | 62 | 21 | 4 | 16 | 42 | 29 |
| No. of milks | 1461 | 580 | 120 | 396 | 1081 | 684 |
| RCT, min | 8.03[a] | 7.78[a] | 6.77 | 6.79 | 7.61 | 8.18 |
| $K_{20}$, min | 9.12 | 8.13 | 6.51 | 7.92[a] | 8.07[a] | 7.77[a] |
| $E_{30}$, mm | 29.5 | 31.6 | 37.5 | 34.1[a] | 32.6[a] | 31.9[a] |
| Milk yield | 30.1[a] | 29.4[a] | 26.7[a] | 29.7[a] | 30.1[a] | 29.2 |
| Fat, % | 3.76 | 3.81[a] | 3.94[a] | 3.67[a] | 3.80[a,b] | 3.82[b] |
| Protein, % | 3.49 | 3.58 | 3.70 | 3.40 | 3.53 | 3.60 |
| Log SCC | 2.096[a] | 2.195[a] | 2.205[a] | 2.123[a] | 2.088[a] | 2.191 |
| pH | 6.77[a] | 6.77[a] | 6.76 | 6.77[a] | 6.77[a] | 6.77[a] |
| Ca, % | 0.1219[a] | 0.1230[a] | 0.1180 | 0.1198[a] | 0.1227[b] | 0.1223[a,b] |
| P, % | 0.0964 | 0.1000 | 0.1009 | 0.0916 | 0.0977 | 0.1001 |
| [1]NCM, % | 5.54 | 3.62 | 0.83 | 2.77 | 4.72 | 5.99 |
| [1]$NK_{20}$, % | 17.73 | 10.86 | 4.17 | 12.59 | 14.63 | 17.40 |

[1] percentage of non-coagulated milk samples (NCM) and samples that did not reach $K_{20}$ 30 min after enzyme addition ($NK_{20}$) from samples of respective κ-casein or β-lactoglobulin genotype

[a,b] means with the same superscripts in the same raw inside of κ-casein or β-lactoglobulin genotypes are not significantly different (P>0.05)

Significant differences between κ-casein and β-lactoglobulin genotypes were found in protein and phosphorus contents (AA<AB<BB; P<0.05). κ-Cn and β-Lg genotypes had no significant effect on milk yield, fat and calcium content, pH and somatic cell count. Only κ-Cn AA contained less fat and κ-Cn BB less calcium, and had lower pH than other genotypes.

The favourable effect of κ-Cn B on the renneting properties of milk has also been confirmed in several studies (Jacob, Puhan, 1992). Reviewing results of

different studies, Ng-Kwai-Hang (1998) found that comparing κ-Cn B variant with A variant the decrease in coagulation time was ranging between 10…40%, and the increase in curd firmness was within the range of 20…140%. The positive effect of κ-Cn B may be partly due to higher fat and casein contents in milk containing this variant.

2058 milk samples out of studied samples (n=2161) coagulated and it was possible to record curd firming time in 1731 cases (Table 2). From studied milks 103 samples (4.8%) did not coagulate. At least one non-coagulated milk sample appeared in 34 cows (39% from cows in trial). Coagulation properties of milk from cows of five experimental groups were higher in EN group (RCT=6.9 min; $K_{20}$ =6.3 min; $E_{30}$ =38.7 mm). No noncoagulated milk samples were observed in this group. Estonian Red breed has second-best coagulation properties of milk. Percentage of non-coagulated milk samples in group of ER (3.6%) was lower than in groups of Estonian Holstein and Red-and-White Holstein (percentage of non-coagulated milk samples 5.0 and 7.7%, respectively)

Table 2. Milk coagulation parameters and allele frequencies of κ-casein and β-lactoglobulin for different breeds in trial

| Number of cows | | Farm | EHFt, EHF | RHF | ER | EN |
|---|---|---|---|---|---|---|
| | | 87 | 45 | 12 | 26 | 4 |
| RCT, min | n | 2058 | 974 | 347 | 619 | 118 |
| | $\bar{x}$ | 8.1 | 8.2 | 8.0 | 8.2 | 6.9 |
| | SD | 3.2 | 3.1 | 3.4 | 3.3 | 2.1 |
| $K_{20}$, min | n | 1731 | 804 | 280 | 530 | 117 |
| | $\bar{x}$ | 8.6 | 9.4 | 9.1 | 7.5 | 6.3 |
| | SD | 4.4 | 4.5 | 4.6 | 4.1 | 3.5 |
| $E_{30}$, mm | n | 2161 | 1025 | 376 | 642 | 118 |
| | $\bar{x}$ | 28.9 | 27.6 | 26.0 | 31.1 | 38.7 |
| | SD | 12.7 | 11.9 | 12.9 | 13.2 | 9.2 |
| κ-Cn | A | 0.833 | 0.922 | 0.917 | 0.645 | 0.750 |
| | B | 0.167 | 0.078 | 0.083 | 0.346 | 0.250 |
| β-Lg | A | 0.425 | 0.489 | 0.292 | 0.365 | 0.500 |
| | B | 0.575 | 0.511 | 0.708 | 0.635 | 0.500 |

Several earlier studies (Tervala et al., 1983; Macheboeuf et al., 1993; Auldist *et al*., 2002) asserted better renneting properties among native breeds, comparing with Holstein breed. Differences between breeds in milk coagulation properties may result from the differences in milk composition derived from genotype.



Mentioned studies explain better milk coagulation properties among native breeds with higher frequency of κ-Cn B allele.

On Polula Research Farm the frequencies of κ-Cn A and B allele were 0.833 and 0.167, respectively, and β-Lg A and B allele frequencies 0.425 and 0.575, respectively (Table 2). Results of earlier studies in Estonia (Toome, 1972; Türk, 1998; Orasson, 2000) about allele frequencies of κ-Cn and β-Lg are presented in Table 3. The results of the present study indicate that the κ-Cn B allele frequency has considerably decreased in the Estonian Holstein cows. Frequency of κ-Cn B allele among local native breeds (ER and EN) has remained on the same level.

Table 3. Allele frequencies of κ-casein and β-lactoglobulin in Estonian dairy breeds according to different studies

| Year of study | Breed | n (κ-Cn / β-Lg) | κ-casein | | β-lactoglobulin | |
|---|---|---|---|---|---|---|
| | | | A | B | A | B |
| 1972 | EHF | 114 / 2033 | 0.693 | 0.307 | 0.465 | 0.535 |
| | ER | 86 / 710 | 0.709 | 0.291 | 0.103 | 0.897 |
| 1998 | EHF | 241* | 0.513 | 0.487 | 0.361 | 0.639 |
| 2000 | EHF | 632 | 0.956 | 0.044 | 0.688 | 0.312 |
| Present | EHF+RHF | 57 | 0.921 | 0.079 | 0.447 | 0.553 |
| | ER+EN | 30 | 0.667 | 0.333 | 0.383 | 0.617 |

* daughters of 9 test bulls

**Conclusions**

• Significant differences between κ-casein genotypes were found in renneting properties (AA<AB<BB).

• From measured coagulation parameters β-lactoglobulin had significant effect only on milk coagulation time. Milk coagulation time was the shortest for the β-Lg AA genotype.

• Milk with better coagulation properties from cows of Estonian Native and Estonian Red breed has higher frequencies of κ-casein B allele.

• Frequency of κ-casein B allele, associated with better coagulation properties, has considerably decreased in the Estonian Holstein cows.

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# ESTIMATING THE ADMIXTURE PROPORTIONS OF EXTANT FAROE ISLANDS CATTLE USING MICROSATELLITE DNA

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**Summary**

In this study, admixture proportions of native Faroe Islands Cattle and other four north European cattle breeds in contemporary Faroe Islands Cattle breed at the population and individual level were evaluated using 20 polymorphic microsatellite loci. Population level admixture proportions estimation showed a large genetic contribution from Norwegian Cattle (55.6%) and individual level admixture analysis demonstrated seven nonadmixed indigenous Faroe Islands Cattle individuals. The results suggested only a few purebred Faroe Islands Cattle still remain in the introgressed population. Breeding strategies that preserve the original native genes in Faroe Islands Cattle breed should be considered for preventing the extinction and/or further use of the breed in future breeding programs.

**Introduction**

As a consequence of a strong emphasis on productivity and specialization of breeds, some native cattle breeds have become almost totally displaced by commercial breeds during the last decades (Kantanen et al., 2000).

World-wide, there are more than 1230 cattle breeds, with 482 of these being native to Europe (FAO 2000). It has been shown that European native cattle breeds, most of which have a unique genetic history, represent separate gene pools and some of them possess unique gene combinations and special adaptations such as disease resistance, adaptation to harsh conditions or poor-quality feeds, etc. (MacHugh et al., 1994, 1998; Maudet et al., 2001)

Faroe Islands Cattle, existing on the Faroe Islands, can be traced back to the time when the Norwegian Vikings disembarked the land (Bjørk, 1984). During the 18th century the number of Faroe Islands Cattle was estimated to 2800 (Thorsteinsson, 1981). Imports of Norwegian Cattle breed seem to have suppressed the original Faroe Islands Cattle breed completely during the 20th century for a higher productive breed. The native Faroe Islands Cattle declined rapidly and are now seriously endangered, even facing to the extinction. Only about 40 Faroe Islands Cattle animals are estimated to exist currently. It is currently uncertain about the existence of purebred Faroe Islands Cattle and the contributions of the newly arrived Norwegian Cattle and the native Faroe Islands

Cattle to the development of contemporary Faroe Islands Cattle breed. The population and individual level admixture analysis was carried out to directly quantify the admixture proportions of contemporary Faroe Islands Cattle using data from 20 microsatellite DNA markers typed in five north European cattle breeds.

**Materials and Methods**

The geographical origins and sample size of cattle populations involved are: Faroe Islands Cattle, Faroe Islands (34); Icelandic Cattle, Iceland (44); Blacksided Troender Cattle, Norway (34); Western Fjord Cattle, Norway (41); Norwegian Cattle, Norway (38).

Twenty microsatellite loci chosen for this analysis correspond to the first 20 loci of 30 markers recommended by the International Society for Animal Genetics (ISAG) and a current European project focusing on genetic diversity in European cattle breeds (*http://www.projects.roslin.ac.uk/cdiv/markers.html*).

Exact tests for deviation from Hardy-Weinberg equilibrium (H-WE) were performed using Guo & Thompson's (1992). Fisher's exact tests in GENEPOP *Version 1.2* (Raymond & Rousset) were also applied to genotypic linkage disequlibrium determination between all locus pairs.

Programme STRUCTURE version 2.0 (Pritchard *et al*., 2000) is a model-based Bayesian procedure and is employed in the population and individual level admixture analysis. The value of k=5, which showed the highest probability for the number of populations existing in the samples, was chosen. Then the individual admixture proportions (q) were estimated. A threshold value of $q \geq 0.80$ was chosen and indicated that ≥80% of ancestry could be attributed to the respective breed. The individuals, proportion of whose membership to each cluster was $q < 0.80$, were inferred as admixed ones. Similarly, each sampled group was assigned to one cluster if its average proportion of membership was more than 0.80, or jointly to more than one cluster, if its average proportion of membership to each cluster was less than 0.80.

**Results**

Only eight deviations (8%) significant at 5% level from H-WE were detected and the most deviations (3, 15%) were detected in Faroe Islands Cattle breed. When results were pooled across breeds, three microsatellites (*INRA023, INRA032, INRA035*) showed significant departure from H-WE at $P < 0.05$ for the probability test and when pooled across loci, all five populations were congruent with the H-WE expectations. Observed H-WE deviations were not consistent over loci but generally occurred with different microsatellites in different populations. Over all populations and loci, H-WE ($p = 0.425$) was not statistically significant.



Tests of genetic disequilibrium for locus pairs across populations resulted in no comparisons showed significant disequilibrium across populations at $p < 0.05$.

The average proportions of membership (q) of each sampled breed in the five clusters showed that the cattle from Icelandic Cattle, Western Fjord Cattle, Blacksided Troender Cattle and Norwegian Cattle grouped in their respective breed cluster. However, Faroe Islands Cattle were split between Norweigian Cattle and Faroe Islands Cattle clusters (Data not shown).

For presenting the result of genetic composition of Faroe Islands Cattle individuals, the estimated individual proportions (q-values) for 34 samples were carried out. As a result of the highly admixed proportion ($q \geq 0.80$ in Norwegian Cattle), 13 individuals (approximately 38%) of Faroe Islands Cattle breed would be categorized as Norwegian Cattle breed. It also showed that in the sample of Faroe Islands Cattle, just 7 individuals (approximately 20%) with $q \geq 0.80$ in Faroe Islands Cattle exhibited a substantial proportion of the original Faroe Islands Cattle breed gene pool. The ancestry of admixed Faroe Islands Cattle individuals showed that 14 admixed individuals were significantly associated with the 'Norwegian Cattle' cluster.

**Discussion**

In general, H-WE was observed in all the five north European cattle breeds across all microsatellite loci and the locus-population test combinations showed a deviation (8%, 8/100) comparable to that of previous studies in cattle breeds (Martín-Burriel et al., 1999; Kantanen et al., 2000). The 20 loci analysed may be assumed to be unlinked, as linkage disequilibrium did not yield any significant comparisons for locus pairs across all population.

The strong membership of Faroe Islands Cattle from Norwegian Cattle cluster ($q = 0.409$) suggested there had been an intensive gene flow from Norwegian Cattle to native Faroe Islands Cattle, which occurred as a result of 'forced breeding' between them. The seven contemporary Faroe Islands Cattle individuals ($q \geq 0.80$ in Faroe Islands Cattle) were assumed to be purebred Faroe Islands Cattle. Due to the strong crossbreeding, 14 contemporarily Faroe Islands Cattle individuals with more than 80% ancestry of Norwegian Cattle were comparable to the pure Norwegian Cattle. Admixture analyses allowed the detection of a number of hybrids showing a $q < 0.80$ in any ancestry. These findings suggested that only few Faroe Islands Cattle still remain.

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## BEEF QUALITY OF VARIOUS CROSSBRED ANIMALS

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**Introduction**

Rearing of meat-type cattle started in Latvia in the last century when animals of Hereford (1965), Charolais (1968), Aberdeen Angus (1971) and Limousin [1] breeds were imported. At the moment the animals of these breeds and also crossbred animals are widespread in beef production [2].

The industry, being under severe financial conditions at the moment – low purchase prices (below 0.30 Ls/kg), huge product import to the country, small proportion of animals in the species (0.2%) etc. – has to try to recover by means of product quality. According to the references in the literature [4, 5], the protein content in muscles of carcasses of meat-type cattle is very high (20-22.5%) as well as biological value.

Great differences in growth rate and amount, and the weight of several muscle groups have been noticed in young bulls of different breeds with different genetic nature and of the same age [5].

A rapid development of the industry of crossing the milk and meat-type cattle's should clear up what kind of meat quality these animals display. The quality of a beef carcass is determined by its weight output, quantity of muscles, fat and bones, colour, meat pH and chemical content of meat.

The nutritional value of meat is connected to its chemical content. Muscle protein is considered to be valuable because it contains essential amino acids while connective tissue protein is incomplete - it does not contain many essential amino acids, especially tryptophane, but mostly replaceable amino acids as oxyproline that do not exist in the proteins of valuable meat. Taking into account this regularity, evaluation of valuable protein content has been adopted according to the quantity of tryptophane. Yet it is an incomplete one – as to the oxyproline content or the expression of the ratio of these amino acids [3, 4, and 5].

Live weight of an individual, its gain rate, settling abilities for fat, quantity and the form of muscles, places for fat settling, marbling of beef, thickness of muscle fibres and tenderness of meat are dependent on genetic factors and environmental effects. External conditions of housing and feeding influence mainly the fat quantity of carcass, meat output, fat melting point, odour and flavour of meat and fat.

Meat-type animals, due to higher growth energy and better assimilation ability of nutrients, fatten more successfully than cattle of milk type. This trend also concerns crossbred animals.

In beef production not only pure breed meat-type cattle are used, but crosses of step one and step two are widely used as well.

The goal of our work was to clear up meat quality of various crossbred cattle.

**Materials and Methods**

Crosses of Latvian Brown (LB) breed cows with Aberdeen Angus (AB), Charolais (CA), Hereford (HE), Highland (HA) and Limousin (LI) breed bulls were used in this study. Before slaughter visual evaluation was carried out on the cattle. Carcasses of the studied animals were evaluated as in compliance with EUROP classification, but the level of fat settling as per grades 1-5. For chemical analysis of meat, two samples were taken from each carcass: the first one from hip - thigh part (*m. gluteus medius)* and the second one from spine – loin part (*m. longissimus dorsi)*. In the studied samples dry matter, crude protein, crude fat, tryptophane, oxyproline and cholesterol were determined.

Housing and feeding of animals, included in this part of the study, are not analysed. It should be noted that all animals originated from farms of biological agricultural production. Meat processing of the studied animals took place in a slaughterhouse in Zaube rural municipality cooperative farm, Cesis district, certified by State Food and Veterinary Service.

The chemical analyses of 56 samples were done: dry matter was determined by a drying method, cholesterol by Blur method; oxyproline, tryptophane by a photometric method, fat by Sochlet method and protein by Kjeldahl method.

The studies were carried out in the second half of 2003 and they are still in progress.

**Results and Discussion**

Slaughter weight of the progeny of Latvian Brown breed cows and meat-type breed bulls was on average evaluated at the age of 16 to 17.5 months. On average, their slaughter weight per progeny was as follows: LB x AB -190.7±26.7 kg; LB x CA - 232.4±16.8 kg; LB x HE -232.5±11.0 kg; LB x HA -168.0±9.6 kg; LB x LI - 200±10.0 kg; CA – 219.6±19.6 kg; HE – 221.3±10.8 kg.

In compliance analyses of carcasses as to fat settling and muscle compliance, the following results were obtained: LB x AB – 3 (O), LB x CA – 3.3 (U), LB x HE – 2.8 (R), LB x HA – 2 (O), LB x LI – 3 (R), CA – 2.3 (R); HE -3.7 (R), observing meat evaluation as to the EUROP standard.

The chemical content of the muscles of the hip - thigh part of the studied crossbred animals (*m. gluteus medius)* is shown in Table 1.

Significant differences between the analysed meat samples of different groups were not observed, except for LB/HE crossbred animals. The quantity of oxyproline in this part of muscles was significantly ($p<0.01$) higher than in the analysed muscle samples of the other animal groups. Crude protein content, as it



can be seen in Table 1, was within the range of 19.33 to 21.02% that is appropriate according to the data of our dieticians Z. Zariņš and L. Neimane [5].

Table 1. Composition of beef topside (*m. gluteus medius)*, %

| Progeny Parentage | Crude protein,% | Crude fat,% | Tryptophane/ mg/% | Oxyproline mg/% | Ratio | Cholesterol |
|---|---|---|---|---|---|---|
| LB x AB | 19.33 ±0.42 | 0.72 ±0.19 | 3.33 ±0.18 | 1.42 ±0.05 | 2.34 ±0.09 | 59.37 ±5.36 |
| LB x CA | 20.44 ±0.31 | 0.93 ±0.25 | 3.07 ±0.10 | 0.90 ±0.04 | 3.52 ±0.24 | 59.26 ±4.30 |
| LB x HE | 20.49 ±0.22 | 1.62 ±0.30 | 3.30 ±0.11 | 1.69 ±0.11** | 1.97 ±0.11 | 66.15 ±2.03 |
| LB xHA | 20.47 ±0.26 | 0.92 ±0.37 | 3.35 ±0.23 | 1.16 ±0.21 | 3.00 ±0.30 | 58.40 ±2.70 |
| LB/LI | 21.02 ±0.72 | 0.61 ±0.46 | 3.10 ±0.15 | 1.1 ±0.0 | 2.77± 0.87 | 60.54 ±12.11 |
| CA | 20.73 ±0.53 | 1.19 ±0.41 | 3.2 ±0.14 | 1.04 ±0.16 | 3.28 ±0.48 | 62.50 ±11.09 |
| HE | 19.99 ±0.49 | 0.58 ±0.20 | 3.08 ±0.17 | 1.19 ±0.22 | 2.70 ±0.3 | 64.58 ±4.45 |

Level of differences in meat – type cattle: ** $p<0.01$

Data are means ±SE

Table 2. Composition of beef *(m. longissimus dorsi)* spine thickness, %

| Progeny Parentage | Crude protein,% | Crude fat,% | Tryptophane/ mg/% | Oxyproline mg/% | Ratio | Cholesterol |
|---|---|---|---|---|---|---|
| LB x AB | 20.30 ±0.56 | 0.56 ±0.09 | 3.5 ±0.11 | 1.5 ±0.24 | 2.53 ±0.37 | 56.83 ±2.96 |
| LB x CA | 19.60 ±0.44 | 0.8 ±0.20 | 3.23 ±0.14 | 0.92 ±0.06 | 3.61 ±0.32 | 56.47 ±2.76 |
| LB x HE | 20.23 ±0.28 | 1.51 ±0.30 | 3.55 ±0.07 | 1.63 ±0.14** | 2.24 ±0.14 | 63.28 ±1.97 |
| LB xHA | 20.19 ±0.30 | 0.64± 0.18 | 3.63 ±0.11 | 1.08 ±0.07 | 3.44 ±050 | 57.81 ±3.12 |
| LB/LI | 20.26 ±0.79 | 0.89± 0.63 | 3.22 ±0.12 | 1.20 ±0.04 | 2.69 ±0.19 | 54.69 ±8.59 |
| CA | 20.07 ±0.51 | 0.86 ±0.23 | 3.27 ±0.19 | 0.95 ±0.12 | 3.53 ±0.38 | 59.37 ±8.02 |
| HE | 19.42 ±0.98 | 0.55 ±0.23 | 3.32 ±0.17 | 1.15 ±0.13 | 2.95 ±0.28 | 62.24 ±0.26 |

Level of difference ** $p<0.01$

Data are means ±SE

In the analysis of crude fat quantity of topside (*m. gluteus medius),* it was recognized that there were no significant ($p>0.05$) differences among the analysed

samples. LB/HE animals showed a trend towards a higher content – 1.61±0.30%. The tryptophane content analysis revealed that it was very stable –3.03 to 3.35%. No significant differences ($p>0.05$) were revealed in the data of cholesterol content, but a certain trend towards a higher content was shown by LB/HE animals.

According to N. Gociridze and L. Tortladze [5], the feeding level for cattle (bulls to be fattened) affects the tryptophane content in meat (±7.1%) in a comparatively small degree. Therefore it should be reminded once again that the feeding level (high or low) of the animals under the study was not considered.

Analysing the data of sample contents of beef spine (*m. longissimus dorsi)* (Table 2), it is seen that there are similarities with these of Table 1. LB/HE animals also showed higher oxyproline content ($p<0.01$), but significant differences ($p>0.05$) were not revealed in the other indices of the chemical content.

**Conclusions**

In the analysis of F1 progeny of different meat-type breed bulls' crosses with Latvian brown breed cows, the following trends were observed.

1. There were no significant differences in crude protein, crude fat, tryptophane and cholesterol ($p>0.05$) content.
2. Lower meat quality, i.e. lower ratio of oxyproline and tryptophane, and higher oxyproline content was revealed by LB/HE cross animals ($p<0.01$).

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# THE INFLUENCE OF BREED ON PRODUCTION AND REPRODUCTIVE TRAITS IN THE LITHUANIAN RED AND RED-AND-WHITE CATTLE POPULATION


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**Introduction**

Lithuanian Red (LR) cattle breed has been developed and improved for more than 110 years. Currently Lithuanian Red and Red-and-White cattle stock comprises Lithuanian Red, Danish Red (DR), Angler (A), Swedish (SRW) and Holstein Red-and-White (HRW) breeds and offspring of various generations out of bulls of Swiss breeds with red cows [2, 4, 7, 8].

A. Banys [1] has grouped the Lithuanian red cattle population to different genotypes. The first genotype is represented by the cattle of the Lithuanian Red, Danish Red and Angler breeds and by the offspring born as a result of mating between the above mentioned breeds that have no blood of other breeds. The second genotype is represented by the descendants of various generations of the Red-and-White Holstein breed, as well as Danish Red and Angler breeds that have blood infusion from the Holstein breed. The third genotype is represented by the descendants of various generations out of bulls of the Brown Swiss (BS) breed, sired by bulls of Swiss breed, and Danish red bulls which have blood infusion from the Brown Swiss breed. The fourth genotype is represented by the descendants of various generations out of bulls of the Swedish Red-and-White and Ayrshire (Ay) breeds, sired by Swedish Red-and-White bulls and Angler bulls that have blood infusion from the above mentioned breed.

**Materials and methods**

Researches have been carried out at the State enterprise ŽEMĖS ŪKIO INFORMACIJOS IR KAIMO VERSLO CENTRAS, at The Lithuanian Red Cattle Improvement Association and at the Laboratory of Animal Breeding Value Establishment and Biometry of Lithuanian Veterinary Academy. Data basis for data manipulation and analysis were created on the cows' performance recording data received from the ŽEMĖS ŪKIO INFORMACIJOS IR KAIMO VERSLO CENTRAS at the Laboratory of Animal Breeding Value Establishment and Biometry of Lithuanian Veterinary Academy using the data operating system PostgreSQL 7.2 and Redhat 6.2 OS on LINUX system.

Statistical analyses were carried out using "R" package.

The milk recording data of all cows which had calved from 1st October, 1995 were used for the investigations.

The objective of the present study was to investigate the influence of breed on production and reproductive traits in the Lithuanian Red and Red-and-White cattle population.

**Results and discussion**

According to the data of state enterprise ŽEMĖS ŪKIO INFORMACIJOS IR KAIMO VERSLO CENTRAS [6], 40631 cows of the Lithuanian Red and Red-and-White cattle population are under milk recording. The average milk yield of those cows in 2002/2003 milk recording year was 4805 kg with 4.49% fat and 3.49% protein.

In the last eight years, fat and protein yield of all Red and Red-and-White cows have increased by 41.7% and 50.9%, respectively. The average milk production, fat and protein yield of the Lithuanian Red breed cows have increased only by 41.2, 50.7 and 44.3 %, respectively (Table 1).

The Lithuanian Red cattle has been improved by using other breeds for many years, however, cows of imported cattle breeds make 4.12% only. Most of them are cows of Swedish Red-and-White and Finnish Ayrshire breeds.

Last year the milk production of the Swedish Red-and-White and Finnish Ayrshire cows was higher than that of the Lithuanian Red by 2135 and 930 kg, respectively. The highest protein level was in the milk of the Angler and Danish Red cows (3.58%), and the highest fat level was in the milk of Angler and Finnish Ayrshire cows – 4.83 and 4.61 respectively.

A moderate positive correlation between milk fat and protein ($r_p$=0.44; P<0.01) and a low positive correlation between milk yield and fat percentage ($r_p$=0.01), as well as between milk yield and protein percentage ($r_p$=-0.08), were estimated in the Lithuanian Red and Red-and-White cattle population. We have found high positive and statistically significant correlation coefficients ($r_p$=0.84-0.97; P<0.01) between milk yield and milk fat and protein yields. The correlation coefficients mentioned above varied among different Red and Red-and-White cattle breeds (Table 2).

The analysis of Red and Red-and-White cows in different lactations shows that age at the first calving was 29.0 ±0.01, at the second calving – 42.0±0.03, and at the third calving – 54.6±0.04 months. The oldest age at the first calving (29.8±0.16 months), was in the German Red-and-White (GRW) breed. Age at the first calving of the Lithuanian Red Breed cows (29.1±0.02 months) was close to that of Red and Red-and-White breeds all together. The youngest age at the second calving was in Ayrshire breed (40.1±0.26 months), and the oldest – in Brown Swiss (43.8±0.68 months). The youngest age at the third calving was also in Ayrshire breed (51.7±0.35 months), and the oldest – in Danish Red (56.4±0.44 months).



We have studied the number of inseminations per pregnancy. The number of inseminations before the first calving was 1.76±0.01, before the second – 2.14±0.01 and before the third – 2.05±0.01.

Table1. Milk production of Red and Red-and-White cows in Lithuania

| Years / Breed | Average number of cows | Average production per year | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | Milk fat | | | | Milk protein | | | |
| | | Milk kg | Chan-ge, % | % | Chan-ge, % | kg | Chan-ge, % | % | Chan-ge, % | kg | Chan-ge, % |
| Red and Red-and-White all together | | | | | | | | | | | |
| 1996-1997 | 45684 | 3392 | 100.0 | 4.22 | 100.0 | 143 | 100.0 | 3.39 | 100.0 | 115 | 100.0 |
| 1999-2000 | 30119 | 4215 | 124.3 | 4.46 | 105.7 | 188 | 131.3 | 3.35 | 98.8 | 141 | 122.6 |
| 2000-2001 | 26643 | 4533 | 133.6 | 4.43 | 105.0 | 201 | 140.4 | 3.39 | 100.0 | 154 | 133.9 |
| 2001-2002 | 31634 | 4695 | 138.4 | 4.38 | 103.8 | 206 | 143.9 | 3.43 | 101.2 | 161 | 140.0 |
| 2002-2003 | 40631 | 4805 | 141.7 | 4.49 | 106.4 | 216 | 150.9 | 3.49 | 102.9 | 168 | 146.1 |
| The Lithuanian Red cows only | | | | | | | | | | | |
| 1996-1997 | 44718 | 3373 | 100.0 | 4.22 | 100.0 | 142 | 100.0 | 3.39 | 100.0 | 115 | 100.0 |
| 1999-2000 | 28914 | 4162 | 123.4 | 4.45 | 105.5 | 185 | 130.3 | 3.35 | 98.8 | 139 | 120.9 |
| 2000-2001 | 25374 | 4489 | 133.1 | 4.43 | 105.0 | 199 | 140.1 | 3.39 | 100.0 | 152 | 132.2 |
| 2001-2002 | 30219 | 4648 | 137.8 | 4.38 | 103.8 | 203 | 143.0 | 3.43 | 101.2 | 159 | 138.3 |
| 2002-2003 | 38957 | 4761 | 141.2 | 4.49 | 106.4 | 214 | 150.7 | 3.49 | 102.9 | 166 | 144.3 |
| Production of cows of all breeds and ±, if compared to the Lithuanian Red in 2002/03 milk recording year | | | | | | | | | | | |
| A | 231 | 5499 | +738.0 | 4.83 | +0.34 | 266 | +52.0 | 3.58 | +0.09 | 197 | +31.0 |
| DR | 209 | 5373 | +612.0 | 4.46 | -0.03 | 240 | +26.0 | 3.58 | +0.09 | 192 | +26.0 |
| Ay | 462 | 5691 | +930.0 | 4.61 | +0.12 | 262 | +48.0 | 3.52 | +0.03 | 201 | +35.0 |
| BS | 47 | 5134 | +373.0 | 4.57 | +0.08 | 235 | +21.0 | 3.45 | -0.04 | 177 | +11.0 |
| GRW | 290 | 5320 | +559.0 | 4.34 | -0.15 | 231 | +17.0 | 3.29 | -0.20 | 175 | +9.0 |
| SRW | 413 | 6896 | +2135.0 | 4.52 | +0.03 | 312 | +98.0 | 3.53 | +0.04 | 243 | +77.0 |
| HRW | 22 | 5570 | +809.0 | 4.35 | -0.14 | 242 | +28.0 | 3.38 | -0.11 | 188 | +22.0 |

The smallest number of inseminations for the first pregnancy was in Red Holstein breed (1.24±0.11), and the highest – in Ayrshire breed (2.05±0.07). The smallest number of inseminations before the second and third calving was in Red Holstein breed (1.40±0.16 and 2.00±0.58), and the highest – in Angler cattle herd (2.82±0.19 and 2.82±0.22).

According to the results of the study, the longest calving interval (397.3 ±0.42 days) was estimated between the first and second calving. The shortest calving interval after the first and the third lactations was in the Lithuanian Red cattle breed –

396.7±0.42 and 385.2±0.65 days, respectively. The longest calving interval after the first calving was in the Danish Red (422.8±6.64 days), and after the third lactation – in the Red Holstein (417.5±16.50 days).

Table 2. Phenotypic correlation of the milk production traits of the Red and Red-and-White cows in Lithuania

| Breed | Milk yield – | | | | Fat | |
|---|---|---|---|---|---|---|
| | fat % | fat kg | protein % | protein kg | protein % | kg - protein kg |
| All breeds | 0.01 | 0.91** | -0.08** | 0.96** | 0.44** | 0.93** |
| LR | 0.01 | 0.89** | -0.06** | 0.96** | 0.46** | 0.92** |
| DR | -0.26** | 0.91** | -0.03** | 0.97** | 0.45** | 0.93* |
| A | -0.21** | 0.90** | -0.36** | 0.96** | 0.55** | 0.91** |
| SRW | 0.01 | 0.84** | -0.03 | 0.96** | 0.48** | 0.88** |
| BS | -0.50** | 0.87** | -0.44** | 0.94** | 0.60** | 0.90** |
| GRW | 0.24** | 0.94** | -0.04 | 0.97** | 0.09 | 0.96** |

**P<0.01, *P<0.05

Service period from calving to conception of cows was different, depending on the age of cows: the longest was in the first lactation, shorter in the second and the third lactation. Service period varied also breed to breed. Among the first calvers, the shortest period was in Red Holstein and the longest – in Danish Red breed. And among cows after the third calving the shortest period was in the Lithuanian Red (105.0±0.68 days) and the longest – in the Red Holstein breed (140.0±22.00 days).

The analysis indicated significant effect (P<0.001) of breed on the reproductive traits. The biggest effect of breed on the calving age was obtained. The effect of breed of the first calvers on factorial dispersion in general dispersion of calving age takes 8.14%, of insemination index for the first calving – 4.96, of service period – 3.69% and of calving interval - 2.26%. The influence of breed on the reproductive traits in the second and the third lactations was lower.

**Conclusions**

The changes of milk production of the Lithuanian Red cows and of the cows of imported Red and Red-and White breeds were similar in the last 8 years: milk yield has increased by 41.2 to 41.7%, fat yield – by 50.7 to 50.9, protein yield – by 44.3 to 46.1%.

A moderate positive correlation was revealed between milk fat and protein ($r_p$=0.44; P<0.01) and high positive and statistically significant correlation coefficients ($r_p$=0.84-0.97; P<0.01) between milk yield and milk fat and protein yields. Correlation between milk yield and fat percentage as well as between milk yield and protein percentage were very low. Correlation coefficients varied among different Red and Red-and-White cattle breeds.



Table 3. Reproductive traits of the Red and Red-and-White cows

| Breed | n | The 1st lactation | n | The 2nd lactation | n | The 3rd lactation |
|---|---|---|---|---|---|---|
| Calving age, months | | | | | | |
| LR | 61250 | 29.1±0.02 | 36549 | 42.1±0.03 | 20751 | 54.6±0.04 |
| A | 419 | 27.8±0.19 | 265 | 41.1±0.28 | 178 | 54.1±0.43 |
| DR | 440 | 29.0±0.17 | 273 | 42.9±0.31 | 157 | 56.4±0.44 |
| Ay | 621 | 29.0±0.16 | 431 | 40.1±0.26 | 283 | 51.7±0.35 |
| HRW | 22 | 27.3±0.86 | 10 | 42.0±1.72 | 3 | 56.7±4.67 |
| BS | 78 | 27.6±0.43 | 48 | 43.8±0.68 | 29 | 55.8±0.65 |
| GRW | 452 | 29.8±0.16 | 298 | 42.8±0.26 | 196 | 55.8±0.41 |
| SRW | 535 | 27.2±0.13 | 323 | 41.1±0.24 | 232 | 54.2±0.34 |
| Average | 63819 | 29.0±0.01 | 38198 | 42.0±0.03 | 21829 | 54.6±0.04 |
| No. of inseminations per cow | | | | | | |
| LR | 44574 | 1.77±0.01 | 34206 | 2.12±0.01 | 19355 | 2.04±0.01 |
| A | 382 | 1.60±0.06 | 259 | 2.82±0.19 | 174 | 2.82±0.22 |
| DR | 420 | 1.54±0.05 | 271 | 2.69±0.16 | 157 | 2.67±0.17 |
| Ay | 572 | 2.05±0.07 | 423 | 2.41±0.09 | 280 | 2.20±0.09 |
| HRW | 17 | 1.24±0.11 | 10 | 1.40±0.16 | 3 | 2.00±0.58 |
| BS | 66 | 1.53±0.12 | 48 | 2.46±0.26 | 29 | 2.17±0.27 |
| GRW | 416 | 1.40±0.04 | 290 | 2.39±0.11 | 193 | 2.15±0.12 |
| SRW | 419 | 1.55±0.05 | 318 | 2.48±0.11 | 232 | 2.29±0.09 |
| Average | 46867 | 1.76±0.01 | 38198 | 2.14±0.01 | 20423 | 2.05±0.01 |
| Calving interval, days | | | | | | |
| LR | 36549 | 396.7±0.42 | 20625 | 387.7±0.50 | 11186 | 385.2±0.65 |
| A | 265 | 405.3±4.77 | 177 | 401.3±6.80 | 120 | 399.9±7.47 |
| DR | 273 | 422.8±6.64 | 157 | 410.2±6.72 | 69 | 407.5±8.54 |
| Ay | 431 | 400.0±4.33 | 283 | 376.1±3.78 | 189 | 393.4±5.31 |
| HRW | 10 | 411.0±36.00 | 3 | 417.0±21.40 | 2 | 417.5±16.50 |
| BS | 48 | 403.7.±11.50 | 29 | 390.9±12.90 | 19 | 398.8±17.70 |
| GRW | 298 | 413.1±6.04 | 196 | 401.8±6.23 | 129 | 402.1±8.00 |
| SRW | 323 | 420.1±5.19 | 232 | 397.5±4.42 | 157 | 414.2±7.10 |
| Average | 38198 | 397.3±0.42 | 21702 | 388.1±0.49 | 11871 | 386.2±0.64 |
| Service period after calving, days | | | | | | |
| LR | 34197 | 117.2±0.44 | 19351 | 107.6±0.52 | 10519 | 105.0±0.68 |
| A | 259 | 127.9±4.95 | 174 | 121.4±6.85 | 116 | 118.0±7.34 |
| DR | 271 | 142.0±6.60 | 157 | 131.5±6.83 | 69 | 125.0±8.55 |
| Ay | 423 | 112.0±4.30 | 280 | 100.5±4.15 | 188 | 115.9±5.64 |
| HRW | 10 | 104.6±20.30 | 3 | 129.7±13.10 | 2 | 140.0±22.00 |
| BS | 48 | 119.5±11.20 | 29 | 102.4±13.10 | 19 | 113.3±16.10 |
| GRW | 290 | 135.8±6.27 | 193 | 120.7±6.32 | 129 | 122.5±8.00 |
| SRW | 318 | 140.1±5.29 | 232 | 117.3±4.45 | 156 | 136.4±7.31 |
| Average | 35817 | 117.8±0.43 | 20419 | 108.1±0.51 | 11198 | 106.1±0.67 |

The analysis of Red and Red-and-White cows in different lactations shows that the oldest age at the first calving (29.8±0.16 months) was in the German Red-and-White breed. The youngest age at the second calving was in Ayrshire breed (40.1±0.26 months), and the oldest – in Brown Swiss (43.8±0.68 months).

Studies of the number of inseminations per cow showed that the number of inseminations before the first calving was 1.76±0.01, before the second – 2.14±0.01 and before the third – 2.05±0.01.

The shortest calving interval after the first and the third lactations was in the Lithuanian Red cattle breed – 396.7±0.42 and 385.2±0.65 days, respectively. The longest calving interval after the first calving was in the Danish Red (422.8±6.64 days), and after the third lactation – in the Red Holstein (417.5±16.50 days).

Service-period from calving to conception of cows was different, depending on the breed of cows: among cows after the third calving, the shortest period was in the Lithuanian Red (105.0±0.68 days) and the longest in the Red Holstein breed (140.0±22.00 days).

Milk production and reproductive traits in the Red and Red-and-White cattle population depend on the breed of cows. It shows that the breed should be considered at the breeding value estimation.

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## EFFECTS OF MILK PROTEIN GENOTYPES ON BODY WEIGHT AND MILK PRODUCTION TRAITS IN FINNISH AYRSHIRE COWS

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**Introduction**

Milk with good coagulation properties is expected to give more cheese with desirable composition than milk with poor properties. High casein concentration, especially that of κ-casein and casein number are beneficial in cheese production. Some milk protein genotypes have been reported to have favourable associations with the above characteristics.

It has been proposed that milk protein genotypes could be used as a criterion in selection to improve cheese production properties of milk. Before the milk protein genotypes can be considered in selection of breeding animals, the effects of the genotypes on milk production traits and other related traits have to be established. So far, the effects of the β-κ-casein (β-κ-CN) and β-lactoglobulin (β-LG) genotypes have previously been studied in Finland on the first lactation milk production traits (Ikonen et al., 1999) and on fertility traits (Ruottinen et al., 2004) from data of Finnish Ayrshire cows.

The objectives of the study were to estimate the effects of β-κ-casein and β-lactoglobulin genotypes on body weight and first, second and third lactation milk production traits in Finnish Ayrshire cows.

**Materials and Methods**

The cows in the data set were born in 1984 to 1993. The β- and κ-casein and β-lactoglobulin genotypes were determined using isoelectric focusing in polyacrylamide gels (Erhardt, 1989). Records for body weight and milk production traits were received from the Finnish Animal Breeding Association. After editing, complete information with respect to the model was available for 18 686 cows with the first, 16 274 with the second and 12 636 with the third lactation milk production records. The body weight measured after first calving was available for 13 921 cows. Regardless of culling, the frequencies of β-κ-CN and β-LG genotypes varied only a little in the three consecutive lactations.

For statistical analyses, year of calving was grouped in seven classes (1986 to 1988, 1989, 1990, 1991, 1992, 1993 and 1994) in the analyses of first lactation records and each year in four seasons, which totalled 28 year-season subclasses. Age at first calving was grouped in six classes: ≤ 23, 24, 25, 26, 27 to 28 and ≥ 29 months, and days open in seven classes: ≤ 60, 61 to 80, 81 to 100, 101 to 120, 121 to 160, 161 to 240, ≥ 240 days. Due to close linkage between the β- and κ-casein

loci, they were merged into 14 β-κ-CN composite genotypes (Table 1). Cows originated from 1548 herds in eastern Finland, and were the offspring of 756 sires.

The traits studied were analyzed within the first, second and third lactation assuming the following linear univariate model:

$$y_{ijklmno} = \mu + ys_i + ca_j + do_k + \beta\text{-}\kappa\text{-}CNgen_l + \beta\text{-}LGgen_m + h_n + a_o + e_{ijklmno}$$

where

$y_{ijklmno}$ = an observation on a cow for body weight or for 305-day milk, fat and protein yield, or fat and protein content,

$\mu$ = overall mean,

$ys_i$ = fixed effect of year-season of calving class $_{i,\ i = 1,\ldots,28}$,

$ca_j$ = fixed effect of calving age class $_{j,\ j = 1,\ldots,6}$,

$do_k$ = fixed effect of days open class $_{k,\ k = 1,\ldots,7}$,

$\beta\text{-}\kappa\text{-}CNgen_l$ = fixed effect of β-κ-CN genotype $_{l,\ l = 1,\ldots,14}$,

$\beta\text{-}LGgen_m$ = fixed effect of β-LG genotype $_{m,\ m = 1,\ 2,\ 3}$,

$h_n$ = random effect of herd $_{n,}$ N $(0, I\sigma^2_h)$,

$a_o$ = random additive genetic effect of animal $_{o,}$ N $(0, A\sigma^2_a)$,

$e_{ijklmno}$ = random residual effect, N $(0, I\sigma^2_e)$.

Covariances among herd, animal and residual effects were assumed to be zero.

Variance components for the random effects were estimated using the REML VCE4 program package (Groeneveld, 1997). The **A-** matrix included relationships among a total of 41 360 individuals of which 18 686 were cows with the first lactation records and 22 674 their parents or grandparents. Statistical significance of the fixed effects was tested by F-test using the PEST program package (Groeneveld, 1990).

**Results**

The effect of β-κ-CN genotypes on body weight was statistically significant (at least with $p < 0.05$) and that of β-LG genotypes non-significant. The differences in body weight between the individual β-κ-CN genotypes were, however, negligible.

The effect of β-κ-CN genotypes was statistically significant in all three lactations (at least with $p < 0.05$) for all milk production traits, except fat yield (Tables 1, 2 and 3). The effect of β-LG genotypes was non-significant on fat yield, but significant ($p < 0.001$) on fat content. The effect of β-LG genotypes was significant in most cases in the three lactations on milk and protein yield and protein content (Tables 1, 2 and 3).

Frequencies of the most common β-κ-CN genotypes for cows in the first lactation data set (Table 1) were $A_1A_2AE$ (30%), $A_2A_2AA$ (22%), $A_1A_2AA$



(13%), $A_1A_1EE$ (9%), $A_1A_1AE$ (8%), $A_1A_2AB$ (7%), $A_1A_1BE$ (4%), $A_1A_1AB$ (2%) and $A_1A_1AA$ (2%).

Table 1. Effects of the β-κ-casein (β-κ-CN) and β-lactoglobulin (β-LG) genotypes on the first lactation milk production traits

| Genotype | No. of cows | Milk yield $\bar{y}$=5861kg | Fat yield $\bar{y}$=265kg | Protein yield $\bar{y}$=192kg | Fat content $\bar{y}$=4.54% | Protein content $\bar{y}$=3.28% |
|---|---|---|---|---|---|---|
| | 18 686 | Est. ± se | Est. ± se | Est. ± se | Est. ± se | Est. ± se |
| β-κ-CN | | | | | | |
| $A_1A_1AA$ | 400 | -126 ± 43 | -2.0 ± 2.0 | -6.1 ± 1.3 | 0.07 ± 0.02 | -0.04 ± 0.01 |
| $A_1A_1AB$ | 418 | -194 ± 42 | -0.7 ± 2.0 | -5.0 ± 1.3 | 0.14 ± 0.02 | 0.02 ± 0.01 |
| $A_1A_1AE$ | 1533 | -151 ± 26 | -1.4 ± 1.2 | -7.2 ± 0.8 | 0.10 ± 0.01 | -0.04 ± 0.01 |
| $A_1A_1BB$ | 71 | -294 ± 95 | -5.3 ± 4.5 | -6.4 ± 2.9 | 0.17 ± 0.05 | 0.06 ± 0.02 |
| $A_1A_1BE$ | 738 | -114 ± 34 | 1.9 ± 1.6 | -4.6 ± 1.0 | 0.13 ± 0.02 | -0.01 ± 0.01 |
| $A_1A_1EE$ | 1664 | -99 ± 25 | 0.1 ± 1.2 | -6.3 ± 0.8 | 0.09 ± 0.01 | -0.05 ± 0.01 |
| $A_1A_2AA$ | 2335 | -73 ± 21 | 0.5 ± 1.0 | -3.0 ± 0.7 | 0.07 ± 0.01 | -0.01 ± 0.01 |
| $A_1A_2AB$ | 1291 | -136 ± 27 | -2.5 ± 1.3 | -3.2 ± 0.8 | 0.06 ± 0.02 | 0.02 ± 0.01 |
| $A_1A_2AE$ | 5657 | -12 ± 17 | 1.5 ± 0.8 | -2.0 ± 0.5 | 0.04 ± 0.01 | -0.02 ± 0.00 |
| $A_1A_2BB$ | 36 | -122 ± 132 | -1.4 ± 6.3 | -6.3 ± 4.1 | 0.05 ± 0.08 | -0.04 ± 0.03 |
| $A_1A_2BE$ | 108 | -94 ± 78 | -2.6 ± 3.7 | -4.1 ± 2.4 | 0.05 ± 0.05 | -0.01 ± 0.02 |
| $A_1A_2EE$ | 24 | -145 ± 160 | 0.5 ± 7.6 | -9.2 ± 4.9 | 0.14 ± 0.09 | -0.06 ± 0.04 |
| $A_2A_2AA$[a] | 4159 | 0 | 0 | 0 | 0 | 0 |
| $A_2A_2AB$ | 252 | 74 ± 55 | 1.5 ± 2.6 | 2.5 ± 1.7 | -0.03 ± 0.03 | -0.01 ± 0.01 |
| F-test | | 0.0000 | 0.0830 | 0.0000 | 0.0000 | 0.0000 |
| β-LG | | | | | | |
| AA | 1466 | 52 ± 24 | -1.3 ± 1.2 | 2.4 ± 0.7 | -0.07 ± 0.01 | 0.01 ± 0.01 |
| AB | 7711 | 25 ± 13 | -1.3 ± 0.6 | 1.2 ± 0.4 | -0.04 ± 0.00 | 0.01 ± 0.00 |
| BB[a] | 9509 | 0 | 0 | 0 | 0 | 0 |
| F-test | | 0.0509 | 0.1216 | 0.0010 | 0.0000 | 0.0751 |

[a]The genotype of comparison

The two most common genotypes, the double heterozygote $A_1A_2AE$ and the double homozygote $A_2A_2AA$, were the best and their effect was about equal to each others for milk yield in each lactation (Tables 1, 2 and 3). The most common genotype $A_1A_2AE$ had a tendency for increased fat and decreased protein content relative to the $A_2A_2AA$, the genotype of comparison. The rest of the genotypes, all genotypes homozygous for $A_1$-allele in the β-CN locus and the $A_1A_2AA$ and

$A_1A_2$AB genotypes, were about 70 to 190 kg inferior in milk yield relative to $A_2A_2$AA genotype. In general, the effects of the β-κ-CN genotypes on milk yield tended to decrease in later lactations.

Table 2. Effects of the β-κ-casein (β-κ-CN) and β-lactoglobulin (β-LG) genotypes on the second lactation milk production traits

| Genotype | No. of cows | Milk _yield ȳ=6854kg | Fat _yield ȳ=305kg | Protein _yield ȳ=227kg | Fat content ȳ=4.49% | Protein content ȳ=3.32% |
|---|---|---|---|---|---|---|
| | 16 274 | Est. ± se | Est. ± se | Est. ± se | Est. ± se | Est. ± se |
| β-κ-CN | | | | | | |
| $A_1A_1$AA | 342 | -67 ± 56 | 2.8 ± 2.7 | -2.9 ± 1.8 | 0.08 ± 0.03 | -0.02 ± 0.01 |
| $A_1A_1$AB | 378 | -186 ± 54 | -1.2 ± 2.6 | -4.7 ± 1.7 | 0.10 ± 0.03 | 0.01 ± 0.01 |
| $A_1A_1$AE | 1321 | -88 ± 33 | 2.7 ± 1.6 | -4.1 ± 1.0 | 0.10 ± 0.02 | -0.02 ± 0.01 |
| $A_1A_1$BB | 63 | -126 ± 123 | -5.4 ± 6.0 | -2.5 ± 3.8 | 0.02 ± 0.06 | 0.03 ± 0.03 |
| $A_1A_1$BE | 653 | -95 ± 44 | 1.1 ± 2.1 | -3.4 ± 1.4 | 0.08 ± 0.02 | -0.00 ± 0.01 |
| $A_1A_1$EE | 1429 | -91 ± 33 | -0.1 ± 1.6 | -5.7 ± 1.0 | 0.06 ± 0.02 | -0.03 ± 0.01 |
| $A_1A_2$AA | 2039 | -95 ± 28 | -0.1 ± 1.4 | -3.4 ± 0.9 | 0.06 ± 0.01 | -0.00 ± 0.01 |
| $A_1A_2$AB | 1144 | -100 ± 35 | -1.6 ± 1.7 | -1.8 ± 1.1 | 0.03 ± 0.02 | 0.02 ± 0.01 |
| $A_1A_2$AE | 4933 | -25 ± 22 | 0.4 ± 1.1 | -2.6 ± 0.7 | 0.02 ± 0.01 | -0.02 ± 0.01 |
| $A_1A_2$BB | 32 | -86 ± 172 | 1.4 ± 8.3 | -3.8 ± 5.4 | 0.09 ± 0.09 | -0.00 ± 0.04 |
| $A_1A_2$BE | 92 | -15 ± 103 | 2.6 ± 5.0 | -2.9 ± 3.2 | 0.05 ± 0.05 | -0.03 ± 0.02 |
| $A_1A_2$EE | 20 | 151 ± 215 | 12.8 ±10.4 | 0.6 ± 6.7 | 0.09 ± 0.11 | -0.06 ± 0.05 |
| $A_2A_2$AA[a] | 3612 | 0 | 0 | 0 | 0 | 0 |
| $A_2A_2$AB | 216 | 34 ± 71 | -3.3 ± 3.5 | -0.1 ± 2.2 | -0.08 ± 0.04 | -0.02 ± 0.02 |
| F-test | | 0.0045 | 0.6557 | 0.0001 | 0.0000 | 0.0000 |
| β-LG | | | | | | |
| AA | 1279 | 57 ± 31 | -3.4 ± 1.5 | 2.9 ± 1.0 | -0.09 ± 0.02 | 0.01 ± 0.01 |
| AB | 6668 | 43 ± 17 | -0.8 ± 0.8 | 2.3 ± 0.5 | -0.04 ± 0.01 | 0.01 ± 0.00 |
| BB[a] | 8327 | 0 | 0 | 0 | 0 | 0 |
| F-test | | 0.0287 | 0.0847 | 0.0000 | 0.0000 | 0.0004 |

[a]The genotype of comparison

The effects of the β-κ-CN genotypes on fat content were the opposite of the effects on milk yield. The effects of all β-κ-CN genotypes were about 0.02 to 0.14 %-units superior in fat content relative to the $A_2A_2$AA genotype. The effects of genotypes $A_1A_1$AB and $A_1A_2$AB were about 0.01 to 0.04 %-units superior and the



genotypes $A_1A_1$AE and $A_1A_1$EE about 0.00 to 0.05 %-units inferior in protein content relative to the $A_2A_2$AA genotype.

Table 3. Effects of the β-κ-casein (β-κ-CN) and β-lactoglobulin (β-LG) genotypes on the third lactation milk production traits

| Genotype | No. of cows | Milk _yield ȳ=7350kg | Fat _yield ȳ=325kg | Protein _yield ȳ=241kg | Fat content ȳ=4.46% | Protein content ȳ=3.29% |
|---|---|---|---|---|---|---|
| | 12 636 | Est. ± se | Est. ± se | Est. ± se | Est. ± se | Est. ± se |
| β-κ-CN | | | | | | |
| $A_1A_1$AA | 256 | -62 ± 70 | 2.6 ± 3.4 | -1.8 ± 2.2 | 0.07 ± 0.03 | 0.00 ± 0.01 |
| $A_1A_1$AB | 303 | -139 ± 66 | 2.2 ± 3.2 | -3.1 ± 2.1 | 0.13 ± 0.03 | 0.01 ± 0.01 |
| $A_1A_1$AE | 1034 | -104 ± 41 | 1.8 ± 2.0 | -3.9 ± 1.3 | 0.09 ± 0.02 | -0.00 ± 0.01 |
| $A_1A_1$BB | 53 | -131 ± 146 | 7.2 ± 7.1 | 2.9 ± 4.6 | 0.18 ± 0.07 | 0.10 ± 0.03 |
| $A_1A_1$BE | 506 | -78 ± 54 | 3.0 ± 2.6 | -2.1 ± 1.7 | 0.09 ± 0.03 | 0.01 ± 0.01 |
| $A_1A_1$EE | 1099 | -64 ± 40 | 1.7 ± 2.0 | -3.9 ± 1.3 | 0.07 ± 0.02 | -0.02 ± 0.01 |
| $A_1A_2$AA | 1588 | -69 ± 34 | -0.7 ± 1.7 | -2.1 ± 1.1 | 0.03 ± 0.02 | 0.00 ± 0.01 |
| $A_1A_2$AB | 914 | -83 ± 42 | 0.6 ± 2.0 | -0.2 ± 1.3 | 0.06 ± 0.02 | 0.04 ± 0.01 |
| $A_1A_2$AE | 3765 | 15 ± 27 | 2.5 ± 1.3 | -0.7 ± 0.8 | 0.03 ± 0.01 | -0.01 ± 0.01 |
| $A_1A_2$BB | 22 | 126 ± 225 | 10.4 ±10.9 | 6.3 ± 7.1 | 0.05 ± 0.11 | 0.02 ± 0.04 |
| $A_1A_2$BE | 70 | 6 ± 128 | 1.7 ± 6.2 | 1.0 ± 4.0 | 0.02 ± 0.06 | 0.02 ± 0.02 |
| $A_1A_2$EE | 11 | 245 ± 315 | 5.9 ± 15.3 | 5.4 ± 9.7 | -0.06 ± 0.02 | -0.04 ± 0.06 |
| $A_2A_2$AA[a] | 2861 | 0 | 0 | 0 | 0 | 0 |
| $A_2A_2$AB | 154 | -148 ± 90 | -8.5 ± 4.4 | -4.7 ± 2.8 | -0.04 ± 0.04 | -0.01 ± 0.02 |
| F-test | | 0.0272 | 0.4130 | 0.0354 | 0.0000 | 0.0000 |
| β-LG | | | | | | |
| AA | 1009 | 35 ± 38 | -2.4 ± 1.8 | 2.6 ± 1.2 | -0.06 ± 0.02 | 0.02 ± 0.01 |
| AB | 5160 | 24 ± 21 | -2.1 ± 1.0 | 1.6 ± 0.7 | -0.04 ± 0.01 | 0.01 ± 0.00 |
| BB[a] | 6467 | 0 | 0 | 0 | 0 | 0 |
| F-test | | 0.4533 | 0.0966 | 0.0206 | 0.0000 | 0.0027 |

[a]The genotype of comparison

The β-LG BB genotype was about 0.06 to 0.09%-units superior in fat content relative to the AA genotype (Tables 1, 2 and 3). The β-LG AA genotype was slightly better in milk yield, but the differences between the individual genotypes were small from the practical point of view.

**Discussion and Conclusions**

The results for milk production traits were, in general, in agreement with the results in the comparable studies in the literature (e.g., Bovenhuis et al., 1992; Velmala et al., 1995).

Milk yield was superior for genotypes with $A_2$-allele as opposed to $A_1$-allele in the β-CN locus. Both B- and E-alleles in κ-CN locus increased the fat content. The B-allele in κ-CN locus increased, but the E-allele decreased the protein content. Thus, the β-κ-CN haplotype $A_2A$ was associated with high milk yield and low fat but moderate protein content, the $A_1B$ haplotype with low milk yield and high fat and protein content, and the $A_1E$ haplotype with low milk yield and high fat but low protein content.

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# THE FUNCTIONAL TRAITS, LONGEVITY AND MILK PRODUCTION OF ESTONIAN HOLSTEIN COWS

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**Introduction**

Early culling of cows decreases the efficiency of milk production as their lifetime productivity decreases and expenses on young stock increase. Early culling rate can be decreased by improvement of functional traits and by creation of favourable environmental conditions. In dairy cattle breeding the main attention has been paid for the improvement of milk performance but more often the functional traits are taken into consideration as well to improve the of durability of cows. High-yielding cows have more frequent fertility problems, udder diseases and metabolic disorders. Feet and locomotion problems also occur very often. The cows with stronger feet and legs have longer lifetime (Burke et al, 1993; Ral et al., 1995). Hamonen (1996) reported that cow's lifetime is most strongly affected by udder traits, then by feet and general impression. McDaniel (1995) reported that the rear legs shape has a smaller effect on longevity than foot angle. Sieber et al. (1988) mentioned that the cows with stronger udder attachment, normal teat placement, deeper body and moderate rump angle stay longer in the herd.

**Materials and Methods**

The data of 7314 Estonian Holstein cows culled from 1996 to 2002 were collected from Animal Recording Centre. The data of the culled cows ere randomly collected from 150 different farms. The cows with registered milk performance, conformation scores, birth and culling date, date at first calving and culling reasons were included into database. The cows were divided into three groups by 1st, 2nd, 3rd and older lactations. According to those data the lifetime length, age at first calving and productive lifetime were calculated. Minitab and Excel programs conducted regression and correlation analyses between different items.

**Results**

The analyses revealed that the proportion of culled cows in the 1st and 2nd lactation increased from year to year (Table 1). The culling rate of young cows has increased from 23.6% in 1996 to 40% in 2002. This process can be due to higher selection intensity and also to economic reasons. Unfavourable economical situation in 1997 was the reason why many dairy farms stopped milk production and lot of young cows were culled out. Since 2001 the culling rate of younger cows has decreased. In connection to the above-mentioned reason, the average lifetime of the culled cows decreased from 77 to 63 months (Table 2).

Table 1. The structure of culled cows in 1996 to 2002, (%)

| Lactation | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | Mean |
|---|---|---|---|---|---|---|---|---|
| 1st | 10.8 | 18.6 | 18.1 | 19.3 | 23.2 | 20.6 | 17.5 | 19.13 |
| 2nd | 12.8 | 11.5 | 21.7 | 22.8 | 24.8 | 26.0 | 27.6 | 21.42 |
| ≥ 3rd | 76.4 | 69.9 | 60.2 | 57.9 | 52.0 | 53.4 | 54.9 | 59.45 |
| Mean | 10.4 | 13.1 | 12.9 | 18.7 | 17.5 | 24.1 | 3.4 | 100.0 |

The age at first calving has been 28 months during seven years. The regression analyses showed that the increase of age first calving decreases the lifetime milk production by 10.6 kg.

$b_{y/x}$=-10.58 day, where $_x$-age at first calving, days $_y$-lifetime milk production, kg

Y=28535.6-10.58x

From 49 to 34 months the average age of productive lifetime also decreased during the period. With shorter lifetime the lifetime milk production per cow was decreased over 5,000 kg as well. The average milk production per day in lifetime has changed only by 0.5 kg but that in productive lifetime has increased by 1.5 kg. This is due to the increase of the productivity of cows.

Table 2. The average lifetime, age at first calving, productive lifetime and milk performance of Estonian Holstein cows in 1996 to 2002

| Item | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | Average |
|---|---|---|---|---|---|---|---|---|
| Age at first calving, month | 28.6 | 28.9 | 28.8 | 28.6 | 28.4 | 28.2 | 28.3 | 28.5 |
| Lifetime, month | 77.8 | 76.4 | 74.0 | 69.1 | 64.4 | 63.2 | 62.6 | 69.1 |
| Productive lifetime, month | 49.2 | 47.5 | 45.1 | 40.5 | 36.0 | 35.0 | 34.4 | 40.6 |
| Lifetime milk, kg | 23379 | 21567 | 20784 | 19263 | 17040 | 18350 | 17393 | 19336 |
| Milk per lifetime day, kg | 9.0 | 8.4 | 8.4 | 8.2 | 7.8 | 8.7 | 8.5 | 8.4 |
| Milk per productive day, kg | 15.8 | 15.7 | 16.2 | 16.1 | 16.1 | 17.8 | 17.3 | 16.5 |

Comparison of the culled cows in different lactation showed that the average age at first calving was not significantly different (Table 3). The average durability of the cows culled in the 1st lactation has been 37…38 months over the years. In 1996-1999 the lifetime of the cows culled in the 2nd lactation decreased from 53 to 48 months.

Lifetime was shortened most with the cows culled in the 3rd and later lactations-from 87 to 77 months in 1999 and 2002 respectively. It can be concluded that the average length of durability shortened mainly by more intensive culling of older cows.

The productive lifetime of the cows culled in the 1st lactation has prolonged from 7.9 to 10 months that of the cows culled in the 2nd lactation has remained



around 20 months. The durability of the 3rd and later lactation cows has shortened by 10 months. The milk production per lifetime day and per productive lifetime day has decreased from year to year due to the total increase of milk productivity of cows.

Table 3. The age at first calving, average lifetime, productive lifetime and milk performance of cows culled from 1st to 3rd lactation in 1996 to 2002

| Lact. | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | Mean |
|---|---|---|---|---|---|---|---|---|
| Age at first calving, month | | | | | | | | |
| 1st | 29.4 | 30.1 | 28.0 | 28.0 | 28.0 | 28.1 | 27.7 | 28.3 |
| 2nd | 29.8 | 29.8 | 29.9 | 28.3 | 27.8 | 28.0 | 28.0 | 28.5 |
| ≥ 3rd | 28.2 | 28.4 | 28.7 | 28.9 | 28.8 | 28.3 | 28.6 | 28.6 |
| Lifetime, months | | | | | | | | |
| 1st | 37.3 | 38.9 | 37.8 | 37.5 | 37.4 | 37.9 | 37.7 | 37.8 |
| 2nd | 53.4 | 49.4 | 50.5 | 48.2 | 47.8 | 48.2 | 48.6 | 48.8 |
| ≥ 3rd | 87.6 | 90.9 | 93.3 | 87.9 | 84.3 | 80.2 | 77.6 | 86.5 |
| Productive lifetime, months | | | | | | | | |
| 1st | 7.9 | 8.8 | 9.8 | 9.5 | 9.5 | 9.8 | 10.0 | 9.5 |
| 2nd | 23.6 | 19.6 | 20.6 | 19.9 | 20.0 | 20.2 | 20.7 | 20.4 |
| ≥ 3rd | 59.4 | 62.4 | 64.6 | 58.9 | 55.5 | 51.9 | 49.0 | 57.9 |
| Average lifetime milk production, kg | | | | | | | | |
| 1st | 3992 | 4392 | 5223 | 4816 | 4817 | 6036 | 5985 | 5114 |
| 2nd | 10342 | 9256 | 10128 | 9755 | 9750 | 10768 | 10929 | 10153 |
| ≥ 3rd | 29562 | 29862 | 30573 | 28029 | 26271 | 26695 | 24075 | 27995 |
| Average milk production per lifetime day, kg | | | | | | | | |
| 1st | 3.3 | 3.6 | 4.3 | 4.0 | 4.1 | 5.1 | 5.0 | 4.3 |
| 2nd | 6.5 | 6.0 | 6.5 | 6.5 | 6.5 | 7.2 | 7.2 | 6.7 |
| ≥ 3rd | 10.6 | 10.6 | 10.6 | 10.3 | 10.1 | 10.7 | 10.2 | 10.5 |
| Average milk production per productive lifetime day, kg | | | | | | | | |
| 1st | 15.5 | 15.5 | 16.8 | 16.2 | 16.4 | 20.0 | 18.8 | 17.2 |
| 2nd | 15.6 | 15.4 | 16.0 | 15.9 | 15.7 | 17.3 | 17.2 | 16.3 |
| ≥ 3rd | 15.9 | 15.8 | 16.0 | 16.1 | 16.2 | 17.2 | 17.0 | 16.3 |

An analysis of various culling reasons by different years and lactations revealed that through the years the major problems have been udder diseases, sterility, feet and hoof disorders and metabolic diseases (Tables 4 and 5).

The rate of metabolic diseases has increased most dynamically. In later lactations liver diseases occur more frequently.

Table 4. The culling rate by different reasons in Estonian Holstein cows from 1996 to 2002, (%)

| Culling reason | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | Mean |
|---|---|---|---|---|---|---|---|---|
| Age | 4.4 | 4.6 | 4.3 | 3.7 | 2.7 | 2.4 | 4.1 | 3.5 |
| Low productivity | 5.8 | 6.4 | 6.6 | 6.9 | 8.3 | 5.0 | 4.9 | 6.4 |
| Sterility | 25.0 | 19.7 | 23.1 | 19.5 | 19.7 | 18.3 | 12.2 | 20.1 |
| Udder diseases | 25.9 | 28.6 | 24.2 | 21.9 | 26.4 | 32.2 | 29.7 | 27.0 |
| Gynaecological diseases | 8.3 | 5.6 | 6.1 | 6.1 | 6.9 | 5.5 | 5.3 | 6.2 |
| Feet and hoof disorders | 10.4 | 14.6 | 16.4 | 18.4 | 13.2 | 13.5 | 12.6 | 14.5 |
| Trauma | 3.2 | 3.6 | 3.2 | 4.6 | 4.2 | 3.6 | 7.7 | 3.9 |
| Metabolic diseases | 4.2 | 6.6 | 5.6 | 5.9 | 7.1 | 7.5 | 11.0 | 6.5 |
| Liver diseases | 5.4 | 4.5 | 4.2 | 5.1 | 2.1 | 3.2 | 3.7 | 3.9 |
| Other diseases | 7.4 | 5.9 | 6.4 | 8.1 | 9.2 | 8.7 | 8.9 | 7.9 |

In both cases the reasons were nutritional problems of high- yielding cows. The 1st lactation cows primarily more frequently culled because of sterility and gynaecological diseases high-yielding cows. Those problems are usually related to metabolic disorders in high-yielding cows.

Table 5. Culling rate by reasons and 305-day milk yield in 1st. 2nd and 3rd lactation in Estonian Holstein Cows

| Culling reason | 1st lactation | | 2nd lactation | | 3rd lactation | | Mean |
|---|---|---|---|---|---|---|---|
| | % | kg | % | kg | % | kg | % |
| Age | … | … | … | … | 5.9 | 5485 | 3.5 |
| Low productivity | 13.2 | 4146 | 7.4 | 5012 | 3.9 | 4711 | 6.4 |
| Sterility | 30.0 | 5503 | 21.0 | 6333 | 16.5 | 5898 | 20.1 |
| Udder diseases | 21.3 | 5498 | 26.2 | 6299 | 29.2 | 6228 | 27.0 |
| Gynaecological diseases | 8.7 | 5355 | 6.9 | 6414 | 5.2 | 5985 | 6.2 |
| Feet and hoof disorders | 9.2 | 5360 | 12.8 | 5883 | 16.9 | 6181 | 14.5 |
| Trauma | 4.3 | 5437 | 4.6 | 6232 | 3.6 | 6231 | 3.9 |
| Metabolism disorders | 3.9 | 4685 | 7.6 | 6135 | 7.0 | 6557 | 6.5 |
| Liver diseases | 1.9 | 5837 | 3.5 | 6594 | 4.7 | 6815 | 3.9 |
| Other diseases | 7.5 | 5379 | 10.0 | 5940 | 7.3 | 6174 | 7.9 |

These results prove that in addition to high milk performance, health traits should be more considered in Estonian Holstein selection.



Table 6. Relationships between type traits, durability and milk production in Estonian Holstein cows

| Type traits | Correlation | | | Lactation | | | |
|---|---|---|---|---|---|---|---|
| | Life-time | Productive lifetime | Lifetime milk. kg | 1st | 2nd | 3rd | Mean |
| Body depth | 0.06 | 0.06 | 0.06 | 6.7 | 6.9 | 6.7 | 6.7 |
| Rump angle | -0.11 | -0.1 | -0.05 | 4.6 | 4.7 | 4.5 | 4.6 |
| Rump width | 0.18 | 0.17 | 0.16 | 6.3 | 6.3 | 6.4 | 6.4 |
| Foot angle | 0.21 | 0.22 | 0.22 | 4.5 | 4.5 | 4.8 | 4.7 |
| Rear legs side view | -0.04 | -0.05 | -0.09 | 6.0 | 6.0 | 5.8 | 5.9 |
| Fore udder attachment | 0.08 | 0.07 | 0.07 | 6.2 | 6.2 | 6.2 | 6.2 |
| Udder depth | -0.03 | -0.04 | -0.08 | 6.4 | 6.3 | 6.3 | 6.3 |
| Rear udder height | 0.17 | 0.17 | 0.20 | 5.5 | 5.7 | 5.9 | 5.8 |
| Centre ligament | 0.01 | 0.03 | 0.06 | 5.7 | 5.8 | 5.8 | 5.8 |
| Teat placement | -0.08 | -0.08 | -0.06 | 5.5 | 5.5 | 5.3 | 5.4 |
| Teat length | 0.04 | 0.05 | 0.07 | 5.2 | 5.3 | 5.3 | 5.3 |
| General impression | 0.09 | 0.11 | 0.18 | 26.4 | 26.6 | 26.7 | 26.6 |
| Udder | -0.13 | -0.12 | -0.09 | 36.9 | 37.1 | 36.6 | 36.7 |
| Feet and legs | 0.26 | 0.28 | 0.33 | 15.4 | 15.5 | 15.9 | 15.7 |
| Final score | 0.02 | 0.04 | 0.10 | 78.6 | 79.2 | 79.2 | 79.1 |

The correlation analysis demonstrated a weak relationship between the type traits and the lifetime length (Table 6). The cows with higher rear udder attachment, wide rump and better hooves have longer lifetime (r=0.18…0.26). A stronger correlation was found between lifetime and feet and legs score (r=0.26).

The increase of feet and legs score prolonged the durability by 171.3 days.

$b_{y/x}$=171.3 day, where y – lifetime, days x – feet and legs score

Y=-579.5+171.3x

A negative relationship between udder score and lifetime was found (r=-0.13). The cows with better udder have usually higher milk yield compare to cows with lower udder score. But the high-yielding cows have more health problems and they culled earlier as it became obvious above. The relationship between final score and durability was weak (r=0.02).

**Conclusions**

The durability of culled Holstein cows shortened from 77.8 to 62.6 months in 1996 to 2002, respectively.

The longevity of cows culled in 3rd and later lactations shortened most-15 months.

The average lifetime production per cow has decreased but milk per lifetime day has been stable (10 kg) due to the higher average milk yield per lactation. The average age at first calving of culled cows was 28 months.

A regression analysis revealed that the productive age becomes shorter and the lifetime milk production decreases with advanced age at 1st calving. Investigation of various culling reasons indicated, that most frequently the cows were culled due to sterility, udder diseases, feet and hoof disorders. In the years of investigation the percentage of metabolic and liver diseases increased to the greatest effect.

The cows with better legs and feet have longer lifetime. In selection of cows, more attention should be paid to functional traits in addition to milk performance

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## SEMEN QUALITY IN ESTONIAN HOLSTEIN AND ESTONIAN RED DAIRY BULLS

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**Abstract**

The aim of the current study was to compare sperm morphology and motility in Estonian Holstein and Estonian Red dairy bulls and evaluate their relations to bulls´ in vivo fertility expressed as non-return rate (NRR) of the dairy cows and heifers.

The average proportion of abnormal sperms was slightly higher in Estonian Holstein bulls in comparison to Estonian Red bulls ($P<0.05$). Positive correlation was obtained between the percentage of normal sperms in the fresh semen and 60-days NRR of cows and heifers both on ejaculate and bull level ($r=0.51$, $P<0.01$ and $r=0.49$, $P<0.01$).

Sperm motility characteristics were similar in two breeds except average path velocity (VAP) which was higher in fresh semen of Estonian Holstein bulls if compared to that of Estonian Red bulls ($P<0.05$). Strong positive correlation was obtained between the overall sperm motility in frozen/thawed semen and 60-days NRR of cows and heifers on bull level ($r=0.69$; $P<0.005$).

We conclude that the Estonian AI bull population is rather uniform in relation to sperm morphology and sperm motility characteristics and there are no significant breed differences. Evaluation of sperm morphology and motility characteristics should be continued as a routine in AI station as these parameters correlate well with female fertility.

**Introduction**

Fertilizing capacity of frozen-thawed bull semen affects non-return rates in cows and heifers. Therefore the AI stations need to apply such semen evaluation methods that give the most objective data about the quality of fresh and frozen/thawed semen and correlate well with the NRR. The most reliable approach to predict the fertility of semen is to use a combination of tests to evaluate different sperm attributes. Among the different methods, evaluation of sperm morphology and determination of motility characteristics in fresh and frozen/thawed semen using Computer Assisted Cell Motion Analyser (CMA) are fully applicable in AI stations.

The aim of the current study was to compare sperm morphology and motility in Estonian Holstein and Estonian Red dairy bulls and evaluate their relation to in vivo fertility expressed as NRR of the dairy cows and heifers.

## Material and Methods

Sperm morphology and motility were evaluated in 4306 ejaculates from 141 Estonian Holstein and 424 ejaculates from 30 Estonian Red dairy bulls collected from March 1998 to December 2003 in Kehtna AI station. During that period, 5-8 ejaculates from each proven bull and 2-5 ejaculates from young bulls were collected per month on an average. Frozen/thawed semen from 91 ejaculates of 29 Estonian Holstein bulls was studied to determine the relation between the sperm morphology, motility and NRR. Altogether 6229 test inseminations were done with the semen doses from those ejaculates (average 323 inseminations per bull and 70 inseminations per ejaculate). Bull's *in vivo* fertility estimation was based on 60-days non-return rates of inseminated females.

For sperm morphology evaluation, air dried smears were fixed in ethanol and stained with SPERMAC$^{TM}$ (Stain Enterprises, South Africa) according to the recommendations of the manufacturer. One hundred spermatozoa in each preparation were examined under the phase contrast microscope (x 1000). Different morphological abnormalities (detached heads, abnormal heads, abnormal necks, proximal and distal cytoplasmic droplets, abnormal midpieces and abnormal tails) were registered in each preparation as a percentage of the total number of counted spermatozoa.

Sperm motility in fresh and frozen/thawed semen was determined with a computer assisted sperm motility analyser (CMA, Computer Assisted Cell Motion Analyser, Sperm Vision, Minitüb GmbH&Co, Germany). Fresh semen was prepared by the dilution in ratio 1:10 in Triladyl (Minitüb GmbH&Co, Germany) and egg yolk extender. The frozen semen straw was thawed by plunging it in water at +35°C for 20 sec. The preparations were studied in Makler chamber, evaluating approximately ~400 spermatozoa from 4-5 different fields (x 400) and estimating percentage of motile and progressively motile spermatozoa, velocity average path (VAP, μm/sec), velocity curve line (VCL, μm/sec), velocity straight line (VSL, μm/sec), linearity (LIN; VSL/VCL), beat cross frequency (BCF, Hz) and amplitude of lateral head displacement (ALH, μm).

Analysis of variance was used for statistical analysis of differences between the bulls obtained in frequency of sperm abnormalities. Differences were considered significant when $P \leq 0.05$. Pearson correlation analysis was used to study the relationships between the laboratory tests values and 60-days NRR.

## Results and Discussion

Sperm morphology

The studies showed significant differences in the character and proportions of sperm abnormalities in fresh semen of Estonian Holstein and Estonian Red bulls. The proportion of total sperm abnormalities was higher in Estonian Holstein bulls



than in Estonian Red bulls (12.17 versus 11.37%, $P<0.05$). Semen of the Estonian Red bulls contained more spermatozoa with abnormal midpieces than the semen of the Estonian Holstein bulls ($P<0.001$). At the same time, nearly all the other abnormalities were represented at a higher level in the Estonian Holstein bulls. There were 1.2 times more spermatozoa with abnormal heads ($P<0.001$), 1.9 times more spermatozoa with proximal and distal cytoplasmic droplets ( $P<0.001$) and 2.2 times more spermatozoa with abnormal tails ($P<0.001$) in the semen of the Estonian Holstein bulls in comparison to the semen of the Estonian Red bulls. Morphology of bull spermatozoa gives a good survey of the semen quality changes caused by the season, age of the bull or breed (Söderquist et al., 1996). At the same time several authors have reported about the relations between the proportions of morphologically normal spermatozoa and the other sperm quality characteristics in raw semen (Neild et al., 1998). The influence of the breed on the frequency of pathological spermatozoa has been observed earlier by the other authors. Söderquist et al. (1996) found more abnormal spermatozoa in the semen of Swedish Red and White bulls than in the Swedish Holstein-Friesian bulls. Notling & Arndt (1995) found that the high proportion of morphologically abnormal sperms in Frieseland bull semen caused low non-return rate of the female animals. Slight increase in the frequency of abnormal spermatozoa in the semen of Estonian Holstein bulls could be explained by inbreeding that has caused relative genetic homogeneity of Estonian Holstein bulls. At the same time the difference in the percentage of abnormal sperms between two breeds was less than 1% in our study and cannot affect significantly pregnancy rates of females.

Sperm motility in fresh and frozen/thawed semen

The results of the study showed that the percentages of motile and progressively motile spermatozoa in fresh and frozen/thawed semen were similar in both breeds (Tables 1 and 2).

Furthermore, all the kinetic characteristics of the spermatozoa except VCL in fresh semen were also similar. The latter was higher in the Estonian Holstein bulls in comparison to the Estonian Red bulls while no difference was found in the frozen/thawed semen.

Several researches have found that testing semen motility characteristics with computer assisted analysis enables good survey of frozen-thawed semen quality. Neild et al. (1998) have found positive correlation between sperm progressive motility and intactness of sperm membranes.

The fact that the average path velocity of spermatozoa of Estonian Holstein bulls was a little higher than that of Estonian Red bulls was not explained in our study. According to the data obtained by the other investigators, content of ATP or seminal plasma immunoreactive relaxin (Kohsaka et al., 2003) could influence sperm motility.

Table 1. Sperm motility characteristics in fresh semen of Estonian Holstein and Estonian Red bulls

| Sperm motility characteristics | Breed | |
|---|---|---|
| | Estonian Holstein | Estonian Red |
| No of bulls | 102 | 30 |
| No of ejaculates | 716 | 424 |
| 1. Total Motility % | 94.07 | 93.52 |
| 2. Progressive Motility % | 86.58 | 87.20 |
| 3. Velocity Average Path (μm/sec) | 67.82 | 67.42 |
| 4. Velocity Curve Line (μm/sec) | 107.32* | 104.12* |
| 5. Velocity Straight Line (μm/sec) | 50.91 | 50.81 |
| 6. Linearity (VSL/VCL) | 0.55 | 0.48 |
| 7. Beat Cross Frequency (Hz) | 30.20 | 30.01 |
| 8. Amplitude of Lateral Head Displacement (μm) | 3.34 | 3.30 |

*P<0.05; **P<0.01; ***P<0.001

Table 2. Sperm motility characteristics in frozen-thawed semen of Estonian Holstein and Estonian Red bulls

| Sperm motility characteristics | Breed | |
|---|---|---|
| | Estonian Holstein | Estonian Red |
| No of bulls | 102 | 30 |
| No of ejaculates | 628 | 370 |
| 1. Motility % | 70.18 | 70.58 |
| 2. Progressive Motility % | 61.08 | 61.59 |
| 3. Velocity Average Path (μm/sec) | 57.28 | 58.69 |
| 4. Velocity Curve Line (μm/sec) | 89.87 | 88.31 |
| 5. Velocity Straight Line (μm/sec) | 45.32 | 45.28 |
| 6. Linearity (VSL/VCL) | 0.51 | 0.51 |
| 7. Beat Cross Frequency (Hz) | 29.42 | 29.89 |
| 8. Amplitude of Lateral Head Displacement (μm) | 2.57 | 2.62 |

Correlations between the semen quality characteristics in frozen/thawed semen and 60-days NRR

The results of the study showed medium positive correlation between the morphological quality of semen and NRR on ejaculate (r= 0.51, P<0.01, Table 4) and bull level (r=0.49, P<0.01). This result is similar to Correa et al. (1997) who reported about significant correlation between the morphological quality of semen and NRR on bull level (r=0.59).



The percentage of motile and progressively motile spermatozoa, VAP, VCL and ALH correlated positively with NRR. The strongest correlation was observed for the motility and progressive motility on both ejaculate (r=0.68 and r=0.66, respectively, Table 4) and bull level (r=0.69 and r=0.62, respectively). Correa et al. (1997) and Januskauskas et al. (2003) have found significant positive correlation between the percentage of motile spermatozoa in frozen/thawed semen and NRR (r=0.53 and r=0.61, respectively).

Table 3. Correlation between the percentage of morphologically normal sperms, sperm motility characteristics in frozen/thawed semen and 60-days NRR (ejaculate and bull level)

| Sperm characteristics | Ejaculate level | | Bull level | |
|---|---|---|---|---|
| | r | P | r | P |
| Morphologically normal spermatozoa, % | 0.51 | 0.01 | 0.49 | 0.01 |
| Sperm motility characteristics: | | | | |
| 1. Motility % | 0.68 | 0.005 | 0.69 | 0.005 |
| 2. Progressive Motility % | 0.66 | 0.005 | 0.62 | 0.005 |
| 3. Velocity Average Path, (μm/sec) | 0.32 | 0.05 | 0.36 | >0.1 |
| 4. Velocity Curve Line, (μm/sec) | 0.58 | 0.005 | 0.63 | 0.005 |
| 5. Beat Cross Frequency (Hz) | -0.48 | >0.1 | -0.55 | >0.1 |
| 6. Amplitude of Lateral Head Displacement (μm) | 0.55 | 0.005 | 0.61 | 0.01 |

Several authors have observed positive correlations between the specific motility characteristics and NRR. Revell and Mrode (1994) have found positive correlation between the amplitude of lateral head displacement (ALH) in frozen/thawed semen and NRR (r=0.43). Hallap et al. (2003) have found a medium correlation (r=0.47) between the velocity average path (VAP) in frozen/thawed semen and NRR.

**Conclusion**

The studies showed that there are some more abnormal spermatozoa in the semen of Estonian Holstein bulls than in the semen of Estonian Red bulls. At the same time, no significant differences were recorded in the sperm motility characteristics for the two breeds.

The results of the experiments showed positive medium correlation between the sperm morphology and NRR. Medium positive correlations was also detected between the motility, progressive motility, velocity curve line, velocity average path, amplitude of lateral head displacement and NRR. The strongest correlation was observed for the overall motility of spermatozoa on bull level.

We can conclude that the Estonian AI bull population is rather uniform in relation to sperm morphology and sperm motility characteristics and there are no major breed differences. Evaluation of sperm morphology and motility characteristics should be continued as a routine in AI station as these parameters correlate significantly with the female fertility.

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## ASSOCIATIONS BETWEEN MILK PROTEIN GENOTYPES AND MILK COMPOSITION TRAITS IN THE LITHUANIAN DAIRY CATTLE

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**Introduction**

Milk has been studied scientifically for over 100 years and is hence probably the best characterised of all our major foods. However, milk can be a very variable biological product (4). The milk proteins are the most important components of milk in human nutrition. Today the dairy industry has technological possibilities to produce many different kinds of milk products. It is widely accepted that manufacturing properties of milk are related to the composition of proteins in the milk (5).

Milk yield and composition in cattle are typical quantitative traits, being affected by environmental factors and allelic variations at many loci. κ- Casein and β- Lactoglobulin are proteins expressed in milk and, due to their polymorphism, may serve as informative molecular markers for yield, composition and technological properties of milk (9, 3). In dairy cattle the B variant of κ-Casein is associated with milk renneting properties, quality of curd and yield of cheese, whereas β- Lactoglobulin variants are associated with casein quantity. In both cases, the B variants are favourable (2). BB genotype of $\alpha_{S1}$-Casein significantly influences milk yield and protein yield. The highest protein percentage in milk could be obtained with the genotype BC of $\alpha_{S1}$-Casein (6). It has been suggested that identification of milk protein genotypes could be an economically important selection criteria for dairy herds designated for industrial milk production. Milk protein polymorphism can be used as selection criteria in cattle selection programs.

The aim of the present study was to estimate association between milk protein genotypes and milk composition traits in the Lithuanian dairy cattle.

**Material and Methods**

Blood samples from 70 LLG, 49 LWB, 109 LBW and 168 LR unrelated animals were collected in EDTA-tubes a total of 10 ml blood from each animal. DNA was extracted using standard phenol-chloroform purification method (7). The identification of milk protein genotypes have been tested by methodology based on a polymerase chain reaction (PCR) (8).

**Analysis of $\alpha_{S1}$- Casein genotype.** For PCR reaction $\alpha_{S1}$- Casein primers were used: A primer 5'-GGC ACA CAA TAC ACT GAT GC-3'; B primer 5'-CAG TGG CAT AGT AGT CTT TT-3' and C primer 5'-CAG TGG CAT AGT

AGT CTT TC-3'. DNA was amplified with 34 cycles (94°C 30s, 60°C 30s, 72°C 30s) followed 5 min 72°C. PCR product was carried out electrophoretically using 2% agarose gel.

**Analysis of β- Lactoglobulin genotype.** For PCR reaction β- Lactoglobulin primers were used: JBLG 2-5'-TGT GCT GGA CAC CGA CTA CAA AAA G-3' and JBLG 3-5'-GCT CCC GGT ATA TGA CCA CCC TCT-3'. DNA was amplified with 35 cycles (94°C 40s, 58°C 50s, 72°C 50s) followed 5 min 72°C. The amplified 247 bp-long DNA fragment was digested with Hae III restriction nuclease (MBI Fermentas, Lithuania; 10 units/20ml, 37°C). After restriction the products were separated electrophoretically using 3% agarose gel 35 min at 100V.

**Analysis of κ- Casein genotype.** For PCR reaction κ-Casein primers were used: K346A-5'-CAT-TTA-TGG-CCA-TTC-CAC-CAA-AG-3' and K346B-5'-CAT-TTC-GCC-TTC-TCT-GTA-ACA-G-3'. DNR was amplified with 34 cycles (94°C 30s, 58°C 30s, 72°C 30s) followed 5 min 72°C. The amplified 337 bp-long DNA fragment was digested with *Hae* III and *HinfI* restriction nucleases (MBI Fermentas, Lithuania; 10 units/20ml, 37°C). After restriction the products were separated electrophoretically using 3% agarose gel 35 min at 100V.

Visualisation of the different milk protein genetic variants was carried out after staining the gels in ethidium bromide solution and using Bio Doc 1000 video documentation equipment (BioRad, USA).

**Statistical analysis.** Data for this study were prepared and used by the Access database management system. The R statistical package was used to estimate effects of milk protein genotypes on milk production traits.

**Results and Discussion**

$\alpha_{s1}$-Casein BB genotype is associated with improved daily milk yield over the BC genotype; the difference between BB and BC reached (LWB 3.23kg (P≤ 0.54), LLG 2.40kg (P≤0.45), LR 0.80kg (P≤0.93) and LBW 0.63kg (P≤0.36), respectively). $\alpha_{s1}$-CN BB genotype has a positive influence on milk yield, is most common to the dairy cattle (1) and was observed at the highest frequency in all four studied Lithuanian cattle populations. The CC genotype of $\alpha_{s1}$-CN was found only in LR breed. This genotype was associated with a slightly higher milk fat percentage; the difference between CC, BB and BC genotypes reached 0.03% (P≤0.92); 0.39% (P≤0.25).

Cows of the κ- Casein AA genotype produced more milk daily than those of other κ- Casein genotypes; the difference between AA and AB genotypes were observed in Lithuanian dairy cattle - (LWB 1.10kg (P≤0.62), LLG 0.15kg (P≤0.85), LR 0.10kg (P≤0.67), and LBW 1.8kg (P≤0.004), respectively. Favourable BB genotype was found only in LR and LWB breeds. High fat percentage in milk of BB genotype resulted, compared to milk of AA and AB



genotypes BB-4.3% (P≤0.25), AA-4.0% (P≤0.08) and AB-4.2% (P≤0.08) LWB; BB-4.8% (P≤0.13), AA-4.7% (P≤0.04) and AB-4.6% (P≤0.05) LR), respectively.

Table 1. Individual effects of κ-Casein, $\alpha_{S1}$-Casein and β-Lactoglobulin genotypes on daily milk yield and milk composition

| Geno-type | Breed | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Lithuanian White Back (n=49) | | | Lithuanian Light Grey (n=70) | | | Lithuanian Red (n=168) | | | Lithuanian B&W (n=109) | | |
| | Milk yield, kg | F % | P % | Milk yield, kg | F % | P % | Milk yield, kg | F % | P % | Milk yield, kg | F % | P % |
| $\alpha_{s1}$-Casein | | | | | | | | | | | | |
| BB | 15.6 ±0.58 | 4.3 ±0.06 | 3.3 ±0.03 | 15.7 ±0.38 | 4.2 ±0.06 | 3.3 ±0.02 | 13 ±0.11 | 4.7 ±0.03 | 3.4 ±0.01 | 21.4 ±0.26 | 4.7 ±0.06 | 3.2 ±0.02 |
| BC | 12.3 ±0.79 | 4.1 ±0.06 | 3.4 ±0.09 | 13.3 ±0.70 | 3.8 ±0.29 | 3.3 ±0.08 | 12.2 ±0.94 | 4.3 ±0.07 | 3.2 ±0.19 | 20.8 ±0.44 | 4.6 ±0.08 | 3.3 ±0.03 |
| CC | - | - | - | - | - | - | 10.7 ±0.78 | 4.8 ±0.30 | 3.7 ±0.03 | - | - | - |
| κ-Casein | | | | | | | | | | | | |
| AA | 15.9 ±0.86 | 4.0 ±0.08 | 3.3 ±0.04 | 16.0 ±0.55 | 4.3 ±0.09 | 3.3 ±0.04 | 13.0 ±0.16 | 4.7 ±0.04 | 3.4 ±0.02 | 21.6 ±0.30 | 4.6 ±0.06 | 3.2 ±0.02 |
| AB | 14.8 ±0.90 | 4.2 ±0.08 | 3.2 ±0.05 | 15.8 ±0.56 | 4.1 ±0.07 | 3.2 ±0.03 | 13.0 ±0.17 | 4.6 ±0.05 | 3.5 ±0.02 | 19.6 ±0.33 | 4.6 ±0.10 | 3.3 ±0.04 |
| AE | 15.4 ±2.90 | 4.0 ±0.20 | 3.3 ±0.13 | 12.1 ±0.87 | 4.2 ±0.20 | 3.41 ±0.08 | 12.5 ±0.62 | 4.6 ±0.09 | 3.4 ±0.06 | 21.4 ±0.74 | 4.6 ±0.15 | 3.2 ±0.05 |
| BB | 15.4 ±1.24 | 4.3 ±0.25 | 3.5 ±0.20 | - | - | - | 12.6 ±0.64 | 4.8 ±0.13 | 3.6 ±0.08 | - | - | - |
| BE | - | - | - | - | - | - | - | - | - | 20.2 ±0.89 | 4.7 ±0.31 | 3.2 ±0.09 |
| β-Lactoglobulin | | | | | | | | | | | | |
| AA | 16.0 ±0.89 | 4.3 ±0.07 | 3.3 ±0.05 | 16.2 ±0.47 | 4.3 ±0.08 | 3.3 ±0.04 | - | - | - | 21.0 ±0.48 | 4.7 ±0.13 | 3.3 ±0.04 |
| AB | 12.9 ±1.21 | 4.07 ±0.19 | 3.1 ±0.07 | 14.6 ±0.77 | 4.0 ±0.09 | 3.3 ±0.04 | 13.3 ±0.35 | 4.6 ±0.12 | 3.5 ±0.05 | 20.9 ±0.07 | 4.7 ±0.07 | 3.2 ±0.03 |
| BB | 15.0 ±0.77 | 4.3 ±0.09 | 3.2 ±0.04 | 16.0 ±0.85 | 4.3 ±0.12 | 3.1 ±0.05 | 12.9 ±0.12 | 4.7 ±0.03 | 3.5 ±0.02 | 21.3 ±0.41 | 4.6 ±0.08 | 3.1 ±0.03 |
| BC | - | - | - | - | - | - | 11.5 ±0.24 | 4.8 ±0.17 | 3.5 ±0.17 | - | - | - |

Additionally, BB genotype of κ- Casein contains a higher protein percentage (BB-3.5% (P≤0.20), AA-3.3% (P≤0.04) and AB-3.2% (P≤0.05) LWB; BB-3.6% (P≤0.08), AA-3.4% (P≤0.02) and AB-3.5% (P≤0.02) LR), respectively.

A and B variants of β- Lactoglobulin are associated with milk composition and manufacturing properties. β- Lactoglobulin BB genotype cows contains more casein and fat than the milk produced by β- Lactoglobulin AA genotype cows (2). No significant effect of BB genotype on fat percentage was shown in this study.

AA genotype of β- Lactoglobulin, which has an effect on milk and protein yield, was detected in all studied breeds. The daily milk yield and protein were detected higher in β- Lactoglobulin AA than in cows of remaining β- Lactoglobulin genotypes. AA genotypes affected the higher protein percentage in the milk of AA cows, which reached 3.3% in the of AA genotype milk and 3.1% and 3.2% in AB and BB milks (LWB); 3.3% AA, 3.3% AB and 3.1% BB (LLG); 3.3% AA, 3.2% AB and 3.1% BB (LBW) breeds. This genotype was not detected in LR. The detection of C allele only in Lithuanian Red shows that this breed might belong to the same group as German Red.

**Conclusion**

The results show that identification of different milk protein genotypes is significantly related to milk composition traits, therefore it can be economically important selection criteria for dairy herds designated for industrial milk production.

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# POSSIBILITIES OF MAINTENANCE AND REPRODUCTION OF LOCAL LATVIAN BROWN DAIRY BREED

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Climate in Latvia is suitable for cattle farming, because it provides conditions for cheap grass forage production. Therefore dairy farming is acknowledged as the prior branch in agriculture of Latvia.

The main dairy breed in the state is Latvian Brown. From all dairy cows under the milk recording system about 70% is Latvian Brown.

Latvian Brown dairy breed belongs to the red breeds group. Formation of this breed was started in the end of 19th century by crossing native cattle with Angler breed and in the beginning of 20th century by using animals of Danish Red breed. As a separate dairy breed, Latvian Brown was confirmed in 1922.

Now Latvian Brown breed has already a hundred year history and in this period there were several improving spans.

In the second part of the 20th century not only these two mentioned breeds, but also other breeds as Brown Swiss, Red Holstein, Swedish Red and White were used for improving. The stages of forming and improving are shown in Table 1.

Table 1. Stages of forming and improving of Latvian Brown breed

| Breed for improving | Used from the year |
|---|---|
| Native cattle x Angler breed | The end of the 19th century |
| Native cattle x Danish Red | The beginning of the 20th century |
| Confirmed as breed | 1922 |
| Danish Red *(old type)* | 1961 |
| Angler *(old type)* | 1972 |
| Danish Red with bloodness of Brown Swiss and Holstein Red | 1984 |
| Holstein Red | 1985 |
| Swedish Red & White | 1988 |

As the result of all breeding and animal crossing work, a productive local dairy breed, suitable for present needs, has been formed.

In this improving period some necessary genes of Latvian Brown dairy breed may disappear permanently. It is very important not only to improve domestic animal breeds for the present time necessities but also to preserve genetic multiform of the existing animal breeds, for biological diversity.



The main advantage of Latvian Brown breed is that these have been reared in Latvian conditions for more than a hundred years and therefore they are adapted for local forage, feeding type and keeping system.

Latvian Brown breed animals are enough productive, hardy and frugal. Cows have a possibility to produce much milk with high protein and fat content by consuming mainly grass forage with small portions of concentrates.

Animals have strong building exterior, hard feet and nocks, and good muscles. Dairy cows are with quite good reproductive ability, having good longevity that is better than the animals of other breeds have.

By using various dairy breeds for improving, Latvian Brown animals have got not only good results for various necessary breeding traits. Some dairy breeds used in the breeding work did not improve even cow's milk yield.

As our last investigations of high productive cows breeding value demonstrated, the cows whose sires were purebred Latvian Brown and Swedish Red and White, showed the best results, but the lowest milk yield breeding indexes were shown by the cows whose sires were from Red Holstein and Angler breeds (D. Strautmanis, 2003). The data are represented in Table 2.

Table 2. Breeding indexes of high productivity cows in 2000

| Breed | Milk yield | Productivity |
|---|---|---|
| Swedish Red & White | 140.1 | 140.8 |
| Latvian Brown | 139.4 | 140.2 |
| Danish Red | 136.2 | 137.7 |
| Angler | 136.7 | 135.1 |
| Brown Swiss | 135.9 | 136.9 |
| Holstein Red | 132.1 | 134.9 |

Why is it necessary to maintain the old type Latvian Brown dairy breed:

**1. Increased protein yield**

Latvian Brown cows have high protein level in milk. The milk protein content of the best cows is 3.6-3.8%. The results of cows' milk recording in the last years confirm that Latvian Brown cows, compared with the other dairy breeds reared in Latvia, have one of the highest milk protein content 3.31% (Table 3).

Latvian Brown cow's milk protein has, like that of the other red cows, an increased amount of α and β fractions of casein. Therefore the milk of these cows has very soluble protein components and the whole protein can be used for cheese production.

Table 3. Milk content

| Breed | Fat,% | | | Protein,% | | |
|---|---|---|---|---|---|---|
| Year | 2000 | 2001 | 2002 | 2000 | 2001 | 2002 |
| Latvian Brown | 4.40 | 4.45 | 4.46 | 3.28 | 3.30 | 3.31 |
| Angler | 4.62 | 4.49 | 4.75 | 3.29 | 3.34 | 3.38 |
| Danish Red | 4.27 | 4.39 | 4.41 | 3.23 | 3.24 | 3.29 |
| Holstein Red | 4.32 | 4.28 | 4.36 | 3.19 | 3.23 | 3.26 |
| Holstein Black & White | 4.17 | 4.19 | 4.21 | 3.14 | 3.14 | 3.14 |
| Swedish Red & White | --- | 4.35 | 4.31 | ---- | 3.20 | 3.24 |

*Sources*: Results of Animal Recording in Latvia

**2. Good ability of reproduction**

If we compare Latvian Brown breed with other dairy breeds reared in Latvia, we can establish that from a hundred Latvian Brown cows in milk recording system, 86 calves per year were obtained. This is 1-6 calves more than other red breeds had and 14 calves more than got from Black and White cows. Latvian Brown cows have good conception rate. For getting cows pregnant, 1.7-1.8 inseminations are necessary. It is less than other breeds need. Latvian Brown cows have mainly easy calving without complications (D. Strautmanis, 1999). Comparing stillborn calves of the first calving cows, Latvian Brown heifers had 2 -3% complication; it is less than Black and White cows had (D. Strautmanis, 1999).

In the last 10 years of this breed, culling percent of fertility problems has been about 5%, but for other red breeds this percent is 6-7% and for Black and White cows even 9%.

**3. Cows' longevity.**

In the last years, for Latvian Brown heifers the first calving age was 26 months that is one of the best results between dairy breeds reared in Latvia.

An important factor is how long a cow produces milk. By milk recording results of the year 2000, Latvian Brown cows had the longest life time of all living cows (Table 4).

Table 4. Cows' age in lactations

| Breed | All cows | High productive cows |
|---|---|---|
| Latvian Brown | 3.35 | 4.18 |
| Angler | 2.87 | ---- |
| Danish Red | 2.80 | ---- |
| Holstein Black White | 2.98 | 3.56 |

*Sources*: Results of Animal Recording 2000



It was 3.5 lactations, by 12.4% longer than the other breeds had. Latvian Brown cows of the high productivity group had this index even by 17.4% better than animals of other dairy breeds.

It is very important to achieve that cows have high productivity with their good functional traits and longevity.

**4. Legs and hocks quality**

For all first calving cows, exterior linear assessment was carried out. In 2003, Latvian Brown heifers had average estimation for legs 5.0 score points and for foot angle points 4.9.

These are the best results, compared with the other dairy breeds in the republic. Latvian Brown breed animals have strong legs with normal sloping foot angle. Sole of claw is hard and seldom damaged. Therefore Latvian Brown breed animals are slaughtered because of feet and legs diseases only in a small number, compared with other red Black and White breeds reared in the state.

It should be considering that all Latvian Brown dairy breed animals have some good breeding traits that must be kept up. Therefore in Latvia a programme has been worked out for maintenance and reproduction of the old type of this breed animals in the future.

All Latvian Brown cows that are in the recording system are divided into two groups:

- The first group includes animals of the old type. These are cows and sires that have in their pedigree old Latvian Brown breed bloodness, and in addition up to 40% bloodness of Angler and Red Danish breed bloodness (old type animals). These two breeds have taken part in the formation of Latvian Brown dairy breed from the same start stage. Animals of this group may not contain bloodness from other breeds as Brown Swiss, Red Holstein, Swedish Red and White etc.
- The second part of Latvian Brown breed population are producer animals, in the breeding work of them some various unkindred dairy breeds have been used.

For maintenance and reproduction of the old preserved type in Latvia, the number of cows and bulls semen stock is large enough. At the moment there are 9,567 cows from preserved Latvian Brown group in the milk recording system. The cows are located in all districts of the republic. From these cows 5.000 – 6.000 animals are suitable for breeding work because a part of them have low milk yield.

Requirements in milk yield for preserving the population of cows are the following: for the first calving cows 4,000 kg and for adult cows 4,500 kg in lactation. For maintaining these cows in the semen bank, there is a large sperm stock: more than 300,000 semen doses from 41 sires (Table 5).

Table 5. Sperm bank in 2003

| Name of genealogical groups | Unkindred branches | Number of sires | Semen doses |
|---|---|---|---|
| Potrimpi | 3 | 13 | 81,443 |
| Ullori | 3 | 16 | 120,844 |
| Rudnes | 2 | 9 | 72,506 |
| Odini | - | 2 | 24,404 |
| Ejlekeri | - | 2 | 19,371 |
| Total | 8 | 41 | 318,568 |

Sires concern 5 unkindred genealogical groups. Three from the genealogical groups are divided into 2-3 unkindred branches in which the common forefather is in the $4^{th}$-$6^{th}$ generation, providing the reproduction of all cows without close related mating. Coefficient of inbreeding will not be higher than 1.5% in off-springs pedigree.

In the maintained part of Latvian Brown breed animals, breeding work can be performed as it is universally recognized. Bull mothers for young bull reproduction will be selected from all cows' population by using breeding indexes. These cows will be mated by a special plan in order to produce young bulls for all 5 unkindred genealogical groups. Besides, there are specialists for embryo transplantations in Latvia, if there will be a need for them in the future.

That will be guarantee the maintaining of the Latvian Brown breed old type animals with their genes and that evolution of the breed can be furthered.

**Conclusions**

• Latvian Brown dairy breed cows have several good breeding traits why the breed should be maintained.

• The number of animals and semen stocks insure the preservation of Latvian Brown dairy breed (old type) population and its further development.

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## USE OF TEST DAY RECORDS FOR GENETIC EVALUATION FOR LATVIAN BROWN SIRES

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**Introduction**

The advantages of the use of test day records for breeding value estimation in dairy cattle are easily seen and test day records in genetic evaluation have been used for recent years in many countries [5]. Since last year, studies have been started to use test day records in genetic evaluation in Latvia. The main reason for changing lactation model to test day model is the reduction of generation interval through frequent genetic evaluation with the latest data and prediction of total production more accurately by accounting for time dependant environmental effects [6]. Many studies had shown it and given strategies of different test day models helped to start these studies in Latvia [3]. The aim of the studies was the comparison of two test day models. Genetic parameters, breeding values and reliabilities were compared for three productivity traits using test day model, assuming that test day records within lactation are repeated.

**Materials and Methods**

Two test day models were used: multi lactation – a multi trait animal model and a single trait – single lactation animal model. Both of them were used for estimation of genetic parameters and estimation of breeding values. The statistical model included fixed effects: herd – test day, lactation (3 lactations; for multi lactation model), calving age (7 levels), calving interval (6 levels) and days in milk (412 levels), permanent environmental effect as random and animal as additive genetic effect.

Data for investigation were obtained from state Ltd. Latvian State Information Data Processing Centre of Domestic Animal Pedigree which organizes milk recording in Latvia.

Data from Latvian Brown breed cows with 1. – 3. lactations were used and total 53,329 test day records were collected in studies. In the data there were included cows with at least 3 test day records and the maximum amount of test days of cow per lactation was 11. The average milk yield of three lactations per test day was 14.6 kg, fat yield – 0.66 kg and protein yield – 0.47 kg (Table 1). The higher milk and fat yield per test day were 15.6 kg and 0.71 kg, respectively, in the $3^{rd}$ lactation. The higher protein yield was 0.51 kg in the $2^{nd}$ and the $3^{rd}$ lactation.

Table 1. The average milk productivity of cows in the test day

| Lactation | n (test days) | Milk yield | Fat yield | Protein yield |
|---|---|---|---|---|
| 1. | 33471 | 14.1 ± 4.24 | 0.63 ± 0.206 | 0.45 ± 0.129 |
| 2. | 14312 | 15.5 ± 5.39 | 0.70 ± 0.257 | 0.51 ± 0.163 |
| 3. | 5546 | 15.6 ± 5.62 | 0.71 ± 0.277 | 0.51 ± 0.167 |
| 1. – 3. | 53329 | 14.6 ± 4.78 | 0.66 ± 0.231 | 0.47 ± 0.145 |

The data were processed using SAS 8.2. software [4]. PEST [1] and VCE 4.2.5. [2] software were used to obtain genetic parameters and results of genetic evaluation.

**Results and Discussion**

Using multiple trait – multiple lactation model heritabilities were obtained $h^2 = 0.24$, $h^2 = 0.11$, $h^2 = 0.18$ for milk yield, fat yield and protein yield, respectively (Table 2). Higher genetic correlations were obtained between milk yield and protein yield ($r_g = 0.91$) and between fat yield and protein yield ($r_g = 0.81$).

Table 2. Heritabilities (on the diagonal) and genetic correlations (above diagonal) for productivity traits in three lactations

| Trait | Milk yield, kg | Fat yield, kg | Protein yield, kg |
|---|---|---|---|
| Milk yield, kg | 0.24 (0.02) | 0.72 (0.03) | 0.91 (0.01) |
| Fat yield, kg | - | 0.11 (0.01) | 0.81 (0.02) |
| Protein yield, kg | - | - | 0.18 (0.01) |

Standard errors in parenthesis

As shown in Table 3, higher heritabilities using single trait - single lactation model were in the 3rd lactation for milk yield ($h^2 = 0.50$) and protein yield ($h^2 = 0.25$). Lower heritabilities were in the 1st lactation for milk yield ($h^2 = 0.27$) and for fat yield ($h^2 = 0.12$) and protein yield ($h^2 = 0.18$) in the 2nd lactation. Heritabilities were similar for fat yield in each lactation. The lower standard errors of heritabilities were obtained calculating heritabilities for the 1st lactation, respectively, $s_{h^2} = 0.03$, $s_{h^2} = 0.02$ and $s_{h^2} = 0.03$ for milk yield, fat yield and protein yield.

Table 3. Heritabilities ($h^2$) and standard errors ($s_{h^2}$) for productivity traits for each trait in each lactation ($h^2 \pm s_{h^2}$)

| Lactation | Milk yield, kg | Fat yield, kg | Protein yield, kg |
|---|---|---|---|
| 1. | 0.27 ± 0.03 | 0.13 ± 0.02 | 0.22 ± 0.02 |
| 2. | 0.31 ± 0.04 | 0.12 ± 0.03 | 0.18 ± 0.03 |
| 3. | 0.50 ± 0.11 | 0.13 ± 0.06 | 0.25 ± 0.08 |



Breeding values were estimated for 297 sires of Latvian Brown breed (Table 4). Higher estimated breeding values (EBV) were obtained for milk yield (EBV = 0.11 kg) using multiple trait - multiple lactation model. Using single trait – single lactation model higher EBV were obtained for protein yield (EBV = 0.003 kg). Similar EBV were for fat yield using both models (EBV = 0.002 kg). No significant differences between breeding values using different models ($p < 0.01$) were found. Significant differences are shown between reliabilities (Table 4) using different models ($p < 0.01$).

Table 4. Estimated breeding values (EBV), standard deviations ($s_{EBV}$) and reliabilities (REL) for sires (n = 297)

| Trait | Multi – lactation model | | | Single – lactation model | | |
|---|---|---|---|---|---|---|
| | EBV | $s_{EBV}$ | REL | EBV | $s_{EBV}$ | REL |
| Milk yield | 0.110 | 1.15 | 72* | 0.030 | 0.93 | 58* |
| Fat yield | 0.002 | 0.04 | 63* | 0.002 | 0.03 | 48* |
| Protein yield | 0.002 | 0.03 | 69* | 0.003 | 0.02 | 58* |

* $p < 0.01$

Higher reliabilities were presented using multi lactation - multi trait model for milk yield, fat yield and protein yield, respectively REL = 72%, REL = 63%, REL = 69%, but using single trait – single lactation model reliabilities for each trait were 58%, 48% and 58%, respectively for milk yield, fat yield and protein yield. Higher reliabilities using both models were obtained for milk yield, but lower for fat yield.

**Conclusions**

The introduction of the test day model is necessary for Latvian conditions to get more rapid genetic evaluation of young sires than by using lactation model. Heritabilities obtained for milk yield are higher, from $h^2 = 0.24$ to $h^2 = 0.50$, but for fat yield and protein yield heritabilities are shown lower, from $h^2 = 0.11$ to $h^2 = 0.13$ and from $h^2 = 0.18$ to $h^2 = 0.25$, respectively for fat yield and protein yield using multiple trait - multiple lactation model and using single trait-single lactation model. There are no significant differences calculated between EBV for milk yield (EBV = 0.11 kg and EBV = 0.03 kg), fat yield (EBV = 0.002 kg and EBV = 0.002 kg) and for protein yield (EBV = 0.002 kg and EBV = 0.003 kg), using different models. Significant differences are calculated between reliabilities for all traits ($p < 0.01$). Higher reliabilities are obtained using multiple trait-multiple lactation model for milk yield (REL = 72%), fat yield (REL = 63%) and protein yield (REL = 69%). Using multiple trait – multiple lactation model it is

possible to get estimated breeding values for sires with higher reliabilities and these models are recommendable to use in Latvian conditions.

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## DATA OF ESTONIAN RED BREED FOR INTERBULL AYRSHIRE EVALUATION; GENETIC LINKS AND MODEL VALIDATION

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**Introduction**

Estonia is a member of Interbull since 1995. Since 1998 we have participated with data of Estonian Holstein breed in international evaluation for production traits and since 2001 for udder health traits in Holstein breed. Joining Interbull evaluation in Ayrshire breed with data of Estonian Red breed (EPK) was initiated by our breeding organisation in January 2004. The purpose of this study was to describe the structure of EPK and to validate evaluation models for production and udder health traits.

**Materials and Methods**

Data

For data connectedness the pedigree information of heifer calves and lactating cows of EPK in our animal recording system were used. For model validation the data collected for the last routine evaluation in January 2004 (Table 1) and data collected for the simulated evaluation at the end of 1999 (Table 2 ) according the rules of our genetic evaluation system (Interbull, 2004) were used .

Table 1. Descriptive statistics of the data set of Estonian Red breed for routine evaluation in January 2004

| Lactation | Number of cows | Number of TD records | Number of bulls |
|---|---|---|---|
| 1 | 59383 | 531330 | 621 |
| 2 | 42232 | 369106 | 551 |
| 3 | 28575 | 248152 | 475 |

Table 2. Descriptive statistics of the data set of Estonian Red breed for the simulated evaluation in December 1999

| Lactation | Number of cows | Number of TD records | Number of bulls |
|---|---|---|---|
| 1 | 35751 | 301788 | 436 |
| 2 | 22639 | 181933 | 382 |
| 3 | 12665 | 99219 | 314 |

Data connectedness

There are 11 countries in Interbull Ayrshire evaluation. EPK has daughters of sires of most of these countries (Table 3). Disadvantage of the structure of EPK is, that due to use of leased bulls (mainly from Germany, Denmark and Sweden) the

percentage of cows of imported sires is relatively high but the number of bulls for Interbull evaluation is quite small (Table 4). Thirty-six bulls have been evaluated in Estonia and in one or more countries of Ayrshire evaluation (Table 4).

Table 3. Distributions of active female animals of Estonian Red breed by the country of origin of sires

| Country | Heifer calves | | | Cows | | |
|---|---|---|---|---|---|---|
| | no of sires | number | % | no of sires | number | % |
| AUT | 4 | 31 | 0,1 | 5 | 142 | 0,5 |
| CAN | 10 | 214 | 0,8 | 19 | 259 | 1 |
| DEU | 31 | 2285 | 8,4 | 30 | 3241 | 12,1 |
| DNK | 39 | 6411 | 23,7 | 43 | 6997 | 26,2 |
| EST | 534 | 15012 | 55,4 | 524 | 12021 | 45 |
| FIN | 5 | 418 | 1,5 | 6 | 196 | 0,7 |
| NLD | 7 | 283 | 1 | 11 | 54 | 0,2 |
| NOR | 8 | 74 | 0,3 | 8 | 431 | 1,6 |
| SWE | 3 | 1654 | 6,1 | 8 | 2878 | 10,8 |
| USA | 13 | 708 | 2,6 | 21 | 493 | 1,8 |
| Total | 656 | 27095 | 100 | 675 | 26712 | 100 |

Table 4. Distribution of bulls for Interbull evaluation by the country of origin

| Country | Number of bulls | Number of days | Common bulls |
|---|---|---|---|
| AUT | 4 | 481 | |
| CAN | 2 | 410 | |
| DEU | 11 | 4979 | 5 |
| DNK | 31 | 12241 | 20 |
| EST | 168 | 31516 | |
| FIN | 1 | 260 | |
| NOR | 6 | 534 | 6 |
| SWE | 6 | 3653 | 5 |
| USA | 7 | 498 | |

Model Validation

The fixed regression test day animal model was used for breeding value estimation of production and udder health traits (Reents et al., 1995) having in model for production traits in current evaluation (Interbull, 2004) and in model for udder health traits (Interbull, 2004) 540 and 70 different fixed lactation curve functions respectively. Due to the small number of cows in 1999 evaluation, the model with 70 groups was used.



Approach of Method 1 and Method 3 described by Boichard et al. (1995) and recommended by Interbull (Interbull, 2001) were used for the validation of genetic evaluation model. Method 1 investigates the impact of cow records from different age groups on the genetic trend. Method 3 investigates the random variation associated with new daughters. As described by Weller et al. (2003) in Method 3 the current genetic evaluation of each bull is analysed as a function of its genetic evaluation four years ago, where the analyses model is:

$$Yi = a + bX + \delta t_i + e_i \quad (1)$$

The δ factor is a function of the number of new daughters per bull during the past four years. If the evaluations are unbiased, the expectation of δ is zero. Estimates of parameters b and δ were derived by PROC GLM of SAS (SAS Institute, 1989).

**Results and Discussion**

Results of Method 1 are presented in Table 5. All traits met the Interbull criterion that $|\Delta| < \sigma$ but as shown in Figures 1 and 2, the genetic trend lines of first and all lactations for SCS trait illustrate better acceptance of criterion than trend lines for protein trait.

Table 5. Method 1 results for production and udder health traits

| Trait | $b_t$ | $b_1$ | r | $\sigma_t$ | $\sigma_1$ | Δ | σ |
|---|---|---|---|---|---|---|---|
| Milk | 43 | 33 | 0.92 | 649 | 552 | 10 | 13 |
| Fat | 1.18 | 0.71 | 0.89 | 23.3 | 20.5 | 0.47 | 0.49 |
| Protein | 1.08 | 0.79 | 0.91 | 16.4 | 13.9 | 0.29 | 0.33 |
| SCS | -0.019 | -0.017 | 0.86 | 0.46 | 0.43 | -0.002 | 0.010 |

$\Delta = b_t - b_1$, where $b_t$ and $b_1$ are estimated genetic trends of trait considering all lactations data and first lactation data respectively;
r is genetic correlation between first and all lactations;
$\sigma = 0.02 * (\sigma_t * \sigma_1)**0.5/r$, where $\sigma_t$ and $\sigma_1$ are genetic standard deviations for all lactations and first lactation respectively.

Results of Method 3 are presented in Table 6. The official Interbull criterion for Method 3 acceptance is $|\delta| < 0.02$* genetic SD considering bulls with first crop daughters. Only SCS trait met the criterion. Using in the analyses all bulls with daughters in at least 10 herds in 1999 genetic evaluation, all traits met the criterion. By Weller et al. (2003) the current criterion of Method 3 penalizes small populations since the standard error of δ is a function of the number of bulls returned to the service. In our case that number of bulls was only 30 and therefore the results of Method 3 could be with low reliability.

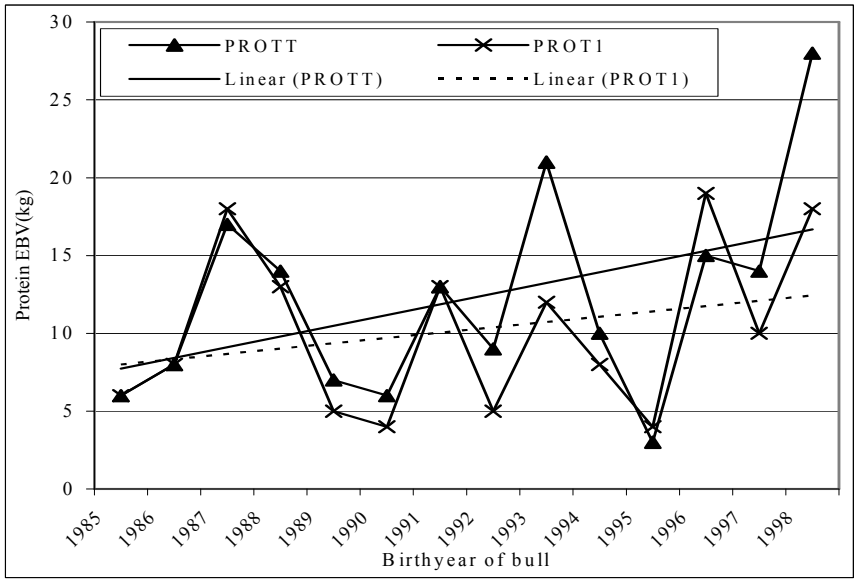


Figure 1. Genetic trends for protein evaluations

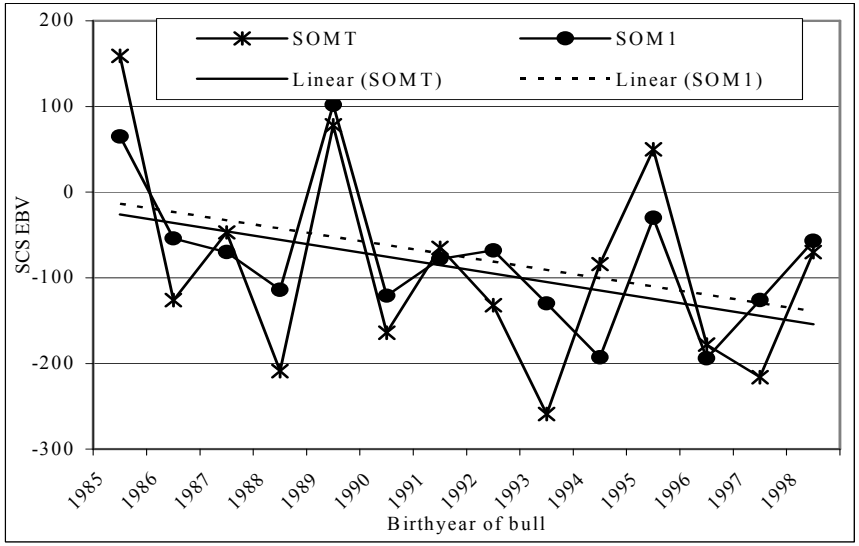


Figure 2. Genetic trends for SCS evaluations



Table 6. Method 3 results for production and udder health traits

| Trait | Official (64 bulls) | | | Non-official (165 bulls) | | |
|---|---|---|---|---|---|---|
| | σ | b | δ | σ | b | δ |
| Milk | 7.26 | 0.96 | 33.4 | 8.32 | 0.88 | -3.6 |
| Fat | 0.26 | 0.81 | 0.51 | 0.33 | 0.80 | 0.21 |
| Protein | 0.17 | 0.95 | 0.71 | 0.20 | 0.92 | 0.009 |
| SCS | 0.010 | 0.98 | -0.009 | 0.010 | 0.97 | 0.009 |

σ= 0.02* genetic SD; b and δ are from (1)

**Conclusion**

Estonian Red breed has genetic links with most populations in Interbull Ayrshire evaluation. Results of model validation indicate some problems but discrepancies may be due to small data set and therefore additional tests are needed for model validation.

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# EFFECT OF CALVING INTERVAL IN HIGH-YIELDING COWS ON MILK YIELD, ITS COMPOSITION AND PRODUCTION COSTS

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## Introduction

From the economical point of view an average milk production per one calving interval (CI) day is highly important. To study CI length influence on milk yield, its composition and production costs, numerous investigations have been carried out and results differ greatly. Perez-Cabal (2003) in his study estimated genetic parameters for lifetime profit and some productive traits. Profit was positively correlated to production traits (0.79 to 0.83), functional herd life (0.38), mature body weight (0.25), and days of milk (0.35), but genetic correlation was found to be close to zero with calving interval. On the basis of the study by Esslemont et al. (2003), and after considering the cost of culling for poor fertility, it was concluded that it is cost-effective to keep the typical average cow in calf until 266 days post calving, whereas the breakeven point for the high-yielding cow is 290 days post calving (Esslemont et al., 2003). In Poland, a study was carried out to evaluate the relations between CI lengths, taking into account the milk yield, milk components and health of high yielding cows. The milk yield of longer CI was by 150 kg higher per 305-day lactation (the difference was not significant). In addition, there were no significant differences in composition. The percentage of mastitis and metabolic disease was lower in the longest CI group of cows (Krzyzewski, 2004). The average loss per cow in the UK is estimated to be poundsterling 183, 3.06 p/litre in the 6000 kg cow. The cost of fertility depends on the stage of lactation and the shape of the lactation curve. Cows normally have a curve that loses 8 to 10% per month after peak. Those rare animals losing 4% or so may justify longer calving intervals (Esslemont, 2003).

Even though several studies suggest an optimum CI of near 12 months, there are studies that have shown an advantage for longer period of days open and, consequently, an extended calving interval. Bar-Anan and Soller (1979) found that maximum production was achieved by inseminating primiparous cows not earlier than 70 days postpartum and multiparous 41 to 90 days postpartum. Weller et al. (1985) stated that the period between calving and insemination affected the milk yield. Arbel et al. (2001) found in their study, that there was an economic advantage in extending lactations by 60 days in high-yielding cows. Ratnayake et al. (1988) showed that a prolongation of the CI up to 18 months may have positive influence on reproduction, in terms of a reduced need for the treatment of ovarian disorders and higher conception rates. Osterman et al. 2003 reported that by combining longer calving intervals with increased milking frequency the milk



production per day from one calving to another might be higher than in traditional calving interval.

**Keywords:** calving interval, structure of expenses, milk production, profitableness.

## Material and Methods

According to methods of experiment 5 test groups were formed from different breeds: 1) Estonian Native (EN), 2) Estonian Red (ER), 3) Red Holstein (RHF), 4) Estonian (SPAV >112) Holstein (EHF), 5) Estonian (SPAV <112) Holstein (EHFt). Current investigation data from years 2000-2003 were used. On the experimental farm a total mixed ration (TMR) was used distributed by feed mixer to ensure constant feed availability. The present investigation was based on individual productivity and cost calculations per feeding days of test cows during lactation and dry period. The herd formation costs and reproductive costs were not included due to partial government support.

The milk production data of 3 years of the Põlula Experimental Farm were obtained from database of the Animal Recording Centre. Least square averages differ from arithmetic mean by year influence. Value of F affirm or disaffirm (*, **, ***) significance of cow´s age (number of lactation) to milk performance data. Economical analysis involves data from cows having calved 3 times – i. e. two calving intervals. Based on the above data it was possible to find out cost effectiveness of cows of different fertility.

## Results and Discussion

Although in EN group none of the cows had finished 3rd lactation, the milk production of test cows was compared (Table 1). On a basis of the milk fat and milk protein production data the ER and RHF groups had a similar productivity, while ER group had higher milk fat and protein content, but lower milk production compared with RHF group. EHF and EHFt groups had equal productivity, since both of them were formed from cows of Estonian Holstein breed with different level of breeding values. Total production of milk fat and protein of two lactations was the greatest in EHF group (1,329 kg) and in EHFt group (1,349 kg) whereas the total of three lactations was greater in EHF group (2,143 kg) and EHFt group (1,972 kg). The highest average production was observed in EHF group in 2nd and 3rd lactation, where 15 cows had finished the 2nd lactation and 5 cows had finished the 3rd lactation (11,085 kg and 12,164 kg, respectively). In this group the number of lactation has highly significant influence on milk yield as well as on milk fat and protein production.

Figures in Table 2 demonstrate the average milk yield per one CI day. According to the data, the milk production per CI day does not vary much in the 1st CI, ranging from 22.0 kg in 421-450 group to 24.5 kg in >450 group. In the 2nd

CI the figures of the milk yield are similar to those of the 1st CI, while exception is the group 391-420, where milk production is significantly lower compared to other groups.

Table 1. Milk productivity of test groups on Põlula Experimental Farm (least square averages)

| Gr. | Lact No | Cows | Milk kg | Fat | | Protein | | F+P kg |
|---|---|---|---|---|---|---|---|---|
| | | | | % | kg | % | kg | |
| EN | 1.# | 6 | 6549 | 4.52 | 296 | 3.68 | 241 | 537 |
| | 2.# | 2 | 8613 | 4.12 | 348 | 3.41 | 288 | 636 |
| F | | | 3.83 | 0.71 | 0.91 | 2.49 | 2.12 | 1.34 |
| ER | 1. | 27 | 7987 | 4.00 | 318 | 3.72 | 297 | 615 |
| | 2. | 21 | 9282 | 3.75 | 348 | 3.56 | 331 | 679 |
| | 3. | 6 | 9364 | 3.93 | 366 | 3.39 | 318 | 684 |
| F | | | 3.97* | 1,39 | 1.73 | 3.83* | 1.95 | 1.86 |
| RHF | 1. | 20 | 8151 | 3.61 | 291 | 3.42 | 279 | 570 |
| | 2. | 12 | 8997 | 3.51 | 313 | 3.42 | 308 | 621 |
| | 3. | 2 | 10986 | 3.60 | 395 | 3.45 | 375 | 770 |
| F | | | 3.23 | 0.13 | 3.19 | 0.01 | 3.69* | 4.05* |
| EHF | 1. | 39 | 8533 | 3.59 | 305 | 3.29 | 280 | 585 |
| | 2. | 15 | 11085 | 3.52 | 387 | 3.22 | 357 | 744 |
| | 3. | 5 | 12164 | 3.59 | 434 | 3.10 | 380 | 814 |
| F | | | 30.85 *** | 0.14 | 21.01 *** | 2.02 | 22.64 *** | 27.63*** |
| EHFt | 1. | 29 | 8853 | 3.70 | 326 | 3.34 | 295 | 621 |
| | 2. | 13 | 10481 | 3.65 | 379 | 3.33 | 349 | 728 |
| | 3. | 2 | 8668 | 3.87 | 339 | 3.26 | 284 | 623 |
| F | | | 4.57* | 0.22 | 3.20 | 0.14 | 5.64** | 4.66* |

# Mean

Due to a high feeding level used on the Experimental Farm, the CI length does not affect the milk yields, taking into consideration that dry period is optimal and under control.

With extended CI, costs increase in both 1st CI and 2nd CI (Table 3). Feed costs in 1st CI are 13,177 EEK per CI in >360 group, increasing to 19,496 in <451 group. Artificial insemination costs increase as well with extended CI in both first and second CI. In 1st CI in 391-420 group there are higher feed costs (42.80 EEK per day), and in 421-450 group there are higher insemination costs (1.58 EEK per day). In 2nd CI feed and insemination costs per CI day vary less.



Table 2. Average milk production per day in calving interval

| Calving interval | 1st calving interval | | | | | 2nd calving interval | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | Cows | per day | | | | Cows | per day | | | |
| | | milk, kg | fat, kg | pr, kg | f + pr, kg | | milk, kg | fat, kg | pr, kg | f + pr, kg |
| <361 | 25 | 23.2 | 0.87 | 0.81 | 1.68 | 6 | 27.7 | 0.98 | 0.96 | 1.94 |
| 361-390 | 18 | 23.5 | 0.88 | 0.82 | 1.71 | 12 | 27.0 | 0.96 | 0.94 | 1.90 |
| 391-420 | 8 | 23.2 | 0.93 | 0.80 | 1.73 | 9 | 24.2 | 0.87 | 0.87 | 1.74 |
| 421-450 | 6 | 22.0 | 0.89 | 0.79 | 1.68 | 5 | 27.7 | 1.05 | 0.93 | 1.98 |
| >450 | 19 | 24.5 | 0.94 | 0.87 | 1.81 | | | | | |

Table 3. Considerable costs in calving interval

| Calving interval | In calving interval (EEK) | | | Per day in calving interval (EEK) | | | |
|---|---|---|---|---|---|---|---|
| | feed | AI | vet costs | feed | AI | vet costs | total* |
| 1st calving interval | | | | | | | |
| <361 | 13177 | 211 | 341 | 37.97 | 0.61 | 0.98 | 73.05 |
| 361-390 | 14313 | 343 | 344 | 38.02 | 0.91 | 0.91 | 73.34 |
| 391-420 | 17300 | 536 | 291 | 42.80 | 1.32 | 0.71 | 78.34 |
| 421-450 | 17508 | 690 | 370 | 40.15 | 1.58 | 0.85 | 76.08 |
| >450 | 19496 | 1042 | 388 | 38.23 | 1.99 | 0.69 | 74.41 |
| 2nd calving interval | | | | | | | |
| <361 | 12897 | 226 | 332 | 37.91 | 0.66 | 0.98 | 73.05 |
| 361-390 | 14053 | 309 | 448 | 37.85 | 0.83 | 1.20 | 73.38 |
| 391-420 | 15769 | 459 | 567 | 39.62 | 1.16 | 1.42 | 75.70 |
| 421-450 | 18080 | 881 | 345 | 41.53 | 2.02 | 0.80 | 77.85 |

*) labour cost 7.70 and other costs 25.80 EEK/day equally to all

Expenditures on medicaments and veterinary treatments vary randomly. Prolong CI increases insemination and veterinary treatment costs. In the first CI, the total costs vary from the shortest CI 73.05 EEK per day to 78.35 EEK per day in 391-420 group (difference 5.29 EEK per day). In the second CI, the total costs increase with extended CI from 73.05 EEK per day in group of the shortest CI to 77.85 EEK per day in group of the cows of the longest CI (difference 4.80 EEK per day). In the second CI the total costs do not vary as much as in the first CI.

Figure 1 illustrates feed and total costs per 1 kg of milk in first and second CI. Feed costs per 1 kg of milk range between 1.56 EEK - 1.84 EEK in the first CI, and between 1.37 - 1.64 EEK in the second CI.

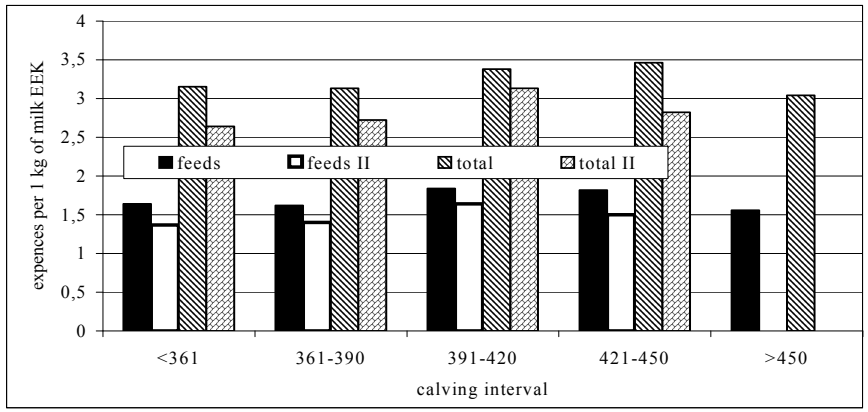

Figure 1. Feed and total costs per 1 kg of milk in first and second CI (I, II)

Total costs range between 3.04 EEK - 3.46 EEK (1st CI) and 2.64 EEK - 3.16 EEK (2nd CI). Feed and total costs are increasing with extended CI per 1 kg of milk, except in group >450 in 1st CI and in group of 421-450 days in 2nd CI. It can be concluded from this study, that optimum calving interval length is up to 390 days: pregnancy in the 3nd and 4th month of lactation.

**Summary**

1. Test groups range on the basis of milk fat and milk protein of two lactations: EHF (1383 kg) > EHFt (1359 kg) > RHF (1266 kg) > ER (1260 kg) > EN (1173 kg).
2. In the first CI, the milk production per CI day does not vary much, ranging from 22.0 kg in 421-450 group to 24.5 kg in >451 group. Due to a high feeding level used on the Experimental Farm, the CI length does not affect the milk yields, taking into consideration that dry period is optimal and under control.
3. The data about cost in CI show that feed costs (37.97-38.23 EEK per CI/d in 1st CI, 37.91-41.53 EEK per CI/d in 2nd CI) and cost for AI (0.61-1.99 EEK per CI/d in 1st CI, 8.98-2.02 EEK per CI/d in 2nd CI) increase with extended CI, per one CI day and totally per CI, while veterinary treatment costs vary randomly.
4. Extended CI increases feed and total costs per one kg of milk – exceptions are cows in the first CI >450 and in the second CI of 421-450 days. Therefore up to 390-day calving interval is considered optimum: pregnancy in third and fourth month of lactation.

**Acknowledgements**

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# GENETIC DIFFERENTIATION AMONG COMMERCIAL AND NATIVE CATTLE BREEDS

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## Introduction

The Food and Agricultural Organization of the United Nations (FAO) has established a global data bank on animal breeds (Scherf, 2000). According to this data bank, the Estonian Native cattle breed is classified as an endangered breed. Currently there are 500 breeding females in the breed. In order to avoid inbreeding, a Finnish native breed, Western Finncattle, has been used for upgrading of the Estonian Native breed. The two breeds have a similar phenotype (whitish-red to red-brown colour and hornless).

In Estonian Holstein cattle breeding, common international elite bulls have been used. Therefore the Estonian Holstein cattle share the same Holstein-Friesian gene pool as the other Holstein-Friesian breeds. In the present study, we have examined genetic divergence of the Estonian Native and Estonian Holstein from two Finnish cattle breeds, Western Finncattle and Finnish Holstein-Friesian using blood groups and transferrin as genetic markers.

## Materials and Methods

Samples The blood samples were taken from unrelated individuals (without common ancestor at least three generations). Number of animals representing the studied breeds varied from 34 to 43 (Table 1). The individuals of Estonian Native cattle were collected from 14 and Estonian Holstein from 17 herds. The Finnish samples analysed here were collected for the previous studies by Kantanen et al. (1999; 2000).

Genetic markers Genetic markers used to characterise the breeds were blood groups and plasma protein transferrin (TF). Breeds were analysed by antigenic factors in 9 blood group systems: EAA, EAB, EAF, EAJ, EAL, EAM, EAS, EAZ and EAR'. EA refers to Erythrocyte Antigen System. Each of studied blood group systems comprises at least one antigenic factor. At EAB, 26 antigenic factors were determined. The erythrocyte antigen detection was based on internationally accepted haemolysis test using monospecific reagents. The TF polymorphisms detection was carried out by separating the blood serum or plasma by electrophoresis.

The blood typing was carried out at the Laboratory of Genetics of Institute of Animal Science, Estonian Agricultural University for Estonian breeds (Tartu, Estonia) and in FABALAB for Finnish breeds (Vantaa, Finland). The laboratories have taken part in comparison tests organized by the International Society for



Animal Genetics. However, some differences in the nomenclature between laboratories were found whereby few reductions were done in allele number. For example, alleles that differed in antigenic subtypes ($A_1$ or $A_2$) were considered as one allele (A). The determination of blood group genotype typically requires family data, except the co-dominant EAF and EAR' systems. The family data were available for most studied animals for genotype determination.

Table 1. Number of breeding females (population sizes), sample sizes and gene diversity estimates within the breeds

| Breed | Pop. size | No. of animals sampled | $H_e$ | No. of alleles |
|---|---|---|---|---|
| Estonian Holstein | 75 000 | 34 | 0.355 | 41 |
| Estonian Native | 500 | 40 | 0.391 | 45 |
| Finnish Holstein-Friesian | 94 000 | 43 | 0.338 | 34 |
| Western Finncattle | 4 000 | 41 | 0.418 | 49 |

He = expected heterozygosity; No. of alleles = the number of alleles detected in each sample.

Statistical analysis The data analysis was based on genotypic data. Genetic variation of studied population was analysed by number of alleles and gene diversities (unbiased expected heterozygosity $H_e$). The observed heterozygosities ($H_o$) were found by direct count from determined individual genotypes. The exact test for deviation from Hardy-Weinberg equilibrium was performed for the breeds and the loci. Also heterozygote deficiency and excess were tested. (GENEPOP version 3.1; Raymond & Rousset, 1995).

Genotypic differentiation between each population pair was performed by GENEPOP program. Fixation index $F_{ST}$ was calculated by the method of Weir & Cockerham (1984) by a weighted analysis of variance as implemented in FSTAT. The 95% confidence intervals for $F_{ST}$ estimates were determined by bootstrapping (Goudet, 1995). Genetic distances between breeds were calculated using $D_A$ distance (Nei et al., 1983). The program DISPAN (Ota et al., 1993) was used for computing the estimates.

## Results and Discussion

The number of alleles per locus ranged from two (6 loci) to 56 (EAB), and expected heterozygosity from 0.048 (EAM) to 0.957 (EAB). This indicates that the EAB blood group system is a highly polymorphic marker exceeding the level of heterozygosity, typically found at microsatellite DNA markers in diversity studies of cattle breeds (e.g. Kantanen et al., 2000; Maudet et al., 2002). The overall expected heterozygosity of the studied loci was 0.317. However, this value is lower than typically found at microsatellites.

The number of alleles found in one breed varied from 34 to 49, and expected heterozygosity from 0.338 to 0.418 (Table 1). At the EAB locus, 28 and 25 different alleles (EAB allele refers to an antigenic complex inherited as one block) were found in Western Finncattle and Estonian Native Cattle, respectively, whereas 17 and 21 EAB alleles, respectively, were detected in Finnish Holstein-Friesian and Estonian Holstein. The number of same EAB alleles found both in Western Finncattle and Estonian Native Cattle was 13. The Holstein-Friesian breeds shared 9 EAB alleles. Most of EAB alleles specific to Western Finncattle or Estonian Native cattle were not found in Holstein-Friesian breeds excluding two alleles that were found in all analysed breeds. One allele, frequently present in Holstein-Friesians was also found in Estonian Native breed. This allele might have been introduced to the Estonian breeds from the crossing with Red Holstein Cattle. In general, the genetic diversity estimates indicated slightly lower intrabreed diversity in the Holstein-Friesian breeds than in the native breeds.

In the HWE testing, each locus-breed combination showed statistically significant agreement with the Hardy-Weinberg proportions. The pooled breed-wise P-values, however, indicated heterozygote excess ($P<0.05$) in Estonian Native Cattle and Western Finncattle. EAB locus ($P<0.01$) deviated from Hardy-Weinberg equilibrium in the pooled breed sample.

The $F_{ST}$ value was 0.040 suggesting that 4% of the total genetic variation can be explained by breed differences. The 95% confidence intervals for $F_{ST}$ ranged from 0.016 to 0.060 indicating that the breed subdivision was statistically significant from zero. $F_{ST}$ values between Holstein-Friesian breeds and between native breeds were 0.008 and 0.030, respectively, indicating a lower level of divergence between the Holstein-Friesian breeds.

Table 2. Pair-wise $F_{ST}$ values (above the diagonal) and Nei's $D_A$ distances (below the diagonal)

| | WFC | FFR | ENC | EHF |
|---|---|---|---|---|
| Estonian Holstein (EHF) | 0.0312 | 0.0084 | 0.0394 | |
| Estonian Native (ENC) | 0.0302 | 0.0606 | | 0.0871 |
| Finnish Holstein-Friesian (FFR) | 0.0663 | | 0.0979 | 0.0535 |
| Western Finncattle (WFC) | | 0.1128 | 0.0553 | 0.0899 |

Further evidence for the breed divergence was obtained by the exact test for population differentiation (Raymond & Rousset 1995). Statistically significant P-values for genotypic differentiation between the Holstein breeds were found at two loci (EAB and EAA, $P<0.01$) and between the native breeds at three loci (EAB and EAR' $P<0.001$; EAS $P<0.01$).



On the basis of pair-wise $F_{ST}$ values and $D_A$ genetic distances, the breeds can be clustered into two groups: the native breeds and Holstein-Friesian breeds (Table 2).

**Conclusions**

The blood group and transferrin data indicated close genetic relationships between the Finnish and Estonian native cattle breeds, and on the other hand also between the Finnish and Estonian Holstein-Friesian breeds. This low level of divergence of different national breeds is due to the use of same sires in artificial insemination of dairy cows. Although Western Finncattle and Estonian Native cattle are small populations, they exhibited more intrabreed diversity than the commercial breeds. Holstein breeds have a large census size, but their effective population size can be rather limited (see Kantanen et al., 1999).

**Acknowledgements**

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# THE INFLUENCE OF DIFFERENT FACTORS ON THE FEED CONSUMPTION OF PIGS IN LITHUANIA

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## Introduction

In recent years approximately one million pigs are kept in Lithuania. The major pig breed in Lithuania is Lithuanian White. Of the foreign dominating breeds in Lithuania there are Landrace and Yorkshire [10].

Food is a major cost in pig production [11].

The feed consumption in the pork cost price makes up more than 50%, so it is one of the main selected indications for purebred pigs in the country [9].

The aim of pig breeding programs is to reduce these costs by selecting most efficient pigs. Selection of breeding pigs might be based on the ratio between growth and feed intakes, while these traits are measured over a fixed weight or time intervals. If there are any differences between animals in performance patterns during the test period, they are not taken into account when animals are selected using this strategy [2,8,9].

## Materials and Methods

The analysis was carried out in the Laboratory of Animal Breeding Value Establishment and Biometry of Lithuanian Veterinary Academy on the national postgreSQL database. Records from the database of the stations test included a total of 9191 sows' and boars' progenies born between 1998 and 2002.

Statistical analyses were carried out using "R" package.

The multivariate mixed animal model was used to estimate heritability [3,4].

The fixed effects in the model were used: breed, year - season, sex; random effect: herd, litter, additive-genetic effect of animals.

The aim of this study was to estimate the influence of different factors on the feed consumption and their correlations with the pigs´ fattening and meat quality traits.

## Results and Discussion

According to the results derived from the control fattening the influence of different factors on feed consumption was estimated. The results are shown in Table 1.

The analysis indicated a significant influence of breed on the feed consumption of pigs (24.9%, P< 0.001).



Table 1. Influence of different factors on feed consumption per 1 kg gain

| Factor | Influence of different factors on feed consumption |
|---|---|
| Bred | 24.9*** |
| Sex | 0.7*** |
| Litter | 1.1** |
| Year - Season | 10.6*** |
| Farm | 6.5*** |

P< *** - 0.001; ** - 0.01; * - 0.05.

The feed consumption of the Lithuanian White pigs was 3.56-3.60 kg of the standard fodder. Moreover, among all breeds of pigs in Lithuania, the Duroc and Pietrain breeds distinguish themselves having the best feed consumption – 2.77±0.07 kg and 2.80±0.05 kg, respectively.

According to the results of the study, the highest influence of all non-genetic factors on feed consumption have had the year - season – 10.6 % (P<0.001) and herd – 6.5% (P<0.001).

The large negative genetic correlation coefficient of the feed consumption was determined with the daily gain ($r_g$=-0.64); moderate negative – with the lean meat ($r_g$=-0.43); moderate positive – with the backfat ($r_g$=0.49) and age ($r_g$=0.45); small positive – with the carcass length ($r_g$=0.14). The results are shown in Table 2.

Table 2. The genetic and phenotypic correlation coefficients of the feed consumption

| Trait | $r_g$ | $r_p$ |
|---|---|---|
| Daily gain, g | -0.64 | -0.72 |
| Age at achieving 100 kg live weight, days | 0.45 | 0.40 |
| Carcass length, cm | 0.14 | -0.04 |
| Backfat, mm | 0.49 | 0.11 |
| Lean meat, % | -0.43 | -0.10 |

Correlated characters are of interest for three chief reasons. Firstly, in connection with the genetic causes of correlation through the pleiotropic action of genes: pleiotropy is a common property of major genes, but we have as yet had small opportunities to consider its effects in quantitative genetics. Secondly, in connection with the changes brought about by selection: it is important to know how the improvement of one character will cause simultaneous changes in other characters. And thirdly, in connection with natural selection: the relationship between a metric character and fitness in the primary agent that determines the genetic properties of that character in a natural population [1].

A large negative genetic correlation coefficient of the feed consumption was determined with the daily gain; moderate negative – with the lean meat; moderate positive – with the back fat and age; small positive – with the carcass length by other authors [5-8].

The phenotypic correlations of the feed consumption with daily gain ($r_p$=-0.72) and lean meat ($r_p$=-0.10) were found also negative, whereas with age ($r_p$=0.40) and back fat – positive ($r_p$=0.11). Though genetic coefficient of correlation with carcass length was small positive ($r_g$=0.14), the estimate phenotypic correlation was small negative ($r_p$=-0.04). The phenotypic correlation coefficients of the feed consumption are shown in Table 2.

We have studied a heritability coefficient of feed consumption. The heritability coefficient was determined according to multivariate analysis.

The heritability of a metric character is one of most important properties. It is important to recognize that the heritability is a property not only of a character but also of the population, of the environmental circumstance to which the individuals are subjected, and of the way in which the phenotype is measured. [1].

The results of the heritability coefficients are shown in Table 3.

Table 3. The coefficients of the heritability

| Trait | $h^2$ |
|---|---|
| Feed consumption, kg | 0.46 |
| Daily gain, g | 0.51 |
| Age at achieving 100 kg live weight, days | 0.30 |
| Carcass length, cm | 0.47 |
| Backfat, mm | 0.33 |
| Lean meat, % | 0.43 |

Comparing to other indicators, the largest heritability coefficient presented daily gain ($h^2$=0.51) and carcass length ($h^2$=0.47). The least heritability coefficient was found for the back fat thickness ($h^2$=0.33) and feed consumption ($h^2$=0.46).

For lean meat the moderate heritability was estimated ($h^2$=0.43). The heritability coefficients for the age at achieving 100 kg live weight and backfat were 0.30 and 0.33, respectively.

Similar heritability for feed consumption was estimated by A. Hofer [5], J. Remeikiene [9] and other authors [11,12]

In this study the coefficient of feed consumption heritability was $h^2$ = 0.46. A significant influence of pig breed shows the possibilities of effective pig selection on this trait in Lithuania.



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## CHANGES IN SELECTION OF PUREBRED LITHUANIAN WHITE PIGS

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### Introduction

The purebred Lithuanian White pigs are prolific, milk productive and fairly good in fattening, however their carcass traits are worse. According to the data of phenotypic evaluation by ultrasonic apparatus *Piglog 105*, average lean meat percentage of progeny of this type, being raised in breeding centres at the beginning of the year 2003, reached 51.9%; when that of progeny, raised in the stables of control fattening of the State Pig Breeding Station – 50.1% (Klimas *et al.*, 2003; Pig breeding records, 2003). Namely because of that reason, rapid decrease in their numerousness is in progress, as they are not withstanding the competition with imported pig breeds.

Having a purpose to preserve the base of Lithuanian White pigs in conditions of up-to–date market, till 2005 it is necessary to increase their muscularity no less than by 3-5% (Animal breeding program, 2001). This became especially relevant after introducing EUROP standard for pigs being slaughtered. For more rapid improvement of genetic potential of the population of purebred Lithuanian Whites the most purposeful is to use the boars of English Large White breed. Whereas namely English Large Whites had the biggest influence on nurture of Lithuanian Whites (Makoveckas, 1986), therefore additional infusion of blood of the above-mentioned breed may be considered as pure breeding. According to prepared schemes of breeding this work has been started in nine breeding centres of purebred Lithuanian White pigs. Lithuanian Association of Pig Producers also approved this decision. Leanness of boars of English Large White breed, used for infusion of blood, must be no less than 58-60%.

The purpose of this work was to determine an influence of English Large White breed on reproductive performance of sows of Lithuanian White and on fattening performance and carcass traits of received first generation progeny ($F_1$).

### Materials and Methods

The work has been carried out in the years 2002-2003. In order to investigate reproductive performance, two groups of sows (of the first and second farrow) were formed in "Berka" (Kelmė district) and Skėmiai (Radviliškis district) breeding centres, using methods of analogues by parentage and age: Lithuanian White x Lithuanian White (LW x LW) and Lithuanian White x English Large White (LW x ELW). In both breeding centres control groups (LW x LW) and experimental groups (LW x ELW) were formed from 48 sows, respectively. Analysis of litter size and milk yield of sows, coupled with the boars of Lithuanian White and English Large White breeds was fulfilled for 192 sows in total.



Pigs of improved first generation ($F_1$): 84 from "Berka" breeding centre and 14 from Skėmiai breeding centre were tested in stables of control fattening of State Pig Breeding Station. Besides that, fattening performance and carcass traits of 98 LW x ELW – $F_1$ pigs from the above-mentioned breeding centres were compared with 2002 analogous parameters of control group of pigs (n=149). During the control fattening (from 30 to approx. 95 kg weight), conditions of housing and feeding were equal for all groups of pigs. Pigs were fed with special dry compound feed KRET- KOM58-1404, containing 1.1 feed units, 13.84 MJ of metabolizable energy and 16% of proteins per kilogram. After finishing control fattening of pigs, their age in days (from the birth until reaching 100 kg weight), average daily gain and feed consumption per kg gain (during the fattening period from 30 kg to approx. 95 kg weight) was calculated. Before realization (slaughtering), lean meat percentage was determined for live pigs according to accepted methods (Piglog 105 User's Guide, 1991). Half carcass length, backfat thickness at the last rib, loin lean area and ham weight of cooled carcasses (at 0…+4$^0$ C in 24-hour period) were recalculated at 100 kg weight, using accepted coefficients of regression.

The investigation data were processed biometrically (Sakalauskas, 1998). The difference was considered significant when $P<0.05$.

### Results and Discussion

It was indicated (Table 1), that litter size and milk yield of Lithuanian White sows, coupled with boars of ELW breed, when compared with purebred Lithuanian Whites (control group) was not reliably different in breeding centres.

Table 1. Reproductive performance of sows

| Family name | LW x LW | | | LW x ELW | | |
|---|---|---|---|---|---|---|
| | n | Litter size | Milk yield, kg | n | Litter size | Milk yield, kg |
| Breeding centre of "Berka" | | | | | | |
| Drąsuolės | 12 | 11.0±0.2 | 61.1±2.1 | 12 | 10.8±0.2 | 62.8±0.7 |
| Dobilės | 12 | 10.6±0.2 | 59.2±1.7 | 12 | 11.3±0.2 | 62.7±0.8 |
| Razetos | 12 | 10.2±0.2 | 57.0±1.9 | 12 | 10.7±0.2 | 61.4±0.9 |
| Rūtos | 12 | 10.8±0.2 | 64.2±1.2 | 12 | 10.8±0.1 | 57.9±1.3 |
| Total | 48 | 10.6±0.1 | 60.4±0.8 | 48 | 10.9±0.1 | 61.2±0.6 |
| Breeding centre of Skėmiai | | | | | | |
| Drąsuolės | 12 | 10.5±0.3 | 52.9±1.4 | 12 | 11.1±0.4 | 56.0±2.3 |
| Dobilės | 12 | 10.6±0.2 | 55.2±1.6 | 12 | 11.0±0.3 | 59.0±1.9 |
| Razetos | 12 | 10.2±0.3 | 51.7±1.1 | 12 | 10.3±0.3 | 53.0±2.0 |
| Rūtos | 12 | 11.0±0.4 | 54.8±1.7 | 12 | 9.8±0.5 | 52.6±1.9 |
| Total | 48 | 10.6±0.1 | 53.6±0.7 | 48 | 10.6±0.2 | 55.2±1.0 |
| All sows | 96 | 10.6±2.4 | 57.0±5.1 | 96 | 10.7±2.1 | 58.4±4.9 |

Consequently, English Large Whites have no significant influence on reproductive performance of Lithuanian White sows.

According to the data of control fattening and slaughtering (Table 2), boars of English Large White breed have positive influence not only on carcass traits, but also on fattening performance of Lithuanian Whites.

Table 2. Control fattening performance and carcass traits of pigs

| Item | 2002 | 2003 | 2003/2002 (±) |
|---|---|---|---|
| | LW x LW | LW x ELW – $F_1$ | |
| Breeding centre of "Berka" | | | |
| No. of pigs | 120 | 84 | * |
| Age at 100 kg weight, d | 183±1 | 179±1 | –4 |
| Daily gain, g | 782±6 | 825±7 | +43 |
| Compound feed conversion per kg gain,kg | 3.19±0.02 | 2.74±0.03 | –0.45 |
| Half carcass length, cm | 95.6±0.2 | 94.3±0.2 | –1.3 |
| Backfat thickness at last rib, mm | 24.0±0.4 | 18.2±0.3 | –5.8 |
| Loin lean area, $cm^2$ | 32.1±0.3 | 36.6±0.3 | +4.5 |
| Ham weight, kg | 11.0±0.1 | 11.4±0.1 | +0.4 |
| Lean meat % (*Piglog 105*) | 51.9±0.3 | 56.0±0.2 | +4.1 |
| Breeding centre of Skėmiai | | | |
| No. of pigs | 29 | 14 | * |
| Age at 100 kg weight, d | 196±1 | 189±3 | –7 |
| Daily gain, g | 716±7 | 718±13 | +2 |
| Compound feed conversion per kg gain,kg | 3.31±0.03 | 2.77±0.07 | –0.54 |
| Half carcass length, cm | 95.9±0.3 | 94.7±0.5 | –1.2 |
| Backfat thickness at last rib, mm | 22.3±0.8 | 19.3±0.5 | –3.0 |
| Loin lean area, $cm^2$ | 30.0±0.4 | 34.5±0.8 | +4.5 |
| Ham weight, kg | 10.7±0.1 | 10.8±0.2 | +0.1 |
| Lean meat % (*Piglog 105*) | 51.1±0.5 | 53.7±0.7 | +2.6 |

Comparing with purebred pigs (LW x LW), Lithuanian Whites of "Berka" and Skėmiai breeding centres, having 50% of English Large White blood, reached 100 kg weight by 4 and 7 days earlier ($P<0.05$), gained daily by 43 g ($P<0.01$) and 2 g more, and consumed 0.45 kg and 0.54 kg less ($P<0.001$) of compound feed per kg gain, respectively. Backfat at the last rib of the last-mentioned was, respectively,



by 5.8 and 3.0 mm thinner ($P<0.05$-$0.001$), and the loin lean area - 4.5 and 4.5 $cm^2$ ($P<0.005$-$0.001$) as well as lean meat percentage - 4.1 and 2.6% ($P<0.05$-$0.001$) higher compared with old type Lithuanian White pigs. Altogether, pigs selected from "Berka" breeding centre showed better fattening performance and leanness.

Although half carcass of improved first generation progeny (LW x ELW - $F_1$) shortened by 1.2 – 1.3 cm, however this difference is not reliable. Besides that, in up-to-date pig selection in Europe each time less attention is paid on the half carcass length. Main indicator of evaluation of carcasses is their lean meat percentage, which is closely related to the backfat thickness.

The essence of this work – to select first generation progeny ($F_1$), muscularity of which would be no lesser than 53 – 55%, and them bred *inter se*. This way 50% of the blood of English Large White breed will be infused in separate lines and families. Infusion of 75% of blood can be applied exclusively.

Tendency shows itself, that in the breeding centres of purebred Lithuanian Whites more numerous will remain 4 improved lines of boars and 8 improved families of sows.

**Conclusions**

Though English Large Whites had no significant influence on the litter size and milk yield of Lithuanian White pigs, they improved their fattening performance, and especially carcass traits. Leanness of improved first generation progeny ($F_1$) in separate breeding centres was from 2.6% ($P<0.05$) to 4.1% ($P<0.001$) higher than that of old type Lithuanian Whites.

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# OSTEOCHONDROSIS IN RELATION TO THE PERFORMANCE TRAITS OF THE DIFFERENT PIG BREEDS

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## Introduction

The syndrome of leg weakness that is directly related to osteochondrosis has become quite widespread in pig husbandry. The problem has become acute because, from exterior view point, long and muscular pigs are being raised (Draper *et al.*, 1992; Jorgensen, Andersen, 2000; Yazdit *et al.*, 2000). Besides, this disease is more revealed in pigs of weaker constitution (Reiland *et al.*, 1978). Osteochondrosis is a hereditary degenerative joint disease of bone and cartilage tissue that leads to leg weakness of pigs. The heritability coefficient of leg weakness defect varies from 0.2 to 0.6 for different pig breeds (Nagel, Seifert, 1980; Lundeheim, 1987; Andersson–Eklund *et al.*, 1998). Feeding and housing conditions (floor type, humidity, etc.) have influence on more intensive development of osteochondrosis in pigs susceptible to this disease (Nakano *et al.*, 1987; Jorgensen, 2000).

As the defect is hereditary, it should be controlled in the course of selection. The studies of osteochondrosis are successfully carried out in Sweden, Denmark, Finland, Norway, Germany, Holland, the USA and other countries.

The monitoring of pig osteochondrosis in Lithuania was started in 2001 (Klimienė, Klimas, 2002). More or less severe osteochondrotic lesions in pigs have been found in all the tested breeding centres. The occurrence of osteochondrosis among all the tested pigs (n=1009) of various breeds made up 48.1%. Lithuanian White pigs were least affected by osteochondrosis in the joints (32.7% of pigs), while osteochondrotic lesions were registered in 78.7% of crossbreds out of imported breeds. The study indicated that castrated males were more inclined to have the leg weakness syndrome than gilts (51.6% vs. 44.5%). Front legs were more affected by joint lesions. The investigation data indicated that osteochondrosis should be controlled in the course of selection of pigs bred in Lithuania.

The purpose of this work was to determine the influence of osteochondrosis on fattening and carcass traits of some pig breeds raised in Lithuania.

## Materials and Methods

Pigs of various breeds chosen from different breeding centres and raised (from 30 to approx. 95 kg weight) at the stables of control fattening of State Pig Breeding Station were checked for osteochondrosis. Housing and feeding conditions were the same for all pigs. The piglets were kept in individual pens**.** Area of pen 1.9 $m^2$, floor of concrete, littered by peat. The average air



temperature was 18-20 $^0$C and relative humidity was not higher than 70 %. During the control fattening, the animals were twice daily fed special dry compound feed. Feed was weighed individually for each pig. A kilogram of compound feed contained 1.1 feed unit, 13.39 MJ of metabolizable energy and 16.76% of crude protein. The pigs had free access to water for 24 hours.

When the pigs were fattened to approx. 95 kg weight, their length of fattening, average daily gain and feed consumption (metabolizable energy) per kg gain were estimated. Before realization (slaughtering), lean meat percentage was determined for live pigs according to accepted methods (Piglog 105 User's Guide, 1991).

The pigs were slaughtered at meat–processing plants and osteochondrosis was measured according to the methods applied in Sweden by the cut surface of distal femur and humerus (Reiland *et al.*, 1978; Andersson – Eklund *et al.*, 1998). The severity of this disease was scored in elbow and knee joints on a 0-5 point scale. The scores range from 0 (no joint lesions), to 5 (severe joint lesions), with 1 indicating weak joint lesions. Half carcass length, backfat thickness at the last rib, loin lean area and ham weight of cooled carcasses (at 0…+4° in 24 hours period) were recalculated at 100 kg weight of pigs, using accepted coefficients of regression.

Analysis of fattening and carcass traits was fulfilled for 58 pigs of various breeds with osteochondrotic lesions in leg joints and for 78 pigs without this defect. The investigation data were processed biometrically (Sakalauskas, 1998). The difference was considered significant when $P< 0.05$.

## Results and Discussion

When analyzing influence of osteochondrosis on fattening performance of pigs of some breed, significant differences were not found (Table 1). Fattening length of healthy pigs and those having hereditary leg weakness defect, daily gain and feed consumption (metabolizable energy) per kg gain statistically were not reliably different ($P>0.1$-$0.5$). Looking at the growth rate in fattening period, Swedish Yorkshire and Lithuanian White bacon (LW-B1) type were pre-eminent among other tested pig breeds. It is necessary to mention, that LW-B1 type was created by immigration crossbreeding, using boars of Swedish and Finnish Yorkshire breed. Therefore in this case influence of breed predetermined better fattening performance of the above-mentioned pigs. Though Yazdit *et al.* (2000) had indicated that pigs having leg weakness syndrome are growing more slowly in the second part of fattening.

According to the Piglog 105 measurements (Fig. 1), lean meat content of pigs of different breed, having osteochondrotic lesions in leg joints, ranged from 51.0 to 54.2%, or was 0.5-3.0% higher than for pigs not having such defect. This tendency especially manifested itself for purebred Lithuanian Whites ($P<0.05$).

Table 1. Control fattening performance

| Breed | No. of pigs | Initial weight, kg | Finish weight, kg | Fattening length, d. | Daily gain, g | Metabo-lizable energy per kg gain, MJ |
|---|---|---|---|---|---|---|
| Normal joints (0 score) | | | | | | |
| Purebred Lithuanian White (LW) | 22 | 30.9±0.4 | 95.6±0.7 | 91±2 | 717±10 | 43.25±0.94 |
| Lithuanian White bacon type (LW-B1) | 16 | 30.4±0.2 | 97.4±0.7 | 84±2 | 810±23 | 41.51±0.94 |
| Lithuanian White meat type (LW-M1) | 5 | 30.0±0.0 | 95.8±1.9 | 104±6 | 637±29 | 47.67±2.81 |
| Swedish Yorkshire (SY) | 27 | 30.0±0.0 | 96.5±0.5 | 86±2 | 777±23 | 41.24±1.07 |
| German Landrace (GL) | 8 | 30.0±0.0 | 94.1±0.9 | 91±4 | 715±32 | 40.71±0.80 |
| Osteochondrotic joint lesions | | | | | | |
| Purebred Lithuanian White (LW) | 10 | 30.0±0.0 | 99.1±1.4 | 94±3 | 740±24 | 43.65±0.94 |
| Lithuanian White bacon type (LW-B1) | 12 | 30.3±0.2 | 94.7±0.5 | 85±2 | 766±16 | 42.31±1.34 |
| Lithuanian White meat type (LW-M1) | 4 | 30.0±0.0 | 98.7±1.3 | 109±4 | 635±26 | 45.53±2.01 |
| Swedish Yorkshire (SY) | 26 | 30.8±0.4 | 95.2±0.3 | 85±2 | 770±23 | 42.98±0.94 |
| German Landrace (GL) | 6 | 30.0±0.0 | 94.7±0.6 | 90±2 | 735±23 | 42.31±0.94 |

Similar dependence of osteochondrosis on muscularity was indicated in other countries for Durocs (Draper *et al.*, 1992), Swedish Landraces and Swedish Yorkshires (Yazdit *et al.*, 2000), Danish Landraces and Danish Yorkshires (Jorgensen, Andersen, 2000).

When investigating whether osteochondrotic diseases depend on carcass traits of pigs, certain tendency was indicated (Table 2). Carcass traits of pigs of all groups having osteochondrotic lesions in leg joints (except the half carcass length) were better than those of pigs, not having this defect.



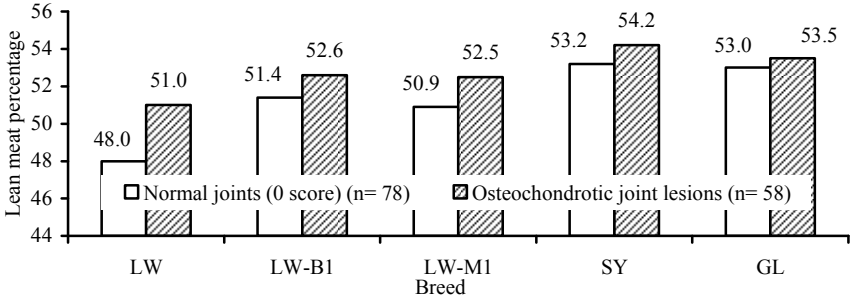


Figure 1. Measurements of leanness in pigs (n =136) of different breed with *Piglog 105*

Table 2. Carcass traits

| Breed | No. of pigs | Half carcass length, cm | Backfat thickness at last rib, mm | Loin lean area, $cm^2$ | Ham weight, kg |
|---|---|---|---|---|---|
| Normal joints (0 score) | | | | | |
| Purebred Lithuanian White (LW) | 22 | 98.06±0.41 | 25.70±0.99 | 31.80±1.14 | 9.90±0.23 |
| Lithuanian White bacon type (LW-B1) | 16 | 98.78±0.61 | 23.05±1.17 | 32.70±1.28 | 9.90±0.06 |
| Lithuanian White meat type (LW-M1) | 5 | 99.44±1.28 | 21.30±1.68 | 32.54±1.43 | 9.64±0.55 |
| Swedish Yorkshire (SY) | 27 | 98.00±0.61 | 21.10±1.08 | 33.20±1.24 | 10.34±0.16 |
| German Landrace (GL) | 8 | 99.20±0.75 | 22.30±1.11 | 36.50±2.23 | 10.24±0.33 |
| Osteochondrotic joint lesions | | | | | |
| Purebred Lithuanian White (LW) | 10 | 99.30±0.71 | 23.20±1.37 | 34.10±1.17 | 10.70±0.31 |
| Lithuanian White bacon type (LW-B1) | 12 | 98.70±1.05 | 22.23±0.87 | 33.03±1.26 | 10.22±0.11 |
| Lithuanian White meat type (LW-M1) | 4 | 96.50±1.19 | 20.13±2.47 | 32.90±1.20 | 9.70±0.27 |
| Swedish Yorkshire (SY) | 26 | 98.50±0.47 | 19.40±1.33 | 35.70±1.26 | 10.50±0.17 |
| German Landrace (GL) | 6 | 98.70±0.82 | 20.90±1.08 | 37.90±2.30 | 10.30±0.53 |

Backfat thickness at the last rib for pigs of different breed, having syndrome of leg weakness was 0.8-2.5 mm less than that of healthy pigs, whose loin lean area and ham weight were 0.3-2.5 $cm^2$ and 0.1-0.8 kg, respectively, higher.

However, statistically reliable difference (P<0.05), according to comparison of ham weight data, was indicated only for purebred Lithuanian Whites.

**Conclusions**

When analyzing influence of osteochondrosis on the fattening performance of purebred Lithuanian White, bacon-type (LW-B1) and meat-type (LW-M1) Lithuanian White, Swedish Yorkshire and German Landrace pigs, significant differences were not found (P>0.1-0.5). However, dependence of this defect on muscularity and other carcass traits of pigs was indicated. Lean meat percentage, loin lean area and weight of ham of pigs, having osteochondrotic lesions of leg joints were higher than that of pigs not having this defect, when backfat thickness was lower.

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# FEED INTAKE, GROWTH AND BODY COMPOSITION IN A THREE GENERATION FULL SIB DESIGN IN SWINE TO IDENTIFY QTL


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**Introduction**

Genetic regulation of protein deposition and energy partitioning in different stages of growth is of high interest in pig breeding, because future selection strategies should concentrate on biological growth models using protein accretion and minimum lipid to protein deposition ratio to optimize feed intake capacity (De Vries and Kanis, 1992; Schinckel and de Lange, 1996). To examine the relationships between energy intake and growth of pigs, daily feed intake and body composition has to be measured. Combined with reference method serial slaughter trial with chemical analysis of empty body (CAEB) the isotope dilution technique (IDT) is a capable non-invasive method to measure body composition based on body water content (Ellis, 2000; Wang, 1999; Susenbeth, 1984; Shields *et al.*, 1983). Objective of the present study was to characterize chemical body composition and daily energy intake of female and castrated fattening pigs between 30 and 140 kg of body weight in the context of a three generation full sib design to identify QTL for these traits.

**Material and Methods**

In founder generation ($F_0$) 7 unrelated boars (heterozygous at MHS locus) of a sire line and 16 unrelated sows of a crossbred dam line were mated. Then, 8 boars and 41 sows from $F_1$ generation were selected and mated under avoiding of inbreeding to produce $F_2$ generation. $F_2$-pigs were tested on station with IDT to obtain protein, lipid and ash deposition at 30, 60, 90, 120 and 140 kg of body weight (BW). In this study, 325 pigs were analysed, whereas 95 pigs were single housed in performance test pens and manual fed with weekly determination of feed intake. 230 pigs were housed in identical straw bedded pens with an electronic feeding station of type ACEMA 48 which provides records of every single visit of the feeding station. Animals were allowed to ad libitum access to a series of pelleted diets to provide expression of maximum protein accretion.

8 pigs from every weight class of F1 (a total of 48) were taken for a serial slaughter trial. Left carcasses were dissected to apply a chemical analysis of single fractions viscera, fat-meat and bones to calculate chemical composition of entire body. To all pigs IDT with use of Deuterium oxide was applied at 30, 60, 90, 120 and 140 kg BW to obtain total body water content (TBW). Based on serial slaughter trials, empty body water content (EBW) was estimated and thereafter

functions to predict fat-free content of empty body (FFC) (Table 2) were fitted. Basic principle for determination of living pigs body composition was based on a two-compartment-model with assumption of partition of empty body in lipid and FFC (Susenbeth, 1984), whereas chemical composition of FFC is unaffected by lipid content. Lipid content of empty body is therefore calculated as difference between empty body weight and FFC.

Table 1: Composition of diets used in different phases of growth (%, MJ ME)

| | Diet 30-60 kg | Diet 60-90 kg | Diet 90-140 kg |
|---|---|---|---|
| ME‡ (MJ/kg) | 13.8 | 13.8 | 13.4 |
| Lysine (%) | 1.2 | 1.1 | 1.0 |
| Lysine : ME (g : MJ) | 0.87 | 0.82 | 0.75 |

‡ME (MJ/kg) calculating according to GFE (1987).

Table 2: Allometric functions to predict chemical body composition

| Trait | Function | R | R.MSE |
|---|---|---|---|
| Empty body water content (EBW) (%) | $17.096 \bullet TBW_{D2O}^{0.4131} \bullet BW^{-0.1141}$ | 0.93 | 2.91 |
| Fat free substance (FFC) content(%) | $3.327 \bullet EBW^{0.7730}$ | 0.86 | 4.37 |
| Protein content of FFC (%) | $972.81 \bullet FFS^{-0.8804}$ | 0.83 | 1.05 |
| Ash content of FFM (%) | $255.77 \bullet FFM^{-0.9619}$ | 0.65 | 0.32 |

Change in chemical components during growth determined by isotope dilution technique were studied in relation to BW using allometric model $y = a \cdot x^b$ (model 1), whereas y is the measured amount of considered trait in kilograms, a the intercept, x the body weight of measured pigs and b the allometric regression coefficient. Model was linearized as $\log_{10}(y_i) = \log_{10}(a) + b\ P \log_{10}(x_i) + e_i$. Sex effect was tested to show differences between genders. Therefore, linearized allometric model $\log_{10}(y_{ij}) = \log_{10}(a_i) + b_i \log_{10}(X_{ij}) + e_{ij}$ with independent estimation of a- and b values was used. Regression equations were developed using the GLM procedure of SAS (SAS Inst. Inc., Cary, NC). Daily accretion rates of lipid and protein were calculated as differences between two measurements of chemical masses divided by days between these two dates. Associations between chemical body composition (IDT), accretion rates, energy intake as well as slaughterhouse test performance traits were calculated as pearson correlation coefficients between residuals after using the following model:

$$Y_{ijklmno} = \mu + S_i + G_j + BF_k + B_l + HT_m + b_{1n}(SBW) + b_{2O}(BW) + e_{ijklmno}$$

$Y_{ijklmno}$ = observation value
$\mu$ = Intercept



$S_i$ = fixed effect of sex (i = 1, 2)
$G_j$ = fixed effect of MHS-Genotype (j = 1, 2, 3)
$BF_k$ = fixed effect of birth farm (k = 1, 2)
$B_l$ = fixed effect of batch (l = 1-9)
$HT_m$ = fixed effect of housing type (m = 1,2)
$b_{1n}$ = linear regression on weight at start
$b_{2o}$ = linear regression on weight at slaughter day
$e_{ijklmno}$ = random residual error

For the traits such as daily feed intake, food conversion and accretion rates as well as daily gain in different weight ranges, linear regression on weight at slaughter day was excluded from the model. Because of offering additional food in feeding troughs to group housed pigs, first analysed weight range begins at 48 kg instead of 30 kg BW for group housed pigs. Therefore daily accretion rates for body weight, lipid and protein are calculated from 48 to 60 kg body weight for group housed pigs by estimating protein and lipid mass from third degree polynomial function for a single pig at 48 kg BW.

**Results**

Calculation of body composition was based on knowledge about content of fat free substance estimated from empty body water content (Table 2). Strong increase of lipid content in process of growth is indicated by decrease of percentage of fat free substance of empty body. Allometric function for FFC of empty body related to BW is $y = 132.321\ BW^{-0.119}$ and $y = 136.533\ BW^{-0.129}$ (r = 0.93, R.MSE = 2.448%) for gilts and barrows, respectively. Average protein content of fat free substance related to BW can be described with allometric function $y = 13.012 \cdot BW^{0.108}$ and $y = 12.562 \cdot BW^{0.118}$ (r = 0.95, R.MSE = 0.4334%) and resulted in 18.6, 20.1, 21.1, 21.8 and 22.2% for gilts and 18.7, 20.2, 21.3, 22.1 and 22.5% for barrows at 30, 60, 90, 120 and 140 kg BW, respectively. Composition of fat free substance was used to calculate body composition as shown in Table 3. Protein content of empty body decreased from 16.64 to 16.26% in gilts, and slightly stronger from 16.64 to 16.22% in barrows. Therefore, lipid content in empty body of castrated pigs increased noticeably more from 11.1 to 28.0%, compared to the increase from 11.1 to 26.7% in female pigs. In general, lipid mass showed much larger variance than protein mass within the different weight ranges.

Table 4 shows LSQ-means for daily gain, lipid and protein accretion rates, daily feed intake and food conversion ratios for the weight ranges I (30 or 48 to 60 kg BW), II (60 to 90 kg BW), III (90 to 120 kg BW) and IV (120 to 140 kg BW) corrected for housing type and sex. Maximum of protein deposition was

observed in weight range II, whereas barrows deposited more protein per day than gilts in this range.

Table 3: Prediction of protein and lipid content and mass of the empty body from empty body weight using allometric functions (n = 325)

| | | Coefficients of model | | | | |
|---|---|---|---|---|---|---|
| | Sex | log a | b | R | CV (%) | R.MSE |
| Protein content | Female | 1.2418 | - 0.0142 | 0.92 | 1 | 0.06% |
| | Castrated | 1.2434 | - 0.0155 | | | |
| Protein mass | Female | - 0.7582 | 0.986 | 0.99 | 1 | 0.05 kg |
| | Castrated | - 0.7566 | 0.984 | | | |
| Lipid content | Female | 0.1785 | 0.592 | 0.92 | 12 | 2.57% |
| | Castrated | 0.1191 | 0.632 | | | |
| Lipid mass | Female | - 1.8215 | 1.592 | 0.99 | 10 | 1.97 kg |
| | Castrated | - 1.881 | 1.632 | | | |

Table 4: LSQ-means of daily feed intake (DFI), food conversion ratios (FCR), daily gain (DG), protein (PAR) and lipid (LAR) accretion rates (n = 325)

| Weight Range | Housing Type | Sex | DFI (kg) | FCR (kg) | DG (g) | PAR (g) | LAR (g) |
|---|---|---|---|---|---|---|---|
| I | Indiv. | Female | 1.526 | 2.20 | 698 | 114 | 169 |
| | | Castrated | 1.718 | 2.32 | 745 | 120 | 187 |
| | Group | Female | 2.044 | 2.76 | 770 | 123 | 223 |
| | | Castrated | 2.271 | 2.86 | 819 | 132 | 239 |
| II | Indiv. | Female | 2.316 | 2.80 | 830 | 134 | 262 |
| | | Castrated | 2.563 | 3.10 | 844 | 136 | 284 |
| | Group | Female | 2.342 | 2.91 | 813 | 131 | 254 |
| | | Castrated | 2.602 | 3.06 | 861 | 139 | 285 |
| III | Indiv. | Female | 2.745 | 3.38 | 824 | 133 | 279 |
| | | Castrated | 2.938 | 3.69 | 811 | 130 | 309 |
| | Group | Female | 2.683 | 3.70 | 739 | 119 | 249 |
| | | Castrated | 2.927 | 3.79 | 784 | 124 | 282 |
| IV | Indiv. | Female | 2.697 | 4.02 | 724 | 118 | 250 |
| | | Castrated | 2.816 | 4.08 | 763 | 126 | 274 |
| | Group | Female | 2.833 | 4.18 | 712 | 113 | 272 |
| | | Castrated | 2.846 | 4.39 | 701 | 111 | 267 |

A stronger decrease in protein deposition at later stage was observed for group housed pigs compared to individual housed, especially for group housed barrows.



Females showed growth depression around 120 kg BW denoted by remarkable decrease of lipid deposition in weight range III for group and in weight range IV for individual housed gilts. Noticeable was strong adiposis of group housed barrows between 90 and 120 kg. In general, castrates had a higher DFI than females and group housed animals had higher feed intake than individual housed pigs, whereas residual feed intake (corrected for maintenance, protein and lipid deposition) was also higher for these pigs as demonstrated by worse FCR. Correlations between residuals of DFI and PAR were 0.68, 0.68, 0.69, 0.74 and correlations between residuals of DFI and LAR were 0.71, 0.69, 0.64, 0.62 in the weight ranges I, II, III and IV, respectively.

Table 5 shows correlations between residuals of carcass traits and DFI, FCR, body composition and growth rates.

Table 5: Correlations between residuals of growth, feed intake and carcass traits

| | Lean area | Fat area | Sidefat thickness | Backfat thickness |
|---|---|---|---|---|
| DG | - 0.14 | 0.13 | 0.15 | 0.13 |
| LAR | - 0.21 | 0.31 | 0.35 | 0.29 |
| DFI | - 0.30 | 0.31 | 0.34 | 0.25 |
| Lipid mass | - 0.22 | 0.46 | 0.51 | 0.43 |

Higher correlations between growth and carcass traits were obtained by using lipid accretion instead of body weight gain. Sidefat thickness showed a higher correlation to growth and feed intake traits compared to backfat thickness. Due to the fact of composition of lipid in the viscera, moderate correlations were found between carcass fat traits and empty body lipid mass. Correlation between residuals of lipid to protein ratio and fat to lean ratio in loin eye area was also moderate with 0.54.

**Discussion**

Prediction of body composition determined by $D_2O$ space showed high accuracy. Chemical composition of fat-free mass agreed with those reported by Susenbeth (1984). Percentage and composition of fat-free mass was used to calculate empty body composition. Coefficients of allometric function to predict lipid mass are similar to Wagner *et al.* (1999). Allometric functions fitted well, whereas gradients of b are interpretable on biological base. Daily deposition rates of lipid and protein in this study agreed well with literature. Kemm *et al.* (1995) calculated highest daily protein deposition of boars and gilts at 69 and 54 kg body weight, respectively. Schinckel *et al.* (1996) affirmed highest daily protein accretion between 50 and 60 kg BW. The explanation for noticeable growth depression of gilts around 120 kg BW is expected to be the first oestrus.

According to Bikker *et al.* (1996), protein and lipid deposition increased linearly with increasing energy intake. Therefore, even in the weight range 60 to 90 kg, feed intake is the determining factor for maximum protein accretion per day. Due to higher residual feed intake, maintenance requirement seems to be higher for group housed pigs, whereas the lower feed intake for individual housed pigs was in contrast to literature (De Haer and Merks, 1992; von Felde, 1996).

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## CARCASS QUALITY ESTIMATION OF YOUNG BOARS

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**Introduction**

At the beginning of 2002, within the frames of the programme ”Marble Pork“ for producing high-quality pork, a new quality estimation system of young boar carcasses was started in the Estonian Pig Breeding Association. Based on the above system, the culled young boars of the tested sows of the nucleous breeding farms are being estimated at the meat industry. Thus, the meat performance data regarding the A.I. station boars as well as the siblings of the boars sold to farms are being obtained. The collected data will be recorded in the database of the Animal Recording Centre in order to be used for further breeding value estimation.

**Materials and Methods**

The young boars were slaughtered at the slaughter department of the Valga Meat Factory. At least 45 minutes post mortem the hot carcasses were weighed and lean content was determined by lean meat meter Ultra FOM 100. Distribution of carcasses into sale classes on the basis of lean content was carried out according to SEUROP system (Tapasigade..., 1994).

The cooled carcasses were estimated in the cold storage 24 hours after slaughter. Carcass length was measured at two points, and the backfat thickness at the thinnest point of withers (at $6^{th}$...$7^{th}$ rib) and loin (*m. glutaeus medius*). The right half of the hanging carcass was dissected between the $13^{th}$ and $14^{th}$ ribs, and the area of *musculus longissimus dorsi* was photographed using a Kodak digital camera set on a tripod. Digital photos were downloaded in the computer and using a special Scan Star program for measuring the area of *musculus longissimus dorsi*, the loin eye area, fat area and sidefat thickness on and in front of loin muscle (*m. glutaeus medius*) were determined. The Estonian Pig Breeding Association obtained the Scan Star system from Rudolf Matthäus Engineering Bureau, Germany.

pH-value of lean meat was estimated in musculus longissimus dorsi within 24 hours after slaughter.

Proceeding from the pH-value of the muscular tissue, PSE-meat pH<5.59, normal meat pH was 5.6...6.29 and DFD- meat pH > 6.3 (Talonen, 1977).

In 2002...2003, the meat performance traits of 850 young boars were estimated; 175 of the Estonian Landrace, 592 of the Estonian Large White, and 81 of the Pietrain breed. A total of 76 young boars were tested; 16 of the Estonian Landrace, 47 of the Estonian Large White, 13 of the Pietrain breed.

A majority of the estimated young boars were the offspring of the boars Fram 4398 (32 pigs), Motor 756 (26), and Asse 7398 (23) of the Estonian Landrace breed; Jommi 2864 (83), Rino 392 (71), Hudson 2958 (67), and Curry 2651 (66) of the Estonian Large White breed, and those of the boars Valor 598 (23), Julius 2343 (16) and Caesar 2345 (13) of the Pietrain breed. The boars of the Estonian Landrace breed originated from the Kehtna Mõisa OÜ, the boars of the Estonian Large White breed from Saimre Farmstead and Pihlaka Farm OÜ, and the boars of the Pietrain breed originated from Pihlaka Farm OÜ.

The data was statistically processed.

Abbreviations: CL, cm – carcass length; BFT, mm - backfat thickness at $6^{th}$ - $7^{th}$ rib; LEA, $cm^2$ - loin eye area; FI - fleshing index; $pH_{24}$- pH- value; FOM, % - lean meat content, fixed using Ultra FOM 100; n - number; std - standard deviation.

**Results and Discussion**

The data presented in Table 1 demonstrate high carcass quality traits of all the estimated young boars. It is a positive result of using the semen imported from Finland, Norway and Austria.

The carcasses of the Estonian Landrace young boars were heavier (73.8 kg), and those of the Pietrain boars were lighter (70.7 kg). As expected, the carcass length of the boars of the Estonian Landrace and the Estonian Large White breed was 101.6 and 99.4 cm, respectively, whereas the carcasses of the Pietrain boars were shorter (92.6 cm).

The backfat of the white breeds (Estonian Landrace, Estonian Large White) was thinner (from 18.1 to 19.2 mm), and that of the Pietrain breed boars slightly thicker (20.4 mm). The offspring of the Pietrain breed boars, however, were remarkable for a high-quality flesh (loin eye area – 49.9 $cm^2$, lean meat content – 59.6%). Moreover, the meat characteristics of the offspring of the Estonian Landrace and the Estonian Large White boars was also good: large loin eye area (45.6 and 46.7 $cm^2$, respectively), and high lean meat content in a carcass (58.7%). Flesh index, i.e. backfat area : loin eye area was better in the carcasses of the Pietrain and the Estonian Large White boars (0.28 and 0.30, respectively). According to the SEUROP classification, the carcasses of young boars are distributed to S, E and U sale classes. To S-class belonged 34% of the carcasses of the offspring of the Estonian Landrace breed boars. The respective data for the Pietrain and the Estonian Large White breed were 32% and 28%. A majority of the carcasses of the evaluated boars belonged to E-class: 68% of the Estonian Large White and the Pietrain boars, and 56% of the Estonian Landrace boars.

As an average of all breeds, the offspring of the boars of the Tartu A.I. Station and nucleous breeding stations are characterized by their thin backfat (18.6 mm), a large loin eye area (46.8 $cm^2$) and a high lean meat content of carcass (58.8%).



Table 1. Carcass quality traits of young boars by breeds

| Traits | Breed | | | |
|---|---|---|---|---|
| | Estonian Landrace | Estonian Large White | Pietrain | Total/ average |
| No. of boars | 16 | 47 | 13 | 76 |
| No. of offspring | 175 | 592 | 81 | 850 |
| Carcass weight, kg | 73.1 | 73.8 | 70.7 | 73.4 |
| Std | 6.61 | 5.64 | 6.70 | 6.0 |
| Carcass length, cm | 101.6 | 99.4 | 92.6 | 99.2 |
| Std* | 3.32 | 3.71 | 3.23 | 4.26 |
| Backfat thickness at $6^{th}$ –$7^{th}$ rib, mm | 18.1 | 19.2 | 20.4 | 19.1 |
| Std | 4.49 | 4.31 | 4.49 | 4.40 |
| Average backfat thickness, mm* | 18.5 | 18.5 | 20.0 | 18.6 |
| Std | 2.9 | 3.1 | 6.5 | 3.1 |
| Loin eye area, $cm^2$ | 45.6 | 46.7 | 49.9 | 46.8 |
| Std | 4.44 | 5.21 | 5.55 | 5.22 |
| Flesh index ** | 0.38 | 0.30 | 0.28 | 0.30 |
| Std | 0.12 | 0.09 | 0.06 | 0.10 |
| $pH_{24}$ value of lean meat | 5.70 | 5.71 | 5.76 | 5.71 |
| Std | 0.13 | 0.13 | 0.21 | 0.13 |
| Share of carcasses with defective lean meat (PSE; DFD), % | 0.2 | 3.0 | 7.0 | 3.1 |
| Lean meat content, fixed using Ultra FOM 100, % | 58.7 | 58.7 | 59.6 | 58.8 |
| Std | 2.6 | 2.4 | 2.2 | 2.4 |
| Distribution of carcasses by lean meat content according to SEUROP-classification, % *** | | | | |
| S | 34 | 28 | 32 | 29 |
| E | 56 | 68 | 68 | 65 |
| U | 10 | 4 | 0 | 6 |
| R, O, P | 0 | 0 | 0 | 0 |

* - mean of four measurements; ** - backfat area : loin eye area; ***- Distribution of carcasses by lean meat content according to SEUROP-classification: S (lean content 60% and more), E (55...60%), U (50...55%), R (45...50%), O (40...45%), P (less than 40%).

According to SEUROP-classification, out of 850 carcasses of the evaluated young boars 29% were distributed into S-class, 65% into E-class, and 7% into U-class.

The results of the evaluation indicate that the carcass flesh of all the boars has improved (Table 2). A majority of the offspring of the evaluated boars had a thin backfat and a large loin eye area, as expected. The largest loin eye area (70.3 $cm^2$) had the offspring of the parental pair of the Pietrain breed (Ego 5074 (boar) x 212 (sow) from the Pihlaka Farm OÜ. As regards the Estonian Landrace breed, the largest loin eye area (58.2 $cm^2$ ) had the carcasses of the descendants of the parent pair Motor 756 x 1158, and regarding the Estonian Large White breed, those of the parent pair Hudson 2958 x Rinkka 3093 (66.1 $cm^2$).

The best meat tissue quality was observed in the offspring of the Estonian Landrace breed boars Orden 916 (lean content of carcass 62.4%), Ofir 965 (61.0%), Akab 112 (59.5%), Novo 113 (59.4%); the offspring of the Estonian Large White boars Jospel 2242 (60.2%), Hudson 2958 (59.7%), Jallis 3348 (59.6%), Opel 3374 (59.2%); and those of the Pietrain boars Cro 218 (63.5%), Umag 1512 (60.3%), Valor 598 (59.5%) and Julius 2343 (59.4%).

Based on the published experimental information (Glodek, 1985; Rei, Kirikall *et al*., 1994) and the earlier results obtained by the author of the present article (Põldvere *et al*., 1990, 1997), the improvement in pig carcasses (increase in loin eye area and share of lean meat) may result in lower meat quality, as a negative correlation was observed between the above data.

To test the meat quality of young boars, the pH value of the *musculus longissimus dorsi* of all the carcasses was determined. The meat tissue of most of the boars appeared to be of normal quality (pH value from 5.6 to 6.3). In smaller number of the carcasses of the Estonian Landrace and the Estonian Large White boars (0.2 and 3%, respectively) a pale, soft and exudative PSE meat (pH < 5.6) was found. In the carcasses of the more stress-susceptible boars of the Pietrain breed a higher incidence (7%) of PSE meat was observed. The DFD meat was not detected in the evaluated carcasses.

**Summary**

As a result of using the semen of the Estonian Landrace and the Estonian Large White breed boars for insemination of sows, the offspring with thin fat, large loin eye area and high lean percentage of a carcass can be obtained.

The Pietrain breed has particular fat build-up areas, since more fat can be found on the back, less on sides. The carcasses of the offspring of the Pietrain breed boars predominate among others for their good flesh quality parameters (large loin eye area, high lean percentage, low flesh index, large hams). The semen of the Pietrain boars should be used in crossbreeding of white breeds to get the crossbred piglets with high lean meat content.

On the whole, the meat of young boars was of normal quality (low PSE meat percentage).



Table 2 Carcass quality traits of the offspring of young boars

| Boar's name, No. | n | CL cm | BFT mm | $pH_{24}$ | FOM % | Distribution of carcasses | | | LEA $cm^2$ | FI |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | S | E | U | | |
| Estonian Landrace breed | | | | | | | | | | |
| Fram 4398 | 32 | 100.0 | 14.6 | 5.83 | 58.8 | 28 | 66 | 6 | 43.7 | 0.40 |
| Motor 756 | 26 | 101.0 | 20.6 | 5.68 | 58.0 | 42 | 35 | 23 | 46.0 | 0.35 |
| Asse 7398 | 23 | 102.2 | 16.1 | - | 58.6 | 26 | 70 | 4 | 45.1 | 0.47 |
| Novo 113 | 14 | 104.7 | 18.4 | 5.69 | 59.4 | 29 | 71 | - | 45.9 | 0.30 |
| Ofir 965 | 14 | 101.9 | 19.4 | 5.73 | 61.0 | 71 | 29 | - | 48.2 | 0.35 |
| Notar 880 | 10 | 98.1 | 21.0 | 5.72 | 57.3 | 20 | 60 | 20 | 43.1 | 0.36 |
| Palaani 1147 | 10 | 103.3 | 18.8 | 5.77 | 57.8 | 30 | 50 | 20 | 46.6 | 0.41 |
| Akab 112 | 9 | 105.3 | 19.7 | 5.75 | 59.5 | 22 | 78 | - | 47.6 | 0.33 |
| Orden 916 | 8 | 101.0 | 16.8 | 5.74 | 60.2 | 50 | 50 | - | 46.8 | 0.36 |
| Estonian Large White breed | | | | | | | | | | |
| Jommi 2864 | 83 | 97.8 | 19.0 | 5.78 | 58.6 | 25 | 70 | 5 | 45.5 | 0.31 |
| Rino 392 | 71 | 99.6 | 20.0 | 5.7 | 58.5 | 25 | 74,9 | 0,1 | 48.2 | 0.30 |
| Hudson 2958 | 67 | 98.0 | 20.9 | 5.87 | 59.7 | 43,0 | 55,5 | 1,5 | 50.1 | 0.29 |
| Curry 2651 | 66 | 98.1 | 17.6 | 5.70 | 58.5 | 27,0 | 65,5 | 7,5 | 45.8 | 0.29 |
| Jallis 3348 | 36 | 100.8 | 18.3 | 5.73 | 59.6 | 42 | 58 | - | 47.4 | 0.26 |
| Riksu 3300 | 35 | 100.6 | 19.9 | 5.71 | 59.1 | 34 | 60 | 6 | 47.0 | 0.33 |
| Jommi 757 | 28 | 99.4 | 17.1 | 5.67 | 57.8 | 14 | 75 | 11 | 46.2 | 0.27 |
| Opel 3374 | 20 | 102.6 | 17.6 | 5.7 | 59.2 | 30 | 70 | - | 45.9 | 0.30 |
| Jospel 2242 | 11 | 100.5 | 22.3 | 5.83 | 60.2 | 55 | 45 | - | 48.1 | 0.29 |
| Hudson 2862 | 12 | 96.9 | 20.4 | - | 58.7 | 33 | 50 | 17 | 45.0 | 0.34 |
| Pontos 7134 | 9 | 98.2 | 17.4 | - | 57.4 | 11 | 89 | - | 46.1 | 0.27 |
| Solid 3277 | 8 | 99.6 | 24.9 | 5.67 | 56.2 | - | 87 | 13 | 45.4 | 0.37 |
| Pietrain | | | | | | | | | | |
| Valor 598 | 23 | 92.4 | 21.0 | 5.76 | 59.5 | 22 | 78 | - | 50.5 | 0.28 |
| Julius 2343 | 16 | 92.7 | 19.2 | 5.73 | 59.4 | 25 | 75 | - | 50.2 | 0.26 |
| Caesar 2345 | 13 | 91.8 | 20.9 | 5.74 | 59.2 | 46 | 54 | - | 47.9 | 0.28 |
| Umag 1512 | 5 | 91.4 | 24.2 | 5.97 | 60.3 | 60 | 40 | - | 48.8 | 0.32 |
| Charly 2259 | 4 | 93.0 | 23.8 | 5.74 | 59.2 | 50 | 50 | - | 51.9 | 0.34 |
| Valor 400 | 4 | 94.0 | 22.3 | 5.65 | 58.6 | - | 100 | - | 48.0 | 0.30 |
| Cro 218 | 4 | 89.5 | 15.8 | 5.90 | 63.5 | 100 | - | - | 51.3 | 0,21 |
| Ego 374 | 3 | 90.7 | 18.3 | 5.6 | 58.4 | - | 100 | - | 48.9 | 0.22 |

Selection of young boars by means of both carcass evaluation (length and thickness, Scan Star system) and the quality traits of meat (pH-value) enable the breeders to improve the carcass and pork quality of offspring.

The meat performance data of young boars provide the pig breeders with additional information necessary for decision-making.

In 2003…2008, the objective of the crossbreeding programme "Marble Pork" is to suggest ways to improve the flesh and meat quality of the Estonian breeds of swine. Based on this, the lean share in the carcasses of the breeding pigs of the white breeds should increase 63% in boars and 62% in sows, whereas the loin eye area should increase up to 48 $cm^2$.

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## REPRODUCTIVE PERFORMANCE OF LITHUANIAN INDIGENOUS SOWS IN SMALL CLOSED POPULATION

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**Introduction**

Conservation of genetic diversity is of fundamental concern to conservation biology, as genetic diversity is required for evolutionary change [5]. Biological and genetic diversity in agriculture is essential for the sustainable development of agricultural production and of rural areas. A decreasing number of international breeds responsible for a growing percentage of the food production has resulted in a growing number of rare breeds or a decline in the number of breeds overall. Therefore, conservation efforts are strongly needed. In general, *in-situ* conservation is preferred as a mechanism to conserve genetic resources. In order to be successfully conserved a breed has to evolve and adapt within its changing environment and the best way to conserve a breed is to create a current need for its product or function and to develop the breeds in the desired direction [1, 2].

The most likely use of Lithuanian indigenous wattle pigs should be slaughtering at lower weight, terminal crossbreeding or organic production. The selection of these unique pigs as dam breed should be aimed at preservation of genetic variation, of solid constitution and high prolificacy, because sow productivity is a major objective for genetic improvement of pigs [3]. For a small and closed population, such as that of Lithuanian indigenous pigs, the negative effects on prolificacy may increase due to inbreeding. Therefore, the objective of this study was to examine the reproductive performance of Lithuanian indigenous sows.

**Materials and Methods**

Data were obtained from farrowing records and performance test of the conserved herd of Lithuanian indigenous pigs between April 1994 and December 2003. The material comprised 3342 piglets weighed at birth, 3 weeks and 2 months. The weight was recorded to the nearest 10 g (at birth) and 100 g (at 3 weeks and 2 months). Piglets came from 316 litters (142 dams and 38 sires) (Table 1).

Records from crossbred parities were excluded. Sows were culled for the following reasons: failure to conceive, poor litter performance, health or injury problems, absence of right sire, change of generation.

The population of Lithuanian indigenous pigs was restored from 19 founders, of which 5 were non-related males and 14 females from 5 non-related groups.

It was impossible to establish all non-related groups at the same time due to the lack of males. Each generation was maintained using single pair mating. Due

to the lack of the sires in founder generation, next generations became interlaced.

Table 1. Summary of data by generation and parity showing the numbers of litters

| Generation | Parity | | | | | |
|---|---|---|---|---|---|---|
| | 1 | 2 | 3 | 4 | 5 | 6 |
| Founder | 55 | 28 | 5 | - | - | - |
| II-III | 64 | 48 | 29 | 14 | 4 | 1 |
| III-V | 11 | 9 | 8 | 4 | - | - |
| VI-VII | 9 | 12 | 9 | 6 | - | - |

The data were computed by *Snedecor* and *Cochran* [7].

**Results and Discussion**

It was noted that the prolificacy of Lithuanian indigenous sows in the 6-7$^{th}$ generations after 10 years of closed breeding has decreased (P<0.050) in comparison with the founder and first generations (Table 2). The same pattern was observed in total numbers born, which is likely to be a reflection of higher rate of stillbirth or mummified piglets. Until the 5$^{th}$ generation, the sows were more prolific in all parities (Table 3).

Table 2. Reproductive and performance data of sows by generation

| Generation | Parity | | | |
|---|---|---|---|---|
| | Founder I | II-III | III-V | VI-VII |
| Total born / litter | 10.78±0.26 | 10.91±0.17 | 10.48±0.48 | 9.69±0.45$^{x}$ |
| Born alive / litter | 10.10±0.22 | 10.21±0.17 | 9.68±0.44 | 8.81±0.39$^{x}$ |
| Stillborn, % | 5.98 | 6.54 | 7.69 | 9.17 |
| Weight of piglets, kg: | | | | |
| at birth | 1.25±0.01 | 1.35±0.01$^{5x}$ | 1.34±0.03$^{3x}$ | 1.31±0.01$^{5x}$ |
| at 3 weeks | 4.7±0.02 | 4.87±0.03$^{5x}$ | 4.6±0.06 | 4.74±0.07 |
| at 2 months | 13.2±0.11 | 13.71±0.09$^{5x}$ | 15.47±0.25$^{3x}$ | 16.35±0.21$^{5x}$ |
| Survivality until 3 weeks, % | 82.1 | 84.2 | 78.7 | 76.7 |

Data are means ± SE: $^{x}$P < 0.050; $^{3x}$P < 0.010; $^{5x}$P < 0.001.

Prolificacy was increased with increasing parity number in accordance with studies of other authors [3, 4, 8]. Högber *et al.* [4] and others have found that large litters have lighter piglets than small litters at birth. Low weight at birth means a higher risk of dying before weaning. In the present study mean weight of piglets at birth in the founder and first generation was lower than in subsequent generations (P<0.025 – P<0.001), but the survival of piglets decreased from generation to generation. Survivality of piglets in 6-7$^{th}$ generation was by 5.4%



lower than that in the founder generation. Mean weight of piglets at 3 weeks was similar to that in other generations, but mean weight of piglets at 2 months increased (P<0.001).

Table 3. Number of piglets total born and born alive by generation and parity

| Gene-ration | Parity | | | | |
|---|---|---|---|---|---|
| | 1 | 2 | 3 | 4 | 5 |
| Total born | | | | | |
| Founder I | 9.98±0.33$^{5x}$ | 10.68±0.35$^{5x}$ | 15.0±0.90 | - | - |
| II-III | 9.53±0.23$^{5x}$ | 11.4±0.28 | 11.99±0.42$^{3x}$ | 13.08±0.57$^{5x}$ | 13.25±1.74$^{4x}$ |
| III-V | 9.50±0.94 | 11.0±0.86 | 10.50±1.07$^{3x}$ | 12.5±1.08 | - |
| VI-VII | 9.67±0.92 | 9.00±0.70$^{x}$ | 10.67±0.82$^{x}$ | 9.67±1.85 | - |
| Born alive | | | | | |
| Founder I | 9.38±0.25$^{5x}$ | 10.11±0.35$^{5x}$ | 14.0±0.79 | - | - |
| II-III | 9.09±0.24$^{5x}$ | 10.85±0.29 | 10.77±0.38$^{5x}$ | 11.54±0.72$^{3x}$ | 12.0±1.37$^{4x}$ |
| III-V | 9.0±0.86 | 10.10±0.80 | 9.38±0.95$^{3x}$ | 11.50±0.97 | - |
| VI-VII | 8.67±0.88 | 8.25±0.54$^{x}$ | 9.89±0.73$^{x}$ | 8.50±1.58 | - |

Data are means ± SE: $^{x}$P<0.050; $^{2x}$P<0,025; $^{3x}$P<0.010; $^{4x}$P<0,005; $^{5x}$P<0.001.

Application of a circular mating scheme prepared by Šveistys [9] with four disconnected pedigree pig groups allows to minimize inbreeding with the coefficient (by Wright) of only 6.2% after four generations. The population of Lithuanian indigenous pigs has five pedigree groups, but generations overlap each other and this increases the risk of inbreeding. Montgomery *et al.* and others [5] have noted that captive breeding programs for endangered species are generally designed to maintain 90% of initial heterozygosity for 100 years with the required population size. Reed *et al.* [6] have evaluated the effect of the rate of inbreeding in populations of *Drosophia milanogaster* at effective population sizes (Ne) of 10 and 20 and have found that populations of Ne = 20 that remained extant after 60 generations, showed inbreeding depression, with the mean fitness of these populations being only 45% of the outbreed controls. These results can be extrapolated to other species.

Lower prolificacy in the last generation of Lithuanian indigenous pigs of Ne = 30 is probably not yet the sign of inbreeding depression, but pigs are sensitive to inbreeding and it is necessary to avoid further increasing the rate of inbreeding.

**Conclusions**

In order to minimize the increasing level of inbreeding, it is necessary to maintain the threatened breed with larger population size or develop new lines. It is critical to maintain indigenous pigs with large size. The most right way would be to develop a line with required founders-migrants.

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# COMPARATIVE STUDY OF REPRODUCTIVE PERFORMANCE CHARACTERISTICS OF DIFFERENT GENOTYPE SOWS

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## Introduction

Most European pig improvement programmes have concentrated on growth and carcass traits. The reasons were high heritability and economic value of such characteristics. As fat levels approach an economic optimum, improvement of feed efficiency must therefore slow down, giving greater importance to reproductive efficiency [13]. Today there is renewed interest in the genetic improvement of functional traits, which in animal breeding are defined as traits which reduce the costs on the input side and also may play a role for the marketability of the animal product. The main functional traits are health, fertility, feet and leg traits and longevity as a "natural index" combining those traits. Up to now, in most breeding programmes the main problem in the improvement of functional traits is their poor recording [11]. As far back as 1980, with the aim to improve the quality of carcasses of Lithuanian White pigs, the breed was divided into 5 populations and 2 of these populations have been improved with immigration of German Landrace (meat-type) and Swedish Yorkshire (bacon-type). Recently there was only one herd of Lithuanian White meat-type pigs, but nowadays Lithuanian White meat-type pigs are on the verge of extinction, because the genetic gain of Lithuanian White pigs was accelerated only by absorptive immigration of lean breeds [7]. The selection of Lithuanian White pigs as a dam breed should be aimed at increasing not only lean meat content but also at preservation of solid constitution, high prolificacy and good mothering qualities [10]. Webb [13] has reported that use of different objectives in sire and dam lines can speed up genetic improvement by up to 20 percent. Immigration of lean breeds can accelerate improvement of growth and carcass traits of Lithuanian White pigs and affect prolificacy and other reproductive traits. Therefore, the objective of this study was to examine the reproductive performance of endangered Lithuanian White meat-type and new (Lithuanian White x Landrace) genotype sows.

## Materials and Methods

Data used in the comparisons were obtained from the performance test and farrowing records from the pig breeding farm "Rugiagėlė" stored in the database of state pig breeding station between January 2002 and February 2004.The herd of "Rugiagėlė" is located in the west part of Lithuania about 20 km from the Baltic sea in former breeding area of Lithuanian White meat-type pigs. Only this herd has the remaining examples of Lithuanian White meat-type pigs.

The material comprised 1089 piglets weighed at 3 and 8 weeks. These piglets came from 99 litters (95 sows and 24 boars). Two dam groups included in the study were Lithuanian White meat-type (LWM1) (47sows) and Lithuanian White x Landrace (48sows). Gilts and sows were mated using single pair mating to the Lithuanian White, Lithuanian White meat-type, Landrace, Yorkshire and Pietrain boars. Reproductive measurements of numbers born alive and total numbers born were taken on each sow. Litter weight at 3 and 8 weeks, and survival rate to weaning were analysed. In addition measurements of backfat depth, eye-muscle depth and lean meat content of sows were taken by ultrasonic equipment Piglog 105 at the age of 6-8 months when the sows were of 85-105 kg live weight. Statistical calculations were based on the methods of Snedecor and Cochran [8].

**Results and Discussion**

Immigration of new pigs into the Lithuanian White meat-type population showed that Lithuanian White meat-type sows in all parities were more prolific than crossbred Lithuanian White x Landrace sows (Table 1). Lithuanian White meat-type sows in the first parity had by 0.4 piglet higher mean of total born piglets and by 0.3 piglet higher mean of born alive than crossbred Lithuanian White x Landrace sows.

In both groups prolificacy was increased in second and later parities in accordance with studies of other authors [2, 4, 12]. The advantage of Lithuanian White meat-type in mean of total born and born alive piglets respectively decreased to the means of 0.3 and 0.1 piglet per litter in second and later parities. But all these differences were not significant. Damgard *et al.* and others [2, 6] have noted that selection for sows capacity to give birth to homogenous litters may be advantagenous for piglet survival, piglets´ growth, and litter homogeneity at weaning. There are no field records on piglets´ weight at birth in Lithuanian Pig Registry of pig testing system. And it was not possible to evaluate the effect of weight at birth. Lithuanian White meat-type and Lithuanian White x Landrace sows in second and later parities had more stillborn piglets than in first parity. Survival rate of piglets from Lithuanian White meat-type sows in first parity until 3 weeks was higher (P<0.025) than that of piglets from crossbred sows. Alfonso *et al.* [1] have estimated insignificant different correlations and low heritability between parities. In our study the estimates of correlations between first and second and later parities ranged from 0.000 to 0.230 for Lithuanian White meat-type and from 0.007 to 0.233 for Lithuanian White x Landrace sows. The maternal capacity of sows has a great influence on piglet growth and litter size at weaning. Until weaning, the effect of mother genes on piglet weights is greater than that of piglet´s own genes [9]. The litter weight at 3 weeks could be used to estimate the breeding value of the maternal qualities of sows. Litter weight as a combination of piglet number and weight were larger for Lithuanian White meat-type sows than for crossbred sows, but significant difference (P<0.005) was estimated only for litter weight between the



groups in the first parity. Average weight of piglets at 8 weeks in first and second and later parities of both groups were similar, but due to the larger number of piglets from Lithuanian White meat-type sows, their litter weight at 8 weeks was higher (P<0.001) than that of Lithuanian White x Landrace sows.

Table 1. Reproductive traits of Lithuanian White meat-type and Lithuanian White x Landrace sows

| Traits | Lithuanian White meat-type | | | Lithuanian White x Landrace | | |
|---|---|---|---|---|---|---|
| | Total | First parity | Second and later parities | Total | First parity | Second and later parities |
| Number of litters | 50 | 26 | 24 | 49 | 28 | 21 |
| Total born/litter | 10.9± 0.16 | 10.8± 0.21 | 11.0± 0.24 | 10.5± 0.20 | 10.4± 0.28 | 10.7± 0.25 |
| Born alive/litter | 10.2± 0.44 | 10.2± 0.33 | 10.2± 0.55 | 10.0± 0.49 | 9.9± 0.60 | 10.1± 0.38 |
| Stillborn, % | 7.1± 3.34 | 6.5± 1.89 | 7.8± 4.50 | 5.3± 2.61 | 5.0± 2.74 | 5.6± 2.69 |
| Number of piglets at 3 weeks | 9.7± 0.43 | 9.7± 0.44[2x] | 9.6± 0.50 | 9.3± 0.76 | 9.0± 0.66 | 9.6± 0.48 |
| Weight of piglets at 3 weeks, kg | 5.24± 0.25 | 5.21± 0.36 | 5.27± 0.58 | 5.19± 0.42 | 5.3± 0.35 | 5.07± 0.63 |
| Weight of litter, kg | 50.5± 1.80 | 50.5± 1.83[4x] | 50.8± 1.79 | 48.1± 2.88 | 47.5± 2.84 | 48.7± 3.03 |
| Number at weaning | 9.1± 0.21 | 9.2± 0.20 | 9.0± 0.22 | 8.5± 0.25 | 8.1± 0.29 | 9.1± 0.20 |
| Weight of piglet at weaning, kg | 11.89± 0.83 | 11.74± 1.26 | 12.07± 1.43 | 11.95± 0.91 | 11.84± 1.03 | 12.06± 0.97 |
| Litter weight at weaning, kg | 107.8± 2.48 | 107.4± 3.8[5x] | 108.2± 3.12 | 102.1± 2.67 | 95.6± 3.42 | 109.7± 3.31 |
| Survival rate, % | 89.2± 1.25 | 90.5± 1.21 | 87.7± 1.28 | 85.6± 2.13 | 81.7± 2.26 | 90.1± 2.04 |

Data are means±SE: [2x]P<0.025; [4x]P<0.005; [5x]P<0.001.

The best reproductive performance in comparison with Lithuanian White meat-type sows was shown by three way breed (Lithuanian White x Landrace x Pietrain) crossing.

Table 2. Reproductive traits of Lithuanian White meat-type and Lithuanian White x Landrace sows mated with boars of different breeds

| Group | No of litters | No born/ litter | No born alive/ litter | Still-born. % | No of piglets at 3 weeks | Litter weight at 3 weeks. kg | No weaned/ litter | Litter weight at weaning. kg | Survival rate. % |
|---|---|---|---|---|---|---|---|---|---|
| First parity | | | | | | | | | |
| LWM1 | 8 | 10.8 ±0.34 | 10.1 ±0.42 | 6.2 ±2.08 | 9.6 ±0.34 | 50.9 ±2.46 | 8.9 ±0.57 | 102.5 ±6.58 | 87.7 ±6.46 |
| LWM1xLW | 5 | 11.0 ±0.80 | 10.6 ±0.55 | 3.8 ±2.40 | 9.8 ±0.90 | 51.2 ±3.90 | 9.6 ±0.85 | 116 ±15.60 | 90.6 ±4.95 |
| LWM1xY | 5 | 11.0 ±0.35 | 9.8 ±0.55 | 12.2 ±3.40 | 8.8 ±0.65 | 47.4 ±3.75 | 8.2 ±0.90 | 102.8 ±11.35 | 83.7 ±7.55 |
| LWM1xL | 8 | 10.5 ±0.45 | 10 ±0.34 | 5 ±1.97 | 9.8 ±0.19 | 51.5 ±0.87 | 9.4 ±0.34 | 109.9 ±4.84 | 93.8 ±6.73 |
| LWxLxLWM1 | 9 | 10.4 ±0.60 | 9.9 ±0.71 | 5.6 ±2.33 | 9.0 ±0.53 | 49.2 ±3.18 | 8.1 ±0.53 | 94 ±3.85 | 82 ±6.01 |
| LWxLW | 6 | 10.0 ±0.94 | 9.8 ±0.89 | 1.7 ±1.83 | 8.7 ±0.54 | 46.2 ±2.82 | 7.8 ±0.67 | 92.2 ±6.31 | 79.2 ±8.94 |
| LWxLxY | 4 | 10.3 ±0.75 | 9.5 ±0.98 | 7.9 ±7.79 | 9.3 ±0.87 | 49.0 ±4.62 | 8.7 ±0.87 | 105 ±10.68 | 91.2 ±6.06 |
| LWxlxL | 5 | 9.6 ±0.55 | 8.8 ±0.80 | 9.1 ±6.80 | 7.2 ±0.80 | 38.6 ±2.95$^{x}$ | 7.0 ±0.80$^{3x}$ | 78.8 ±10.75 | 79.6 ±12.40 |
| LWxLxPi | 4 | 12.0 ±0.92 | 11.8 ±0.98 | 2.1 ±2.60 | 11.3 ±0.58 | 55.5 ±3.23$^{x}$ | 10.3 ±1.67 | 118.5 ±16.57 | 87.2 ±10.91 |
| Second and later parities | | | | | | | | | |
| LWM1 | 7 | 11.1 ±0.45 | 10 ±0.82 | 11.4 ±7.47 | 9.4 ±0.61 | 50 ±2.12 | 8.9 ±0.65 | 106.9 ±5.96 | 88.6 ±4.61 |
| LWM1xLW | 5 | 11.2 ±0.40 | 10.8 ±0.40 | 3.7 ±2.60 | 10 ±0.35 | 52.4 ±1.30 | 8.4 ±0.75 | 103.8 ±8.25 | 77.8 ±8.40 |
| LWM1xY | 12 | 10.8 ±0.42 | 9.6 ±0.63 | 13 ±4.37 | 9.6 ±0.48 | 50.5 ±2.02 | 9.3 ±0.51 | 111 ±4.82 | 96.8 ±3.65 |
| LWxLxY | 15 | 10.8 ±0.33 | 10.4 ±0.30 | 3.4 ±1.36 | 10 ±0.33 | 49 ±3.74 | 9.4 ±0.48 | 112.3 ±4.43 | 89.3 ±3.95 |
| LWxLxPI | 4 | 10.5 ±0.35 | 8.8 ±0.58 | 20 ±4.16 | 8.5 ±0.35 | 47.8 ±0.75 | 8.3 ±0.29 | 98.5 ±2.25 | 94.3 ±3.52 |

Data are means±SE: $^{x}$P<0.050; $^{3x}$P<0.010.



Table 3. Field performance of Lithuanian White meat-type (LWM1) and Lithuanian White x Landrace (LWxL) replacement gilts

| Traits | Number | Age, days | Weight, kg | Backfat depth at point FAT-1, mm | Backfat depth at point FAT-2, mm | Muscle depth, mm | Lean meat content, % |
|---|---|---|---|---|---|---|---|
| LWM1 | 47 | 216.3± 3.68 | 98.8± 0.48 | 16.8± 0.23 | 16.3± 0.59 | 45.2± 1.34 | 53.8± 0.25 |
| LWxL | 48 | 199.3± 2.79$^{5x}$ | 95.9± 0.54$^{3x}$ | 16.9± 0.20 | 16.1± 0.44 | 45.9± 1.03 | 54.0± 0.19 |

Data are means±SE: $^{3x}$P<0.010; $^{5x}$P<0.001.

The worst variant was absorptive crossing of Lithuanian White x Landrace x Landrace, but significant differences were estimated only for litter weight at 3 weeks (P< 0.050) between Lithuanian White meat-type and Lithuanian White x Landrace x Pietrain, Lithuanian White x Landrace x Landrace. Though the absorptive crossing of Lithuanian White with Landrace resulted in the smallest litter size, a significant difference was only for the number of weaned piglets (P<0.010). There were no significant differences between the groups of sows in the second and later parities (Table 2).

**Conclusion**

Immigration of different breeds into the population of Lithuanian White meat-type pigs did not significantly affect their field reproductive performance.

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## FACTORS AFFECTING PERFORMANCE OF GILTS

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### Introduction

The number of piglets in litter is an important trait to achieve economic success. Different breeds vary by litter size; breeders must carefully select breeds to realize heterosis. To select breeding gilts, it is important to consider all information a breeder has because the characteristic data about gilts are limited.

The aim of the research was to analyse different factors affecting the litter size of gilts.

### Material and Methods

2389 gilts were raised in 41 farms over Estonia at 1998 to 2003. The gilts average litter size at birth was 10.45 piglets and length of pregnancy 115.78 days. The gilts were inseminated at 180 to 290 days of age. Paterson (1989) recommended management strategy, by witch gilts are mated at about 200 days of age with a body weight of >100 kg.

Table 1. Characterization of the analyzed dataset (n = 2389)

| Traits | Mean | Std. Dev. | Min. | Max. |
|---|---|---|---|---|
| Piglets born alive, no. | 10.45 | 1.83 | 5.00 | 14.00 |
| Mating age, days | 233.62 | 23.79 | 180.00 | 290.00 |
| Gestation length, days | 115.78 | 1.69 | 110.00 | 122.00 |
| Live weight at test, kg | 100.55 | 8.95 | 85.00 | 125.00 |
| Gilt X1, mm | 13.36 | 2.48 | 7.00 | 20.00 |
| Gilt X2, mm | 52.92 | 5.25 | 39.00 | 69.00 |
| Gilt X3, mm | 13.45 | 2.28 | 7.00 | 21.00 |
| Gilt Y, % | 60.66 | 2.09 | 54.08 | 68.24 |

Dataset was obtained from of Animal Recording Centre and included breed, sex, birth and testing date, weight, backfat thickness, area of loin eye and lean meat percentage, insemination and fertility data on gilts and their parents which was collected by PC program DB-Planer.

Gestation length was divided into three classes - 110…114, 115…117 and 118…122 days.

Meat traits were measured by ultrasonic equipment Piglog 105. Meat traits recorded were: backfat thickness at last (X1) and 11...12th (X3) rib, 7 cm from midline (mm), and diameter of loin eye (X2), 7 cm from midline (mm). Lean meat percentage (Y) was calculated using the formula (Piglog 105, 1991).

Calculating the effect of breed combination and gestation length on litter size of gilts, the following general linear model (GLM) was used (SAS, 1991):

$$Y_{ijkem}=\mu+T_i+M_j+K_k+S_e+A_m+P_n+e_{ijkem},$$

Y= dependent variable;
$\mu$ = general mean;
$T_i$ = breed combination (n=1...5);
$M_j$ = insemination year (n=1...6);
$K_k$ = insemination season (n=1...4);
$S_e$ = gestation length classes (n=1...3);
$e_{ijkem}$ = random residual effect

Calculating the effect of insemination traits and gilt breed on gestation length, the following GLM model was used:

$$Y_{ijkem}=\mu+T_i+M_j+K_k+S_e+A_m+P_n+e_{ijkem},$$

Y= dependent variable;
$\mu$ = general mean;
$T_i$ = gilt breed (n=1...3);
$M_j$ = insemination year (n=1...6);
$K_k$ = insemination season (n=1...4);
$S_e$ = insemination method (n=1...2);
$e_{ijkem}$ = random residual effect

Calculating the effect of breed and technician on meat traits of live gilts, the following GLM model was used:

$$Y_{ijklemn}=\mu+T_i+M_j+K_k+S_e+A_m+P_n+e_{ijklemn},$$

Y= dependent variable;
$\mu$ = general mean;
$T_i$ = gilt breed (n=1...3);
$M_j$ = technician (n=1...7);
$K_k$ = test year (n=1...6);
$S_e$ = test season (n=1...4);
$F_l$ = farm (1...41);
$W_m$ = weight at test;
$e_{ijklemn}$ = random residual effect



The results are given as least-square means (Parring *et al.*, 1997). Level of significances expressed conventionally: *** - P<0.001, ** - P<0.01, * - P<0.05, # - P<0.1. a, b, c … – least square, within each effect with one letter in common do not differ significantly.

**Results and Discussion**

Usually farmers feed gilts intensively to prepare them for lactation period. According to the results, this could slightly decrease the litter size on the first parity as backfat thickness and number of live piglets in litter are negatively correlated (Table 2). Rozeboom's (1996) results agreed with these results, where body composition at first mating did not affect litter size of primiparous sows. As expected, meat traits were significantly correlated. Gilts with thin backfat had somewhat larger loin eye. Cleveland (1988) concluded, that selection for lean growth should have little effect on litter size, but may have beneficial effect on carcass traits.

Table 2. Phenotypic correlations between meat and fertility traits

| Traits | Gilt Y | Gilt X3 | Gilt X2 | Gilt X1 |
|---|---|---|---|---|
| Piglets born alive | 0.041* | -0.036# | -0.005 | -0.064** |
| Gilt X1 | -0.827*** | 0.725*** | -0.165*** | |
| Gilt X2 | 0.511** | -0.172*** | | |
| Gilt X3 | -0.904*** | | | |

Due to heterosis effect, achieved through crossbreeding, significantly larger litters were found on EL and ELW gilts crossed with white boars (Tabe 3). Number of piglets in purebred litters of EL and ELW gilts was about same – 10.43 and 10.36 respectively. Significantly smaller litters were found in purebred P gilts.

Gestation length does not affect litter size significantly, although somewhat larger litters were found on gestation length 115...117 days.

Gestation length was highly influenced by insemination method, being longer in artificial insemination (Table 4). Significant breed effect was calculated on gestation length as well. Pietran gilts had shorter gestation period (115.03 days) than white breeds, whose gestation was shorter in Estonian Landrace breed (115.66 days). Gilts, inseminated in fall, had much longer gestation, than those inseminated in other seasons and shortest gestation was found in spring and summer.

Table 3. Effect of breed combination and gestation length on litter size of gilts

| Traits | n | piglets born alive, no. |
|---|---|---|
| Piglets breed | | |
| EL | 656 | 10.43a |
| ELW | 1150 | 10.36a |
| P | 39 | 8.99c |
| EL♀ x ELW♂ | 404 | 10.69b |
| ELW♀ x EL♂ | 140 | 10.76b |
| Gestation length, days | | |
| 110…114 | 511 | 10.19a |
| 115…117 | 1538 | 10.32a |
| 118…122 | 340 | 10.22a |

Table 4. Effect of insemination traits and gilt breed on gestation length

| Traits | n | Gestation length, days |
|---|---|---|
| Insemination method | | |
| Artificial | 560 | 115.94a |
| Natural | 1829 | 115.22b |
| Gilt breed | | |
| EL | 797 | 115.66a |
| ELW | 1553 | 116.04b |
| P | 39 | 115.03c |
| Insemination season | | |
| Winter | 699 | 115.62a |
| Spring | 671 | 115.34b |
| Summer | 487 | 115.47ab |
| Fall | 532 | 115.89c |
| Insemination year | | |
| 1998 | 67 | 114.82a |
| 1999 | 474 | 115.41b |
| 2000 | 559 | 115.65c |
| 2001 | 618 | 115.69cd |
| 2002 | 548 | 115.87de |
| 2003 | 123 | 116.03e |

Gestation length increased from 114.82 days in 1998 to 116.03 days in 2003. One reason for this could be wider use of artificial insemination of pigs.

Pietran and Estonian Landrace gilts, whose lean meat percentage was over 6% had superior meat quality (Table 5).



Table 5. Breed effect on meat traits of gilts

| Traits | Gilt breed | | |
|---|---|---|---|
| | EL | ELW | Pi |
| n | 797 | 1553 | 39 |
| X1, mm | 13.36a | 13.83b | 13.85a |
| X2, mm | 50.70a | 50.16a | 56.81b |
| X3, mm | 13.16a | 14.02b | 13.51ab |
| Y, % | 60.51a | 59.83b | 61.04a |

Landrace pigs had thinner fat, but showed modest results in diameter of loin eye, compared with Pietrain gilts who were a little fatter, but with large loin eye. The worst results were shown by Estonian Large white breed. Superiority of Landrace breed was found also by Tummaruk *et al.* (2000).

Lean meat percentage, measured by different technicians, differed about 4% (Table 6).

Table 6. Technician effect on meat traits of gilts

| Traits | Technician | | | | | | |
|---|---|---|---|---|---|---|---|
| | A | B | C | D | E | F | G |
| n | 776 | 488 | 373 | 582 | 143 | 18 | 9 |
| X1, mm | 13.66abc | 12.02ac | 15.49bd | 13.34ab | 14.10cd | 11.88ac | 15.25abc |
| X2, mm | 55.03a | 53.57ac | 50.99ad | 55.29a | 53.88bcd | 48.32bd | 50.82bcd |
| X3, mm | 13.74abc | 11.40ac | 16.05b | 13.63abc | 13.85ab | 11.19c | 15.10b |
| Y,% | 60.71a | 62.26a | 58.36b | 60.90a | 60.37ab | 61.67ac | 58.93bc |

Technician F measured the thinnest backfat and the smallest diameter of loin eye. Fatter were the gilts with technician C and loin eye was larger with technicians A and D.

**Conclusions**

Meat traits (backfat thickness and diameter of loin eye) do not affect litter size of gilts and they are not closely related to each other.

Large difference between white and colour breeds on litter size, whereas crossing white breeds give larger litters in the first parity.

Insemination method and gilt breed affect gestation length highly. Gestation length increases year by year.

Differences between colour meat type breeds and white breeds will decrease.

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# USE OF BREEDING METHODS FOR IMPROVING PRODUCTION OF PIG FARM

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Estonian agriculture is facing major economic difficulties. Many enterprises have been closed down, swine production farms among them. Hereinafter is described a farm, where grain growing used to be the main branch of production. It sold grain or meal to the farmers nearby.

Several new businesses, among them a full-cycle pig farm, were established in the territory of a former collective farm. Rises and falls in a price policy, however, resulted in bankruptcy of the above-mentioned pig farm that comprised only 400 pigs of the former 3,000 heads. The farm was acquired by a grain producing farm which started with pork production. It has 800 ha of arable land.

**Introduction**

Already in 1980s the possibilities of increasing the sows' fertility and survival were studied. Timmi (1985) reported that the fertility and milkability of crossbred sows, and the growth and longevity of their piglets are better, compared with purebred ones. The crossbred sows are stronger and of higher fertility and lower culling rate than the purebred sows. The best reproductive qualities have shown the Estonian Large White/Estonian Landrace crossbred sows (Y/L), whereas in backcrossing, the use of L boars has been more effective. The crossings have resulted in obtaining piglets of heavier live weight and more uniform properties.

Another study (Tänavots, 1997) has also proven, that the number of piglets in a litter can be increased by crossing as well as changing the environmental factors of litters and piglets. To raise the profitability of production, the crossbred sows that give larger litters, shall be used for producing slaughter pigs. Feeding conditions must be improved to realize the heterosis effect on daily gain, litter size and pig weight in the result of crossing. Analyzing the fertility of sows, the effect of a farm and a year must definitely be considered.

High fertility properties were observed in Estonian Large White breed (10.66 piglets), whose fertility increased even further by crossing with Estonian Landrace boars (Tänavots *et al.*, 2001). However, the heterosis effect by crossbreeding was smaller than that found in previous study by the same author (Tänavots, 1997). The lowest fertility was detected in white breeds and in their combination Y boar x L sow.

Steinheuer *et al.* (2002) reported that the breed of swine had an impact on a litter size in Germany as well. The share of the piglets born alive was bigger in German Landrace and German Large White crossbred sows. The number of

piglets born alive in a litter, in the result of double insemination by two different boars, was above average (10.03).

Based on the meat performance data of alive pigs, the best local breed among others appeared to be the Estonian Landrace, the lean meat share of which was by 1.25% higher than that of the Estonian Large White breed (Tänavots *et al.*, 2001). Positive results were also obtained from the crosses of white breeds, where the combination Estonian Large White boar x Estonian Landrace sow, however, had smaller diameter of loin eye area, while the backfat was thinner compared with the Estonian Landrace boar x Estonian Large White sow crosses.

**Material and Methods**

The herd comprises 250 sows and 10 boars. The replacement sows are produced in the same herd, the boars are obtained from other farms. Feeds are produced on the same farm, while feed concentrates, sunflower- and soybean oil meal, and limestone are purchased. The main sow breed is the Estonian Large White (Y) and its crosses with the Estonian Landrace boars (L/Y). The production is focused on producing marble pork. The L/Y sows were inseminated either with Pietrain (P) or crossbred boar, since the crossbreds have better fattening and pork qualities.

A low saleprice of pork did not enable the farm to invest neither in forming the breeding herd nor buying additional breeding sows. Thus, with the aim of increasing the number of pigs, some crossbred sows with unknown parentage were brought in the breeding herd. Their offspring will only be used for fattening.

The performance testing of the breeding herd sows were started two years ago. The breeding herd was formed from the sows, whose parentage was recorded in the database of the Animal Recording Centre. However, the origin of a part of the basic herd sows is still unknown.

The Estonian Pig Breeding Association is offering to its members as well as to other pig farms an opportunity to test young pigs with an ultrasonic apparatus Piglog-105. At 100 kg live weight 3 measurements (mm) were taken: 2 backfat thickness – x1 and x3, and the diameter of the *musculus longissimus dorsi* – x2. On a basis of these measurements the lean meat content in a carcass (%) will be calculated. According to body weight (based on weighingtape) and age, an average lifetime daily gain (g) was calculated.

In 2002 and 2003, the reproduction performance of sows was quite similar, whereas the intensiveness of using breeding sows has improved (Table 1).

Although the number of sows increased only by 10, the number of litters increased by 56 on the farm. The average production of a sow has increased by 1.7 piglets a year. However, the improvement in farrowing frequency was accompanied by significant losses in the number of piglets, thus only one more weaned piglet was received per sow a year.



Table 1. Reproduction performance of sows of the production farm in 2002…2003

| Year | No. sows | No. litters | Piglets born alive | | | Weaned piglets | | |
|---|---|---|---|---|---|---|---|---|
| | | | total | per litter | per sow/year | total | per litter | per sow/year |
| 2002 | 190 | 345 | 3424 | 9.9 | 18.0 | 2828 | 8.1 | 14.8 |
| 2003 | 200 | 401 | 3946 | 9.8 | 19.7 | 3168 | 7.9 | 15.8 |

The database of sows recorded at the Animal Recording Centre in 2002 and 2003, and the results of testing the initial data of young sows selected for the basic herd, were studied.

GLM procedure of SAS program was used for determining the significance of the factors and estimating the least square means (LSM) to compare the breeds and their combinations.

The following combinations of sows were compared:

1. Pure-breed: Y
2. Crossbred: L x Y
3. Backcrosses: Y x LY; L x LY.
4. P-combinations: P x Y; PY x Y; Y x PY.

Moreover, an analysis was carried out to compare the maternal and paternal breeds of sows as well as their combinations. All the studied traits – x1; x2; x3; lean meat %; daily gain; fertility – were analyzed on a basis of the same model, whereas besides the impact of maternal and paternal breeds, the effect of test year, age and live weight were also considered:

$y_{ijkl} = \mu + \text{test year}_i + b_1 \text{ x age}_{ijkl} + b_2 \text{ x weight}_{ijkl} + \text{paternal breed}_j + \text{maternal breed}_k + e_{ijkl}$

**Results and Discussion**

Reproduction performance of the purebred sows (Y) was significantly lower, and that of the sows with unknown parentage remained on the same level. Superiority of the crossbred sows (L/Y) was demonstrated by the litter size, and by the number of alive and weaned piglets (Table 2).

Table 2. Reproduction data of sows farrowed in 2003

| Sow breed | No. litters | Piglets per litter | | | Loss of suckling pigs, % |
|---|---|---|---|---|---|
| | | born | alive | weaned | |
| Y | 130 | 11.3 | 9.6 | 7.8 | 18.9 |
| L/Y | 66 | 12.1 | 10.2 | 8.3 | 18.8 |
| P/Y | 27 | 12.3 | 10.1 | 8.0 | 20.5 |
| Unknown | 34 | 11.8 | 9.4 | 7.4 | 21.3 |

The loss of suckling pigs was similar in both groups, whereas the number of weaned piglets was by 0.5 larger in the group of crossbred sows. Surprisingly larger litters were obtained from the crossbred sows of the Pietrain and the Large White breed, however, as a rule, the so-called meat-type swine breeds have reduced productivity. During a lactation period, the losses in the number of piglets were not related to their dam's parentage. The crossbred sows (L/Y and Pi/Y) had considerably larger litter size, which is typical to the white breed crosses. It is not usual, however, that the use of Pietrain boars did not lower the fertility.

For breeding herd replacement, the young sows of the Estonian Large White breed or their crosses with Estonian Landrace boars were predominantly selected. Therefore, the data presented in Table 3 is mostly related to the sows above. In addition, the herd comprised the sows obtained in the result of backcrossing (Y/LY and L/LY), and a few sows from some other combinations.

Table 3. Comparison of parentage and test data of 2002 and 2003 (least square means)

| Sow's breed | | Backfat, mm | | Depth of loin eye,mm | Lean meat, % | Daily gain, g | Fertility, piglets |
|---|---|---|---|---|---|---|---|
| paternal | maternal | x1 | x3 | | | | |
| Y | Y | 15.1 | 16.4 | 53.6 | 58.7 | 519.6 | 9.5 |
| L | Y | 13.3 | 13.5 | 54.6 | 60.9 | 517.2 | 10.2 |
| L | LY | 14.9 | 15.5 | 52.3 | 59.0 | 518.1 | 11.0 |
| Y | LY | 14.7 | 15.8 | 52.1 | 58.9 | 518.7 | 10.9 |
| Pi | Y | 12.0 | 13.0 | 59.1 | 62.2 | 515.6 | 12.3 |
| Y | PY | 14.2 | 16.0 | 52.1 | 58.7 | 513.9 | 9.9 |
| PY | Y | 14.5 | 14.8 | 55.6 | 60.0 | 520.6 | 9.7 |
| F | | 2.91** | 7.24*** | 1.91 | 6.98*** | 0.59 | 0.76 |
| Test year | | ** | ** | n.s. | ** | * | n.s. |
| Age | | *** | ** | *** | *** | *** | n.s. |
| Body weight | | *** | *** | *** | * | *** | n.s. |

Results proved a significant effect of sow's parentage on backfat thickness and lean content (P<0.01...0.001). The thickest backfat was observed in the purebred sows of the Estonian Large White breed, while the thinnest was found in the crosses of the Pietrain breed. A completely opposite tendency was revealed in the lean content (P<0.001). The daily gain variability of young sows was low. Major differences were observed in fertility of different sow groups. However, it was not statistically significant, due to small number (n = 86) of litters.

A separate analysis of sows' parentage (Table 4) showed that a sow's maternal breed did not have a significant effect on any of the studied traits, whereas a significant effect of paternal breed on backfat thickness and lean meat content was



found (P<0.01...0.001), similarly to the breed combination of a sow's parents (Table 3).

Table 4. Comparison of test data of paternal and maternal breeds of sows

| Sow's breed | | Backfat, mm | | Depth of loin eye, mm | Lean meat, % | Daily gain, g | Fertility, piglets |
|---|---|---|---|---|---|---|---|
| paternal | maternal | x1 | x3 | | | | |
| Y | x | 15.1 | 16.5 | 52.1 | 58.4 | 517.8 | 10.1 |
| L | x | 13.4 | 13.8 | 53.1 | 60.5 | 515.4 | 10.7 |
| P | x | 12.0 | 13.3 | 57.6 | 61.8 | 513.8 | 12.8 |
| PY | x | 14.5 | 15.0 | 54.1 | 59.6 | 518.8 | 10.2 |
| F | | 5.13** | 13.03*** | 1.93 | 12.11*** | 0.83 | 1.02 |
| x | Y | 13.7 | 14.4 | 55.7 | 60.4 | 518.3 | 10.4 |
| x | LY | 14.5 | 15.4 | 53.7 | 59.4 | 518.4 | 11.6 |
| x | PY | 12.9 | 14.2 | 53.2 | 60.4 | 512.6 | 10.8 |
| F | | 0.62 | 0.54 | 1.84 | 0.36 | 0.52 | 0.70 |

The analysis of sow's maternal breed showed that the reproduction performance (11.6 piglets per litter) of the crossbred dams (L/Y) was significantly higher than that of the daughters of the sows of the Estonian Large White breed (10.4). This tendency has been described earlier by other researchers.

As for side-factors, the test results were statistically significantly affected by both age and body weight of sows, and less by a test year (Table 4). Based on the test results, the sows selected to replace the breeding herd, showed relatively good performance, as the breeding material for selection was quite limited. The higher age at testing resulted from the fact that the pigs were tested once a month. Due to this, one test procedure comprised young gilts, whose age may differ by one month.

Moreover, within the last year the daily gain has increased as a result of modernization of farm technology, which in its turn, improves the selection objectivity. Fertility of sows has also increased. In 2003, due to animal recording system, it was possible to form 85% of the breeding herd from the sows with known parentage.

The fertility data of the Estonian Large White sows of the breeding herd correspond with those published in the literature (Tänavots *et al.*, 2001). The same goes for the fertility of crossbred sows (L/Y). Superiority and higher efficiency of crossbred sows was also revealed (Timmi, 1985).

The test data related to young sows of the Estonian Large White breed were practically the same, compared with published results (Tänavots *et al.*, 2001). The loin eye diameter of sows (53.9) was a little larger, probably due to the use of

better boars. It appeared, that the crossbred sows had thicker backfat (x3). This could be caused either by the boar lines or some other factors.

**Summary**

Pig industry is focusing on both breeding and fattening pig production. In the breeding herd, both purebreeding and crossbred sows (L/Y) will be applied. Regarding purebreeding, further attention shall be paid to increasing the fertility of sows. The share of purebred sows in a herd should constitute 35% and that of crossbred ones 65%. Once an appropriate breeding sows herd will be formed, the sale of sows can be considered.

Considerable attention must be paid to selection of boar lines aimed to reduce backfat thickness, and increase muscle depth and lean meat percentage. Along with the above characteristics, the fertility of the offspring of boars (sows) must be followed. The representatives of the most appropriate lines for the herd shall be found, whereas import of the "new blood" is also very important.

As the number of sows will be increasing, artificial insemination shall also be applied. At present the ratio of mating to artificial insemination is 70:30. It would also be feasible to start with semen collection from some boars of the farm to increase the efficiency of young sows. A similar system is in use on several European pig farms.

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# GENETIC STUDY OF VARIABILITY AND SIMILARITY IN THREE DIFFERENT POULTRY SPECIES

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## Introduction

The order *Galliformes* join many of wild bird species and the entire row of domestic species and breeds, the majority of which is well known by their morphophysiological and productive qualities. Plenty of experiments are described were various molecular - genetic markers are used for evaluation of genetic variability in different poultry species and breeds. The DNA utilization as genetic marker to evaluate genetic variability of poultry breeds and lines was reported by Semionova et al. (1996). The use of biochemical markers is also significant (Cywa-Benko et al., 1994; Inafukuk et al., 1998).

The characteristic features of biochemical markers are high stability and conservativity. That is the reason why the research of these markers gave an opportunity to evaluate intra- and inter-line genetic variability and also calculate inter-line similarity values. The allelic variants of protein visualized after electrophoresis are the products of certain genes. Studies of such polymorphic proteins may provide additional information on the genetic differences among separate individuals, populations, breeds or species and on the influence of natural or artificial selection to genetic processes, which occur in populations and breeds – gene drift, gene flow and etc. (Kuznetsov, 1995).

In Lithuania, the biochemical markers were used to evaluate intra-specific genetic variability of several poultry species. The genetic differentiation, genetic similarity and genetic difference were defined for Japanese quail breeds (Tubelytė et al., 2000), chicken cross Lohman White (Sruoga et al., 2002) and turkey crosses and hybrids (Juodka et al., 2003). Nevertheless, there is no data according to the use of biochemical markers for evaluation of the intra-specific genetic differentiation of domestic species, especially in the order *Galliformes*.

The purpose of present research was to evaluate the genetic variability, genetic similarity and genetic distances among three poultry species – chicken, turkey and Japanese quail, based on genetically determinate blood serum protein allele frequencies.



## Material and Methods

Blood samples were collected from 171 chicken cross Lohman White individuals, 267 Japanese quail individuals and 65 turkey cross individuals: BIC-6, BUT-9 and their hybrids. Blood was taken by venipuncture of the wing vein. Clear supernatants were obtained by centrifugation at 3000 g for 10 min. These samples were frozen at -20°C for future storage in laboratory.

Vertical polyacrilamide gel electrophoresis was conducted after conventional methods with few modifications to increase separation. For isozyme separation was used Tris-Glycine buffer system. Blood serum proteins were visualized using staining system indicated by Brewer (1970) with few modifications.

Multiloci protein systems were numbered in accordance with their mobility from anode to cathode. Allele marking is response to their expression product migration rate in gels - A (fast) and B (slow). Indistinct polymorphic loci were not included in further analysis.

Genetic variability analysis – allele frequency, allele number per locus, mean heterozygosity (direct-count and Hardy-Weinberg expected) was investigated. A genetic similarity and genetic distance among populations was evaluated by using Nei (1972) calculations. All evaluations were performed using BIOSYS-2 software (Swofford & Selander, 1981).

## Results and Discussion

After investigation of blood samples from different poultry species by using non-specific protein system, 8 loci which were polymorphic in all investigated species were identified: *PreAl-1, PreAl-2, Al, PostAl, PreTf, PostTf, Mc ir Tf*. Allele frequencies of analysed loci are given in Table 1. A majority allele frequency has no statistically significant difference between turkey and quail. For these species was detected the smallest difference of allele frequencies in the albumin locus: in turkey allele $Al^A$ frequency was 0.5645, $Al^B$ - 0.4355. In quail population these alleles were found with frequencies 0.5356 and 0.4644, respectively. Closely related values of allele frequencies were observed in the other homological diallelic *PreAl-1, PreTf* and polyallelic *Tf* loci. The rare variant of allele $Tf^E$ was found only in chicken population with frequency 0.0117. In turkey and quail populations this allele was not detected, although the number of birds examined is sufficient (65 turkey and 267 quail individuals). In general, the allele frequencies of chicken population differ from turkey and quail in much more loci examined. Statistically significant differences were observed in three diallelic *PreAl-1, Al, PostTf* loci and one polyallelic *Tf* locus (alleles $Tf^A$, $Tf^B$, $Tf^C$, $Tf^D$) in chicken. The chicken population differs significantly from turkey population in three diallelic loci. The similar allele frequencies were found in the same loci in chicken and quail populations, although the allele $Tf^D$ was identified in chicken population with frequency 0.1404, but not identified in quail population.

Table 1. Allele frequencies of blood serum homologic loci in different poultry species

| Allele | Allele frequency | | |
|---|---|---|---|
| | Turkey (65)* | Chicken (171) | Quail (267) |
| *PreAl–1*$^A$ | 0.4071 | 0.5322 | 0.3557 |
| *PreAl–1*$^B$ | 0.5929 | 0.4678 | 0.6443 |
| *PreAl–2*$^A$ | 0.5593 | 0.5936 | 0.4679 |
| *PreAl–2*$^B$ | 0.4407 | 0.4064 | 0.5321 |
| *Al*$^A$ | 0.5645 | 0.4064 | 0.5356 |
| *Al*$^B$ | 0.4355 | 0.5936 | 0.4644 |
| *PostAl*$^A$ | 0.4531 | 0.4971 | 0.5302 |
| *PostAl*$^B$ | 0.5469 | 0.5029 | 0.4698 |
| *PreTf*$^A$ | 0.4841 | 0.4591 | 0.4511 |
| *PreTf*$^B$ | 0.5159 | 0.5409 | 0.5489 |
| *PostTf*$^A$ | 0.5797 | 0.4123 | 0.4663 |
| *PostTf*$^B$ | 0.4203 | 0.5877 | 0.5337 |
| *Mc*$^A$ | 0.4429 | 0.4620 | 0.4963 |
| *Mc*$^B$ | 0.5571 | 0.5380 | 0.5037 |
| *Tf*$^A$ | 0.3939 | 0.3304 | 0.5356 |
| *Tf*$^B$ | 0.4167 | 0.3070 | 0.4532 |
| *Tf*$^C$ | 0.1061 | 0.2105 | 0.0112 |
| *Tf*$^D$ | 0.0833 | 0.1404 | 0.0000 |
| *Tf*$^E$ | 0.0000 | 0.0117 | 0.0000 |

* Number of birds examined

The values of heterogeneity (Table 2) show the influence of natural and artificial selection, intra-population breeding or inbreeding for the separate loci and also the whole population. The highest deficit of heterozygotes was detected in three loci - *Al, PostAl, PreAl-2,* in turkey population. Also for the other loci observed heterozygosity was lower than expected heterozygosity. Such great heterozygote deficiency in separate loci is the main reason of low value of mean observed heterozygosity (0.2800) in turkey. However, the expected heterozygosity in this population was 0.5160. Significant excess of heterozygosity in many loci was found in quail population. The highest excess was detected in two diallelic loci - *PreAl-1* and *PreAl-2.* In all population examined, the observed heterozygosity was higher than expected in *Tf* locus (Table 2); this difference is statistically reliable. The mean observed heterozygosity in quail was higher than in chicken population, even both means are lower than expected. The level of heterozygosity and heterozygote deficiency values shows that those genetic and



selective criteria, as mentioned above, has strongly influenced non-specific diallelic genetic systems.

Table 2. Observed and expected heterozygosity of blood serum homologic loci in different poultry species

| Locus | Heterozygosity | | Mean heterozygosity | |
|---|---|---|---|---|
| | Observed $H_O$ | Expected $H_{ex}$ | Observed $\hat{H}o$ | Expected $\hat{H}_{ex}$ |
| Turkey | | | | |
| *PreAl–1* | 0.3000 | 0.4862 | | |
| *PreAl–2* | 0.2712 | 0.4972 | | |
| *Al* | 0.0968 | 0.4957 | | |
| *PostAl* | 0.1563 | 0.4995 | 0.2800 | 0.5160 |
| *PreTf* | 0.2698 | 0.5035 | | |
| *PostTf* | 0.2319 | 0.4908 | | |
| *Mc* | 0.1714 | 0.4970 | | |
| *Tf* | 0.7424 | 0.6580 | | |
| Chicken | | | | |
| *PreAl–1* | 0.2690 | 0.4994 | | |
| *PreAl–2* | 0.2865 | 0.4839 | | |
| *Al* | 0.3684 | 0.4839 | | |
| *PostAl* | 0.3275 | 0.5014 | 0.4108 | 0.5232 |
| *PreTf* | 0.3216 | 0.4981 | | |
| *PostTf* | 0.3333 | 0.4860 | | |
| *Mc* | 0.3977 | 0.4986 | | |
| *Tf* | 0.9825 | 0.7346 | | |
| Quail | | | | |
| *PreAl–1* | 0.1423 | 0.4593 | | |
| *PreAl–2* | 0.1283 | 0.4989 | | |
| *Al* | 0.3596 | 0.4984 | | |
| *PostAl* | 0.2679 | 0.4991 | 0.3362 | 0.4950 |
| *PreTf* | 0.2932 | 0.4962 | | |
| *PostTf* | 0.2060 | 0.4987z | | |
| *Mc* | 0.3783 | 0.5009 | | |
| *Tf* | 0.9139 | 0.5086 | | |

According to all genetic markers examined, Nei‘s coefficients of genetic similarity and distance were calculated (Table 3). The highest genetic similarity coefficient (0.9868) and the shortest genetic distance (0.0133) were observed between turkey and quail populations. However, genetic similarity between turkey

and chicken is 0.9773, between quail and chicken - 0.9673. Respective values of genetic distances are presented in the same table.

Table 3. Nei's (1972) coefficients of genetic distance (D) and genetic similarity (I) between different poultry species

| I / D | Turkey | Quail | Chicken |
|---|---|---|---|
| Turkey | *** | 0.9868 | 0.9773 |
| Quail | 0.0133 | *** | 0.9673 |
| Chicken | 0.0230 | 0.0333 | *** |

Cluster analysis of the obtained data revealed that turkey and quail populations form one cluster, while chicken population forms another one (Figure 1).

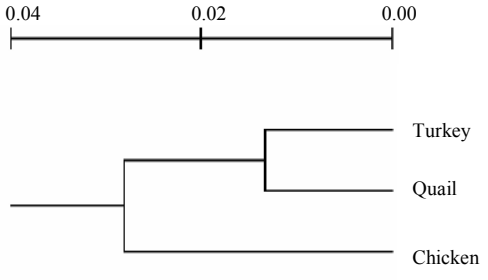


Figure 1. Unweighted pair-group clustering analysis, according to Nei's (1972) genetic distance coefficients.

Those data of cluster analysis coincide with Helm-Bychowski (Helm-Bychowski, Wilson, 1986) DNA restriction analysis data. According to the data of restriction analysis turkey and family Phasianidae (which includes Japanese quail) form the same cluster. Chickens and other birds from genus *Gallus* form another cluster.

**Conclusions**

▪ It was established, that in turkey and quail populations the allele frequencies in three diallelic loci (*PreAl-1, Al, PostTf*) and one polyallelic *Tf* locus $Tf^{E}$ allele are similar, however, in the chicken population allele frequencies differ statistically significantly from turkey and quail populations in the most loci examined.

▪ The highest deficit of heterozygotes was detected in turkey population and the mean observed heterozygosity for this population is 0.2800. However, the



mean observed heterozygosity in Japanese quail and chicken populations are 0.3362 and 0.4108, respectively.

▪ The highest genetic similarity coefficient (0.9868) was calculated between turkey and quail populations. The longest genetic distance was observed between quail and chicken populations. Cluster analysis revealed that turkey and quail populations form one cluster, while chicken population forms another one.

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# INDICATORS OF NON-SPECIFIC IMMUNITY IN BLOOD SERUM, THEIR CONNECTION WITH THE GROWTH INTENSITY OF THE RAMS

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## Introduction

Natural non-specific immunologic reactivity performs the protective function of body's first early stages. Non-specific immunity description is an important component for the assessment of the whole immunologic status. Lysocym has an important role in the characterisation of non-specific immunity. Lysocym is one of the most significant and the widest spread natural factors for the antibacterial protection of people and animals. It is secreted in the intercellular space mainly from macrophages and neutrophils, and it participates in the hydrolysis of the cell membranes polysaccharide component molecule's glicosides. Lysocin destroys the membranes of microbes at the last stage of phagocytosis and thus ensures the non-specific protection of body. It has been widely applied in medicine to improve the non-specific resistance of body (Phillips, 1965).

Lysocym or muramidase is a ferment that belongs to the group of hydrolyses that lyses cell wall of many grampositive and gramnegative bacteria and it is thermally resistant up to even 100 $^0$C in the acid and neutral environment. There are about 50 different lysocyms known, which have similar features, but they differ according to the structure of amino acids. Therefore it is appropriate to speak about lysocyms (Каулиньш , 1982).

As we know, within the appropriate reaction of the body's immunity system the interaction of antigens and antibodies occur, the result of which is the formation of the circulating immune composites (CIC) (Бахановский, Рудых, 1982).

The research carried out in Latvia concerning the dairy goats show that the amount of lysocym and CIC in milk is related to the animal feeding (Sprūžs, Šeļegovska, 2003) and breed (Sprūžs, Beča, 2003).

**The aim of the present research** – to find out the amount of the non-specific immunity indicators in the blood serum of various origin rams, find out their interrelations and relation to the rams' growth intensity.

## Material and Methods

Research has been carried out at the farm "Mežkalēji", Platone Rural Municipality, Jelgava District. Up to 12-month-old rams of various origin were used. In order to find out the indicators of non-specific immunity in the blood of slaughtered animals, we chose from each group the animals, with similar weight and age. Before slaughtering these animals we took the blood samples from their jugular veins and sent these samples to the Laboratory of Food Control at the



State Veterinary Medicine Diagnostics Centre of the Republic of Latvia and to the Animal Biochemistry and Physiology Laboratory at the University of Latvia.

Table1. Research scheme

| Research groups | Origin of the animals under the research |
|---|---|
| 1st control group | ♀ LT x ♂LT |
| 2nd research group | ♀ LT x ♂VM |
| 3rd research group | ♀ LT x ♂IF |

LT – Latvian dark-headed; VM – German black-headed; IF - Il–de–France.

Indicators found in blood serum:

- Total albumen, including albumin and globulin- method of spectrophotometry (Cornall, Bardawill, David, 1949);
- Activity of lysocym - non-pholometrical method (Грант, Яворковский, Блумберга, 1972; Дорофейчук, 1968);
- Amount of CIC - method of spectrophotometry (Барановский, Рудых,1982);
- Carotene and Vitamin A - method of photocolorimetry.
- The findings have been processed using SPSS (Backhaus, 2000).

## Results and Discussion

The estimated rams' average age in groups before slaughter was from 278 to 318 days or 9 – 10 months, but the average live weight was from 44.0 to 47.2 kg. The estimated increase of live weight from birth till slaughter differed from 120 to 226 g, but the average of groups was from 137 to 151 g. Best results were achieved in the 3rd research group, in which the rams with the blood of Il-de-France breed were included

The results of the biochemical analysis of blood, obtained from the laboratories are shown in Table 2. The total amount of the albumen in the blood serum of the rams from all groups corresponded to the physiological norms and differed from 6.73 to 7.57 g/100g. The least correlation of albumin and globulin was found in the blood of the 2nd research group rams.

The best correlation of calcium and phosphorus – 1.19 – was found in the blood of the above mentioned group rams. In other groups the correlation of calcium and phosphorus deviated from the norm, and therefore we can conclude that insufficient attention in the process of feeding was paid to the provision of mineral substances, in spite of the fact that the mineral substances are very important for the appropriate regulation of metabolism.

In the blood serum of the rams from 1st research group was found the lowest level of lysocym (0.76 mkg/ml), but the highest amount of CIC (4.25 c.u.).

Table 2. Separate biochemical indicators of blood (n=3)

| Indicators | Units | Physiological norm | Groups | | |
|---|---|---|---|---|---|
| | | | 1. | 2. | 3. |
| | | | $\bar{x} \pm s_{\bar{x}}$ | $\bar{x} \pm s_{\bar{x}}$ | $\bar{x} \pm s_{\bar{x}}$ |
| Total protein | g/100g | 5.9-7.8 | 6.83 ± 0.625 | 7.57 ± 0.650 | 6.73 ± 0.405 |
| Albumin | g/100g | 2.7-3.7 | 3.08 ± 0.635 | 3.20 ± 0.950 | 3.03 ± 0.755 |
| Globulin | g/100g | 3.2-5.0 | 3.76 ± 0.775 | 4.37 ± 1.260 | 3.71 ± 0.615 |
| Albumin vs. globulin | | 0.74-0.84 | 0.81 | 0.73 | 0.82 |
| Calcium | mmol/l | 2.3-2.9 | 2.55 ± 0.150 | 2.85 ± 0.500 | 2.30 ± 0.200 |
| Phosphorus | mmol/l | 1.3-2.4 | 2.85 ± 0.850 | 2.40 ± 0.200 | 3.60 ± 0.500 |
| Calcium vs. phosphorus | | 1.21-1.77 | 0.89 | 1.19 | 0.64 |
| Carotene | mg% | | 0.21 ± 0.055 | 0.20 ± 0.023 | 0.21 ± 0.040 |
| Vitamin A | mg% | | 13.35 ± 1.765 | 12.87 ± 1.870 | 11.00 ± 3.000 |
| Lysocym | mkg/ml | | 0.76 ± 0.197 | 0.82 ± 0.136 | 0.85 ± 0.080 |
| CIC | c.u. | | 4.25 ± 1.032 | 3.91 ± 1.501 | 3.85 ± .109 |

None of the groups had significant differences regarding the mentioned indicators, therefore we can say that the non-specific resistance indicators in the blood of the animals from all groups were similar. Similarly to the research carried out in Russia, where it was found out that the hybrid animals have higher resistance under the same keeping and feeding conditions (Абонеев, Скорых, 2002), we found out that the amount of lysocym is higher in the blood of hybrid rams. The hybrid sheep have the increased impulse of life processes that is characterised by the increased lambs' vitality and growth intensity (Монастырёва, 1992).

Using the estimated correlation coefficients of indications we found out that there are close interrelations between several biochemical indicators of blood (Table 3).

Table 3. Interrelations between separate biochemical indicators of blood

| Indicators | Total protein | Albumin | Globulin | Carotene | Vitamin A | Lysocym |
|---|---|---|---|---|---|---|
| Total protein | 1.00 | | | | | |
| Albumin | 0.981*** | 1.00 | | | | |
| Globulin | 0.944*** | 0.957*** | 1.00 | | | |
| Carotene | 0.430 | -0.084 | 0.212 | 1.00 | | |
| Vitamin A | 0.330 | -0.993 | -0.916 | -0.242 | 1.00 | |
| Lysocym | -0.957** | -0.875 | -0.825 | -0.977 | -0.401 | 1.0 |
| CIC | -0.920** | -0.967*** | -0.986*** | 0.157 | 0.999** | -0.165 |

**p<0.05; ***p<0.01



As we can see, the total protein of blood has a significant positive correlation with the found albumen of blood – albumin and globulin, the main albumen of blood. Close significant negative correlation for the protein of blood is found with the level of lysocym (r= -0.957**) and CIC (r= -0.920**) in blood, because all the mentioned indications are related to the body resistance. Significant positive correlation for the vitamin A is found with CIC (r= 0.999).

The main grounded indicator of lamb breeding is growth rate, i.e. the ability of animals to reach the live weight necessary for sale within the certain period of time. The close negative correlation between the live weight per twenty-four hours and the animal age has been found, but the positive – with the live weight. It is important to analyse, which of the biochemical indications in a particular case were related to the rams' growth intensity (Table 4).

Table 4. Interrelations between separate biochemical indicators of blood and live weight increase from the time of birth till slaughter

| Indications | Calcium | Phosphorus | Vitamin A | Lysocym | CIC |
|---|---|---|---|---|---|
| Phosphorus | -0.109 | 1.00 | | | |
| Vitamin A | 0.511 | 0.239 | 1.00 | | |
| Lysocym | -0.257 | 0.112 | -0.401 | 1.0 | |
| CIC | -0.808 | 0.886 | 0.999** | -0.165 | 1.0 |
| Increase of live weight within 24 hours from time of birth till slaughter | 0.684 | 0.522 | 0.316 | 0.718* | -0.297 |

*p<0.1; **p<0.05

According to the obtained results, the amount of the lysocym in the animals' blood (r= 0.718*) influenced the increase of the live weight per twenty-four hours. This influence was statistically credible and positive. Close, however, insignificant influence on the mentioned indication had the level of calcium and phosphorus in blood – 0.684 and 0.522, respectively. In addition, in the particular case, if the level of phosphorus in the blood increases, the level of non-specific resistance indicators may also increase. This can be explained by the greater deviation of mineral substances' correlation from the norm.

**Conclusions**

1. In the blood serum of the Latvian dark-headed rams was found the lowest level of lysocym (0.76 mkg/ml), but the highest amount of CIC (4.25 c.u.). The highest amount (0.85 mkg/ml) of lysocym was found in the blood samples of the 3rd group rams – Il-de-France bred rams. No significant difference was found in the biochemical indicators of the blood samples of groups, therefore we can

conclude that the status of the non-specific resistance of the rams from all groups was similar.

2. Close significant negative correlation for the protein of blood is found with the level of lysocym (r= -0.957**) and CIC (r= -0.920**) in blood. Significant positive correlation for the vitamin A is found with CIC (r= 0.999**).

3. The amount of the lysocym in the animals' blood (r= 0.718*) influenced the increase of the live weight per twenty-four hours. This influence was statistically credible and positive. The level of calcium and phosphorus in blood – 0.684 and 0.522, respectively, had a close, however insignificant effect on the mentioned indicator. In research groups No. 1 and 3 the correlation of calcium and phosphorus in the animals' blood deviated from the norm, therefore we can conclude that insufficient attention in the process of feeding was paid to the provision of mineral substances.

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# MITOCHONDRIAL DNA DIVERSITY OF LITHUANIAN ŽEMAITUKAI HORSES

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## Introduction

The Zemaitukai - an indigenous Lithuanian horse breed is known since the 6th-7th centuries (Gleβ, 1989). This breed became famous especially in the 14th century as excellent warhorses during the Lithuanian-Crusader battles. Later, the Zemaitukai developed into a utility horse. Horses are small in size, their withers height is 128-142 cm, chest girth 165-180 cm, oblique body length 136-148 cm and the weight is 360-420 kg (Macijauskiene, 2002). The FAO Mission Conference for Central and Eastern European countries recognized the Zemaitukai horse breed as watched internationally and included into the FAO World Watch List for domestic animal diversity (Scherf, 2000).

Genetic polymorphism at protein and DNA-level has been widely used to study genetic variation within- and genetic relationships between the domestic animal breeds. One of the genetic markers, the mitochondrial DNA (mtDNA) D-loop region is known to be hyper variable (Cann et al., 1984) and has been used in many phylogenetic studies. Ishida et al. (1995) used mtDNA to determine phylogenetic relationships between Przewalskii wild horse and other domestic horse breeds. Also other studies based on mtDNA variation in horses have been published (Ishida et al., 1994; Marklund et al., 1994; Dovc et al., 1996; Kavar et al., 1999; Bowling et al., 2000).

The characterization of the Zemaitukai breed was traditionally based on morphology and just recently analyses performed on biochemical and microsatellite markers have been introduced (Juras et al., 2003). Here we present genetic relationships between Zemaitukai and some other breeds based on mtDNA sequence variation. This knowledge might be of interest for conservation measures that may be implemented for this rare breed.

## Materials and Methods

Hair samples of Zemaitukai horses were collected from Vilnius Stud farm and private farmers. To perform a phylogenetic analysis of Zemaitukai, mtDNA D-loop sequences from GenBank (http://www.ncbi.nlm.nih.gov/GenBank), representing some other horse breeds were included.

DNA was extracted from hair roots using the DNEasy® Tissue Kit (Qiagen) following the manufacturer‘s procedure. To amplify a 1,280 bp fragment of mtDNA D-loop, primers were designed according to the published horse sequence



(X79547, Xu and Arnason, 1994). The amplification was carried out in PTC-100™ termocycler (MJ Research, Inc., USA) under the following conditions: an initial denaturation step at 94 °C for 4 min, followed by 31 cycles each consisting of 40 s at 94 °C, 60 s at 62 °C and 55 s at 72 °C and 4 °C hold. Amplified products were sequenced using a Thermo Sequenase fluorescent labelled primer cycle sequencing kit with 7-deaza-Dgtp (Amersham Biosciences, Germany). Products were sequenced in both forward and reverse directions separately. Sequencing was performed on a LI-COR® 4200S-2 automated sequencer (LI-COR Inc., Lincoln, Ne, USA). Sequencher v 4.1.4. (Gene Codes Corporation, USA) software package was used to generate the actual DNA sequence for each of the animals.

Multiple alignments of sequences were performed with CLUSTAL X 1.8 (Thompson et al., 1997) Sequence variation was quantified by the number of haplotypes and polymorphic sites. The Neighbor-joining tree (Saitou and Nei, 1987) of mtDNA sequences was constructed from Jukes-Cantor distances, performed on the pairwise deletion using the MEGA software (Kumar et al., 1993). Bootstrap analysis (1000 data sets) was used to assess confidence in the branching order.

## Results and Discussion

*Sequence variation*. Sequence data of 3 Zemaitukai horses were compared with the published sequences of a 243 bp mtDNA D-loop fragment available in the GenBank. Two representatives from Icelandic (ISL) and Noriker (NOR) domestic horse breeds, 1 Przewalskii’s (PRZ) wild horse and 1 ancient (ANC) horse mtDNA sequence from North European area were selected. Zebra (*E. grevyi*), Asiatic wild ass (*E. hemionus*) and wild ass of Mongolia (*E. kiang*) sequences were used as an out-group. Analysis of the 243 bp sequences revealed 46 polymorphic positions representing 18.9 % of the total sequence (Table 1). These variable sites defined 12 haplotypes in total. Within Zemaitukai breed 11 (4.5 %) polymorphic sites were detected. No share of haplotypes was observed neither between individuals or breeds. All haplotypes were represented by a single sequence. In both wild ass sequences one deletion at the positions 36-61 was present (Table 1), however, it was absent in domestic horse and zebra sequences. Other polymorphic sites were caused by transitions or transversions.

*Phylogenetic relationships*. To test phylogenetic relationships between Zemaitukai and other horse breeds, an unrooted neighbour-joining tree was constructed. However, results indicated that individuals from the same breed did not tend to form separate clusters on the tree (Figure 1).

Table 1. Polymorphic sites within the 243 bp mtDNA D-loop sequence

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | 1 1111111111 | 122222 | |
| | | 22223333 | 4444455555 | 5667778990 | 0003556888 | 801234 |
| | h | 3924691679 | 1245901245 | 6193788890 | 5678239678 | 962913 |
| **cons** | | **TGCGTTCATT** | **ACCCCCCACT** | **GGTGGGAAAA** | **TCGCGAGCCA** | **ATCGTA** |
| ISL1 | **1** | ........C. | .......... | ......G... | .TA.A..... | .C.A.G |
| ISL2 | **2** | .......... | .......... | .......... | .......... | ...... |
| NOR1 | **3** | ........C. | G......... | .......... | .T..AG.... | ..T... |
| NOR2 | **4** | .......... | .......... | .......... | C......... | ...... |
| ZEM1 | **5** | ........C. | .......... | ......G..G | .TA.AG.... | .C.A.. |
| ZEM2 | **6** | ........C. | ...T...... | ......G..G | .T.TA.A... | .C.... |
| ZEM3 | **7** | .......... | .......... | ......G... | .......... | ...... |
| PRZ | **8** | ........C. | ...T...... | ......GG.. | .T..AGA... | ...... |
| ANC | **9** | .....CT.C. | ..T....... | ......G..G | .T.TAGA... | .C.... |
| E.gre | **10** | .ATAA..TCC | GTT.TTAGTC | AACC.CT... | .T.TAGA... | ....C. |
| E.hem | **11** | C.TAA..--- | ---------- | --CT.CG... | .T.TA..TT. | ...A.. |
| E.kia | **12** | C.TAA..--- | ---------- | --CTAC..C. | .TAT..AT.G | G..... |

Both breeds included in the analysis, Icelandic and Noriker, are old horse breeds. The Noriker horse might have its origin as a Roman legion horse in the province Noricum that was in the modern-day Austrian territory, while the history of the Icelandic horse goes back to the late 9th century. Vikings who settled in Iceland brought with them horses of various origins, though mostly of Germanic descent.

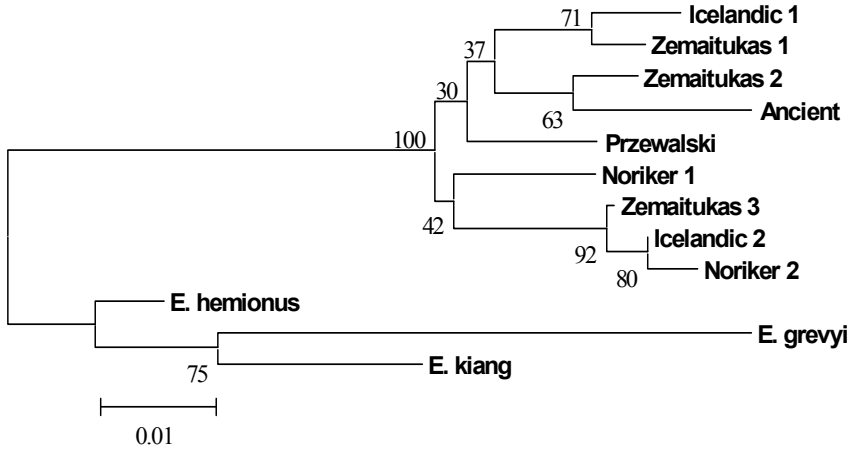


Figure 1. Unrooted Neighbor-joining tree of 12 mtDNA haplotypes. The numbers above the branches represent bootstrap values.



Zemaitukai haplotypes showed closer genetic relationships to the Icelandic rather than to the Noriker horse haplotypes (Figure 1). In addition, one of the haplotypes detected in Zemaitukai breed formed a separate branch with the ancient DNA haplotype, supported by relatively high bootstrap value (63 %).

Here we provide the first results of mitochondrial sequence variation in the Zemaitukai horse breed. Despite the small population size and endangered status of this breed, the phylogenetic analysis reflects the presence of diversity among the mitochondrial maternal lines within Zemaitukai breed. In addition to that, detected similarity with the ancient mtDNA sequence indicates that a similar haplotype to an old haplotype, which was present in horse breed(s) of North European area, is still present in native Lithuanian horse population.

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## GENETIC POLYMORPHISM OF B-LACTOGLOBULIN IN LITHUANIAN BLACKFACE SHEEP

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### Introduction

In the last years milk protein gene polymorphisms have been widely studied due to their potential use as genetic markers to improve the efficiency of selection for quantitative traits (Bolla, 1989). The β- lactoglobulin (β-LG), the major whey protein in milk, is one of the markers to investigate genetic diversity in sheep. Three genetic variants of this protein: A, B (Kolde and Braunitzer, 1983; Schlee et al., 1993) and C (Erhardt, 1989) have been identified. Differences in genetic composition of β-LG have effect on the properties of milk. The genotype BB is linked with higher milk yield, while AA and AB genotypes seem to be superior in protein and casein content and curd yield (Gazon and Martinez, 1992). In addition, Бочкарев (1998) found associations between β-LG variant AB with higher body weight, while genotype AA could be linked with sheep wool density.

Lithuanian Blackface is a modern meat-wool type sheep breed, created in the middle of the 20$^{th}$ century by crossing Lithuanian Coarsewooled ewes with wool type Shropshire and meat type German Blackface rams. The productivity traits of the animals have been continuously studied (Zapasnikiene, 2002). Also the genetic diversity within this breed using microsatellite markers and mitochondrial DNA sequencing has been evaluated (Grigaliunaite, 2003). However, the polymorphism of β-LG in Lithuanian Blackface sheep so far has not been studied.

We have recently started a study to analyse the associations between β-LG genotypes and production traits in sheep. The present study is the first phase of the work. Here we describe the polymorphism of the β-LG milk protein locus in the Lithuanian Blackface sheep breed obtained using isoelectric focusing (IEF) method.

### Materials and Methods

Milk samples of 21 sheep were collected from the state enterprise 'Šeduvos veislininkystė'. Phenotyping of skim milk was carried out by isoelectric focusing (IEF) in 0.3 mm thin polyacrylamide gel using carrier ampholytes according to the method developed by Erhardt (1989). Identification of the genetic variants was carried out after staining the gels with Coomassie Brilliant Blue R-250 according to Erhardt (1989).

The frequencies of A and B alleles and β-LG genotype frequencies were calculated by direct counting.

The mean expected unbiased and mean observed heterozygosities were calculated using Pop100gene program: (http://www.ensam.inra.fr/URLB/pop100gene/pop100gene.html).

**Results and Discussion**

In Lithuanian Blackface sheep two genetic variants A and B with allele frequencies of A=0.52 and B=0.48 were identified. The most frequent genotype in Lithuanian Blackface breed, detected in 66.4% of studied individuals, was heterozygous genotype AB (Figure 1). Homozygous genotypes AA and BB were observed at frequencies of 19.5% and 14.1%, respectively. Mean observed heterozygosity value ($H_{obs}$=0.511) was slightly lower than mean expected heterozygosity ($H_{exp}$=0.667), but deviation from Hardy-Weinberg equilibrium was not detected.

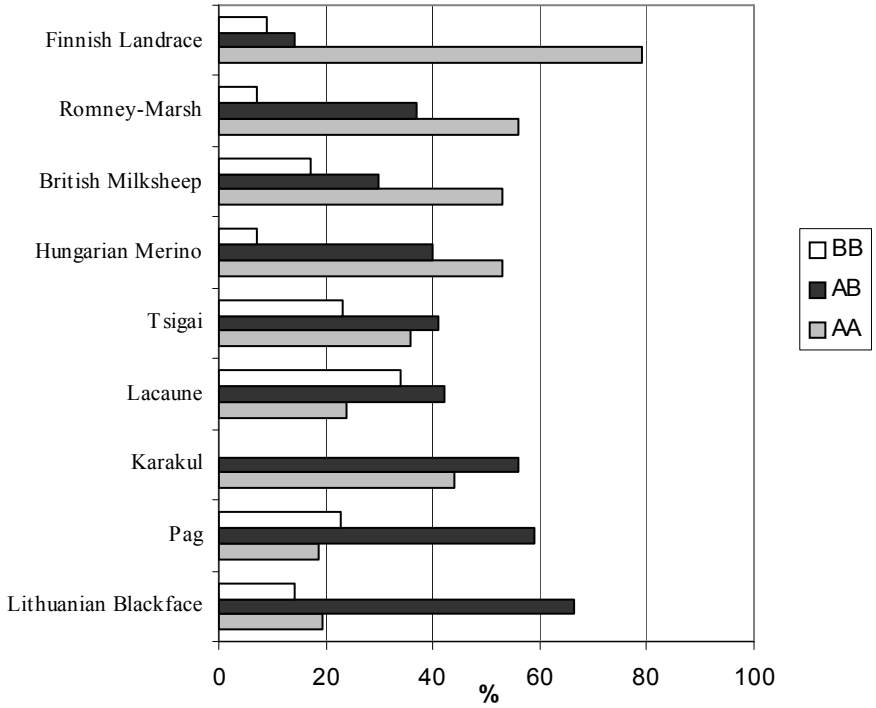


Figure 1. The distribution of β-LG genotypes in Lithuanian Blackface sheep breed and other sheep breeds, represented in literature.



The polymorphism of the β-LG locus in Lithuanian Blackface sheep breed is comparable to the results for some dairy and wool type sheep breeds described in literature. Relatively similar amount of heterozygous individuals (>50%) was observed also in Pag (Cubric-Curik, 2002) and Karakul (Нассири, 2000) breeds (Figure 1). However, the frequency of AA genotype in Lithuanian Blackface was relatively small in comparison with the group of sheep, represented by Romney-Marsh (Бочкарев, 1998), British Milk sheep, Hungarian Merino (Anton, 1997) and Finnish Landrace (Нассири, 2000), in which the AA genotype was detected in 79% of studied individuals. The BB genotype was not frequent in any of studied breeds, with the exception of Lacaune (Anton, 1997) where the frequency was highest and Karakul in which this genotype was absent. Results obtained for BB genotype in Lithuanian Blackface sheep were similar with observations in British Milk sheep breed (Anton, 1997).

The detected high frequency of genotype AB in meat-wool type Lithuanian Blackface sheep might be in agreement with the observations made by Бочкарев (1998). Since the priority in the development of this breed is given to the improvement of the meat traits, the associations between β-LG variant AB and higher body weight are possible. However, in order to prove this observation, further analyses are needed.

**Acknowledgements**

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## CHANGES IN SIZE, VALUE AND STRUCTURE OF ŽEMAITUKAI HORSE POPULATION UNDER CONSERVATION PROGRAMME

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### Introduction

Since ancient times Lithuania has been famous for its small in size and structure, yet strong and hardy horse, that under the name Žemaitukai, was known far from Lithuania's boundaries [1; 3]. Since 1554, the Žemaitukai horse has become the object of interest for Russian, German, Polish and Lithuanian scientists [2]. The unique nature of the breed is justified by the latest research findings. Very rare allele T has been detected in the serum carboxylasis system (ES) of the breed [5[ ]. By the frequency of antigenic factors and alleles of most genetic systems, Žemaitukai horses are different from related heavy-type Žemaitukai and Lithuanian Heavy Draught horses [4]. Such findings have been determined after as many as four times when the Žemaitukai were at the risk of total disappearing.

Though Žemaitukai horses have retained their unique phenotypic and genotypic traits, a very small population and narrowed genealogical structure of the breed might have seriously led to inbreeding depression. Therefore, since 1994, when the breed conservation programme was started [11], our aim has been to broaden the genealogical structure of the breed without changing its genetic characteristics.

### Materials and Methods

The year 1994 gave the start for preparation and implementation of the programme on the conservation of the Žemaitukai horse breed at the Lithuanian Institute of Animal Science. The programme was based on ten main conservation measures [2; 8; 11]. One of them was formation of the genealogical structure of the breed in two ways. The first one was to extend as many as possible lines of breeding with distinct traits within each zootechnical line, and the second one was to develop new unrelated lines.

The two lines in possession ─ those of Erelis 3 and Astūras 634 – were dispersed into lines of pure breeding by circular mating scheme [10]. Several mares from each of the five mare families in possession were selected for mating with heavy-type Žemaitukai, Arab and Estonian Native stallions with the aim to find out the founders of the new lines. The first lines under development are presented in Figure 1.

Our study was based on the material of breed monitoring and status analysis [8], circular mating scheme by prof. J. Šveistys [10], and FAO system of breed classification [6; 9]. The effective population size was expressed as Ne = 4NmNf /

(Nm + Nf), where Nm is the number of breeding mares, Nf – the number of breeding females [7]. Horse selection was carried out following the evaluation rules for the Žemaitukai horse breed [2].

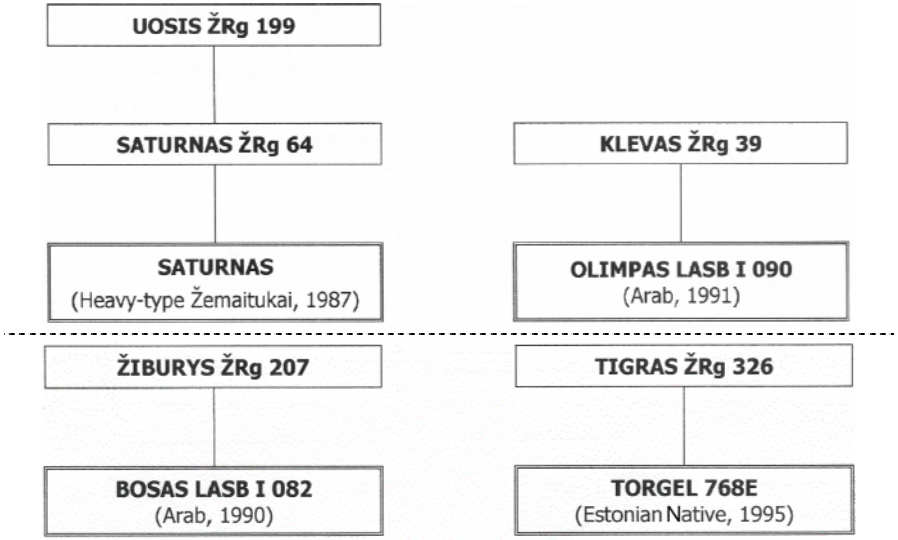


Figure 1. The Žemaitukai lines under development

**Results and Discussion**

At the start of the Žemaitukai conservation programme, there were only 30 adult and 12 progeny horses left in Lithuania. The monitoring of the breed indicated that the system of the undertaken measures was effective not only for the increase of the horse number but also for the increase of the number of the effective population, i.e. for the formation of the proper ration of stallions and mares that influences the breeding efficiency of the population. The literature survey indicates that the breed is considered as endangered when the effective population number Ne is lower than 50 (Ne < 50), as vulnerable when Ne < 100 and cared when Ne < 200 [7; 9].

The changes in size of the Žemaitukai horse population and effective population from 1999 to 2004, presented in Table 1, indicate that the breed is no longer in its critical status but still endangered (Table 1).

The increase in the population and Ne numbers does not reveal the value of the population that had been determined by a complex of traits and selection. Figure 2 indicated that in 2004 the whole Žemaitukai population comprised 149 horses of which 81 were evaluated as elite class, 17 – as first class and there were 51 young not yet evaluated horses.



Table 1. The size of the Žemaitukai horse population in 1994-2004

| Year | Žemaitukai | | | Total popu-lation | Breed status | Effective population number Ne |
|---|---|---|---|---|---|---|
| | Sires | Dams | Breeding progeny | | | |
| 1994 | 4 | 26 | 12 | 42 | Critical | 13.8 |
| 1995 | 6 | 29 | 12 | 47 | Endangered | 19.8 |
| 1996 | 7 | 31 | 16 | 54 | Endangered | 22.8 |
| 1997 | 7 | 33 | 28 | 68 | Endangered | 23.1 |
| 1998 | 8 | 33 | 35 | 76 | Endangered | 26.4 |
| 1999 | 9 | 33 | 52 | 94 | Endangered | 25.1 |
| 2000 | 17 | 40 | 44 | 101 | Endangered | 47.7 |
| 2001 | 20 | 44 | 54 | 118 | Vulnerable | 55.0 |
| 2002 | 20 | 52 | 57 | 129 | Vulnerable | 57.7 |
| 2003 | 22 | 67 | 57 | 146 | Vulnerable | 62.6 |
| 2004 | 22 | 70 | 149 | | Vulnerable | 66.9 |

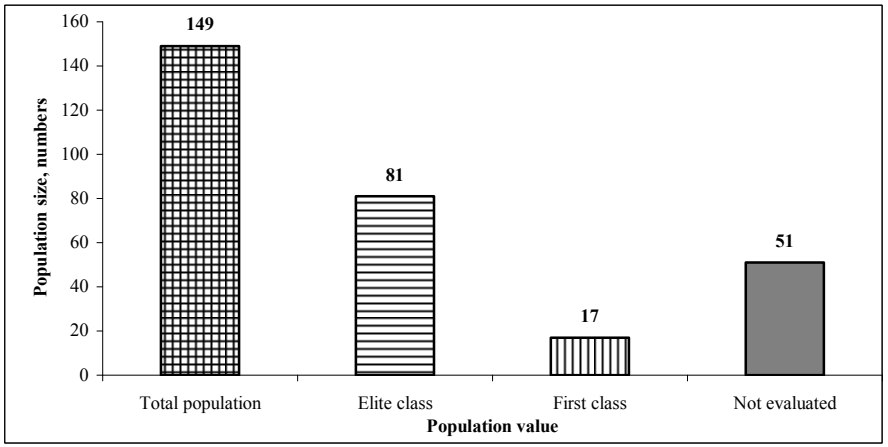


Figure 2. The size and value of the Žemaitukai horse population by Jan 1, 2004

As the nucleus of the population comprises elite class horses given at evaluation from 80 to 100 points on a 100-point scale, it was interesting to find out the value of the breed nucleus expressed in points.

As seen in Figure 3, 29.6% of horses were evaluated at minimum of 80 points, the larger part of the population was given from 81 to 92 points and only separate specimens of the Žemaitukai were worth from 93 to 97 points.

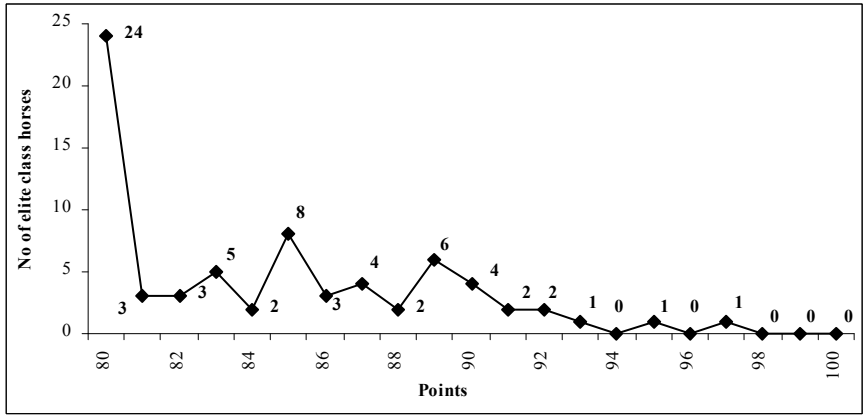


Figure 3. Distribution of elite class horses according their evaluation score in points

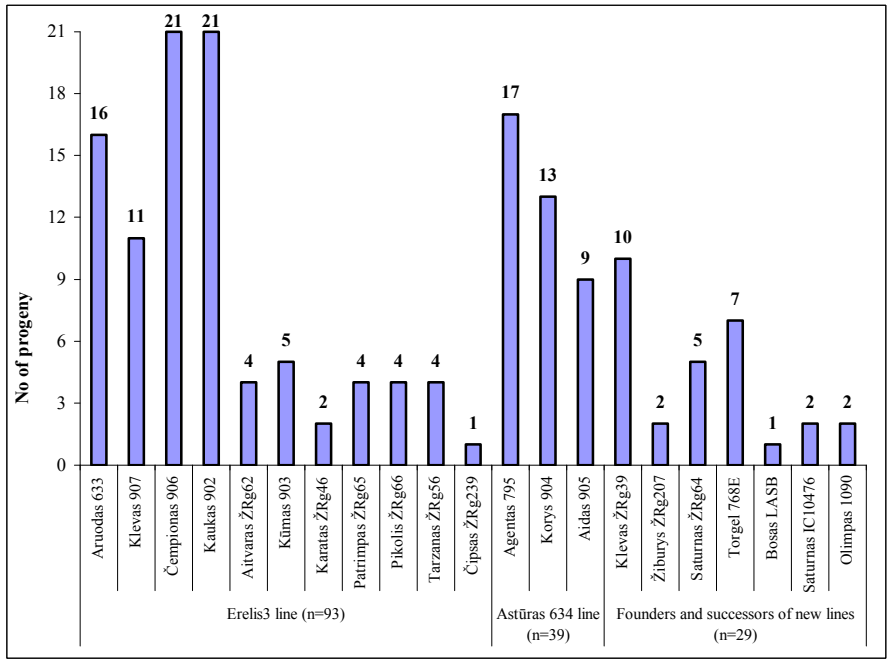


Figure 4. The genealogical structure of the Žemaitukai progeny born in 1994...2003



Figure 4 indicates the genealogical structure of the breed in development from 1994 to 2003. In this period 161 foals in total were born, 57.7% of which were sired by the stallions from Erelis 3 and 24.3% from Astūras 634 lines. 18.0% of foals were born from the stallions of newly developed lines. The old Erelis 3 line the progeny of which was produced by eleven licensed stallions, has been developed most successfully. The progeny in Astūras 634 line was produced by three licensed stallions, and the progeny founders of the new genealogical lines will be chosen among them. Only the most typical foals out of 29 newborns, belonging to the newly developed lines, will be used for breeding, and their influence on the genetic structure of the breed will be observed.

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# MICROSATELLITE ANALYSIS OF GENETIC DIVERSITY IN RUSSIAN AND UKRAINIAN SHEEP BREEDS

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## Introduction

Genetic markers such as blood groups, plasma proteins and DNA markers can be used to examine genetic variation and population structure within domestic animal breeds and genetic relationships between them. Breeds showing genetic distinctiveness have a potential value in the maintenance of genetic diversity at the species level (Eding et al., 2002). Microsatellites are useful markers for genetic diversity studies on domestic animals as they are polymorphic and ubiquitous throughout the domestic species genome (Tautz, 1989; Zhao et al., 2000; Tapio et al., 2003). The Finnish and Russian research groups have established an international collaboration to study genetic diversity and history of North and East European sheep breeds by DNA marker analyses.

## Materials and Methods

The following Russian sheep breeds were studied: Grozney, Edilbaev, Karakul, Oparino, Romanov, Romney-Marsh, Stavropol, Tsigai. Additionally, two Ukrainian breeds (Mountain Carpathian sheep and Sokolskaya) were included into the study. A total of 16 microsatellites were analyzed: MAF65, OarHH47, MAF214, OarVH72, McM527, MAF48, OarFCB304, OarFCB48, OarFCB128, BM4621, BM0757, BM1314, BM6506, BM6526, BM8125, INRA023. The PCR typing methods have been described by Tapio et al. (2003). Within population variation was quantified using mean observed and expected heterozygosities and the average number of alleles per microsatellite (POPGENE 1.32 software package available at *http://www.ualberta.ca/~fyeh/download.htm*). *f* estimates ($F_{IS}$ in Wright's terminology) values for the breeds and population subdivision Θ ($F_{ST}$ in Wright's terminology) were estimated using FSTAT (Goudet, 1995; Weir & Cockerham, 1984). The level of breed differentiation and Hardy-Weinberg equilibrium were tested using the exact test (GENEPOP package version 3.1; Raymond & Rousset, 1995). $D_A$ genetic distances (Nei et al., 1983) were calculated and neighbor-joining tree (Saitou & Nei, 1987) was constructed from the distance matrix using DISPAN program (Ota, Pennsylvania State University, PA, USA). The significance of the branching pattern of the tree was evaluated using 1,000 bootstrap replication of loci.



## Results and Discussion

The number of alleles detected at the loci varied from 8 (MAF214) to 23 (OarFCB304) (Table 1). Mean observed and expected heterozygosity within the sheep breeds indicated that the breeds in general showed a similar level of intrabreed genetic variation (Table 2). Majority of the breeds have been genetically isolated with no recent effect of gene flow from other breeds and some of them, such as the Oparino breed, have very low census sizes (less than 100 individuals), but they still displayed a high level of allelic diversity and intrabreed heterozygosity.

Table 1. The number of alleles at 10 sheep breeds by 16 microsatellite loci

| Breeds | Romney-Marsh | Romanov | Mountain Carpathian | Karakul | Edilbaev | Grozney | Oparino | Sokolskaya | Stavropol | Tsigai | Total |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ***Loci:*** | | | | | | | | | | | |
| *MAF65* | 8 | 8 | 8 | 6 | 6 | 4 | 6 | 6 | 4 | 10 | 11 |
| *OarHH47* | 9 | 8 | 9 | 8 | 5 | 2 | 6 | 10 | 7 | 8 | 14 |
| *MAF214* | 3 | 4 | 6 | 4 | 4 | 3 | 4 | 7 | 5 | 4 | 8 |
| *BM4621* | 15 | 7 | 13 | 14 | 8 | 7 | 5 | 11 | 15 | 11 | 19 |
| *INRA023* | 11 | 9 | 11 | 11 | 9 | 7 | 7 | 12 | 7 | 10 | 16 |
| *OarVH72* | 7 | 6 | 8 | 5 | 4 | 4 | 5 | 8 | 7 | 9 | 10 |
| *McM527* | 6 | 6 | 9 | 10 | 5 | 4 | 5 | 8 | 7 | 9 | 11 |
| *OarFCB304* | 9 | 9 | 13 | 11 | 7 | 4 | 6 | 9 | 12 | 12 | 23 |
| *MAF48* | 5 | 4 | 7 | 5 | 6 | 4 | 6 | 8 | 5 | 7 | 10 |
| *BM6526* | 9 | 5 | 8 | 9 | 7 | 4 | 3 | 11 | 8 | 6 | 14 |
| *BM6506* | 8 | 3 | 7 | 4 | 3 | 2 | 4 | 6 | 5 | 7 | 9 |
| *BM8125* | 5 | 6 | 8 | 5 | 7 | 4 | 3 | 6 | 5 | 6 | 9 |
| *BM1314* | 10 | 7 | 13 | 10 | 8 | 6 | 6 | 13 | 9 | 12 | 16 |
| *BM0757* | 6 | 8 | 5 | 6 | 5 | 4 | 5 | 6 | 5 | 6 | 10 |
| *OarFCB48* | 8 | 6 | 10 | 8 | 6 | 5 | 7 | 9 | 8 | 10 | 14 |
| *OarFCB128* | 6 | 7 | 8 | 8 | 4 | 4 | 7 | 8 | 6 | 8 | 13 |
| *Total alleles:* | 125 | 103 | 143 | 124 | 94 | 68 | 85 | 138 | 115 | 135 | 207 |

The Θ estimate indicated that genetic differences between the breeds explained 5.3% of the total genetic variation. The remaining 94.7% was due to differences among individuals within the breeds. This estimate was higher than

typically found e.g. in studies on cattle (88.6%) and goats (85.7%) (Kantanen, 1999; Barker et al., 2001). The data indicated the highest positive *f* ($F_{IS}$) estimate for Karakul which can be attributable to inbreeding within the breed (the parents in the Karakul breed have been more related than expected under random mating). For the other breeds, the $F_{IS}$ values showed a lower probability of inbreeding or no effect of inbreeding ($F_{IS}$ estimates close to zero) (Table 2).

In the Hardy-Weinberg equilibrium testing, exact P-values for single breeds were pooled (Table 2). After adjusted to the Bonferroni correction (P=0.05/16= 0.003125), all investigated breeds were in Hardy-Weinberg equilibrium (also Sokolskaya and Tsigai breeds).

Table 2. Mean observed and expected heterozygosities within the breeds, P-values showing agreements with Hardy-Weinberg expectations and $F_{IS}$ estimates for the breeds.

| Breed | Heterozygosity | | P | *f* |
|---|---|---|---|---|
| | Observed | Expected | | |
| Romney-Marsh | 0.73367 | 0.73855 | 0.4019 | -0.011 |
| Romanov | 0.71654 | 0.71794 | 0.4148 | -0.018 |
| Mountain Carpathian | 0.79613 | 0.80087 | 0.2046 | 0.006 |
| Karakul | 0.78633 | 0.79848 | 0.0773 | 0.082 |
| Edilbaev | 0.77121 | 0.78225 | 0.7849 | 0.013 |
| Grozney | 0.72396 | 0.74479 | 0.9282 | -0.026 |
| Oparino | 0.70952 | 0.72863 | 0.7802 | 0.021 |
| Sokolskaya | 0.80583 | 0.81046 | 0.0469 | 0.020 |
| Stavropol | 0.74944 | 0.76095 | 0.3557 | -0.011 |
| Tsigai | 0.77799 | 0.78245 | 0.0137 | -0.015 |

When the Hardy-Weinberg testing was performed for the loci, departure from the Hardy-Weinberg equilibrium was found only at MAF214. Although the present breed samples did not allow an examination of the inheritance of microsatellite alleles, it is assumed that the result obtained for MAF214 is due to a presence of undetected null alleles at MAF214.

The $D_A$ genetic distances (Table 3) demonstrated close genetic relationships between Tsigai and Mountain Carpathian (0.09) and between Tsigai and Sokolskaya (0.1). This can be explained by the history of the breeds. Tsigai rams were used to mate the local coarse wool sheep in Carpathian mountains, as the crosses had the highest productivity and vitality (Сулыма, 1963). Moreover, Sokolskaya was probably formed using genetic material from Tsigai sheep (Люцканов, 1990).



The highest genetic distances were found between Grozney and Romanov (0.31) and Grozney and Edilbaev breeds (0.32). Genetic distances within other breeds ranged from 0.12 to 0.30.

Table 3. The $D_A$ genetic distances between the sheep breeds

| Breed | *Romney-Marsh* | *Romanov* | *Mountain Carpathian* | *Karakul* | *Edilbaev* | *Grozney* | *Oparino* | *Sokolskaya* | *Stavropol* |
|---|---|---|---|---|---|---|---|---|---|
| *Romanov* | 0.266 | | | | | | | | |
| *Mountain Carpathian* | 0.126 | 0.234 | | | | | | | |
| *Karakul* | 0.210 | 0.248 | 0.209 | | | | | | |
| *Edilbaev* | 0.240 | 0.295 | 0.226 | 0.252 | | | | | |
| *Grozney* | 0.286 | 0.314 | 0.265 | 0.259 | 0.325 | | | | |
| *Oparino* | 0.165 | 0.284 | 0.195 | 0.229 | 0.256 | 0.273 | | | |
| *Sokolskaya* | 0.157 | 0.248 | 0.109 | 0.196 | 0.217 | 0.297 | 0.206 | | |
| *Stavropol* | 0.193 | 0.236 | 0.149 | 0.214 | 0.277 | 0.192 | 0.228 | 0.168 | |
| *Tsigai* | 0.128 | 0.196 | 0.088 | 0.205 | 0.199 | 0.256 | 0.164 | 0.103 | 0.141 |

The neighbor joining tree demonstrated that studied sheep breeds were grouped into 3 clusters (Figure 1).

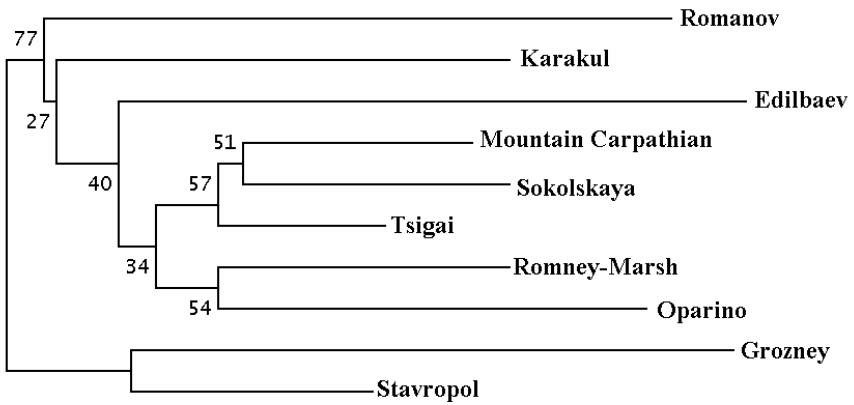


Figure 1. Neighbor joining tree showing relationships between 10 analysed sheep breeds. The numbers at the nodes represent the percentage of group occurrence in 1000 bootstrap replicates.

The first cluster was formed by fine wool sheep – Grozney and Stavropol. The second group consisted of semi fine wool breeds – Romney-Marsh and Oparino. Oparino sheep was created in Kirov region by crossing local coarse wool sheep with Romney-Marsh rams. The third group was formed by the Tsigai, Sokolskaya and Carpathian Mountain breeds. The rest of breeds form each their own branches. Edilbaev is meat-fat production sheep. The name of this breed has the origin from the old name of Volga river – "Itil". Romanov has been developed for the fur production and according to one hypothesis it was created in Yaroslavl region. An alternative hypothesis assumes that this breed came with Mongol-Tatar people and was bred long time in Central part of Russia (Марзанов & Магомадов, 1997). Karakul is one of the oldest breeds in the territory of the former Soviet Union, and it was reared with Romanov and Edilbaev sheep in Volga river region for a long time.

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# COMPARISON OF THE GENEALOGICAL LINES AND GROUPS OF LATVIAN HORSE BREED BY QUALITY OF PROGENIES

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## Introduction

With increasing number of people who take interest in riding, increases demand for high quality horses. Therefore each horse breeder must search for the best methods in horse breeding. One of the most important rules to gain high quality horses is using high-quality stallions. The most effective method to evaluate the stallions is evaluation of their progeny. The most important parameter of horses' quality is performance.

## Material and Methods

In our research we included evaluated stallions in Latvia, whose progeny were born during years 1996-2001 and had evaluated performances. The performance of 764 progeny from 201 stallions was evaluated in this period.

The stallions were in related groups according to their common progenitor in father's line. Schemes of related groups and lines of stallions were worked out. In the clarification of stallions' progenitors the Latvian Horse Studbook was used. In the research stallions, whose progenies were entered in Latvian Horse Breed were included. The progenies of stallions were evaluated at the age of 2 - 3 years. Evaluated parameters were quality of walk, trot, gallop and free jump. On the basis of these parameters performance index for each offspring were calculated. In the research only those related groups were included, in which there were at least 3 stallions and at least 20 performance evaluated progenies.

## Results

We compared 12 different related groups of stallions:

- Flagmanis Lb 703 line - Latvian Horse Breed stallions' line;
- Cor De La Bryere 210398168, Ramiro Z 210389565 H, Duo H 2410, Valerik, Han., Alme Z 310077466 P.B., Voltaire 356 STB, Gardegeneral H 180 - German warmblood stallions' related groups;
- Lady Killer 064000861, 1573 Duglass, Dekret Ang. - English Thoroughbred stallions' related group;
- Absatz T 4025 - Trakehner stallions' related group.

An example of the related the group of the well-known French stallion Cor De La Bryere and the old line of Latvian horse breed - Flagmanis Lb 703 line is shown below. In bold are marked those stallions, whose progenies are included in the research (Figures 1 and 2).



Horse breeders from Holstein bought stallion Cor de la Bryere in France. In 1971 in Elmshorn in stallions' performance testing, Cor de la Bryere was recognized as a winner. Already in 1974 four sons of this stallion became breeding sires. By the autumn of 1998 from Cor de la Bryere 1456 colts were obtained. Among his progenies 48 stallions and 483 mares were positively evaluated.

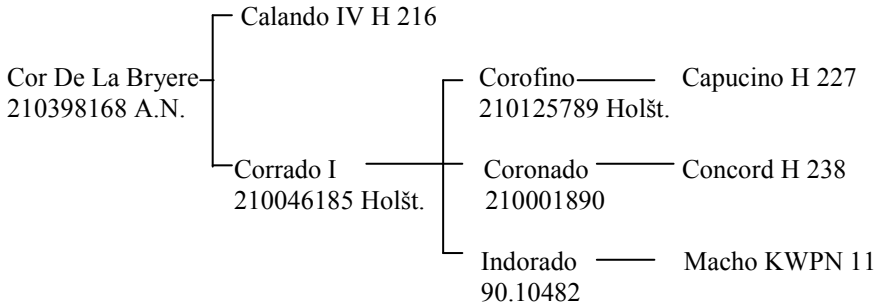


Figure 1. Related group of stallion Cor De La Bryere 210398168 A.N.

In 1977 son of Flagmanis Finmāls L 891 became the winner of exhibition in Latvia and in 1980 it became the breed champion in Soviet Union. Grandson of Flagmanis Lb 703 - Finmāls L 1429 has shown good results in jumping competitions, taking part in Seula Olympic games in in 1988.

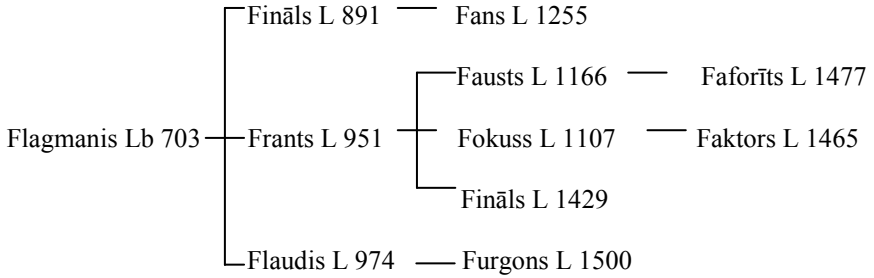


Figure 2. Flagmanis Lb 703 line

Results of assessment of young stallions and young mares in the related groups are given in Tables 1 and 2. Mean index of all young stallions (101.5) is

higher than index of all young mares (99.5), because the worst young stallions were sold before evaluation.

Table 1. Comparison of related groups and lines by performance index of sons

| Related group or line | Number of stallions in group[1)] | Number of evaluated young stallions (sons) | Index of sons | |
|---|---|---|---|---|
| | | | x ± sx | rank |
| Flagmanis Lb 703 | 1 | 5 | 94.9±3.30 | 11 |
| Cor De La Bryere 210398168 | 3 | 8 | 113.0±8.16 | 1 |
| Ramiro Z 210389565 H | 12 | 30 | 101.7±2.45 | 6 |
| Lady Killer 064000861 | 8 | 26 | 110.0±4.17 | 2 |
| Duo H 2410 | 5 | 10 | 97.4±6.77 | 9 |
| Valerik, Han. | 9 | 17 | 90.9*±3.79 | 12 |
| Alme Z 310077466 P.B | 6 | 20 | 109.7*±2.86 | 3 |
| Voltaire 356 STB | 5 | 13 | 98.8±4.20 | 7 |
| Gardegeneral H 180 | 3 | 13 | 105.2±5.05 | 4 |
| Absatz T 4025 | 4 | 18 | 102.7±5.02 | 5 |
| 1573 Duglass | 5 | 6 | 95.3±6.37 | 10 |
| Dekret Ang. | 3 | 5 | 98.6±3.79 | 8 |
| All evaluated young stallions[2)] | x | 262? | 101.5±1.10 | x |

*[1)] number of stallions with evaluated sons*

*[2)] young stallions from related groups and other young stallions born in this period*

** p < 0.05 (in comparison with all evaluated young stallions)*

As seen in Table 1 the best young stallions come from Cor De La Bryere 210398168, Lady Killer 064000861 and Alme Z 310077466 P.B related groups. In our research we clarified, that 5 of the best 10 young stallions come from Lady Killer 064000861 related group. Evaluation results of young stallions Alme Z 310077466 P.B related group are significantly better than the results of all evaluated young stallions together.

The results presented in Table 2 indicate that the best young mares are in Duo H 2410, Alme Z 310077466 P.B, Voltaire 356 STB and Cor De La Bryere 210398168 related groups (significantly higher results are shown by Alme and Duo related groups).

Unsatisfactory results are shown by Flagmanis Lb 703 line, because horses from old Latvia Horse Breed lines are for universal use and must be evaluated otherwise than sport horses.



Table 2. Comparison of related groups and lines by performance index of daughters

| Related group or line | Number of stallions in group[1)] | Number of evaluated young mares (daughters) | Index of daughters | |
|---|---|---|---|---|
| | | | x ± sx | rank |
| Flagmanis Lb 703 | 6 | 17 | 91.3±5.06 | 12 |
| Cor De La Bryere 210398168 | 4 | 32 | 102.5±2.68 | 4 |
| Ramiro Z 210389565 H | 19 | 63 | 96.6±2.08 | 9 |
| Lady Killer 064000861 | 12 | 49 | 98.7±2.54 | 5 |
| Duo H 2410 | 10 | 20 | 110.0*±3.07 | 1 |
| Valerik, Han. | 15 | 42 | 96.5±2.38 | 10 |
| Alme Z 310077466 P.B | 8 | 37 | 105.4*±2.60 | 2 |
| Voltaire 356 STB | 6 | 13 | 104.1±4.44 | 3 |
| Gardegeneral H 180 | 3 | 15 | 92.6±4.24 | 11 |
| Absatz T 4025 | 5 | 20 | 97.5±4.17 | 7.5 |
| 1573 Duglass | 10 | 14 | 97.5±5.62 | 7.5 |
| Dekret Ang. | 4 | 15 | 98.1±4.66 | 6 |
| All evaluated young mares together [2)] | x | 501? | 99.5±0.77 | x |

*[1)] number of stallions with evaluated daughters*

*[2)] young mares from related groups and other young mares born in this period*

** p < 0.05 (in comparison with all evaluated young mares)*

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## ON BREEDING VALUE OF THE ESTONIAN NATIVE BREED HORSES

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### Introduction

The objective of the study was the estimation of breeding value of the outstanding stallions, used in Estonian Native breed, on the basis of their 2-year-old offspring.

The breeding value is expressed by indexes. The study is based on the results of the experiments carried out during 1996-2003 with the stallions of the Estonian Native Horse. On the basis of the results of 8 years, the average indexes have been calculated. The ranking of stallions, both improvers and impairers, used in the period mentioned above, is presented according to breed. The attached diagrams show the yearly indexes of the best stallions.

### Material and Methods

The most important qualities have been considered: general index of stallions, indexes of type, body, feet, pace, trot and free jump. Average indexes per year and per 8 years were calculated.

176 offspring tests with the foals of 44 stallions (3 stallions were tested twice) have been carried out during 8 years. Results of 61 tests were not calculated as some stallions had only one foal per one or couple of years which were not included. In 1996-2003, there were 18 native stallions in use (Table 2). A total of 173 (+3) offspring have been estimated but in this case we calculated 112 only.

The indexes of stallions were calculated using the following formula:

$$I=100+b_1x\ (EL_1-VG_1)+b_2x\ (EL_2-VG_2)...+b_6x\ (EL_6-VG_6)$$

where $EL_1$- estimate of horse in trait 1,
$VG_1$- comparison value in trait 1,
$b_1$- share of index for trait 1,
$EL_6$- estimate of horse in trait 6,
Share of index was calculated as follows:

$$b_1=\frac{\text{relative share of index}}{\text{phenotypical standard deviation of trait}}$$

Determination of relative share has been based on major qualities in horseracing, according to which the relative share comprised: type 1, body 1, feet 1.5, pace 2, free jump 2.5.

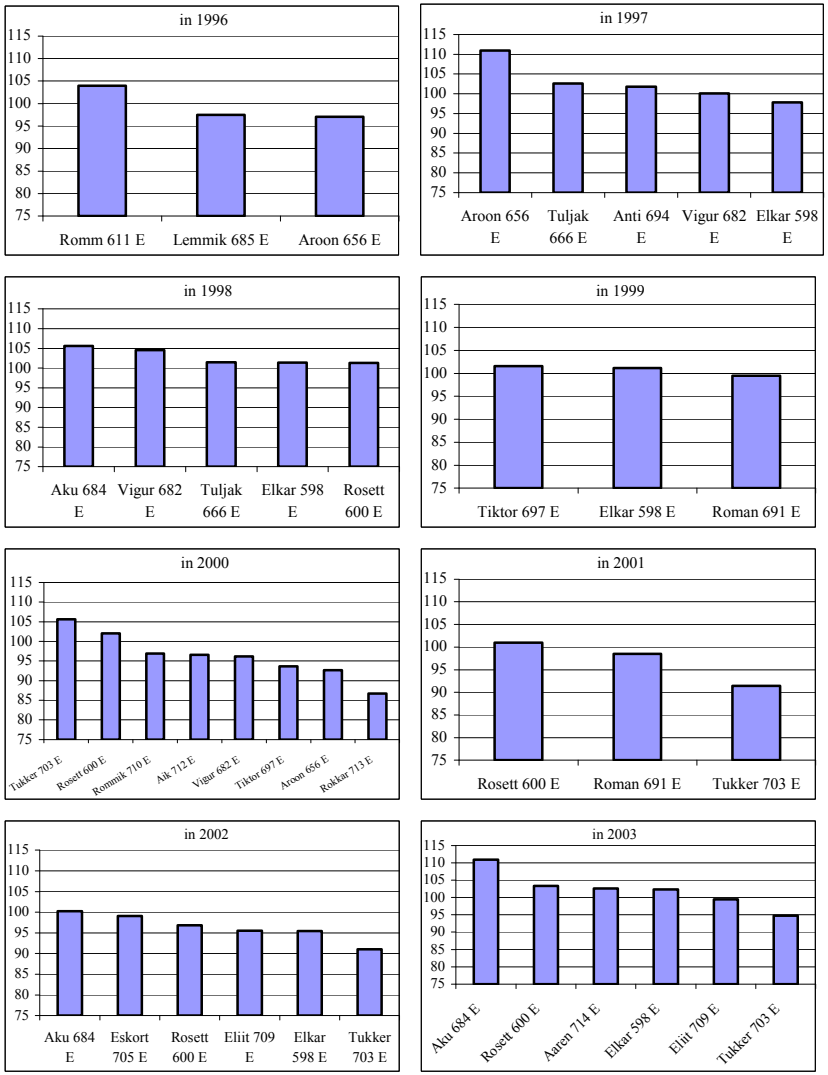
Indexes of stallions used in the Estonian Native Horse, based on tests carried out every year, are presented in Table 1. Stallions Rosett 600 E, Eskort 705 E, Elkar 598 E, Vigur 682 E were used more (4-7 tests per year) and others less (2–3 per year).



Table 1. Indexes of stallions used in the Estonian Native Horse, based on tests carried out every year

| Year | Horse name | No.of tests | Index | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | | General | Type | Head, neck, body | Feet | Pace | Trot | Free jump |
| 1996 | Aroon | 2 | 97.03 | 100.03 | 99.88 | 100.17 | 100.07 | 99.69 | 99.15 |
| 1996 | Lemmik | 2 | 97.46 | 99.86 | 99.88 | 99.0 | 99.74 | 99.86 | 100.48 |
| 1996 | Romm | 2 | 103.95 | 100.53 | 100.2 | 100.5 | 100.07 | 101.0 | 99.48 |
| 1997 | Anti | 2 | 101.80 | 99.36 | 99.88 | 100.17 | 100.57 | 100.2 | 99.98 |
| 1997 | Aroon | 2 | 110.96 | 100.86 | 100.4 | 100.17 | 101.07 | 100.7 | 100.98 |
| 1997 | Elkar | 4 | 97.85 | 99.74 | 100.1 | 99.92 | 100.07 | 99.44 | 99.86 |
| 1997 | Tuljak | 3 | 102.61 | 100.19 | 99.88 | 99.84 | 100.4 | 100.2 | 100.31 |
| 1997 | Vigur | 7 | 100.10 | 99.72 | 99.31 | 99.74 | 100.92 | 99.9 | 99.76 |
| 1998 | Aku | 2 | 105.61 | 100.36 | 100.9 | 100.67 | 99.90 | 100.5 | 100.31 |
| 1998 | Elkar | 2 | 101.42 | 99.86 | 99.88 | 100.34 | 100.57 | 99.52 | 100.15 |
| 1998 | Rosett | 2 | 101.34 | 100.69 | 100.1 | 100.67 | 100.07 | 100.0 | 99.48 |
| 1998 | Tuljak | 4 | 101.50 | 99.94 | 100.2 | 100.17 | 100.24 | 100.0 | 99.98 |
| 1998 | Vigur | 3 | 104.52 | 100.19 | 99.21 | 99.84 | 100.4 | 100.2 | 101.31 |
| 1999 | Elkar | 2 | 101.12 | 99.11 | 99.38 | 99.55 | 100.7 | 100.7 | 99.98 |
| 1999 | Roman | 2 | 99.48 | 99.99 | 100.0 | 100.42 | 99.95 | 99.44 | 100.11 |
| 1999 | Tiktor | 2 | 101.54 | 99.99 | 100.1 | 100.05 | 100.2 | 99.94 | 100.23 |
| 2000 | Aroon | 3 | 92.63 | 99.19 | 99.88 | 99.95 | 98.63 | 99.41 | 100.2 |
| 2000 | Rokkar | 2 | 86.68 | 98.86 | 98.88 | 99.34 | 99.74 | 99.69 | 97.81 |
| 2000 | Aik | 2 | 96.54 | 99.53 | 99.55 | 99.34 | 100.40 | 99.69 | 99.65 |
| 2000 | Rommik | 3 | 96.93 | 100.64 | 100.3 | 99.95 | 99.74 | 99.52 | 99.31 |
| 2000 | Rosett | 2 | 102.04 | 99.69 | 100.1 | 100.5 | 100.07 | 100.0 | 100.31 |
| 2000 | Tiktor | 2 | 93.64 | 99.36 | 99.21 | 100.17 | 99.40 | 99.69 | 99.48 |
| 2000 | Vigur | 4 | 96.13 | 99.69 | 100.1 | 99.92 | 100.07 | 99.44 | 99.31 |
| 2000 | Tukker | 2 | 105.60 | 100.36 | 100.9 | 99.84 | 100.57 | 99.86 | 100.81 |
| 2001 | Roman | 2 | 98.53 | 100.11 | 100.3 | 99.42 | 100.7 | 99.57 | 99.36 |
| 2001 | Rosett | 8 | 101.00 | 100.36 | 100.4 | 100.39 | 99.79 | 100.2 | 99.73 |
| 2001 | Tukker | 2 | 91.45 | 99.11 | 99.38 | 99.17 | 99.45 | 99.94 | 99.23 |
| 2002 | Aku | 3 | 100.23 | 100.08 | 99.99 | 99.84 | 99.62 | 100.5 | 100.09 |
| 2002 | Eliit | 2 | 95.54 | 100.03 | 99.38 | 99.84 | 100.24 | 99.69 | 98.98 |
| 2002 | Elkar | 4 | 95.41 | 99.76 | 99.88 | 99.67 | 99.67 | 99.49 | 99.78 |
| 2002 | Eskort | 4 | 99.10 | 100.61 | 100.1 | 99.67 | 99.82 | 100.2 | 99.61 |
| 2002 | Rosett | 2 | 96.81 | 99.86 | 100.1 | 100.0 | 100.4 | 99.69 | 98.81 |
| 2002 | Tukker | 4 | 91.03 | 99.96 | 99.78 | 99.47 | 99.37 | 99.29 | 98.98 |
| 2003 | Aaren | 2 | 102.62 | 100.19 | 100.2 | 100.5 | 100.24 | 100.4 | 99.65 |
| 2003 | Aku | 2 | 110.94 | 101.49 | 101.1 | 101.05 | 100.20 | 100.4 | 100.86 |
| 2003 | Eliit | 2 | 99.50 | 99.66 | 99.68 | 99.57 | 100.27 | 99.59 | 100.58 |
| 2003 | Elkar | 4 | 102.28 | 100.36 | 100.1 | 99.86 | 100.01 | 100.0 | 100.61 |
| 2003 | Rosett | 5 | 103.30 | 100.36 | 100.2 | 100.12 | 100.02 | 100.4 | 100.28 |
| 2003 | Tukker | 3 | 94.70 | 99.86 | 99.63 | 98.92 | 99.40 | 99.61 | 100.4 |
| | Average | 112 | 99.68 | 100.01 | 99.97 | 99.96 | 100.06 | 99.96 | 99.90 |
| | s | | 3.830 | 0.394 | 0.346 | 0.366 | 0.364 | 0.344 | 0.535 |

Total of 112 tests were calculated, because 61 tests were not taken into account, as referred to in Material and Methods.




Figures 1…8. General indexes of the Estonian Native breed stallions in 1996-2003



Higher general index in 1996 got Romm 611 E (103.95), in 1997–Aroon 656 E (110.96), in 1998–Aku 684 E (105.61), in 1999–Tiktor 697 E (101.54), in 2000–Tukker 703 E (105.60), in 2001–Rosett 600 E (101.00), in 2002–Aku 684 E (100.23), in 2003–again Aku 684 E (110.94).

On the one hand, Aku 684 E had rather good results, whereas on the other hand, he had very small number of foals.

Higher index for type (101.49) and for body (101.1) got Aku 684 E in 2003. Highest index for feet (101.05) obtained also Aku 684 E in 2003.

The best pace (101.07) had Aroon 656 E in 1997. Higher index for trot was observed in Elkar 598 E in 1999.

Free jump is very important characteristic of Estonian Native Horse. The best (101.31) in this field was Vigur 682 E in 1998. General indexes of Estonian Native Breed Horse are illustrated in Figures 1…8.

Average indexes of 18 more intensively used stallions in Estonian Native Horse during a 8-year period are presented in Table 2.

Table 2. Average indexes of 18 more intensively used stallions in Estonian Native Horse (during 8 years)

| Year | Horse name | No. of tests | Avg. gen. index (by years) | Type | Head, neck, body | Feet | Pace | Trot | Free jump |
|---|---|---|---|---|---|---|---|---|---|
| 1996/97/00 | Aroon | 7 | 100.20 | 100.03 | 100.05 | 100.10 | 99.92 | 99.93 | 100.11 |
| 1996 | Lemmik | 2 | 97.46 | 99.86 | 99.88 | 99.0 | 99.74 | 99.86 | 100.48 |
| 1996 | Romm | 2 | 103.95 | 100.53 | 100.2 | 100.5 | 100.07 | 101 | 99.48 |
| 1997 | Anti | 2 | 101.80 | 99.36 | 99.88 | 100.17 | 100.57 | 100.2 | 99.98 |
| 97/98/99/02/03 | Elkar | 16 | 99.62 | 99.77 | 99.87 | 99.87 | 100.20 | 99.83 | 100.08 |
| 1997/98 | Tuljak | 7 | 102.06 | 100.07 | 100.04 | 100.01 | 100.32 | 100.1 | 100.15 |
| 1997/98/00 | Vigur | 14 | 100.25 | 99.87 | 99.55 | 99.83 | 100.46 | 99.85 | 100.13 |
| 1998/00/03 | Aku | 7 | 105.59 | 100.64 | 100.66 | 100.52 | 99.91 | 100.47 | 100.42 |
| 98/00/01/02/03 | Rosett | 19 | 100.90 | 100.19 | 100.18 | 100.34 | 100.07 | 100.06 | 99.72 |
| 99/01 | Roman | 4 | 99.00 | 100.05 | 100.15 | 99.92 | 100.33 | 99.51 | 99.74 |
| 99/00 | Tiktor | 4 | 97.59 | 99.68 | 99.66 | 100.11 | 99.80 | 99.82 | 99.86 |
| 2000 | Rokkar | 2 | 86.68 | 98.86 | 98.88 | 99.34 | 99.74 | 99.69 | 97.81 |
| 2000 | Rommik | 3 | 96.93 | 100.64 | 100.3 | 99.95 | 99.74 | 99.52 | 99.31 |
| 2000 | Aik | 2 | 96.54 | 99.53 | 99.55 | 99.34 | 100.40 | 99.69 | 99.65 |
| 2000/01/02/03 | Tukker | 11 | 95.69 | 99.82 | 99.92 | 99.35 | 99.70 | 99.68 | 99.86 |
| 2002/03 | Eliit | 4 | 97.52 | 99.85 | 99.53 | 99.71 | 100.26 | 99.64 | 99.78 |
| 2002 | Eskort | 4 | 99.10 | 100.61 | 100.1 | 99.67 | 99.82 | 100.2 | 99.61 |
| 2003 | Aaren | 2 | 102.62 | 100.19 | 100.2 | 100.5 | 100.24 | 100.4 | 99.65 |

In different years more matings and more tested pedigree had Rosett 600 E (19), Elkar 598 E (16), Vigur 682 E (14), and Tukker 703 E (19). Aroon 656 E, Aku 684 E and Tuljak 666 E (7) and others (2-4 were used less).

**Conclusions**

The highest average general index during a 8-year period had Aku 684 E (105.59), the second was Romm 611 E (103.95) and the third was Aaren 714 E (102.62). Unfortunately they were in moderate use only. The first two of them had rather good type and body indexes. Good feet indexes are characteristic of the Estonian Native Horse Breed. Gallop and free jump are also very important for this breed, but variation in movements especially in free jump is bigger.

**Acknowledgements**

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## EXTERNAL FEATURES OF BEES AND THE USE OF THEM IN SELECTION FOR REPRODUCTION OF QUEENS

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**Introduction**

According to statistics, in Estonia commonly the Carniolan (*Apis mellifera Carnica*) and Italian (*A.m. ligustica*) beeraces (22%) are kept. In many aparies (56%) native crossbred bees descended from unknown parentage are used. Reproduction of Queens from crossbred $F_1$ colonies is giving the Queens $F_2$ whose honey production is by 30....50% lower compared to that of purebred or crossbred $F_1$ colonies. Investigations in 1997-1999 indicated that purebred Italian or their crossing $F_1$ bees were bigger, they had longer proboscis and they produced by 8-25 kg more honey than Carniolan, Nigra or crossbred $F_2$ bees (Nõmmisto, 2002).

The winter of 2002/2003 was very cold and temperatures varied in great range, causing the perishing of many Italian colonies, and as a result of this, many beekeepers preferred defection from Italian bees to Carniolan bees. This emerged the need to reproduce Carniolan bees.

As the reproduction of Queens should take place in purebred colonies, it is very important to determine the raciality of bees. That is determined by external features, mainly by the colour of tergites and cubital index of bees.

As the yellow colour of tergites (Italian bees) is dominant, some crossbred drones and workers have yellow tergites. Thus the colour of tergites of workers does not indicate the relationship with purebred or crossbred ($F_1$ or $F_2$) bees (Carniolan or Nigra bees). In that case the raciality can be determined by the cubital index (%). The cubital index of Italian bees was 40% to 45% and their tergites were yellow, Carniolan and Nigra bees had dark tergites and their cubital index was 45% to 50% and 60% to 65%, respectively. The cubital index is not subject to seasonal changes (Bilaš and Krivtsov, 1991).

In selection of bees for reproduction some external features of bees play an important role. In literature there are some data about the external features of bees of different races (Bilaš and Krivtsov, 1991; Balžekas and Balžekas, 1996; Amsiejus and Straigis, 1998; Krivtsov et al., 2000; Nõmmisto, 2001 a, b).

The body weight and length of proboscis are subjects to seasonal changes. The length of wing and the first paw segment, and the width of wing, tergite and the first paw segment are not subjects to seasonal changes. The size of wing, length of proboscis and the width of tergite are important in respect of nectar and pollen. The measurements of the first paw segment are expressed by the tarsal index (%). The bees with wider paws are carrying more pollen, their colony is bigger and

they may produce more honey. The width of wing and tergite, and the length of wing and tergite have great heritability, $h^2$ = 0.75...0.77. Between honey production and the width of tergite, and honey production and the length of wing there are significant correlations, r = 0.63...0.69 (Krivtsov et al., 2000).

In selection of colonies for reproduction such characteristics as honey production, winter losses (wintering), anger and external features of bees play an important role. It should be considered that usually the colonies of bees are reproduced in the second year of Queen's life. But the determination value of Queen may be done in the first year of Queen's life by external features of workers and drones as they all are the daughters and sons of Queen.

**Material and Methods**

In 2003 the external features and raciality of bees were determined in one apiary and 23 colonies. The number of bees was 1380. Ten colonies of bees were purebred Carniolan and 13 colonies crossbred $F_1$ bees (Carniolan x Italian, Carniolan x Nigra). From each colony 60 bees were measured. The bees were collected from a winter debris. The Carniolan bees were imported from Austria.

The raciality was determined by the colour of tergites and the cubital index (%). The cubital index was found as the ratio (%) measurements of neighbour obstructions of cubital obstruction on wing. The length of proboscis, wing and the first paw segment were measured with a gauge (mm, exactness 0.1). The tarsal index (%) was found as the ratio (%) measurements of the first paw segment.

The wintering of bees was determined by the 5-point system, where the debris under the glass gave 5 points. One to 2 glasses gave 4 points, 2 to 3 glasses gave 3 points, 3 to 4 gave 2 points and more than 4 glasses gave 1 point.

The data were analyzed using the methods of Pearson and the t-test.

**Results and Discussion**

The results of measurements of external features of 600 purebred Carniolan and 780 crossbred $F_1$ bees are presented in Table 1.

The width of tergite of purebred Carniolan and crossbred $F_1$ bees was not different. The wings of crossbred $F_1$ bees were by 0.07 mm ($P< 0.01$) longer and by 0.05 mm ($P< 0.01$) wider than these of Carniolan bees.

The proboscis of Carniolan purebred bees was by 0.09 mm ($P< 0.01$) longer than that of crossbred $F_1$ bees.

The tarsal index, cubital index, wintering of bees and honey production of purebred Carniolan and crossbred $F_1$ bees were not significantly different in 2003.

Table 2 presents the external features and honey production of Carniolan bees of 10 colonies in 2003. The wings of the high-yielding bees in 4 colonies were by 0.1 mm ($P< 0.01$) longer and proboscis by 0.3 mm ($P<0.001$) longer than these of the low-yielding in 6 colonies. The high-yielding colonies produced only 7 kg honey per a colony.



Table 1. Differences in external features of bees

| Indices | Purebred | Crossbred | Differenses |
|---|---|---|---|
| | n = 600 | n = 780 | |
| | mean | mean | |
| Width of tergite, mm | 4.82 | 4.82 | 0.00 |
| Length of wing, mm | 9.82 | 9.89 | 0.07** |
| Width of wing, mm | 3.22 | 3.27 | 0.05*** |
| Length of proboscis, mm | 6.44 | 6.35 | 0.09** |
| Tarsal index, % | 58.77 | 58.07 | 0.70*** |
| Cubital index, % | 52.24 | 52.39 | 0.15 |
| Wintering (1-5) | 3.20 | 3.23 | 0.03 |
| Honey production, kg | 21.55 | 21.42 | 0.13 |

Correlation between external features, wintering and honey production are presented in Table 3. The correlations between the characteristics ranged from r = 0.01 to r = 0.25. All correlations were weak. The bees with bigger wings had longer proboscis (r = 0.21...0.25; $P< 0.001$). Honey production was in correlation with the cubital index (r = 0.14; $P< 0.001$) and wintering of bees (r = 0.21; $P<0.001$).

Table 2. The external features of Carniolan bees in 2003

| No of Hive | Width (mm) | | Length (mm) | | Tarsal index % | Cubital index % | Honey production, kg |
|---|---|---|---|---|---|---|---|
| | tergite | wing | wing | proboscis | | | |
| 1 | 4.8 | 3.2 | 9.8 | 6.8 | 59 | 51 | 35 |
| 2 | 4.8 | 3.3 | 10.0 | 6.5 | 57 | 53 | 6 |
| 3 | 4.9 | 3.2 | 9.7 | 5.8 | 61 | 57 | 41 |
| 4 | 4.9 | 3.2 | 9.6 | 5.7 | 61 | 50 | 8 |
| 5 | 4.9 | 3.3 | 9.6 | 5.8 | 59 | 50 | 8 |
| 6 | 4.8 | 3.2 | 10.1 | 7.0 | 57 | 54 | 48 |
| 7 | 4.9 | 3.2 | 9.9 | 6.9 | 59 | 58 | 8 |
| 8 | 4.7 | 3.1 | 9.8 | 6.5 | 59 | 51 | 6 |
| 9 | 4.8 | 3.2 | 10.0 | 6.7 | 58 | 49 | 50 |
| 10 | 4.8 | 3.2 | 9.9 | 6.8 | 56 | 50 | 6 |
| Mean | 4.82 | 3.22 | 9.82 | 6.44 | 58.77 | 52.24 | 21.55 |

Table 3. Correlations between the external features of bees

| Indices | Tergite width | Wings length | Wings width | Proboscis length | Tarsal index % | Cubital index % | Wintering | Honey kg |
|---|---|---|---|---|---|---|---|---|
| Tergite w. | | 0.06* | 0.05 | -0.04 | 0.02 | 0.08** | -0.04 | 0.03 |
| Wings l. | 0.06* | | 0.21*** | 0.25*** | -0.07** | -0.02 | 0.04 | 0.05 |
| Wings w. | 0.05 | 0.21*** | | 0.07** | 0.04 | 0.00 | -0.04 | 0.05 |
| Proboscis l. | -0.04 | 0.25*** | 0.07** | | -0.09** | -0.01 | 0.02 | 0.05* |
| Tarsal in. | 0.02 | -0.07** | 0.04 | -0.09** | | 0.06* | 0.02 | 0.04 |
| Cubital in. | 0.08** | -0.02 | 0.00 | -0.01 | 0.06* | | 0.04 | 0.14*** |
| Wintering | -0.04 | 0.04 | -0.04 | 0.02 | 0.02 | 0.04 | | 0.21*** |
| Honey | 0.03 | 0.05 | 0.05 | 0.05* | 0.04 | 0.14*** | 0.21*** | |

**Conclusions**

1. The purebred Carniolan and crossbred $F_1$ bees (Carniolan x Italian; Carniolan x Nigra) did not differ in the width of tergite, cubital index, wintering and honey production in 2003. Crossbred $F_1$ bees had longer and wider wings than the purebred bees. The purebred Carniolan bees had longer proboscis and higher tarsal index (wide paw).

2. The Carniolan bees in high-yielding colonies (4) had longer wings by 0.01 mm ($P< 0.01$) and proboscis by 0.3 mm ($P< 0.001$) and their honey production was high - 44 kg. These 4 colonies indicated their suitability for reproduction of Queens. Six colonies were low-yielding (7kg) and the bees had shorter wings and proboscis.

3. Correlations between external features, wintering and honey production were weak.

**Acknowledgement**

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# EFFECTS OF FLAX CAKE AND FLAXSEED OIL IN GOAT DIET ON OMEGA -3 FATTY ACID CONTENT OF GOAT MILK

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## Introduction

Human consumption of mammalian milk and meat products has been a matter of concern during the last few years. Milk has been criticized because it contains more saturated fatty acids (SFA) and less polyunsaturated fatty acids (PUFA) than vegetable oil or fish oil (Petit et al., 1998). Monounsaturated and polyunsaturated fatty acids are recommended to replace saturated fats in the diet of humans as much as possible, because evidence suggests that they may reduce blood cholesterol levels and lower the risk for heart disease. An increase in the consumption of products with high saturated fatty acids content is associated with a rise in cardiovascular diseases while intake of PUFA has been associated with the decrease of cholesterol and due to that having less heart problems. The rise in cardiovascular diseases has been linked to the effects of saturated fats, in particular myristic (C 14:0) and palmitic (C16:0) acids, in elevating the plasma concentration of low density lipoprotein cholesterol, which is recognized as a risk factor for coronary heart disease (American Heart Association…, 1990). Human consumption of dairy products containing elevated proportions of mono- (MUFA) and polyunsaturated fatty acids reduces the content of cholesterol in plasma low density lipoproteins (Ashes J.R. et al., 1997). Especially important among polyunsaturated fatty acids are essential omega-3 fatty acids. Alpha-linolenic acid (ALA, C18:3n3) is the parent compound of the omega-3 fatty acid family and it is required in the diet because humans cannot manufacture it. The richest source of ALA is flaxseed which constitutes about 57% of the total fatty acid in flaxseed. ALA is also found mainly in fats and oils of canola, wheat germ and soybeans, currant seeds and nuts such as walnuts (http://www.wadsworth...). Recommended daily intakes of ALA have been determined as 1.6 grams for men and 1.1 grams for women (http://www.wadsworth...). Flax is nature's richest and safest source of omega-3 fatty acids. Flax contains 18 to 24% omega-3 compared to fish at 0 to 2% (http://www.flax...). Flax can be used in animal nutrition by supplementing flax products (flax cake, flaxseed oil) in the normal animal diet. Omega-3 enriched eggs are available at a sale in Estonia (Hämmal et al., 2001), but we have no information whether by feeding goats with omega-3 enriched diets could change the goat milk composition. The aim of this study was to investigate the content and composition of goat milk by feeding goats with omega-3 enriched diets supplemented with flax cake and flaxseed oil. Flaxseed oil is available and a



relatively cheap product. Flax cake is valuable for the high protein content (30.6%) as well.

## Materials and Methods

Study was carried out in April, 2001 on Tubri goat farm, Läänemaa, Estonia with nine Estonian local lactating goats. Goats were selected for similar pedigree, age (3-4 years) and lactation month (3rd month). After adaptation period lactating goats were divided into three groups (Table 1).

Table 1. Experimental scheme

| Group | No. of animals | Diet | No. of milk samples | | |
|---|---|---|---|---|---|
| | | | Day 0 | Day 14 | Day 28 |
| Control | 3 | Conventional diet | 3 | 3 | 3 |
| First Experimental (1. Experim.) | 3 | Plus 30g daily intake of flax-seed oil mixed into barley meal | 3 | 3 | 3 |
| Second Experimental (2. Experim.) | 3 | Plus 180 g daily intake of flax cake | 3 | 3 | 3 |

Normal daily diet included 1.5 kg hay, 1.5 kg forages and 0.7 kg barley meal (control group). The first Experimental group was fed conventional diet supplemented with 30 g of flaxseed oil (Table 1). Flaxseed oil 30 g was mixed into barley meal twice a day (15 g in the morning, plus 15 g in the evening). Conventional diet was supplemented with 180 g flax cake in feeding the second Experimental group. Milk samples were collected from each goat at the beginning of experiment (day 0), after 2 weeks (day 14) and after 4 weeks (day 28). Fatty acid content (16 different fatty acids) of each goat milk sample was analysed using gas chromatography by the Laboratory of Ecochemistry, Department of Chemistry at the Institute of Animal Science. Data were analysed with statistical package Excel.

## Results and Discussions

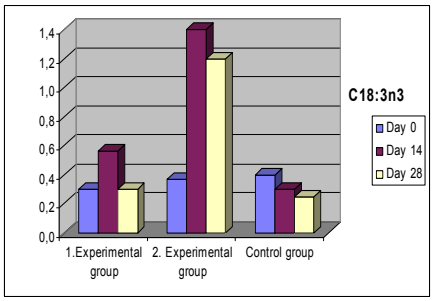
Fatty acids content of goat milk by feeding goats with conventional diet and/or omega-3 enriched diets is given in Table 2.

The total SFA content in goat milk before supplementation was 58.2…64.4% and total MUFA content in the milk was 31…37.3%. The goat milk contained considerable amount of myristic acid (C14:0)-8.10…10.25%, palmitic acid (C16:0)-27.17…30.6%, stearic acid (C18:0)-12.9…14.3% and oleic acid (C18:1)- 29.1…35.3% of the total lipids.

It became clear that goats of the first Experimental group disclaimed to eat barley meal enriched with flaxseed oil after first week from the beginning of the

experiment. There could be two reasons why goats refused to eat this diet. One reason could be because flaxseed oil is fast rancidity oil with low storage stability and therefore goats refused to eat this diet probably because of high rancid taste. Secondly, goats are the animals who are very selective about feed and they might have refused to eat the because of a strange taste. So we found it quite difficult to add flaxseed oil to the goats diet because flaxseed oil is highly rancidity and if there is a wish to use flaxseed oil in goat feeding it would be necessary to find a method which avoids flaxseed oil from becoming rancid and provides it storage ability.

On the other hand, goats ate flax cake eagerly during the whole experiment and this changed the content of goat milk in the second Experimental group in a very positive way (Table 2). The total content of SFA in the second Experimental group decreased from 64.5% (day 0) to 55.5% (day 14) and to 58.9% (day 28), and the total content of MUFA increased from 31% to 38% and 35.5%, respectively. Flax cake in the diet of goats increased the total content of omega-3 fatty acids (C18:3n3 + C18:4n3 + C20:4n3) and essential alpha-linolenic acid (ALA, C18:3n3) content, which is an acid that humans cannot manufacture (Figure 1, Figure 2). For example, the total content of omega-3 fatty acids was 0.97 on day 0, 2.50% on day 14 and 2.13% on day 28 (increase 258% and 220%, respectively). The increase in the content of alpha-linolenic acid was even higher, from 0.37% at the beginning of experiment to 1.40% on day 14 and to 1.20% on day 28. So the increase was 378 % and 324%, respectively.



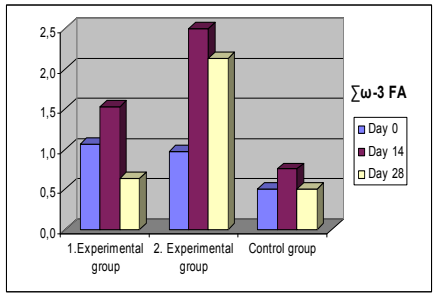




Figure 1, (on the left). Change in alpha-linolenic acid (ALA, C18:3n3) content of goat milk from goats fed with flax cake (2nd experimental group) ration or with ration supplemented with flaxseed oil (1st experimental group) compared with that of goats fed conventional diets (control group).

Figure 2, (on the right). Change in total omega-3 fatty acids content of goat milk from goats fed with flax cake (2nd experimental group) ration or with ration supplemented with flaxseed oil (1st experimental group) compared with that of goats fed conventional diets (control group).



Many investigators had shown the need to protect different oilseeds from ruminal metabolism (Ashes et al.., 1997; Gulati et al., 1997). Supplements with lower protection invariably suppress fiber degradation, reduce acetate production and lower milk yield and fat content.

Table 2. Fatty acid content of goat milk (% of total lipids)

| Fatty acids | Day 0 | | | Day 14 | | | Day 28 | | |
|---|---|---|---|---|---|---|---|---|---|
| | Cont-rol | 1st Expe-rim. | 2nd Expe-rim. | Cont-rol | 1st Expe-rim. | 2nd Expe-rim. | Cont-rol | 1st Expe-rim. | 2nd Expe-rim. |
| C10:0 | 6.30 | 5.30 | 8.94 | 6.50 | 6.97 | 5.23 | 6.05 | 5.27 | 5.20 |
| C12:0 | 2.70 | 2.70 | 3.43 | 2.85 | 2.70 | 2.17 | 2.80 | 2.40 | 2.23 |
| C14:0 | 10.25 | 8.10 | 9.37 | 10.1 | 8.43 | 6.47 | 11.3 | 8.43 | 6.37 |
| C16:0 | 30.6 | 27.17 | 29.17 | 31.75 | 25.10 | 24.03 | 32.65 | 27.93 | 24.33 |
| C18:0 | 12.9 | 14.33 | 13.10 | 12.35 | 15.10 | 17.23 | 14.15 | 8.47 | 20.63 |
| C16:1 | 1.40 | 1.50 | 1.40 | 1.45 | 1.50 | 1.37 | 1.15 | 1.53 | 1.00 |
| C18:1 | 30.35 | 35.27 | 29.07 | 30.35 | 36.30 | 32.60 | 28.05 | 38.33 | 34.20 |
| C20:1 | 1.25 | 0.53 | 0.50 | 0.15 | 0.30 | 0.30 | 0.05 | 0.03 | 0.20 |
| C22:1 | 0 | 0.03 | 0.03 | 0.9 | 0.03 | 0.03 | 0 | 0.0 | 0.07 |
| C18:2n6 | 2.50 | 2.60 | 2.73 | 2.35 | 4.13 | 3.50 | 2.25 | 2.27 | 3.33 |
| C18:3n3 | 0.40 | 0.30 | 0.37 | 0.30 | 0.57 | 1.40 | 0.25 | 0.30 | 1.20 |
| C18:4n3 | 0.10 | 0.63 | 0.40 | 0.25 | 0.87 | 0.93 | 0.20 | 0.27 | 0.80 |
| C20:2n6 | 0.25 | 0.27 | 0.23 | 0.10 | 0.60 | 0.13 | 0.65 | 0.0 | 0.0 |
| C20:3n6 | 0.2 | 0.23 | 0.23 | 0.10 | 0.27 | 0.13 | 0.0 | 0.03 | 0.0 |
| C20:4n6 | 0.40 | 0.23 | 0.40 | 0.20 | 0.23 | 0.30 | 0.1 | 0.23 | 0.13 |
| C20:4n3 | 0.0 | 0.13 | 0.20 | 0.20 | 0.10 | 0.17 | 0.10 | 0.07 | 0.13 |
| Fatty acids % | 1.95 | 2.13 | 2.30 | 2.0 | 2.53 | 2.43 | 1.85 | 2.53 | 2.50 |
| ∑SFA | 63.15 | 58.17 | 64.47 | 63.95 | 58.63 | 55.47 | 67.25 | 56.97 | 58.90 |
| ∑MUFA | 33.00 | 37.33 | 31.00 | 32.85 | 34.40 | 38.00 | 29.25 | 39.90 | 35.47 |
| ∑ω-3 FA | 0.50 | 1.07 | 0.97 | 0,75 | 1.53 | 2.50 | 0.50 | 0.63 | 2.13 |
| ∑ω-6 FA | 3.35 | 3.33 | 3.60 | 2.75 | 5.23 | 4.07 | 3.0 | 2.53 | 3.47 |
| ∑ω-3 FA/∑ω-6 FA | 7.0 | 3.43 | 3.73 | 3.70 | 3.43 | 1.60 | 6.4 | 4.03 | 1.73 |

In this context use of flax cake in goat feeding is a good possible way to alter the content and composition of milk fat with omega-3 fatty acids without special protection of oilseed feeds. This helps to fulfil guidelines for human health.

**Conclusions**

Feeding goats with flax cake improves goat milk fatty acid content and composition as this improves the total content of omega-3 fatty acids, particularly

the content of essential alpha-linolenic acid. As goat is a mini model of milking cow, a similar experiment could be carried out on milking cows to find a possible way to alter the omega-3 fatty acid content in cow's milk and produce healthier milk which has maintained the quality of milk.

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## MILK QUALITY AND CHEMICAL CONTENT OF LATVIAN BREEDING GOATS

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**Abstract.** The chemical composition of goat's milk is better and more valuable, compared with that of cow's milk. The concentrate feeding elevates protein, fat, sugar, amino acid, and macro- and microelement content in goat's milk. The total amount in experimental group was 34.85 g/kg and 32.72 g/kg or 6.5 % more compared with control group. The goat's milk is usable for processing.
**Key words:** goats, milk chemical content.

**Introduction**

The excellent quality of goat's milk shows that it is valuable as a medical product and only from very qualitative and pure goat's milk it is possible to prepare high quality food products – kefir, cream, butter, cheese, yoghurt, etc.

Today in developed countries like the USA, England, France, Germany, Belgium, Italy, Poland and others, the number of goats increases every year. In many countries there is a tendency to establish health resorts and hospitals, where diseases are successfully treated by goat's milk.

The products we received from one goat per annum exceeded the value of goat itself eight to ten times. This situation has not yet been properly estimated. The major products we can receive from goat are milk and cheese. Cottage cheese has appeared in small quantities on the market recently, but it is used mostly by goat breeders themselves at home.

In all countries the regulations are prepared and implemented concerning the goat's milk quality standards – provisions of milk the processing enterprises buy up from producers. In Latvia, the provisions of goat's milk have been drafted but not yet implemented.

In order to attain pure and qualitative goat milk one has to:

a) keep a healthy nanny-goat;
b) apply proper feeding, keeping and care;
c) pay attention to bacteriological purity of milk, obtained from healthy goat in the hygienic circumstances;
d) get fresh milk, without odours and contaminants;

It is important for Latvia to range the goat-breeding issues, because from economic point of view it is very profitable both to keep the pedigree breed and produce cheese and goat's milk for sale.

To produce high quality and pure goat's milk and prepare high quality products, the following conditions should be observed:

• feed should be of great value and quality; it differs from feed used for other domestic animals, e.g. roughages, wood-fibre tree, bush sprouts and branches of trees;

• a stall must be dry and clean, well ventilated and with plenty of litter, draught is not allowed;

• paddocks must have water facilities, which always deliver a fresh water;

• there has to be a disinfectant carpet at a paddock door;

• in the stalls working conditions for milking, feeding and mucking out a dung should be comfortable; the stalls should be big enough – at least 1.5 $m^2$ for one goat and 0.5 $m^2$ for one kid;

• the nanny-goats must be kept separately from he-goats, stalls for he-goat have to be 2.0 – 3.0 $m^2$;

• separate site is necessary for milk refrigerator ( 2.0-5.0$^0$ C).

**Materials and Methods**

Goat's milk from "Apiņi" and "Līcīši" farms in Jelgava region, , where goats had received a special mixed concentrated feed was analysed. The chemical content of milk was determined using Milko-Scan 133 B analyzer. Amino acids (exc. tryptophane) were determined by automatic analyser of amino acids T 229[1], and triptophane - by spectrometer [2]. Macro- and micro elements - by atom absorption spectrophotometer on 403 Perkin - Elmar spectrophotometer model.

The total amount of protein was determined by biuret reaction spectrophotometer [3],and the amount of albumin by spectrophotometer [4].

The amount of lysocym was determined by the nephelometric methods [7], and the circulation amount of immune by spectrophotometer [6].

The analyses were determined in the Laboratories of Animal Biochemistry and Physiology of Biological Institute of the Latvia University, and in milk factory in Riga .

**Results**

The chemical composition of goat's milk is a little better and more valuable than that of cow's milk( Table 1).

We can see, that the content of goat's milk is similar to that of cow's milk, but it has more variations depending on goat breed, age, lactation, keeping and care, feed quality, amount of food and other factors [5].

The goat's milk is of white colour, while cow's milk is yellow. The carotene in the goat feed transforms into vitamin A in the milk. There is 2075 IV vitamin A in one litre of goat's milk, but in cow's milk only 1500 IV. People who are allergic to cow's milk, can use the goat's milk without any threat of allergy.



Table 1. The chemical content of goat's and cow's milk

| Type of animal | Chaff | Include: | | | |
|---|---|---|---|---|---|
| | | fat | protein | milk sugar | mineral substances |
| Cow's milk | 13.0 | 4.0 | 3.3 | 4.7 | 0.7 |
| Goat's milk on average | 13.0 | 4.5 | 3.2 | 4.8 | 0.8 |
| Variations | 10.0-14.6 | 2.9-6.8 | 2.5-4.2 | 4.2-5.2 | 0.8-0.9 |

The goat's milk is rich in albumin and casein not so compact and undigested as that in cow's milk, i.e. it did not penetrate the intestine wall, but is transformed to light flakes by operations of gastric juice and organism revises it easily (Table 2).

Table 2. The content of protein in goat's milk, g/100 g *($x \pm Sx$)*

| Indicator | Content of | | |
|---|---|---|---|
| | total protein | albumin | casein |
| Saanen goat | 3.84 ± 0.16 | 0.66 ± 0.04 | 3.16 ± 0.21 |
| Latvian local goat | 3.92 ± 0.07 | 0.61 ± 0.01 | 3.31 ± 0.10 |

Calculating from total protein content in the Saanen goat's milk, casein constituted 85 %, but in Latvian local goat's milk – 84.4%, about 2.5 % more.

It is known from the literature, that in the goat's milk the greater part of protein is casein ~ 80 %, and lesser part albumin ~ 13-15 %, followed by globulin and other proteins ~ 1 % [5].

In Saanen breed the content of fat is always lower, but in Latvian and Alps – higher. The fat content depends not only on breed, but also on age of animal, lactation and amount of eaten feed. The variations of fat in goat's milk are more sensitive than in the cow's milk, but it is not standardised and depends on determined conditions. The fat content in the goat besting can exceed 14.0% or more, besides balls of fat are very small and equable in the milk and fat and equably digestible and resoluble.

The goat's milk contains all types of amino acids that goats receive with special mixed feed for goats. (Table 3).

Feeding more mixed feed increased the amount of amino acids in milk (lysine, methionine, tryptophane, histidine, leucine + isoleucine, phenylalanine, glycine, alanine, serine, aspartic acid, glutamic acid, tyrosine, proline).

The total sum of amino acids in the test group was 34.85 kg against to 32.72 kg of control group, or 6.5% more compared with the control group.

Table 3. Content of amino acids

| Amino acids | Group | |
|---|---|---|
| | Control | Test |
| Lysine | 1.99 | 2.07 |
| Methionine | 0.89 | 0.93 |
| Tryptophane | 0.64 | 0.82 |
| Arginine | 1.10 | 1.14 |
| Histidine | 1.25 | 1.21 |
| Leucine + isoleucine | 4.89 | 5.17 |
| Phenylalanine | 1.52 | 1.65 |
| Treonine | 2.17 | 2.23 |
| Valine | 1.58 | 1.39 |
| Glycine | 0.92 | 0.96 |
| Alanine | 0.72 | 0.76 |
| Serine | 1.14 | 1.22 |
| Aspartic acid | 2.25 | 2.41 |
| Glutamic acid | 6.79 | 7.73 |
| Tyrosine | 1.85 | 1.91 |
| Proline | 3.02 | 3.25 |
| Sum of amino acids | 32.72 | 34.85 |

Feeding the required amount of mixed feed the amount of macro- and microelements increased in the milk (Table 4).

From minerals in goat's milk, approximately 0.5% are phosphoric acid and calcium (in the cow's milk ~ 0.3%) which can be used easily.

Table 4. Content of macro- and microelements in milk

| Group | Microelements mg/ml | | Microelements mkg/ml | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | Ca | Mg | Zn | Cu | Mn | Fe | Co | Cd | Ni | Pb |
| Control | 0.35 | 0.12 | 4.60 | 0.5 | 0.12 | 1.26 | 0.47 | 0.22 | 0.0 | 2.5 |
| Test | 0.35 | 0.13 | 6.26 | 1.4 | 0.17 | 1.69 | 0.50 | 0.34 | 0.05 | 2.6 |

Our tests indicate that goat's milk contains protective matters. One of them is lysocym, the basic function of which is regulation of permeability of biological membrane and barrier of tissue. Lysocym has high enzyme activities and it operates on the cell membrane of micro-organism. Lysocym at the set level can operate on several infection diseases (staphylococci, streptococci, salmonella, etc.).



The test demonstrated that Latvian local goat's milk contains more protective factors than is shown for possibilities on immunostimulant (medical) effect (5.tab.).

Table 5. Goat's milk unspecific resistance indicators (x± Sx)

| Indicators | Saanen | Local | % against to Saanen | Coefficient of variation S % | |
|---|---|---|---|---|---|
| Lysocym, mkg/ml | 15.17±1.30 | 37.00±3.79* | 243.9 | 14.84 | 17.73 |
| CIC conditioned units | 4.33± 0.73 | 8.35±0.53* | 192.8 | 29.09 | 11.02 |

* $p < 0.05$

The amount of Circulated immune complex (CIC) characterises, that in goat's body and in milk there exists "antigens - antibody ". In the Circulated immune complex usually exists globulin, that fulfils antibody role, but in any case the synthesis of globulin is connected with presence of antigen in the body.

Samples of goat's milk, especially those of the local breed of goats, contains enough lycotin, that can be used in the organism as unspecific protection instrument especially for diseases of stomach.

The analyses were performed also on frozen goat's milk (frozen one week in a refrigerator at $-5^0$ C) (Table 6).

Table 6. Indicators of protein and unspecific resistance in unfrozen and frozen goat's milk

| No. of sample | Milk sample | Total protein quantity g/100g | Albumin quantity g/100 g | Casein quantity g/100 g | Lysocym quantity mgk/ml | CIC in conditioned units* |
|---|---|---|---|---|---|---|
| 1. | unfrozen | 4.05 | 0.56 | 3.49 | 43.0 | 7.30 |
| | frozen | 3.98 | 0.50 | 3.48 | 38.0 | 6.0 |
| 2. | unfrozen | 3.80 | 0.66 | 3.14 | 38.0 | 8.70 |
| | frozen | 3.68 | 0.58 | 3.10 | 32.0 | 8.40 |
| 3. | unfrozen | 3.92 | 0.61 | 3.31 | 30.0 | 9.05 |
| | frozen | 3.83 | 0.54 | 3.29 | 24.0 | 8.50 |
| Average | unfrozen | 3.92 | 0.61 | 3.31 | 37 | 8.35 |
| | frozen | 3.83 | 0.54 | 3.29 | 31 | 7.63 |

* the units of extraction x 100

Various products can be made of goat's milk -- butter, yoghurt, several kinds of cheese – while those are with better taste and flavour, compared with similar products prepared of cow's milk.

## Conclusions

1. Feeding special mixed feed will increase :
   a) milk yield about 15- 20 %;
   b) chaff content in the milk about 1.22 %;
   c) fat content in the milk about 0.71 %;
   d) protein content in the milk about 0.012 %;
2. Feeding special mixed feed for goats increases amino acid content in the milk. The total sum of amino acids for the test group was 34.85 g/kg against 32.72 g/kg or 6.6% more compared with the control group.
3. In Latvian local goat's milk greater part of protein constitutes casein (78.2-87.4% of total protein content), albumin (14.5 – 20.4% of total protein content), globulin and other proteins (1% ).
4. The goat's milk contains the protective matters lysocym Un es ftufdtuyf. 13 – 43 mkg/ml, and circulated complex of immune (CIC) 3.5 – 9.05 conditioned units.
5. Frozen milk loses neither biologically active matters nor its nutritional value.

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# SOME ASPECTS OF PHYLOGENESIS OF LITHUANIAN VISHTINES GEESE


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## Introduction

The order Anseriformes join many wild bird species and the entire row of domestic species and breeds, the majority of which is well known by their morphophysiological and productive qualities. Plenty of experiments are described were various molecular-genetic markers are used for evaluation of genetic variability in different poultry species and breeds. The DNA utilization as genetic marker to evaluate genetic variability of poultry breeds and lines was reported by Semionova et al. (1996), Sruoga et al. (1998). The use of biochemical markers is also significant (Cywa-Benko et al., 1994; Inafukuk et al., 1998; Sruoga et al., 1999).

The characteristic features of biochemical markers are high stability and conservativity. That is the reason why the research of these markers gave an opportunity to evaluate intra- and inter-line genetic variability and also calculate inter-line similarity values. The allelic variants of protein visualized after electrophoresis is the products of certain genes. Studies of such polymorphic proteins may provide additional information on the genetic differences among separate individuals, populations, breeds or species and on the influence of natural or artificial selection to genetic processes, which occur in populations and breeds – gene drift, gene flow and etc. (Kuznetsov, 1995). To date application of biochemical markers for evaluation of plylogenesis of inter- and intra-specific genetic differentiation of wild and domesticated species of Anseriformes is insufficient. Thus, the purpose of present research was to evaluate the genetic variability, genetic similarity and genetic distances among White-fronted goose (*Anser albifrons*) and Touluse Landaise, Rheinish White, Italian, commercial hybrid line and Lithuanian Vishtines domestic geese breeds based on genetically determinated blood serum and liver protein allele frequencies.

## Matherial and Methods

Blood samples were collected from migratory White-fronted geese and Touluse Landaise, Rheinish White, Italian, commercial hybrid line and

Lithuanian Vishtines geese breeds. Blood was taken by venipuncture of the wing vein and plasma was obtained by centrifugation at 3000 g for 10 min. Samples collected were frozen at -20°C for future storage in the laboratory.

Disk-electrophoresis was carried out in a two layer vertical block of polyacrilamide slides following the methods suggested by Brewer (1970), Murphy (1996) with some modifications. Proteins were stained with Coomassie Blue G-250. All parameters and distances were calculated using Biosys-1, Biosys-2 and PopGene 1.32. Dendrogram was performed using TFPGA computer program for population genetic analysis.

**Results and Discussion**

Investigated geese breeds belong to Touluse and Embden phenotype subgroups of European phenotype group. Wild geese – White-fronted geese (*Anser albifrons*) belong to the most numerous and distributed all around the world wild geese species. Hybrids derived from Italian White and Touluse Landaise breed crossing as well as native Lithuanian Vishtines and Italian breeds were examined according to genetic variability of non-specific blood serum proteins. Using electrophoresis 8 polymorphic protein systems were investigated: macroglobulin (Mc), posttransferin (Ptf), transferin (Tf), Pretransferin (Prtf), postalbumin (Pa), albumin (Al), prealbumin 1 (Pr-1) and prealbumin 2 (Pr-2). Gene frequencies of investigated wild geese and domesticated geese hybrids are presented in Table 1, from which we can see that all investigated domestic and hybrid breeds differ from white-fronted geese at least by four (*PreTf, PostTf, Mc* and *Tf*) loci allele frequencies. The most conspicuous difference was detected between White-fronted geese and domestic geese in poliallelic *Tf* locus rear $Tf^D$ allele frequency. This allele was not detected in Italian White and Lithuanian Vishtines breeds at all, while frequency of this allele in White-fronted geese is 0.125. Pronounced difference in $Tf^A$ and $Tf^B$ allele frequencies (0.304, 0.694 and 0.725, 0.275) between White-fronted geese and Touluse Landaise geese was detected.

Heterozygosity, heterozygote deficiency and deviation from Hardy-Weinberg equilibrium analysis shows (Table 2) that natural selection and domestication, breeding in close populations, and sometimes even inbreeding had influence on different geese breeds and species. Very high heterozygote deficiency and deviation from Hardy-Weinberg equilibrium is detected in Touluse Landaise and Rheinish White geese. Significant deficiency of heterozygotes was detected at *PreAl, PostAl, Mc* and *Tf* loci for Touluse Landaise breed and at *PreAl, PreTf, PostTf* and *Tf* loci for Rheinish White breed.



Table 1. Alelle frequencies of Italian, Touluse Landaise, Hybrid geese, Rheinish, Lithuanian Vishtines breeds and White-fronted geese

| Alleles | Geese breeds and species | | | | | |
|---|---|---|---|---|---|---|
| | Italian (n=20) | Touluse-Landaise (n=20) | Hybrid geese (n=20) | Rheinish White (n=36) | Lithuanian Vishtines (n=26) | White-fronted geese (n=28) |
| $PreAl\text{-}1^A$ | 0.525 | 0.400 | 0.575 | 0.583 | 0.419 | 0.500 |
| $PreAl\text{-}1^B$ | 0.475 | 0.600 | 0.425 | 0.417 | 0.481 | 0.500 |
| $PreAl\text{-}2^A$ | 0.550 | 0.525 | 0.425 | 0.556 | 0.538 | 0.411 |
| $PreAl\text{-}2^B$ | 0.450 | 0.475 | 0.575 | 0.444 | 0.462 | 0.589 |
| $Al^A$ | 0.475 | 0.650 | 0.675 | 0.597 | 0.538 | 0.429 |
| $Al^B$ | 0.525 | 0.350 | 0.325 | 0.403 | 0.462 | 0.571 |
| $PostAl^A$ | 0.575 | 0.475 | 0.575 | 0.542 | 0.654 | 0.429 |
| $PostAl^B$ | 0.425 | 0.525 | 0.425 | 0.458 | 0.346 | 0.571 |
| $PrtTf^A$ | 0.500 | 0.725 | 0.500 | 0.417 | 0.423 | 0.304 |
| $PrtTf^B$ | 0.500 | 0.275 | 0.500 | 0.583 | 0.577 | 0.694 |
| $PostTf^A$ | 0.400 | 0.575 | 0.500 | 0.306 | 0.577 | 0.679 |
| $PostTf^B$ | 0.600 | 0.425 | 0.500 | 0.694 | 0.423 | 0.321 |
| $Mc^A$ | 0.400 | 0.450 | 0.425 | 0.306 | 0.327 | 0.571 |
| $Mc^B$ | 0.600 | 0.550 | 0.575 | 0.694 | 0.673 | 0.429 |
| $Tf^A$ | 0.250 | 0.200 | 0.475 | 0.552 | 0.346 | 0.107 |
| $Tf^B$ | 0.375 | 0.350 | 0.250 | 0.345 | 0.385 | 0.304 |
| $Tf^C$ | 0.375 | 0.375 | 0.250 | 0.086 | 0.269 | 0.464 |
| $Tf^D$ | 0.000 | 0.075 | 0.025 | 0.017 | 0.000 | 0.125 |

Table 2. Nei's (1972) genetic identity (below diagonale) and genetic distance (above diagonale) between different geese breeds and White-fronted geese species.

| Breed | Italian | Touluse Landaise | Hybrid geese | Reinish White | Lithuanian Vishtines | White-fronted geese |
|---|---|---|---|---|---|---|
| Italian | * * * | 0.037 | 0.028 | 0.021 | 0.016 | 0.055 |
| Touluse Landaise | 0.963 | * * * | 0.041 | 0.072 | 0.047 | 0.075 |
| Hybrid geese | 0.972 | 0.960 | * * * | 0.024 | 0.020 | 0.072 |
| Reinish White | 0.980 | 0.930 | 0.977 | * * * | 0.026 | 0.104 |
| Lithuanian Vishtines | 0.984 | 0.954 | 0.980 | 0.974 | * * * | 0.057 |
| White-fronted geese | 0.946 | 0.928 | 0.931 | 0.901 | 0.944 | * * * |

In Italian White and Lithuanian Vishtines breeds gene equilibrium was broken only at two loci – *PreAl* and *Tf*. In hybrid geese statistically significant gene disequilibrium was detected only for one diallelic *PreTf* locus. It shows that crossbreeding plays an important role in recovering of equilibrium of genes. For wild White-fronted geese population significant heterozygote deficiency was detected only in two diallelic *PreAl-1* and *PreAl-2* loci. Moreover, expected heterozygosity was not diverged from observed at the majority of loci investigated. This allows us to predicate that gene equilibrium and high heterozygosity level are maintained at naturally existing numerous panmictic populations. High level of heterozygosity increases potentiality of adaptation of species.

Genetic distances and genetic identity analysis shows that wild White-fronted geese are most differentiated from Reinish White (genetic distance is 0.104). The least genetic distance was detected between Italian and Lithuanian Vishtines geese breeds (D=0.016).

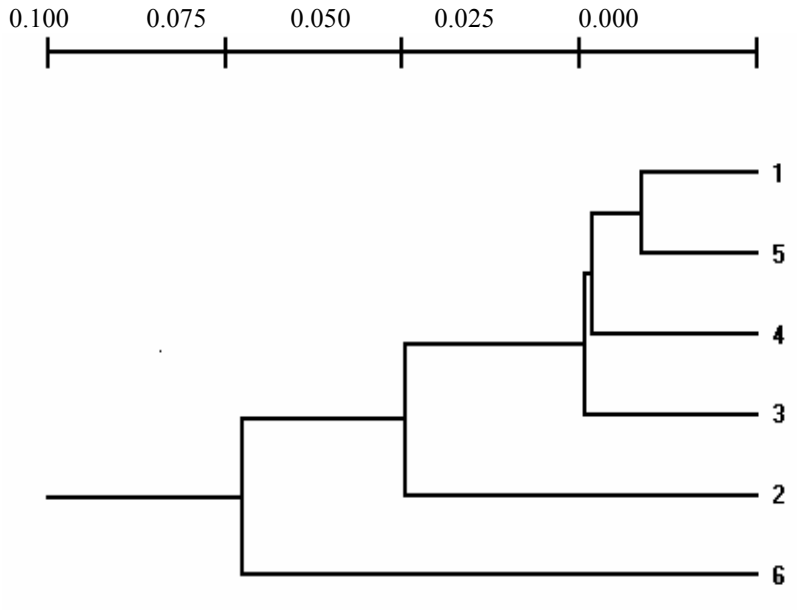


Figure 1. UPGMA cluster analysis of different geese breeds and White-fronted geese species using Nei's (1972) original distance. 1 – Italian; 2 – Touluse-Landaise; 3 – Hybrid geese; 4 – Reinish White; 5 – Lithuanian Vishtines; 6 – White-fronted geese.



Cluster analysis of investigated geese breeds and White-fronted geese (Figure 1) shows, that Touluse Landaise phenotype geese form separate cluster, differentiated separately from other investigated breeds and hybrids. Whereas Italian and Lithuanian Vishtines geese of Embden phenotype form one cluster in dendrogram. Hybrid geese occupy intermediary place between Lithuanian Vistines and Rheinish White geese. White-fronted geese form separate line in dendrogram and it is the most close to Touluse Landaise geese and hybrids. The highest distance is detected between wild geese and Embden phenotype Italian and Native Vistines geese breeds. The last ones have common origin and similar phenotype.

In general, results of the investigation show, that geese breeding in closed population as well as man-maid selection affect domestic geese gene equilibrium and lower heterozygosity. In White-fronted geese population panmictic natural selection maintains genetic equilibrium and high level of heterozygosity.

**Conclusion**

1. Lithuanian Vishtines geese have original morpho-physiological, productive and genetic characteristics and differentiate from wild White-fronted geese more than by four polymorphic loci allele frequencies. The lowest genetic distance (0.016) was detected between Lithuanian Vishtines and Italian geese breeds, and the highest genetic distance coefficient (0.104) was calculated between White-fronted geese species and Rheinish White geese breed.

2. Lithuanian Vishtines geese form separate common with Italian geese cluster in dendrogram, whereas White-fronted geese form separate branch, which is more related to Touluse Landaise and hybrid geese.

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# GENETIC STRUCTURE AND VARIATION BETWEEN THE LINES AND FAMILIES OF LARGE-TYPE ŽEMAITUKAI HORSES

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## Introduction

The large-type Žemaitukai horse was developed in Eastern Lithuania at the end of the 19th century by crossbreeding old-type Žemaitukai horses with North Swedish and Orlov Trotter horses. Later, the horse was called the harness horse of East Lithuania. They are most suitable draft horses, easy manageable, not shy, highly disease resistant and undemanding as regards feeding. In 1949, the horses of this type and the Žemaitukai horses were given one name – the Žemaičiai horses. In the same year, the improvement of the large-type Žemaitukai horse was started at the Vilnius Stud, where stallion lines and mare families have been formed. Employing the remaining three main stallion lines, i.e., Šachtioras, Agrastas and Kalmanas, line breeding at the studs has been carried out. Besides, the Klintas and Listeris lines of the North Swedish horse were used. Blood polymorphism facilitates to describe the genetic variation within breed and its structural units (lines). The objective of our study was to examine the genetic differences and genetic variation between the lines and families.

## Material and Methods

The pedigree of large type Žemaitukai horses was analysed on the basis of state stud books and stud documentation. The level of inbreeding was calculated by the formula of S. Wright [1931].

The blood of large-type Žemaitukai horses was analysed at the Blood Typing Laboratory of the LIAS. The pedigree and blood samples were collected from 25 horses from Šachtioras line, 15 from Agrastas line, 12 from Kalmanas line, 6 from Klintas line, 9 from Niemka family, 5 from Gulbė family, 4 Danutė family and 3 from Mėta family. Two 10 ml samples were obtained from each horse, one on ACD anti-coagulant and another to a dry tube to be used as a source of red cells and serum, respectively. Standard immunological procedure involving hemagglutination and complement-mediated heamolysis [Stormont and Suzuki, 1964] were used to detect red cell alloantigens at six internationally recognized blood group loci: A, D, C, Q, P and K [Sanberg, 1995]. The reagents used to detect the antigenic properties were obtained by alloimmunization. Assigment of alleles was based on reagent reaction patterns and followed the internationally accepted terminology.

Standard methods of horizontal polyacrylamide gel electrophoresis [Juneja et al., 1978] were used to identify inherited variants at the following protein loci:

albumin (Al), esterase (Es), vitamin D-binding protein (Gc), AlB glycoprotein (Xk) and transferrin (Tf). Frequency of antigenic factors, allele frequency, genetic similarity and degree of homozygosity (Ca) were computed by conventional methods described by Maijala and Lindstrom [1966], Rendel [1967], Matousek [1964], Nei [1972], and Zhivatovski and Mashurov [1974].

**Results and Discussion**

The genealogical analysis of large-type Žemaitukai horses indicated that inbreeding produced 43.4% of investigated breeding horses. The average inbreeding coefficient of these horses was 5.1% (0.8-14.1%) by the method of S. Wright. Currently, we have the progeny of the three main stallion lines, namely, Šachtioras, Agrastas and Kalmanas as well as of the North Swedish stallion Klintas line and Listeris line.

53.3% of horses of Agrastas line were obtained by inbreeding, the average inbreeding coefficient is 4.43%. 80% of horses of the Agrastas line have North Swedish horse blood. Currently, stallions and mares belonging to the Agrastas line are energetic and have solid constitution. The stallions and mares of Šachtioras line are noted for high heritage. The body conformation and development traits of Šachtioras line horses are very similar, yet the representatives of this line are large in size and heavy. 72% of horses of this line were obtained by inbreeding. The average inbreeding coefficient is 5.8%. 84% of horses of the Šachtioras line have North Swedish horse blood. The mares and stallions of the Kalmanas line are very uniform in development and exterior. The resemblance of the representatives of this line to the large-type Žemaitukai horse is very high. 50% of horses this line were obtained by inbreeding, the average inbreeding coefficient is 6.9%. 25% of horses of the Kalmanas line have North Swedish horse blood. 67% of horses of Klintas line were obtained by inbreeding. The average inbreeding coefficient is 1.05%.

The genealogical analysis of families indicated that 55% of mares of Niemka family were obtained by inbreeding, the average inbreeding coefficient (F) is 7.04%. 60% of mares of Gulbė family were obtained by inbreeding, the average inbreeding coefficient is 7.2%. 25% of mares of Danutė family were obtained by inbreeding, the average inbreeding coefficient being 7%. The Mėta family was obtained by outbreeding.

The characteristic blood group alleles, serum protein alleles obtained in this study are shown in Table 1. The most effective loci were those having five or more alleles with appreciable frequencies, namely D and Tf. The genetic analysis of alleles indicated that $Al^{AB}$ genotype was typical of large-type Žemaitukai, alleles $D^{dghm}$, $D^{cgm}$, $D^{dk}$, $D^{dl}$ and genotype $Tf^{FF}$, $^{FO}$ were also frequent. The degree of homozygosity ranged from 13.48% (D locus) to 50.67% (Q locus), with mean value of 32.69%. Macijauskienė and Juras [2003] have reported that the genetic



analysis of alleles indicated that $D^{dghm}$ allele was typical of old-type Žemaitukai horses, alleles $D^{adl}$, $D^{cgm}$ and genotype $Tf^{DF}$ were also frequent.

Table 1. Gene frequencies of blood group and serum protein markers in large-type Žemaitukai horses

| Locus | Allele | Allele frequency (n=83) | Locus | Genotype | Genotype frequency (n=83) |
|---|---|---|---|---|---|
| Blood group markers | | | Protein markers | | |
| A | ad | 0.4036 | Al | AA | 0.3133 |
| | bc | 0.0843 | | AB | 0.6024 |
| | b | 0.0843 | | BB | 0.0843 |
| | c | 0.0723 | Ca | 46.82% | |
| | $A^-$ | 0.3555 | Es | FF | 0.1807 |
| Ca | 30.87% | | | FI | 0.3494 |
| D | dghm | 0.1627 | | II | 0.4217 |
| | cgm | 0.1506 | | IS | 0.0361 |
| | dk | 0.1627 | | FS | 0.0120 |
| | ad | 0.006 | Ca | 33.39% | |
| | dl | 0.1566 | Tf | DD | - |
| | bcm | 0.0783 | | FF | 0.3373 |
| | dkl | 0.0482 | | DF | 0.1807 |
| | cdf | 0.006 | | DO | 0.0843 |
| | dfk | 0.012 | | DR | - |
| | cfgkm | 0.0723 | | FO | 0.2048 |
| | $D^-$ | 0.1446 | | FR | 0.1084 |
| Ca | 13.48% | | | OO | 0.012 |
| Q | abc | 0.0422 | | RR | - |
| | bc | 0.0542 | | FM | 0.012 |
| | c | 0.0964 | | HR | 0.012 |
| | b | 0.1145 | | FH | 0.0361 |
| | ac | - | | OR | 0.012 |
| | a | - | | MO | - |
| | $Q^-$ | 0.6925 | Ca | 20.9% | |
| Ca | 50.67% | | | | |

Tables 2 and 3 show the frequencies of alleles within blood group and serum protein systems occurring in the horses of Sachtioras, Agrastas, Kalmanas and Klintas lines. $D^{ad}$, $Q^b$ alleles and genotypes $Tf^{FM,\ HR}$ were detected only in Šachtioras line. Allele $D^{dfk}$ and genotypes $Es^{IS}$, $Tf^{DO,\ FH,\ OR,\ MO}$ were detected only

in Agrastas and genotype $Tf^{DR}$ in Klintas lines. Analysis of allele and genotype frequencies on which the estimation of genetic similarity between the lines should be based showed that the frequencies of alleles varied from 0.02 to 0.83. The most frequent allele at A system was $A^{ad}$ (frequency 0.42-0.47).

Table 2. Allele frequencies of blood group markers in large-type Žemaitukai horses

| Locus | Allele | Stallion lines | | | | Mare families | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | Šach-tioras n=25 | Ag-rastas n=15 | Kal-manas n=12 | Klin-tas n=6 | Niem-ka n=9 | Gulbė n=5 | Danu-tė n=4 | Mėta n=3 |
| | | Allele frequency | | | | | | | |
| A | ad | 0.42 | 0.47 | 0.46 | 0.42 | 0.39 | 0.30 | 0.50 | 0.50 |
| | bc | 0.08 | 0.13 | 0.08 | 0.08 | 0.11 | 0.20 | 0.25 | - |
| | b | 0.14 | - | 0.13 | 0.08 | 0.05 | 0.20 | - | - |
| | c | 0.06 | 0.03 | 0.04 | 0.08 | 0.05 | - | 0.13 | 0.33 |
| | $A^-$ | 0.30 | 0.37 | 0.29 | 0.34 | 0.4 | 0.30 | 0.12 | 0.17 |
| Ca % | | 29.8 | 37.5 | 32.1 | 31.1 | 39.9 | 26.0 | 34.4 | 38.8 |
| D | dghm | 0.10 | 0.23 | 0.08 | - | 0.17 | 0.20 | 0.25 | 0.16 |
| | cgm | 0.12 | 0.17 | 0.33 | 0.17 | 0.22 | 0.20 | 0.25 | - |
| | dk | 0.16 | 0.13 | 0.29 | 0.17 | 0.17 | 0.30 | 0.12 | 0.33 |
| | ad | 0.02 | - | - | - | - | - | - | 0.33 |
| | dl | 0.20 | 0.13 | - | 0.25 | 0.05 | - | - | - |
| | bcm | 0.10 | 0.07 | 0.04 | 0.17 | - | 0.10 | 0.12 | - |
| | dkl | 0.06 | - | 0.08 | - | 0.11 | 0.10 | - | - |
| | cdf | 0.02 | 0.03 | 0.04 | - | 0.05 | - | - | 0.16 |
| | dfk | - | 0.03 | - | - | - | - | - | - |
| | cfgkm | 0.10 | 0.13 | - | 0.17 | - | - | 0.25 | - |
| | $D^-$ | 0.12 | 0.08 | 0.14 | 0.07 | 0.23 | 0.10 | 0.01 | 0.02 |
| Ca % | | 15.9 | 14.6 | 22.9 | 18.3 | 17.6 | 20.0 | 21.6 | 26.9 |
| Q | abc | 0.02 | - | 0.04 | 0.08 | 0.05 | 0.10 | - | 0.50 |
| | bc | - | 0.03 | 0.04 | - | 0.05 | 0.10 | 0.13 | - |
| | c | 0.26 | 0.23 | 0.13 | 0.17 | 0.11 | 0.10 | 0.13 | - |
| | b | 0.06 | - | - | - | - | - | - | - |
| | ac | - | 0.07 | 0.08 | - | 0.05 | 0.10 | 0.13 | - |
| | $Q^-$ | 0.66 | 0.67 | 0.71 | 0.75 | 0.74 | 0.60 | 0.61 | 0.50 |
| Ca % | | 50.7 | 50.7 | 53.1 | 59.8 | 56.7 | 30.0 | 42.3 | 50.0 |



Table 3. Gene frequencies of serum protein markers in large-type Žemaitukai horses

| Locus | Genotype | Stallion lines | | | | Mare families | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | Šach-tioras n=25 | Ag-rastas n=15 | Kal-manas n=12 | Klin-tas n=6 | Niem-ka n=9 | Gulbė n=5 | Danu-tė n=4 | Mėta n=3 |
| | | Gene frequency | | | | | | | |
| Al | AA | 0.20 | 0.33 | 0.33 | 0.17 | 0.33 | 0.40 | 0.25 | 0.33 |
| | AB | 0.76 | 0.40 | 0.67 | 0.83 | 0.55 | 0.60 | 0.50 | 0.33 |
| | BB | 0.04 | 0.27 | - | - | 0.11 | - | 0.25 | 0.33 |
| Ca % | | 61.9 | 34.2 | 55.8 | 71.8 | 42.4 | 52.0 | 37.5 | 32.7 |
| Es | FF | 0.16 | 0.13 | - | 0.17 | 0.22 | - | - | - |
| | FI | 0.56 | 0.53 | 0.17 | 0.50 | - | 0.40 | 0.25 | 0.33 |
| | II | 0.28 | 0.27 | 0.83 | 0.33 | 0.77 | 0.60 | 0.75 | 0.66 |
| | IS | - | 0.07 | - | - | - | - | - | - |
| | FS | - | - | - | - | - | - | - | - |
| Ca % | | 41.8 | 37.6 | 71.8 | 38.8 | 64.1 | 52.0 | 62.5 | 54.5 |
| Tf | DD | - | - | - | - | - | - | - | - |
| | FF | 0.36 | - | 0.58 | 0.33 | 0.44 | 0.40 | - | 0.66 |
| | DF | 0.12 | 0.20 | 0.08 | - | 0.22 | - | 0.25 | - |
| | DO | - | 0.40 | - | - | - | - | 0.50 | - |
| | DR | - | - | - | 0.17 | - | - | - | - |
| | FO | 0.32 | 0.13 | 0.25 | 0.33 | 0.33 | 0.20 | - | 0.33 |
| | FR | 0.12 | 0.07 | - | 0.17 | - | 0.20 | - | - |
| | OO | - | - | 0.08 | - | - | 0.20 | - | - |
| | RR | - | - | - | - | - | - | - | - |
| | FM | 0.04 | - | - | - | - | - | - | - |
| | HR | 0.04 | - | - | - | - | - | 0.25 | - |
| | FH | - | 0.07 | - | - | - | - | - | - |
| | OR | - | 0.07 | - | - | - | - | - | - |
| | MO | - | 0.07 | - | - | - | - | - | - |
| Ca % | | 26.4 | 23.7 | 41.2 | 27.6 | 35.1 | 28.0 | 37.5 | 54.5 |

Tables 2 and 3 show the frequencies of alleles within blood group and serum protein systems occurring in the horses of Niemka, Gulbė, Danutė and Mėta families. $D^{dl}$ allele and genotype $Es^{FF}$ were detected only in Niemka family. Genotype $Tf^{FR,\ OO}$ were detected only in Gulbė family. Allele $D^{clgkm}$ and genotypes $Tf^{DO,\ HR}$ were detected only in Danutė family, allele $D^{ad}$ in Mėta family.

Genetic similarities between Šachtioras and Agrastas, Kalmanas, Klintas lines, and between Niemka and Gulbė, Danutė, Mėta families were determined using the genetic distance coefficients calculated from the allele frequencies within three blood group and three serum protein systems. The higher genetic similarities were detected between Šachtioras and Klintas lines (r=0.914) and the lowest between Šachtioras and Agrastas lines (r=0.514). The lowest genetic similarities r=0.239 were found between Niemka and Danutė families. The higher genetic similarities r=0.567 were found between Niemka and Gulbė families.

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## THE EFFECTS OF HOUSING METHODS ON THE GROWTH RATE AND FEED CONVERSION OF FATTENING MALE LAMBS

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**Introduction**

In 1995 a flock of almost extinct local coarsewooled sheep was started at the Lithuanian Institute of Animal Science. In 1999 these sheep were recognized as pedigree. The Institute conducts research of the biological and farming qualities and selection of local sheep for their further breeding and distribution [10, 12]. Currently, the flock consists of 40 sheep, including 4 breeding rams, 20 ewes and 17 lambs.

Since 2000, local sheep have also been bred by farmer L. Griškevičienė (Širvintai distr.). In 2003 her flock (approx. 30 heads) was recognized as pedigree. Several local sheep are kept by Kaunas Zoo, Open Country Life Museum in Rumšiškės and farmer V. Kondratas (Telšiai distr.).

At present, local sheep are distinguished by higher productivity and earlier maturity, compared to the aboriginal ones, but they also have remained disease resistant and undemanding with regard to housing and feeding conditions, have retained the exterior and non-seasonal estrus peculiar to aboriginal sheep [5, 6].

Sheep at the conservation flock of the Institute are evaluated for their exterior, weight, reproductive performance, milk, wool and meat traits. The purpose of the present paper was to determine the effects of housing methods on the growth rate and feed conversion of fattening ram lambs of the local coarsewooled breed.

**Material and Methods**

In 2003 the trials were carried out in the conservation flock of native coarsewooled sheep belonging to the Lithuanian Institute of Animal Science. All male lambs (n=10) born in 2003 were used in this trial. From birth to the end of the trial (6.5 months of age), the ram lambs were housed in confinement and fed cultivated pasture grass and concentrated feeds. The lambs were kept in pens together with their ewes till weaning at 2.5 months of age. The lambs were allotted to two groups (5 lambs for individual fattening and 5 for group fattening) when the control feeding was started. The lambs were allotted to two groups of animals on the basis of their age, litter size and weight [2, 3, 9].

The fattening of lambs lasted for 60 days (from 2.5 to 4.5 months of age), and later the youngsters were fed in the same way following the feeding standards for lambs [7, 11]. Every day each fattened lamb was offered 500 g of compound feed and 2-3 kg of grass. The amount of offered feeds and the remains of feeds were weighed twice daily [6, 12]. The chemical composition of feeds was determined by conventional methods at the Analytical Laboratory of the Institute.

The growth rate of lambs was determined by weighing lambs at birth, 20 days, 2, 2.5, 3.5, 4.5, 5.5 and 6.5 months of age. All the main data except for feed intake have been processed biometrically [1, 4, 8].

**Results and Discussion**

The weight of newborn lambs and their growth rate were determined every year, but the fattening performance of male lambs was studied for the first time. Fattening in two different ways – group and individual – was also performed for the first time.

It should be noted that the weight of newborn lambs varied from 2.0 to 3.9 kg and such difference could be explained by different age and fertility of ewes. Further growth of male lambs depended on individual traits of the lamb, milk yield of the ewe, feeding level and housing method. The average daily gain of male lambs was 165 g (120-250 g) from birth to 20 days of age and about 120 g (50-200 g) from 20 to 60 days of age.

Table 1. The growth rate of male lambs at different housing

| Item | Group housing (n=5) | Individual housing (n=5) |
|---|---|---|
| Weight of a newborn male lamb, kg | 3.05±0.07 | 2.77±0.27 |
| Weight at 20 days of age, kg | 6.55±0.45 | 5.81±0.44 |
| Daily weight gain till 20 days of age, g | 175.60±23.14 | 152.00±11.54 |
| Weight of a male lamb at 2 months of age, kg | 10.18±0.74 | 9.36±0.52 |
| Daily gain from 20 to 60 days of age, g | 90.0±9.52 | 88.40±17.68 |
| Weight of a male lamb at 2.5 months of age, kg | 14.14 ±0.97 | 13.82±0.41 |
| Daily gain in 14 days of control fattening from 2 to 2.5 months, g | 226.60±37.86 | 253.20±39.40 |
| Weight of a male lamb at 3.5 months of age, kg | 20.0±1.38 | 19.60±0.89 |
| Daily gain in the first 30 fattening days from 2.5 to 3.5 months, g | 201.80±27.41 | 192.0±32.97 |
| Weight of a male lamb at 4.5 months of age, kg | 27.00±2.17 | 25.00±0.94 |
| Daily gain in the second 30 fattening days from 3.5 to 4.5 months, g | 226.60±32.73 | 180.00±16.97 |
| Weight of a male lamb at 5.5 months of age, kg | 32.40±2.29 | 30.40±1.15 |
| Daily gain in 30 days at adequate feeding from 4.5 to 5.5 months, g | 180.00±14.42 | 179.80±8.15 |
| Weight of a male lamb at 6.5 months of age, kg | 35.40±2.50 | 32.90±2.33 |
| Daily gain from birth till 6.5 months of age, g | 154.60±16.96 | 136.40±9.05 |



In order to determine the highest level of feeding for fattening lambs, a 14 – day check of control fattening was carried out (Table 1). At this period, all male lambs (n=10) were kept in a group pen. Afterwards, when 60 – day control fattening was started (from 2.5 to 4.5 months of age), five male lambs were transferred to their group pen, while the other five were kept in individual pens.

The data in Table 1 show that at the beginning the weight of male lambs for individual feeding was only by 32 g lower than that of lambs for group feeding. A small weight difference (60 g) was also recorded after the first 30 fattening days, but at the end of fattening (60 days), weight of individually fattened lambs was by 2 kg (7.4%) lower and their daily gain was 46.6 g (20.6%) lower than that of the lambs fattened in group.

After completion of fattening, the lambs were given only 300 g of compound feed and 3-4 kg of grass and kept in a group of 5 animals. From 4.5 to 5.5 months of age, the difference in weight remained but the daily gain became almost the same. However, from 5.5 to 6.5 months of age, male lambs fed individually weighed by 2.5 kg (7.1%) less and their daily gain was 15 g (18.4%) lower compared with group feeding of male lambs.

Table 2. Economic efficiency of male lamb fattening

| Item | Group feeding (n=5) | Individual feeding (n=5) |
|---|---|---|
| Weight of a male lamb, kg: | | |
| at the beg. (2.5 months of age) | 14.14 ± 0.7 | 13.82 ± 0.41 |
| at the end (4.5 months of age) | 27.00 ± 2.17 | 25.00 ± 0.94 |
| Daily gain, g | 214.20 ± 29.37 | 186.40 ± 14.81 |
| Food consumption in 60 days: | | |
| Cultivated pasture grass, kg | 128.89 | 82.76* |
| Compound feed, kg | 29.33 | 28.94 |
| Metabolizable energy, MJ | 607.53 | 499.92* |
| Feed units | 57.93 | 48.71* |
| Digestible protein, kg | 5.88 | 4.87* |
| Used per 1 kg of gain: | | |
| Metabolizable energy, MJ | 47.24 | 44.72 |
| Feed units | 4.50 | 4.36 |
| Digestible protein, g | 457.23 | 435.60 |
| Price of consumed feeds, LTL: | | |
| Per male lamb in 60 days | 17.71 | 15.92 |
| Per 1 kg gain | 1.38 | 1.42 |

*P < 0.01

The data in Table 2 indicate that the total weight increase in 60 days was 12.86 kg for group fattened lambs and 11.18 kg for individually fattened lambs. However, individually fattened lambs consumed about 20% feeds less and the cost price of feeds was 10% lower. Also these lambs used 5% less energy and nutrients per kg gain, but the cost price of feeds per kg gain was 0.04 Litas (3%) higher than that of the feeds for group fattened lambs.

**Conclusions**

1. Group fattening of male lambs resulted in 1.68 kg (13.1%) higher weight increase in 60 days than individual fattening.
2. On the basis of this study, it is recommended to keep fattening male lambs in group pens (5-10 animals per pen), feed them with green feeds *ad libitum* and up to 500 g of compound feed.

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## COMPARISON OF CYTOPLASMIC AND AUTOSOMAL DNA DIVERSITY PATTERNS IN BALTIC SHEEP


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**Introduction**

Sheep husbandry had spread to British Isles, Scandinavia and Russia already 6000 years ago (Ryder, 1991). There exist two common mitochondrial lines in domestic sheep which diverged from each other approximately 375 000 to 750 000 years ago. One of the mitochondrial types has been found only in European domestic sheep, while the other type is uncommon in Europe, but common elsewhere (Hiendleder *et a.,* 1998).

Recent studies have been unravelling the patterns of molecular genetic variation in Baltic sheep breeds using cytoplasmic (mitochondrial control region sequences) and autosomal (microsatellite length variation) DNA markers (Grigaliunaite, 2003; Grigaliunaite et al*.,* submitted; Tapio et al*.,* in prep). Since the two types of markers might give conflicting results (Mitton, 1994) the present paper compares the reported (Grigaliunaite, 2003) cytoplasmic and mitochondrial diversity results for Baltic sheep and discusses the reasons for the unconcordant results.

**Material and Methods**

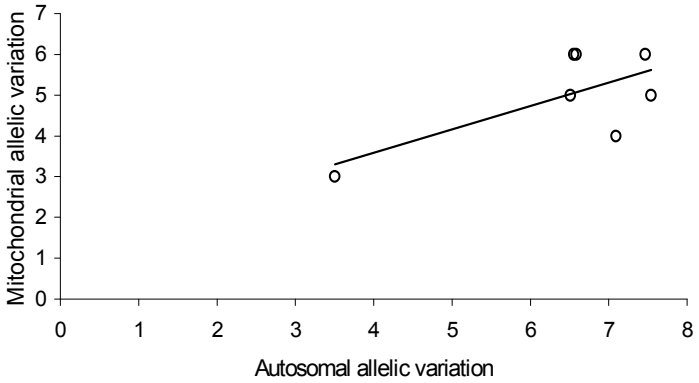
DNA marker information about seven Baltic sheep breeds was used (Estonian Whitehead, Estonian Blackhead, Estonian Ruhnu, Estonian Saaremaa, Latvian Darkheaded, Lithuanian Coarsewooled, Lithuanian Blackface). Data collection and analyses have been described by Grigaliunaite (2003). The sequencing of mitochondrial control region was performed for six sheep per breed except for Ruhnu sheep, where nine individuals were sequenced. The microsatellite genotyping was performed for 21-32 sheep per breed.

**Results and Discussion**

In total, 45 mitochondrial control region sequences were determined and 96% of the sequences belonged to the mitochondrial line that constitutes the majority in Europe. Only two local sheep from Saaremaa possessed the so called Asian type mitochondrion, which is rare in Europe. Mitochondria belonging to this group have been found earlier in breeds of Finnish, Norwegian and Russian origin (Tapio *et a.,* 2002).

The within-breed diversity estimates of mitochondrial and microsatellite variation correlated positively (Figure 1). However, the correlation was caused by Ruhnu sheep, and if it was excluded no significant correlation existed. Similarly, the between breed differentiation estimates (Figure 2) did not correlate significantly.

a) r=0.68




b) r=0.83

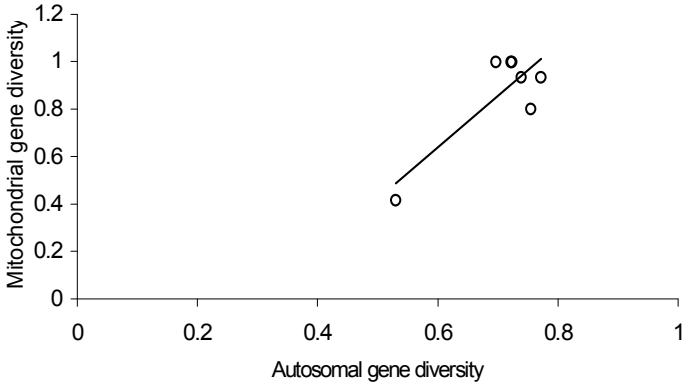



Figure 1. Scatter plot of estimates of allelic variation (a) and gene diversity (b) within the Baltic sheep breeds. Mitochondrial allelic variation (a) refers to the number of haplotypes.



r = 0.255

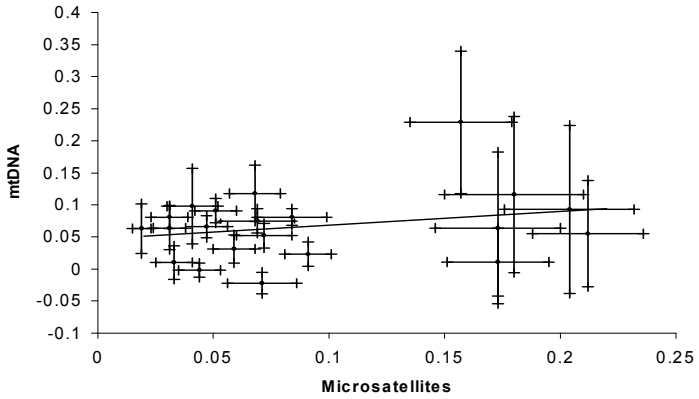



Figure 2. Scatter plot of pairwise differentiation based on autosomal microsatellites (measured as θ) and based on mitochondrial variation (measured as $N_{ST}$). Dots represent the point estimates of θ and $N_{ST}$ estimates. Horisontal dashes are θ standard errors, while vertical dashes represent $N_{ST}$ standard errors.

Differences between mitochondrial variation and autosomal microsatellite variation patterns are often observed (e.g. MacHugh et al., 1997), and they are caused by the different modes of inheritance. Mitochondria are inherited clonally from the mother only and seem to be unaffected by recombination (Piganean and Eyre-Walker, 2004). Mitochondrial variation is especially informative about the primary spreading of domestic species and less disturbed by later gene flow. In the presentation, some simulation results will be shown to demonstrate the effect of inheritance mode when number of flocks or breeding rams in the breeds varies.

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# PROTEIN, DIGESTIVE METHIONINE AND LYSINE MUTUAL CONNECTIONS IN BROILERS MIXED FEED

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## Introduction

Full value poultry feeding provided with a corresponding feed in necessary amount and quality is a basis of high productivity. One of feed quality indices is crude protein level. Crude protein full value is determined by amino acid content and amount. It is of great significance that such essential amino acids as lysine and methionine were in sufficient amount in feed. There are references (Woodham, Deans, 1975) that poultry organism does not synthesize lysine and methionine and receives them by feedstuffs. Moreover, poultry can utilize definite amounts of feed lysine and methionine, the so-called utilizable part of lysine and methionine (Ward, 1989). Therefore it is possible to supply local combined feed with corresponding utilizable lysine and methionine amount instead of feeding with expensive imported protein feedstuffs.

It is believed that protein level is not most important in broilers feeding, but amino acids are of main significance. Therefore the first limiting factor that hinders the growth of broilers is lysine and methionine deficiency in feed. There are data on broiler feeding with decreased crude protein content in feed and corresponding utilizable lysine and methionine level (Woodham and Deans, 1975).

It is possible to ensure the same productivity by feeding out feed with decreased crude protein level and corresponding utilizable lysine and methionine supplement as with optimum protein content in feed (Bornstein, 1979).

The aim of our investigations was to determine optimum utilizable lysine and methionine levels corresponding to crude protein decreasing percentage and their influence on broiler productivity indices.

## Material and methods

The material of investigations was Hibro-G cross broiler chickens aged 1-49 days. Broiler chikens were divided into four groups by 50 in each according to the analogy principle. The investigation was carried out in accordance with scheme (Table 1). Broilers were kept in cages; keeping conditions were the same for all groups and corresponded to the requirements of cross-keeping. Control group broilers were fed according to the Euribrid norms. Total protein content was decreased by 1.5-2 %, but utilizable lysine and methionine levels increased by 1.2-1.5 times to Euribrid Company norms *versus* for trial groups (2.-4.groups).

Table 1. Scheme of the experiment

| Group | Feeding programme | | | | | | Increases utilizable lysine and methionine, in times |
|---|---|---|---|---|---|---|---|
| | Of 0-28 days | | | Of 29-49 days | | | |
| | Crude protein, % | Utilizable lysine, % | Utilizable methionine, % | Crude protein, % | Utilizable lysine, % | Utilizable methionine, % | |
| 1st-control | 23.0 | 1.24 | 0.51 | 21.0 | 0.90 | 0.36 | Norm |
| 2nd – trial | 21.0 | 1.24 | 0.51 | 21.0 | 1.24 | 0.51 | 2% Norm |
| 3rd – trial | 21.0 | 1.49 | 0.61 | 19.5 | 1.08 | 0.43 | 2% and 1.5% 1.2 x |
| 4th – trial | 21.0 | 1.86 | 0.76 | 19.5 | 1.17 | 0.46 | 2% and 1.5% 1.5 x |

The amount of amino acid additives was determined according to Euribrid norms for poultry crosses i.e. necessary utilizable lysine and methionine content in feed rations.

DL-Methionine (France) and L-Lysine (USA) preparations were used for providing amino acids.

The live mass of animals was recorded at the age of 1, 7, 14, 28, 35 and 49 days and feed consumption by weighing daily the fed out feed during the trial period. Live mass, daily gain, feed consumption per 1 kg live mass gain and productivity index were calculated from the obtained data.

The obtained data were statistically processed by the MS Excel 97 computer programme.

**Results**

A comparison of the control and trial group productivity indicated that better productivity indices were obtained with a decreased total protein level (by 1.5-2 %), but with simultaneously increased utilizable lysine (1.2 times) and methionine (1.2 times) levels in broiler feed ration. The live mass of broilers was 2806 g or by 1.3 % higher in comparison with that of the control group ($p>0.1$) (Table 2) at the age of 7 weeks. Their live mass was 2639.0 g or by 4.7 % lower than in the control group at the age of 7 weeks, feeding broilers all the rearing period a feed with the same protein level (21 %), but with utilizable lysine and methionine level that corresponded to Euribrid Company norms (1.24 % and 0.51 % respectively).

Therefore we can conclude that broiler's live mass was influenced mainly by utilizable lysine and methionine level ($p<0.001$) and not so much by protein level in the feed. Feed consumption is dependent of feed utilizability. So feed consumption per 1 kg live mass gain was 2.04 kg in control group broilers and 1.90-2.08 kg in trial groups (Table 3).

Table 2. Development of broiler body weight

| Age in weeks | Group | | | |
|---|---|---|---|---|
| | 1st – control | 2nd – trial | 3rd – trial | 4th – trial |
| 1st day | 40.8±0.83 | 42.7±0.55 | 41.4±0.55 | 39.8±0.95 |
| 14 | 397.4±5.18 | 400.4±7.36 | 406.0±4.80 | 391.8±5.94 |
| 21 | 738.0±9.88 | 721.9±8.54 | 710.8±6.71 | 673.8±10.28 |
| 28 | 1330.0±15.91 | 1274.5±12.91 | 1316.7±15.61 | 1190.8±30.34 |
| 35 | 1898.0±33.76 | 1839.8±18.03 | 1870.0±27.85 | 1759.6±40.52 |
| 42 | 2445.7±23.15 | 2397.7±16.81 | 2413.3±46.13 | 2335.7±44.92 |
| 49 | 2770.4±37.17 | 2639.0±36.31 | 2806.7±83.77 | 2759.0±44.75 |
| % to control | 100.0 | 95.3 | 101.31 | 99.59 |

Table 3. Influence of digestible lysine and methionine on feed conversion and index of productivity

| Parameters | Group | | | |
|---|---|---|---|---|
| | 1st-control | 2nd – trial | 3rd– trial | 4th – trial |
| Feed conversion, kg | 2.04 | 2.08 | 1.90 | 1.98 |
| % to control | 100,0 | 101.9 | 93.14 | 97.06 |
| Index of productivity | 277.1 | 258.9 | 301.4 | 284.3 |
| ± to control | - | -18.2 | +24.3 | +7.22 |
| Profit of 1000 broilers chicks | 586 | 509 | 743 | 608 |
| ± to control | - | -77 | +157 | +22 |

Feed consumption per 1 kg weight gain was the lowest in the 3rd group broilers – 1.90 kg i.e. by 6.9 % lower in comparison with the control group. The highest feed consumption level per 1 kg live mass gain was in the 2nd group broilers (all rearing period the same 21 % total protein level in the feed ration) – 2.08 kg, i.e. by 1.9 % higher than in the control group.

Productivity index calculation includes sale at age, live mass preservation and feed consumption per 1 kg mass gain which characterize in more detail broiler productivity and breeding economics. The 3rd group broilers had the highest productivity index – 301 (total protein content decreased by 1.5-2%, but utilizable lysine and methionine levels in feed increased by 1.2 times), i.e. were by 24.3 higher than in the control group ($p<0.001$). The increased broiler productivity index of the 3rd group confirms that the feeding variant was appropriate for broiler organism requirements, provided the organism with necessary nutritives and promoted live mass gain. Economic effectiveness calculation confirmed that the 3rd group feeding variant provided the highest profit – 743.00 Ls from 1000 sold broilers i.e. by 157 Ls more in comparison with the control group. The second

group feeding variant caused 77 Ls losses. Thus combined feed was not of full value with regard to utilizable lysine and methionine levels in broiler feed composition. The different broiler feeding variants almost did not influence the broilers' meat chemical composition (Table 4): dry matter, total protein, total ash content in 2nd, 3rd and 4th group broiler muscle tissue did not differ essentially from these of the control group. The 2nd, 3rd and 4th group broiler muscle tissue mass contained a little lower levels of total fat (by 0.20-0.65 %) than that of the control group. The total fat content in the liver of these broiler groups had a tendency to be lower too, (by 0.60-1.04 %).

Table 4. The biochemical indices of muscles tissue mass and liver of broilers in 49 days

| Group | Dry matter, % | Moisture, % | Total protein, % | Total fat, % | Ash, % |
|---|---|---|---|---|---|
| The biochemical indices of meat | | | | | |
| 1st control | 24.74 | 75.26 | 21.86 | 1.48 | 1.39 |
| 2nd trial | 22.72 | 77.28 | 20.20 | 1.21 | 1.30 |
| 3rd trial | 23.27 | 76.73 | 20.58 | 1.28 | 1.41 |
| 4th trial | 20.84 | 79.16 | 18.79 | 0.83 | 1.22 |
| The biochemical indices of liver | | | | | |
| 1st control | 25.80 | 74.20 | 21.14 | 1.58 | 3.06 |
| 2nd trial | 24.07 | 75.93 | 18.01 | 0.98 | 2.13 |
| 3rd trial | 22.63 | 77.37 | 19.80 | 0.54 | 2.28 |
| 4th trial | 23.04 | 76.96 | 17.94 | 0.70 | 2.90 |

Table 5. Biochemical analyses of 49 days age broilers

| Group | Total of albumen, g% | Pyruvic acid, mg% | Glucose, mg% | Phosphorus, mg% | Calcium, mg% | Reserve alkaline, mg% |
|---|---|---|---|---|---|---|
| 1st control | 4.2±0.70 | 1.54±0.26 | 139.6±6.25 | 7.6±0.80 | 15.57±0.25 | 712±10.0 |
| 2nd trial | 4.24±0.41 | 1.20±0.07 | 167.5±19,52 | 8.1±0.5 | 11.62±0.25 | 980±20.0 |
| 3rd trial | 3.66±0.06 | 1.26±0.61 | 156.25±18.75 | 7.7±0.70 | 14.46±0.12 | 822±10.0 |
| 4th trial | 3.42±0.42 | 1.13±0.20 | 147.39±2.62 | 6.76±0.56 | 13.47±1.60 | 840±40.0 |

Control and trial groups' metabolism indices in blood were within physiological limits and did not differ among the groups essentially (Table 5). It confirms that applying different feeding variants with decreased total protein content and increased utilizable lysine and methionine content in broilers feeding

did not cause credible departures of metabolism processes from the norm in the organism

**Conclusions**

A comparison of the optimum utilizable lysine and methionine content specified according to total protein decrease percentage in broiler combined feed composition and its influence on the productivity indices in the study and control groups resulted in the following conclusions.

The economically profitable Hibro-G broiler cross feeding variant is:

- combined feed broilers of the first age period (0-28 days) must contain 21 % total protein, 1.49 % utilizable lysine and 0,6% utilizable methionine;
- combined feed of broilers of the second age period (28-49 days) must contain 19.5 % total protein, 1.08 % utilizable lysine and 0.43 % utilizable methionine.

Application of such feeding variants on broilers in comparison with the control group caused the following effects:

- increased broiler live mass at the age of 7 weeks by 1.3%,
- productivity index was higher by 24.3,
- feed consumption per 1 kg live mass gain was lower by 6.9 %,
- profit from 1000 broilers was 743 Ls, that is by 157 Ls higher than for control group broilers,
- combined feed composition price was 219 Ls per ton i.e. by 3.50 Ls lower than for control group,
- increased broiler meat biological value – meat quality index by 1.2 % higher, but meat energetic value by 7.1 % lower.

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# EFFICIENCY OF CONVERTING RATION DRY MATTER, ENERGY AND PROTEIN TO MILK IN DIFFERENT CATTLE BREEDS

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## Introduction

The main purpose of raising livestock is to convert feeds into food products desirable to humans. At the same time feed cost comprises the largest operating expenses in the production of food of animal origin. The effective use of feed dry matter and nutrients of the cattle ration is the key factor in farm profitability. Feed efficiency is not commonly measured in dairy herds as it is done in swine or poultry farms. Feed efficiency is customarily defined as the ratio of feed input to produced animal products, and namely in dairy farming, as the ratio of feed consumption to milk yield.

The purpose of this study was to evaluate besides the feed dry matter (DM) converting efficiency to milk, also the efficiency of feed metabolizable energy (ME) and metabolizable protein (MP) utilization for milk production in different breeds raised in Estonia.

## Materials and Methods

A database necessary for analysis was formed from the data gained during performance experiments with Estonian cattle breeds. Feed intake, milk performance and milk composition were determined twice a month. All data characterizing dry matter intake, ration composition and nutrient utilization were collected on the day when dry matter intake was determined experimentally. The experimental data of four different breeds were analyzed, Estonian Holstein breed being divided into two groups, according to the breeding value. The following groups were formed: Estonian Red breed (ER), Estonian Native Breed (EN), Red-and-White Holstein breed (RHF), Estonian Holstein breed with the breeding value over 112 (EHF-t) and Estonian Holstein breed with breeding value below 112 (EHF). Breeding value is characteristic to an experimental cow at the moment of calving and it is left unadjusted according to its production performance.

All cows were fed *ad libitum* a total mixed ration (TMR) by the same feeding treatment. Feed samples were analyzed for dry matter, crude protein (CP), crude fibre (CF) and crude fat according to the methods recognized in the EU. Neutral detergent fibre (NDF) and acid detergent fibre (ADF) were determined by the method of Van Soest (1994) using ANKOM analyser. MP content in feeds was calculated according the system described by Kärt et al. (2002) and is quite similar to the system used in Finland.

The content of milk protein, fat, lactose and urea were determined using a Combi Foss analyser. Energy corrected milk (ECM) was calculated by a

simplified equation used in the milk recording system in Estonia: ECM = (0.4 x MY) + (0.15 x MY) x F%, where MY – milk yield, and F% - fat content in the milk.

The collected data were analysed using the SAS statistical package. To explain correlations between investigated variables, correlation analysis that take into account repeated measurements, was used.

**Results and Discussion**

In the present study the data of two experimental years are analysed. The number of cows in the experimental groups was not the same but it has been big enough to generalize the results with statistical significance. As all the experimental cows were fed similar ration, according to days in lactation (DIM), it is evident why the indices characterising the composition of ration are almost identical with all experimental groups. The average milk production of the Estonian Holstein experimental groups has been somewhat above 31 kg per day, that of the ER and the RHF groups has been a bit lower. Milk production of the cows of the EN group has been significantly lower than that of the others. Milk fat and protein contents of the experimental groups have been quite equal as well; the exception is the EN group where the content of them have been significantly higher.

Significant differences between the groups were revealed in the efficiency of feed consumption. The most efficient energy and protein utilizers for milk production were Estonian Holstein cows with an average breeding value and the worst utilizers were Estonian Native cows (Tables 1 and 2). Somewhat surprising was the fact that the Estonian Holstein cows with a high breeding value utilized considerably more protein and energy for milk production than the cows with an average breeding value and even more than the Estonian Red cows.

The efficiency of ME utilization is affected by several factors, lactation stage being one of the most important of them (Table 3). A well-known fact is that to produce milk in early lactation, cows use body reserves and in late lactation they begin to restore them. In all experimental groups ME utilization per kilogram FCM increased with the increase of days in lactation.

The efficiency of energy utilization is strongly affected by milk production as well. With the increase of milk production the energy amount needed per one kg of milk production decreases. It is mainly related to the reduced ratio of maintenance energy requirement in the cost of milk production.

Milk fat and protein contents showed an opposite correlation with the efficiency of energy utilization. The amount of ME used for milk production increased with the increase of milk protein content but decreased with the increase of milk fat content. The relationship between milk protein content and ME in the ration can be explained by ruminally synthesized microbial protein. Using silage rich

rations, the amount of degradable protein in the rumen is sufficient but there is a deficiency of fermentable carbohydrates. If we increase the ration energy content by the addition of ruminally fermentable carbohydrates, we increase the amount of amino acids reaching the small intestine and with that the milk protein content (Kärt et al., 2002).

Table 1. Simple statistics of investigated variable

| Variable | | EHF N=749 | EHF-t N=586 | RHF N=444 | ER N=685 | EN N=126 |
|---|---|---|---|---|---|---|
| DIM | Mean | 139.6 | 165.5 | 151.4 | 125.8 | 189.8 |
| | Std.Dev | 115.0 | 133.3 | 119.1 | 90.9 | 102.6 |
| DM in TMR, % | Mean | 58.1 | 58.0 | 58.1 | 58.3 | 57.6 |
| | Std.Dev | 2.4 | 2.2 | 2.4 | 2.5 | 2.1 |
| CP in DM of TMR,% | Mean | 16.7 | 16.5 | 16.4 | 16.7 | 16.2 |
| | Std.Dev | 1.0 | 1.0 | 0.9 | 0.9 | 0.8 |
| MP in DM of TMR,% | Mean | 10.1 | 10.1 | 10.0 | 10.2 | 9.9 |
| | Std.Dev | 0.5 | 0.5 | 0.5 | 0.5 | 0.4 |
| ME in DM of TMR , MJ | Mean | 11.7 | 11.6 | 11.6 | 11.7 | 11.4 |
| | Std.Dev | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 |
| CF in DM of TMR,% | Mean | 14.2 | 14.4 | 14.4 | 14.4 | 15.1 |
| | Std.Dev | 1.9 | 1.8 | 2.0 | 1.8 | 1.6 |
| NDF in DM of TMR,% | Mean | 29.0 | 29.4 | 29.9 | 29.6 | 30.4 |
| | Std.Dev | 3.5 | 3.2 | 3.6 | 3.3 | 2.4 |
| Milk yield, kg/d | Mean | 32.7 | 31.2 | 30.4 | 30.7 | 22.4 |
| | Std.Dev | 8.8 | 8.8 | 8.7 | 8.1 | 6.9 |
| Fat in milk, % | Mean | 3.81 | 3.90 | 3.79 | 3.92 | 4.79 |
| | Std.Dev | 0.68 | 0.66 | 0.78 | 0.64 | 0.98 |
| Protein in milk,% | Mean | 3.37 | 3.47 | 3.55 | 3.55 | 3.79 |
| | Std.Dev | 0.34 | 0.38 | 0.36 | 0.39 | 0.47 |
| Urea in Milk, mg/l | Mean | 251 | 238 | 257 | 264 | 249 |
| | Std.Dev | 59 | 62 | 68 | 69 | 66 |
| Feed DM/ENM, kg/kg | Mean | 0.66 | 0.72 | 0.72 | 0.70 | 0.75 |
| | Std.Dev | 0.18 | 0.22 | 0.34 | 0.25 | 0.24 |
| Feed ME/ENM, MJ/kg | Mean | 7.66 | 8.38 | 8.36 | 8.13 | 8.60 |
| | Std.Dev | 2.00 | 2.48 | 3.76 | 2.89 | 2.66 |
| Feed MP/ENM, g/kg | Mean | 66.56 | 72.83 | 72.17 | 70.90 | 74.50 |
| | Std.Dev | 17.41 | 21.68 | 32.14 | 25.32 | 22.78 |

Table 2. The significance of differences in utilization efficiency of ME and MP in different breeds (P values are given in the Table)

| | EN | RHF | EHFt | EHF |
|---|---|---|---|---|
| ER | 0.0996[a]<br>0.1362[b] | 0.3011<br>0.4810 | 0.0003<br>0.0002 | 0.0003<br>0.0002 |
| EN | | 0.4204<br>0.3592 | 0.3767<br>0.4348 | 0.0002<br>0.0003 |
| RHF | | | 0.9190<br>0.7120 | 0.0003<br>0.0007 |
| EHFt | | | | 0.0000<br>0.0000 |

a) presents the significance of differences in ME utilization between the groups,
b) presents the significance of the efficiency of MP utilization between the groups.

The precursors of milk protein synthesis are free fatty acids in the blood. For milk fat synthesis the lacteal gland uses mainly acetic acid, to a lesser degree butyric acid (for the synthesis of short and medium carbon chain fatty acids) and fatty acids originating from feeds (for the synthesis of long chain fatty acids). This should explain why with the lower energy content of the ration the milk fat content is higher (Kärt et al., 1998). As during cell wall fermentation much acetic acid needed for milk fat synthesis is formed and the energy content of milk fat is higher than that of milk protein, we expected that with the increasing CF and NDF content of the ration, the amount of energy needed for milk production increases as well. However, the present study does not affirm this opinion. It is possible that the reason is in the methods as the rations were quite stable during the two experimental years and their nutrient contents were not very different.

Britt et al. (2003) also studied the factors affecting the efficiency of milk production in Holstein cows but on the contrary to our methods (we took into consideration the amount of consumed feed or nutrients per kg milk produced), they regarded efficiency as the amount of milk production per kg of consumed dry matter. Due to this the correlation coefficients have an opposite direction but are close in meaning. The authors found negative correlation between the efficiency of milk production and days in milk, dry matter intake, grass feed proportion in the ration, ration NDF content (%): r=-0.529, r=-0,316, r=-0.430, r=-0.308, respectively. Positive correlation was found between milk production efficiency and milk production (r=0.707).

As in our experiment the Estonian Holstein cows were divided into two groups according to the relative breeding value (SPAV), it was possible to analyse the effect of SPAV on the efficiency of milk production. Although the equations, on the basis of which the diagrams in Figure 1 are drawn, do not describe the real

situation quite precisely, some tendencies can still be found. In the group with a lower breeding value, with the increase of SPAV, ME utilization per kg of milk production was constantly decreasing; in the group with a high breeding value it began to increase later. This can be related to the increase of feed passage rate in the digestion tract or to the decrease of organic matter digestibility.

Table 3. Simple correlation between ME converting efficiency to milk and investigated variables

| Variable | EHF | EHF-t | RHF | ER | EN |
|---|---|---|---|---|---|
| DIM | 0.4915<br><0.0001 | 0.5245<br><0.0001 | 0.5078<br><0.0001 | 0.3715<br><0.0001 | 0.4117<br><0.0001 |
| DM in TMR, % | -0.0065<br>0.8636 | -0.1521<br>0.0003 | -0.1314<br>0.0070 | -0.0655<br>0.0939 | 0.0300<br>0.7440 |
| CP in DM of TMR,% | 0.0138<br>0.7149 | -0.1338<br>0.0016 | -0.1577<br>0.0012 | 0.0881<br>0.0241 | 0.03229<br>0.7252 |
| MP in DM of TMR, % | -0.0175<br>0.6441 | -0.1732<br><0.0001 | -0.1739<br>0.0003 | 0.0760<br>0.0518 | -0.0180<br>0.8451 |
| ME in DM of TMR, MJ | -0.0097<br>0.7983 | -0.1926<br><0.0001 | -0.1427<br>0.0034 | 0.0507<br>0.1954 | 0.0223<br>0.8082 |
| CF in DM of TMR,% | -0.0397<br>0.2938 | 0.1072<br>0.0117 | 0.0795<br>0.1040 | -0.0666<br>0.0886 | 0.0881<br>0.3368 |
| NDF in DM of TMR,% | -0.0675<br>0.0743 | 0.0009<br>0.9832 | 0.0394<br>0.4212 | -0.0706<br>0.0710 | -0.0380<br>0.6790 |
| Milk yield, kg/d | -0.37861<br><0.0001 | -0.5839<br><0.0001 | -0.6087<br><0.0001 | -0.5104<br><0.0001 | -0.5516<br><0.0001 |
| Fat in milk, % | -0.1732<br><0.0001 | -0.0202<br>0.6361 | -0.1049<br>0.0316 | -0.2104<br><0.0001 | 0.1704<br>0.0618 |
| Protein in milk,% | 0.2425<br><0.0001 | 0.4036<br><0.0001 | 0.3331<br><0.0001 | 0.1836<br><0.0001 | 0.5450<br><0.0001 |
| Urea in Milk, mg/l | -0.0257<br>0.4973 | -0.1213<br>0.0043 | -0.1748<br>0.0003 | -0.0630<br>0.1071 | -0.0711<br>0.4383 |
| SPAV | -0.1872<br><0.0001 | -0.0711<br>0.0857 | NE* | 0.0284<br>0.4574 | NE* |

*NE – none estimated

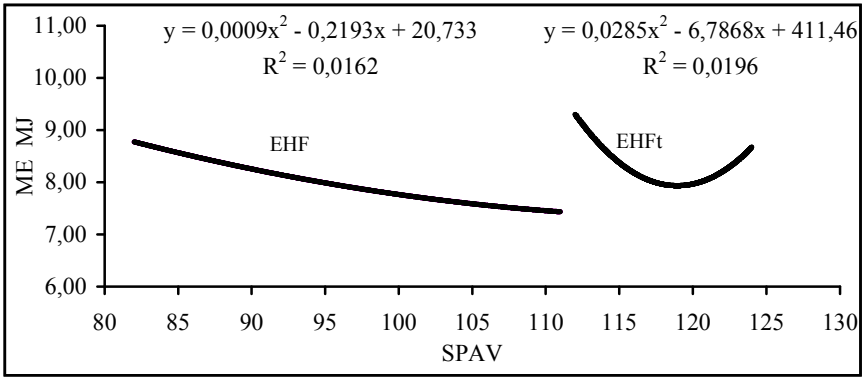


Figure 1. The effect of SPAV on the efficiency of ME utilization for milk production in Estonian Holstein dairy cattle.

The further experiment should reveal whether the breeding value, gained during a cow's lifetime, correlates with the efficiency of ME utilization for milk production better than her parentage index.

**Conclusions**

The efficiency of ME and MP utilization in milk production is affected by several factors – primarily by a lactation stage, milk production and milk composition, and to a lesser degree by the composition of ration. The efficiency of feed consumption in Holstein cows with a very high breeding value has a tendency to decrease.

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# NUTRITIVE VALUE CHANGES IN DIFFERENT STAGES OF GRASS DEVELOPMENT, GREEN MASS AND DIFFERENTLY MADE GRASS SILAGE

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## Introduction

Cows require feed balanced in nutrients. Exactly sufficient levels of energy (NEL) and protein (CP) have the decisive role in cows feed (Ramane, 1999).

Forage grasses differ by their feeding value, production capacity and nutrient availability (Cooper, 1995; James, 1995; Ošmane, 2003). They may be divided into several groups. Dry matter is the sum of grass valuable components. Grass dry matter content below 15 % does not provide cows with necessary nutrients needed for milk production (Osītis, 1998; Ošmane, 2003).

The aim of the experiment was to evaluate feed value in three vegetation stages of grass development, green mass and differently made silage.

## Materials and Methods

Aimed at fulfilling the set goal and target of research, in the summers of 2001 and 2002 (May-July) green grass material from special grass fields with similar agricultural background was harvested in Priekuļi Plant Breeding and Experimental Station. The green grass material was cut and conserved from six grass species at branching, shooting and blooming.

According to the set research goal, the following species of grasses, grown in pure sowing and being little investigated in Latvia, were selected for ensiling:

- perennial ryegrass /*Lolium perenne/,*
- meadow fescue /*Festuca pratensis/,*
- timothy /*Phleum pratense/,*
- meadow foxtail /*Alopecurus pratense/,*
- cocksfoot */Dactylus glomerata/,*
- grass mixture "Havera 1" (SIP Schaap Agro Holland Latvia).

The composition of grass mixture was as follows:

- Perennial ryegrass (*Lolium perenne tetraploid* "Montagne")- 30 %
- Perennial ryegrass (*Lolium perenne tetraploid* "Madera")- 30 %
- Timothy (*Phleum pratense "Goliath")*- 15 %
- Meadow fescue (*Festuca pratensis "Darimo")*- 15 %
- White clover (*Trifolium repens "Retor")*- 10 %

Prior ensiling the green mass was weighed with precision ± 1g and analysed according to below mentioned methods. Samples from each grass species were ensiled at three stages of maturity (branching, shooting, blooming) in four variants, in jars 3 litres of size in three replications under laboratory conditions.

The conservation treatments were as follows:

- control – fresh mass without additives,

- fresh mass silage preservative AIV-2Plus (5 ml $kg^{-1}$),
- fresh mass with biological inoculant SIL-All$^{4x4}$ (0,01 g $kg^{-1}$),
- wilted mass (24 h in the laboratory room) without additives.

Plant harvesting conditions and ensiling technology were similar for all the treatments. The ensiled material was stored under similar conditions at maximum temperature from $10^{o}$ to $12^{o}$ C, in darkness.

SILL-All$^{4x4}$ contains lactic acid bacteria *Lactobacillus plantarum, Streptococcus feacium, Pediococcus acidilactici, Lactobacillus salivarus* and enzymes, such as amylase, cellulose, hemi-cellulose and pento-sanose.

AIV-2Plus contains formic acid – 76 % and ammonium phormiate – 5,5 %.

The norms made and applied into practice were used. In the accredited laboratory of Biochemistry of the RC "Sigra" the following parameters were determined in fresh material and silage (samples were air-dried at $60^{o}$ to $65^{o}$ C):

- dry matter, drying the sample at 103 ± $2^{o}$ C (ISO 6496-1999);
- crude protein by the Kjeldahl procedure (ISO 5983-1997);
- fibre fractions by van Soest;
- digestible nutrients DM (TDN – Total Digestible Nutrients), % was calculated:

  TDN = 88.9 – (ADF % x 0.779);
- net energy lactation in feed (NEL), MJ $kg^{-1}$ was calculated:

  NEL = (0.0245 x TDN % DM – 0.12) x 4.184.

In statistical data processing with SPSS computer programme, GLM model, there were used:

- three-factorial dispersion analysis,
- correlation analysis,
- factorial analysis.

**Results and discussion**

Forage grasses at tiller showed the highest feeding value (1 $kg^{-1}$mass) during vegetation due to low content of fibre fractions (ADF and NDF) and high levels of crude protein and productive energy. In making silage, the preservation of feeding value in green material, cut at branching, is burdened because of difficulties in right fermentation process and with storage of high feeding value. Table 1 presents the effect of ensiling technique on feeding value changes in different grass silages.

The results summarized in Table 1 show increased energy level and crude protein content in silages treated with additives and made of grasses harvested at branching. The highest feeding value in grass silages made from green material (1 $kg^{-1}$) cut at branching, which had the worst ensilage capacity, was mainly provided by the biological inoculant.

Table 1. Feed values of different grasses and their silages, made at branching

| Conservation method | NEL MJ $kg^{-1}$ in DM | TDN, % | Crude protein g $kg^{-1}$ in DM |
|---|---|---|---|
| Perennial ryegrass | | | |
| Grass | 6.92 | 72.46 | 166.90 |
| Silage - control | 6.30 | 65.40 | 155.70 |
| - AIV-2Plus | 6.46 | 68.00 | 161.20 |
| - SIL-All$^{4x4}$ | 6.58 | 68.90 | 164.01 |
| - wilted | 6.40 | 66.92 | 159.0 |
| Meadow fescue | | | |
| Grass | 6.76 | 70.33 | 196.3 |
| Silage - control | 6.41 | 65.12 | 182.2 |
| - AIV-2Plus | 6.66 | 67.82 | 187.6 |
| - SIL-All$^{4x4}$ | 6.74 | 68.52 | 191.0 |
| - wilted | 6.49 | 66.18 | 190.2 |
| Timothy | | | |
| Grass | 7.00 | 73.21 | 227.4 |
| Silage - control | 6.58 | 64.25 | 217.8 |
| - AIV-2Plus | 6.88 | 65.85 | 223.8 |
| - SIL-All$^{4x4}$ | 6.91 | 66.88 | 224.7 |
| - wilted | 6.80 | 64.43 | 218.5 |
| Meadow foxtail | | | |
| Grass | 6.80 | 68.71 | 163.4 |
| Silage - control | 6.47 | 65.13 | 149.7 |
| - AIV-2Plus | 6.69 | 66.79 | 158.0 |
| - SIL-All$^{4x4}$ | 6.62 | 67.57 | 161.4 |
| wilted | 6.54 | 64.19 | 157.0 |
| Cocksfoot | | | |
| Grass | 6.80 | 71.16 | 179.2 |
| Silage - control | 6.42 | 58.28 | 161.9 |
| - AIV-2Plus | 6.55 | 63.42 | 169.7 |
| - SIL-All$^{4x4}$ | 6.73 | 67.14 | 173.9 |
| wilted | 6.60 | 61.48 | 168.9 |
| Grass mix “Havera 1” | | | |
| Grass | 7.01 | 73.0 | 221.2 |
| Silage - control | 6.61 | 62.71 | 202.8 |
| - AIV-2Plus | 6.93 | 65.56 | 210.2 |
| - SIL-All$^{4x4}$ | 6.82 | 66.32 | 212.9 |
| wilted | 6.78 | 62.40 | 204.5 |

At shooting, forage grasses were higher in dry matter content, lower in buffer capacity, more balanced in crude protein to sugars ratio, had lower content of non desirable micro-organisms (better ensilage capacity than that at branching) and

better feeding value preservation. Table 2 presents the summarized data on grasses, cut at shooting and feeding value changes in differently made silages.

Table 2.Feed values of different grasses and their silages, made at shooting

| Conservation method | NEL MJ $kg^{-1}$ in DM | TDN, % | Crude protein $kg^{-1}$ in DM |
|---|---|---|---|
| Perennial ryegrass | | | |
| Grass | 6.67 | 69.99 | 148.7 |
| Silage - control | 6.28 | 64.82 | 138.0 |
| -AIV-2Plus | 6.39 | 67.16 | 144.9 |
| - SIL-All$^{4x4}$ | 6.55 | 68.90 | 144.3 |
| - wilted | 6.36 | 65.06 | 143.3 |
| Meadow fescue | | | |
| Grass | 6.75 | 68.81 | 153.3 |
| Silage - control | 6.25 | 64.14 | 138.9 |
| -AIV-2Plus | 6.51 | 66.54 | 144.2 |
| - SIL-All$^{4x4}$ | 6.59 | 67.28 | 146.5 |
| - wilted | 6.49 | 64.54 | 141.2 |
| Timothy | | | |
| Grass | 6.78 | 71.01 | 179.3 |
| Silage - control | 6.53 | 61.82 | 156.2 |
| -AIV-2Plus | 6.62 | 65.46 | 172.0 |
| - SIL-All$^{4x4}$ | 6.64 | 65.74 | 173.1 |
| - wilted | 6.53 | 63.22 | 159.9 |
| Meadow foxtail | | | |
| Grass | 6.68 | 67.30 | 157.5 |
| Silage - control | 6.28 | 61.89 | 148.8 |
| -AIV-2Plus | 6.37 | 64.23 | 153.2 |
| - SIL-All$^{4x4}$ | 6.43 | 65.63 | 154.9 |
| - wilted | 6.47 | 62.14 | 152.6 |
| Cocksfoot | | | |
| Grass | 6.41 | 67.40 | 158.3 |
| Silage - control | 5.97 | 58.88 | 142.8 |
| -AIV-2Plus | 6.04 | 64.68 | 151.0 |
| - SIL-All$^{4x4}$ | 6.19 | 66.76 | 151.6 |
| - wilted | 6.03 | 61.48 | 148.9 |
| Grass mix “Havera 1” | | | |
| Grass | 6.48 | 68.17 | 172.1 |
| Silage - control | 6.10 | 60.62 | 155.6 |
| -AIV-2Plus | 6.20 | 64.12 | 162.6 |
| - SIL-All$^{4x4}$ | 6.29 | 64.48 | 163.6 |
| - wilted | 6.27 | 62.26 | 159.7 |

SIL-All$^{4x4}$ additive compared to other ensiling techniques.

Data summarized in Table 2 show that higher NEL, organic matter digestibility and crude protein content in silages of grasses harvested at stem elongation were predominantly provided by biological ferment SIL-All$^{4x4}$ additive.

All forage grasses decline in feeding value as they mature (1 kg$^{-1}$). Delayed cutting is connected with NEL and crude protein losses and increase of fibre fractions ADF and NDF DM (worsening of nutrient availability). Changes in feeding value of silages, made of grasses cut at the blooming stage are presented in Table 3.

The feeding value preservation was best provided by AIV-2Plus and SIL-All$^{4x4}$ additives (Table 3).

Mathematical data processing showed the following:

- NEL changes were significantly dependent on:
  - grass species ($p<0.01$: $R=0.544$) (higher for perennial ryegrass, meadow fescue);
  - grass developmental stage ($p<0.01$: $R=0.544$) (highest at branching);
  - ensiling technique ($p<0.01$: $R=0.544$) (highest with AIV-2Plus and SIL-All$^{4x4}$ additives);
  - grass species and plant developmental stage interaction ($p<0.05$: $R=0.544$);
  - grass species and ensiling technique interaction ($p<0.05$: $R=0.544$).

Comparison between control treatment and other ensiling techniques showed significant difference ($p<0.01$).

- Crude protein content in grass silages was significantly affected by:
  - grass species ($p<0.01$: $R=0.629$) (mainly for timothy);
  - grass developmental stage ($p<0.01$: $R=0.692$) (mainly at branching);
  - ensiling technique ($p<0.01$: $R=0.692$) (highest with AIV-2Plus and SIL-All$^{4x4}$ additives);
  - grass species and plant developmental stage interaction ($p<0.01$: $R=0.692$).

The crude protein content, compared to that of the control silage, significantly differed with SIL-All$^{4x4}$ ($p<0.01$) and AIV-2Plus ($p<0.05$) additives made silage. Comparison of crude protein in grass mixture with other grasses showed significant difference only with perennial ryegrass, timothy and cocksfoot grass ($p<0.01$).

Table 3. Feed value of different grasses and their silages, made at blooming

| Conservation method | NEL MJ $kg^{-1}$ in DM | TDN, % | Crude protein g $kg^{-1}$ in DM |
|---|---|---|---|
| Perennial ryegrass | | | |
| Grass | 6.48 | 68.06 | 126.40 |
| Silage - control | 6.12 | 63.26 | 119.8 |
| -AIV-2Plus | 6.32 | 66.78 | 123.5 |
| - SIL-All$^{4x4}$ | 6.38 | 67.48 | 122.9 |
| - wilted | 6.26 | 63.92 | 121.9 |
| Meadow fescue | | | |
| Grass | 6.50 | 66.86 | 119.3 |
| Silage - control | 6.16 | 62.68 | 113.9 |
| -AIV-2Plus | 6.21 | 65.56 | 119.0 |
| - SIL-All$^{4x4}$ | 6.26 | 66.08 | 119.1 |
| - wilted | 6.07 | 63.26 | 116.7 |
| Timothy | | | |
| Grass | 6.54 | 68.69 | 137.1 |
| Silage - control | 6.15 | 60.88 | 129.2 |
| -AIV-2Plus | 6.46 | 64.66 | 130.9 |
| - SIL-All$^{4x4}$ | 6.45 | 64.64 | 134.5 |
| - wilted | 6.32 | 61.80 | 132.0 |
| Meadow foxtail | | | |
| Grass | 6.62 | 65.50 | 145.3 |
| Silage - control | 6.23 | 60.50 | 133.9 |
| -AIV-2Plus | 6.40 | 62.74 | 139.5 |
| - SIL-All$^{4x4}$ | 6.34 | 64.12 | 141.9 |
| - wilted | 6.24 | 61.42 | 136.3 |
| Cocksfoot | | | |
| Grass | 6.31 | 66.48 | 111.8 |
| Silage - control | 5.81 | 58.26 | 103.7 |
| -AIV-2Plus | 5.98 | 63.26 | 108.1 |
| - SIL-All$^{4x4}$ | 6.18 | 65.24 | 106.9 |
| - wilted | 5.96 | 61.36 | 106.1 |
| Grass mix “Havera 1” | | | |
| Grass | 60.24 | 65.75 | 140.5 |
| Silage - control | 5.68 | 60.30 | 123.2 |
| -AIV-2Plus | 5.89 | 62.60 | 128.1 |
| - SIL-All$^{4x4}$ | 5.91 | 63.06 | 130.6 |
| - wilted | 5.79 | 61.54 | 127.9 |

**Conclusions**

Feeding values of grass silages made from green material, cut at three stages of maturity, are different.

- Energy (NEL) and protein values were significantly ($p<0.01$) affected by grass species, grass developmental stage and ensiling technique ($R=0.692$).

- Digestible nutrient content DM in silages is significantly ($p<0.01$) affected by grass species, grass developmental stage and ensiling technique ($R=0.581$).

- Fibre fraction content in silages is significantly ($p<0.01$) affected by grass species, plant developmental stage and ensiling technique ($R=0.661$).

Parameters characterizing grass silage feeding value such as NEL and crude protein content were affected by the stage of vegetation, grass species to be ensiled and ensiling technique.

Fermentation regulators (chemical silage preservative AIV-2Plus and biological inoculant SIL-All$^{4x4}$ additive) provided not only fermentation optimisation but maximum energy ($p<0.01$) and crude protein ($p<0.01$) preservation in grass silage as well.

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# MILK UREA CONCENTRATION AND PBV AS INDICATORS OF EFFECTIVE PROTEIN USE IN FEEDING OF DAIRY CATTLE

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## Introduction

In recent decades in the whole world much attention has been paid to the effective use of feed protein in livestock breeding. This is due to the necessity to protect and enhance natural environment and on the other hand it is related to more rational use of nature resources and animal health, welfare and life period (Shingfield, 2001). Important ways to do that are more accurate rationing of protein as a nutritive factor in the feeding of livestock and considering of the losses in protein metabolism of different animal species.

Since 2002, in Estonia a feed evaluation system based on metabolizable protein (MP) has been applied. In this system the protein supply of dairy cows is treated at the level of amino acids absorbed in the small intestine (Kärt et al., 2002). The feed evaluation system based on MP is based on the total amount of amino acids absorbed in the small intestine. A part of them originates from the feed ruminally undegraded protein that is digested in the small intestine, another part from the microbial mass ruminally synthesized and digested in the small intestine. According to this system, the rumen-degraded protein balance (PBV) is always calculated. The PBV is the balance between the amount of microbial protein that is potentially synthesized from the available rumen-degradable protein and the amount of microbial protein that is potentially possible from the available energy, extracted during fermentation in the rumen. To minimise avoidable nitrogen losses, the PBV should be 0 or slightly above 0.

Protein evaluation systems distinguish between two main sources of nitrogen loss. The first may come from a surplus of nitrogen that is available for microbial growth compared with the available energy and the second from the true protein digested in the small intestine. In both cases toxic ammonia that goes to the blood is in the liver rapidly converted into urea - the end product of protein metabolism. It is evaluated that 50% of excessive nitrogen is quickly excreted via urine (Tamminga, 1992) while urea constitutes 70-80% of it (Bristow et al, 1992). Lactating animals excrete some amount of urea (2.5-3%) with milk (DePeters, Ferguson, 1992). Despite great differences between the urea contents of the above mentioned excretes, several studies have revealed statistically significant relationship between the urea contents of urine, blood and milk contents (Ciszuk and Gebregziabher, 1994; Gonda and Lindberg, 1994; Susmel et al., 1995).

As milk urea concentration can be easily determined, it could potentially be used as a parameter to monitor protein nutrition of the dairy cows. Due to this the

purpose of the present study was to explain how closely is milk urea content related to PBV value and how exactly the relationship between them describes the protein nutrition of a dairy cow, taking into account the MP evaluation system used in Estonia.

**Material and Methods**

The database was formed on the basis of the results of 4 physiological experiments carried out in 4x4 Latin square design (16 diets, 16 cows and 60 observations) at Eerika experimental farm in 1997-2000.

The rations consisted of silage, barley meal, protein feed (sunflower or soybean oil meal) and mineral feed. Roughages as clover and alfalfa silage, and in two experiments clover-timothy hay, which clover content ranged between 25 and 30%, were used. Their average crude protein (CP) content in silage dry matter (DM) was 17.4, 21.9, 11.5 and 13.9%, respectively.

Barley meal and protein feed were fed, considering that the CP content of the ration DM did not remain below 15%. Experimental cows were fed silage *ad libitum* and concentrate constituted 25, 40, 55 or 70% of the metabolizable energy requirement, calculated by the standards of maintenance energy requirements compiled by Oll (1995).

The preliminary periods lasted for 8 and the experimental periods for 6 days. DM and CP content of the feeds and feed residues, sampled in the experimental periods, were determined by the methods accepted by the EU. The calculation of metabolizable energy (ME) content was based on the instruction of calculating energy content of feeds compiled by Ü.Oll and S.Tölp (1997). In evaluating MP and PBV, the Finnish protein evaluation system (Tuori et al., 1996), improved in the Institute of Animal Science of the Estonian Agricultural University (Kärt et al., 2002), was used.

During the experimental period the milk yield of the cows was registered daily and milk samples were taken thrice. Milk samples were analysed at the Milk Analysis Laboratory of Animal Recording Centre by *CombiFoss* automated analyser. In calculating ECM, it was considered that the energy content of the 4% fat milk is equal to 3.14 MJ.

**Results and Discussion**

The experimental cows ate 12.8 to 22.4 kg dry matter per day (Table 1), from which silage DM comprised 6.8 to 16.8 kg per day and concentrate DM 1.1 to 13.0 kg per day. With the increase of barley meal proportion in the ration, the intake of silage DM decreased ($P<0.001$). However, the change of concentrate proportion in the ration had no statistically significant effect on silage DM intake.

The depressive effect of starch-rich barley meal on silage DM intake remained within the same range as described by de Visser et al. (1998) but the effect of

protein content in the concentrate was not revealed due to the fact that according to the methods of the experiment, the ration CP content was held at the same level in all experimental variants.

Table 1. Simple statistics of investigated variables

| Items | Mean | Minimum | Maximum | SD |
|---|---|---|---|---|
| Intake: | | | | |
| Dry matter, kg | 18.5 | 12.8 | 22.4 | 2.3 |
| Silage dry matter, kg | 12.5 | 6.8 | 16.8 | 2.5 |
| Barley dry matter, kg | 5.2 | 1.1 | 10.5 | 2.3 |
| Protein feed dry matter, kg | 0.8 | 0.0 | 2.5 | 0.8 |
| Metabolizable energy, MJ | 189 | 122 | 242 | 27 |
| Crude protein, kg | 2.9 | 1.9 | 4.2 | 0.5 |
| Metabolizable protein, kg | 1.6 | 1.0 | 2.0 | 0.2 |
| PBV[1], g | 295 | -157 | 1307 | 350 |
| ECM[2] yield, kg/d | 21.8 | 13.0 | 30.4 | 4.2 |
| Milk composition: | | | | |
| Fat, % | 4.31 | 2.67 | 6.45 | 0.75 |
| Protein, % | 3.29 | 2.76 | 4.14 | 0.32 |
| Urea, mg/l | 293 | 212 | 459 | 54 |

[1] – Protein balance in the rumen
[2] – Energy corrected milk

With the increase of the concentrate proportion in the rations, both the cows' intake of ME and MP increased statistically significantly ($P<0.001$). It can be concluded that the amount of amino acids absorbed in the small intestine was higher in the cows whose rations were of a higher energy density. On the other hand, when the rations were with lower energy content, the CP intake and PBV were higher. There was a strong, statistically significant correlation between CP intake and PBV ($P<0.001$) but it was absent between PBV and ME intake. In the case of rations with low energy density, the limiting factor of microbial protein synthesis in the rumen was the deficiency of carbohydrates hydrolysing in the rumen.

The ECM production of these experimental cows, whose ration DM had a higher proportion of barley meal, was higher. However, barley meal decreased milk fat content significantly ($P<0.05$). In that experiment no statistical relationship between milk protein content and barley meal proportion was found.

Milk urea content correlated significantly with CP intake ($r=0.451$; $P<0.001$) but had no statistical correlation with ME intake ($r=-0.245$; $P<0.059$). The ratio of ME and CP of the consumed ration gave an expected strong significant

correlation with milk urea content (r=0.730; P<0.001). The gained data are in accordance to the data found in literature, e.g. Hof et al. (1997) revealed that the right protein-energy ratio in the ration enables to use these nutrients for microbial protein synthesis with the highest efficiency and enables to diminish nitrogen losses from the organism as well.

According to the data found in literature, there is a very strong correlative relationship between urea content of blood, urine and milk. Thus in recent years milk urea content has been widely used in protein metabolism evaluation, mainly because it is easy to determine in routine milk analysis during performance test system.

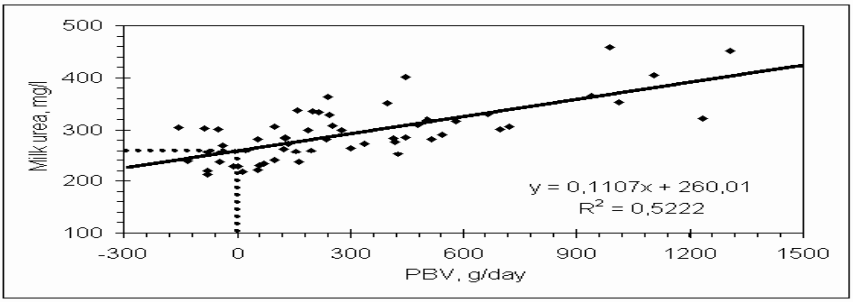


Figure 1. Relationship between PBV and milk urea concentration

As PBV characterizes energy and protein utilization by the ruminal micro-organisms more precisely than the ratio of utilized ME and crude fibre of the ration, it can be concluded that PBV correlates better with milk urea concentration as well. In our investigation the relationship between milk urea concentration and PBV was significant but the equation (Figure 1) describes the relationship somewhat weaker than the ratio of ME and CP to milk urea content does. By MP evaluation system it is considered that the ration enery: protein ratio is well balanced when PBV value is zero. As in this study the milk urea content with PBV zero value was 260 mg/l, the milk urea content 150…270 mg/l, recommended by Animal Recording Centre, should be regarded critically.

**Conclusions**

The feed evaluation system based on metabolizable protein and the PBV value enables to evaluate feed protein quality in dairy cattle feeding and to predict protein losses during metabolism more precisely than the protein evaluation system based on crude protein. On the basis of milk urea content, the effectiveness of protein utilization in the organism can be expected, as it correlates quite well with the PBV.

**Acknowledgment**

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# FEEDSTUFFS PRODUCED IN ORGANIC FARMING SYSTEM – INFLUENCE ON LAYERS PRODUCTIVITY AND EGG QUALITY

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## Introduction

In organic farms the same crosses of layers as those selected for conventional farms are kept. To ensure economically profitable productivity level for these crosses in organic farms, it is necessary to feed out feed mixtures corresponding to normatives as in conventional farms. Full value composition feed mixtures for conventional poultry farming are industrially produced. Feed mixtures that contain the cheapest possibly locally produced organic feedstuffs should be produced industrially for organic poultry farms. Feed mixtures with such composition are not produced in Latvia. The goal of our investigations was to elaborate the feed mixture composition for feeding organic farms layers that contains the cheapest organic feedstuffs produced in local organic farming enterprises and to evaluate the feeding effect at the above mentioned feedstuffs mixture on layers productivity and especially on egg quality.

## Materials and Methods

The investigations were carried out by cross Lohmann Brown layers at the age of 22 to 47 weeks. Two groups of layers were formed for investigation (n=200, Table 1). Mixtures of the same feed value that contained metabolic energy 11.7 MJ/100 g, total protein 17.6 %, total fat 3.8 %, calcium 3.5 % etc. were fed out.

Table 1. Scheme of the trial

| Group | Mixed feed content | Crude protein, % |
|---|---|---|
| 1st – control | Feedstuffs produced by conventional farming system | 17.6 |
| 2nd – trial | Feedstuffs produced by organic farming system | 17.6 |

The feed mixture of the trial group layers contained the following feedstuffs produced in organic farming system: wheat, barley, buckwheat, rapeseed oil cake, rapeseed oil and permitted additives: vitamins, trace elements, chalk etc.

Feed mixture fed out to the control group layers contained analogical conventionally produced wheat, barley, rapeseed oil as well as soybean cakes. Soybean cakes were replaced by buckwheat meal and rapeseed oil cakes in organic feedstuffs mixture. The layers of both groups were kept in the same conditions according to domestic animals welfare requirements in organic farms (Rules of the Council of Ministers of the Republic of Latvia N 514, Latvijas Vēstnesis 03.12.2002).

Feed mixture composition, consumption, expenses, hens laying, egg mass and biochemical composition, were recorded, calculated and analyzed during the trial period. Feedstuffs and egg biochemical analyses were carried in the Laboratory of Biochemistry of the Research Centre "Sigra" according to accepted methods during the accreditation process.

**Results and discussions**

After elaboration of the same feed value feed mixtures for the 1st and 2nd group layers feeding it was ascertained, that wheat and barley grown in organic farming system had an equivalent content of dry matter, total protein, total fat and ash than conventionally grown wheat and barley (Table 2). On the other hand organic rapeseed oil cakes contained by 2.13 % and buckwheat meal by 1.6 % less total protein, but had correspondingly by 2.28 % and 0.30 % higher total fat level than in conventionally produced feedstuffs ($p<0.05$).

Table 2. Chemical indices of feedstuffs produced by local conventional and organic farming systems

| Parameters | Dry matter, % | Total protein, % | Total fat, % | Total ash, % |
|---|---|---|---|---|
| Wheat – convent.*) | 86.15±0.94 | 12.19±0.51 | 1.70±0.09 | 2.49±0.24 |
| Wheat – organic**) | 86.03±0.84 | 12.08±0.53 | 1.83±0.08 | 2.11±0.31 |
| Barley – convent.*) | 82.31±0.95 | 13.45±0.59 | 1.31±0.09 | 2.86±0.30 |
| Barley – organic**) | 82.04±0.91 | 13.06±0.61 | 1.34±0.02 | 2.15±0.29 |
| Buckwheat meal – convent.*) | 83.66±0.85 | 13.27±0.38 | 1.52±0.05 | 2.18±0.11 |
| Buckwheat meal – organic**) | 82.57±0.89 | 11.67*** ±0.33 | 1.82*** ±0.04 | 2.01±0.15 |
| Rapeseed oil cake – convent.*) | 86.53±0.98 | 30.72±0.22 | 14.67±0.03 | 6.00±0.38 |
| Rapeseed oil cake – organic**) | 85.94±0.93 | 28.59*** ±0.27 | 16.95***±0.02 | 5.91±0.42 |

*) convent. – produced by conventional farming system; **) organic. – produced by organic farming system; ***) $p<0.05$

The high productivity level of the layers was reached by feeding out to the 2nd group layers the elaborated feed mixture that contained feedstuffs produced in organic farming system. The laying intensity of the second group hens was in average 91.90 %, average egg mass – 57.92 g and feed consumption per 1 kg egg mass production – 2.27 kg. The productivity of trial group layers was equivalent to the control group layers productivity (Table 3).

Table 3. Productivity of laying hen, consumption and expenses of feed

| meters | Group | | ± to control |
|---|---|---|---|
| | 1st – control | 2nd – trial | |
| Laying intensity, % | 90.71±1.01 | 91.90±0.97 | + 1.19 |
| Average egg weight, g | 58.24±0.26 | 57.92±0.38 | -0.32 |
| Shell thickness, μ | 372.50±3.20 | 380.00±3.22 | +7.5 |
| Feed consumption per 1000 eggs, kg | 132 | 131 | -1,0 |
| Feed conversion, kg $kg^{-1}$ | 2.26 | 2.27 | +0.01 |
| Expenses of feed, Ls: | | | |
| Per 1000 eggs | 22.68 | 22.56 | -0.12 |
| Per 1 kg egg mass | 0.39 | 0.39 | - |

Table 4. Content of fatty acids (% of total lipids) and cholesterol (g $kg^{-1}$) in layers' eggs

| meters | Group | | ± to control | % to control |
|---|---|---|---|---|
| | 1st- control | 2nd – trial | | |
| Saturated fatty acids | | | | |
| Myristic acid C14:0 | 0.34±0.03 | 0.32±0.02 | -0.02 | 94.12 |
| Palmitic acid C16:0 | 24.47±0.21 | 23.22±0.22 | -1.25 | 94.89 |
| Stearic acid C18:0 | 8.09±0.11 | 9.93±0.10 | +1.84 | 122.74 |
| Total | 32.90 | 33.47 | +0.57 | 101.73 |
| Monounsaturated fatty acids | | | | |
| Palmitoleic acid C16:1 | 3.94±0.06 | 3.50±0.04 | -0.44 | 88.83 |
| Oleic acid C18:1 | 43.39±0.94 | 42.34±0.95 | -1.05 | 97.58 |
| Eikosenic acid C20:1 | 0.26±0.03 | 0.25±0.02 | -0.01 | 96.15 |
| Total | 47.59 | 46.09 | -1.50 | 96.84 |
| Polyunsaturated fatty acids | | | | |
| Linoleic acid C18:2, n-6 | 14.14±0.12 | 14.29±0.11 | +0.15 | 101.06 |
| Linolenic acid C18:3, n-3 | 1.38±0.03 | 2.04±0.02 | 0.66 | 147.83 |
| Arahidonic acid C20:4, n-6 | 1.14±0.01 | 1.21±0.02 | +0.07 | 106.14 |
| Eicosapentaenoic acid C20:5, n-3 | 0.10±0.001 | 0.12±0.001 | +0.02 | 120.0 |
| Docosapentaenoic acid C22:5, n-3 | 0.27±0.01 | 0.27±0.01 | - | 100 |
| Docosahexaenoic acid C22:6, n-3 | 2.38±0.04 | 2.42±0.02 | 0.04 | 101.68 |
| Total | 19.41 | 20.35 | +0.94 | 104.84 |
| Cholesterol | 4.50±0.02 | 4.33±0.03 | -0.17 | 96.22 |
| Σ Polyunsaturated fatty acids : Σ Saturated fatty acids | 1:0.58 | 1:0.61 | | |

Though the average egg mass of the 1st and 2nd group layers was practically similar the egg mass biochemical composition between groups was a little different. So organic feedstuffs mixtures, fed out to the 2nd group layers, increased dry matter content (by 5.93 %, $p<0.05$) and total fat (by 7.68 %, $p<0.05$), but decreased total protein (by 5.18 %, $p< 0.05$) level in egg mass.

The level and ratio of fatty acids were evaluated by taking into account that the eggs of the 1st and 2nd group layers had different total fat amount.

The egg yolk of the control and trial group layers contained in average 32.90 up to 33.47 % saturated, 46.09-47.59 % monounsaturated and 19.41-20.35 % polyunsaturated fatty acids of total lipids amount (Table 4).

Feedstuffs produced in organic farming system, fed out to the 2nd group layers, did not influence saturated and monounsaturated fatty acids percentage level in egg yolk lipids, but increased polyunsaturated fatty acids content by 4.84 %. As a result, the ratio of polyunsaturated and saturated fatty acids in the 2nd group layers' egg is more favourable for food and human health – 1:0.61 (Farrell, 1997).

The content of total n-3 fatty acids group was in average 4.13 % from total lipids amount of the control group's egg yolk but for the trial group it was 4.85 %, that is by 0.72 % ($p<0.01$) higher than the control group layers' egg yolk had (Table 5).

Table 5. The content of n-3 (omega-3) and n-6 (omega-6) fatty acids in the egg yolk (% of total lipids)

| Parameters | Group | |
|---|---|---|
| | 1st – control | 2nd – trial |
| n-3 (omega-3) fatty acids: | | |
| Linolenic acid | 1.38±0.01 | 2.04*±0.02 |
| Eicosapentaenoic acid | 0.10±0.001 | 0.12±0.001 |
| Docosapentaenoic | 0.27±0.01 | 0.27±0.01 |
| Docosahexaenoic acid | 2.38±0.04 | 2.42±0.02 |
| Total n-3 fatty acids | 4.13 | 4.85* |
| Total eicosapentaenoic and docosahexaenoic acid | 2.48 | 2.54 |
| n-6 (omega-6) fatty acids: | | |
| Linoleic acid | 14.14±0.12 | 14.29±0.11 |
| Arachidonic acid | 1.14±0.01 | 1.21±0.02 |
| Total n-6 fatty acids | 15.28 | 15.55 |
| Σn-6:Σn-3 | 3.69:1 | 3.21:1 |
| Linoleic acid:linolenic acid | 10.25:1 | 7.00:1 |

* $p<0.01$

Organic farming system feedstuffs fed out to the 2nd group layers improved egg quality i.e. increased the content of n-3 group fatty acids, necessary for human health, in egg yolk: linolenic acid content by 0.66 % ($p<0.01$), eicosapentaenoic acid and docosahexaenoic acid content by 0.06 % ($p<0.05$) in comparison with of the control group.

In the 1st and 2nd group layers' egg yolk n-6 fatty acids content was almost the same. The fed out feedstuffs mixture did not affect n-6 fatty acids level in egg yolk. In the second group layers' egg yolk the sum of n-6 and n-3 fatty acids as well as linoleic acid and linolenic acid ratio, are very close to the recommended norms of healthy food (Clayton, 2001).

The cholesterol level in egg yolk of the layers who were fed a conventionally produced feedstuffs mixture was in average 4.50 g $kg^{-1}$ (the 1st group, Table 4). By feeding out organic farming feedstuffs mixture to the 2nd group layers, a cholesterol level in egg yolk was 4.33 g $kg^{-1}$ i.e. by 0.17 g $kg^{-1}$ lower than that of the control group.

**Conclusions**

1. Feeding out the permitted full value feedstuffs mixture, produced in organic farming system, to cross Lohmann Brown layers ensured high productivity level: laying intensity of the hens in average 91.90 %, average egg mass 57.92 g and feed conversion 2.27 kg $kg^{-1}$.

2. Feeding out the feed mixture containing organic farming feedstuffs significantly improved egg quality: in the egg yolk the content n-3 fatty acids group increased by 0.72 (calculated from total lipids amount $p<0.01$), but cholesterol level decreased by 0.17 g $kg^{-1}$ in comparison with conventionally produced egg composition.

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# SELECTION AND PRODUCTIVITY EVALUATION OF DOMESTIC ANIMALS IN LATVIA

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## Introduction

The development of agriculture is determined by climate and soil fertility conditions in Latvia. Therefore milk production, pig breeding and partly beef production have priority over other branches of animal husbandry in the country.

According to Central Statistics Board data of January 1, 2004 there were 186 thousand dairy cows with the average annual milk yield 4397 kg per cow in farms of Latvia. From the total number of cows 39% was under recording and their average milk yield was 4767 kg. Latvian Brown and improving breeds comprise 72% and Holstein Black and White – 28% of the total number of cows reared in Latvia. Milk recording data in 2002 / 2003 are shown in Table 1.

Table 1. Milk recording in 2002/2003

| Breed | n | Milk yield, kg | Milk fat | | Protein | | Fat + protein, kg |
|---|---|---|---|---|---|---|---|
| | | | % | kg | % | kg | |
| Red | 44 338 | 4568 | 4.44 | 203 | 3.22 | 147 | 350 |
| Black & White | 17 377 | 5296 | 4.21 | 223 | 3.09 | 164 | 387 |
| Latvian blue | 68 | 4364 | 4.35 | 190 | 3.19 | 139 | 328 |
| Total | 64 143 | 4764 | 4.37 | 208 | 3.18 | 152 | 360 |

The main selection traits of cattle are productivity and body constitution, but functional traits have economical significance as well. Our latest investigations were carried out on cattle reproduction: fertility, burdened delivery, unborn calves count, and also on functional traits: temperament and milking rate of cows. All these properties influence the length of production life. The longer lifetime of a cow is more profitable. Young cow's breeding expenses are high. The price of one pregnant heifer is about 500–700 LVL. Such a sum can be obtained by eliminating 4-5 dairy cows. Therefore the length of production life of dairy cows has great economic significance and during recent years it is considered as the second important selection trait after cows' milk yield.

## Milk production of Latvian cattle breeds

Latvian basic breed, Latvian Brown, has many outstanding properties. The main advantage of the Latvian Brown breed is that during 100 years of development it has adapted to local keeping and feeding conditions. Therefore Latvian Brown breed population should be maintained by developing its good

properties: sufficiently high productivity, strong bone constitution, strong legs and feet, early-maturing animals, high-quality feed (especially forage) conversion ability, good fertility and longevity (Tables 2 and 3) (investigations by D. Strautmanis).

Table 2. High-yielding herds in 2003

| Breed code | Number of cows | Breed | Milk yield, kg | Milk fat | | Protein | | Milk fat + protein, kg |
|---|---|---|---|---|---|---|---|---|
| | | | | % | kg | % | kg | |
| 0488992 | 53 | HM | 9716 | 4.21 | 409 | 3.25 | 316 | 725 |
| 0383101 | 85 | LB+HM | 7838 | 4.45 | 349 | 3.25 | 255 | 604 |
| 0124604 | 641 | HM | 7802 | 4.10 | 320 | 3.19 | 249 | 569 |
| 0327350 | 109 | LB | 7252 | 4.21 | 305 | 3.23 | 234 | 539 |

LB – Latvian Brown; HM – Holstein Black & White

Table 3. High-yielding cows

| No. of cows | Breed | Lac-tation | Milk yield, kg | Milk fat | | Protein | | Milk fat + protein, kg |
|---|---|---|---|---|---|---|---|---|
| | | | | % | kg | % | kg | |
| 7444 | HM | 2 | 12932 | 4.02 | 520 | 3.08 | 399 | 919 |
| 9780 | HM | 1 | 11509 | 3.47 | 400 | 3.27 | 377 | 777 |
| 0019 | LB | 3 | 9871 | 5.03 | 497 | 3.55 | 350 | 847 |
| 0026 | LB | 1 | 9251 | 4.45 | 412 | 3.20 | 296 | 708 |

The keeping plan of Latvian Blue cows is being elaborated as of an exotic breed that can arouse great interest of tourists.

**Milk quality regularities in Latvia cows' milk in connection with breeds and welfare**

The aim of the investigations was to clear up milk quality regularities for Latvian Brown and Holstein Black and White breed cows' milk, depending on animals' age and environmental conditions. The main tasks were to determine the content of protein, fat and cholesterol in cows' milk, to evaluate milk quality changes, affected by cows' breed, lactation and keeping conditions.

The obtained results confirm that protein and fat contents in the milk of the compared breeds differ significantly ($p<0.05$). It was ascertained that the milk samples of Latvian Brown breed cows had in average by 0.8% higher fat and by 0.3% higher protein content than those of Holstein Black and White breed. Average cholesterol indices in the milk of both breed cows differed a little - 0.85 mg per 100 ml. Lactose and somatic cells count did not differ significantly ($p<0.05$).

Somatic cells count fluctuated from 100 thousands per ml to 5 millions per ml in analysed milk samples. Cholesterol content fluctuated from 10 to 20 mg per 100 ml in most samples. Differences in milk chemical composition of Latvian Brown and Holstein Black and White breed cows are shown in Table 4 (investigations by V. Sterna).

Table 4. Chemical composition of the milk of Latvian Brown, and Holstein Black and White breed cows

| Milk constituents | Breed | Samples count | Average value |
|---|---|---|---|
| Cholesterol content, mg per 100 ml | LB | 127 | 16.05 |
| | HM | 68 | 15.20 |
| Fat content, % | LB | 127 | 4.82 |
| | HM | 68 | 4.02 |
| Protein content, % | LB | 127 | 3.39 |
| | HM | 68 | 3.08 |
| Lactose content, % | LB | 127 | 4.72 |

Average cholesterol content is higher in Latvian Brown breed cows' milk samples but cholesterol specific content in fat is higher in these of Holstein Black and White (Figure 1) (investigations by V. Sterna).

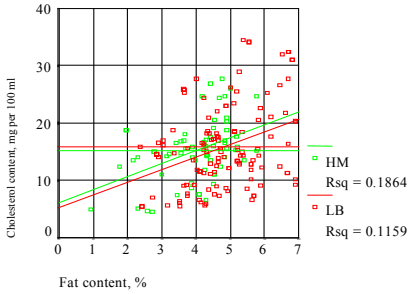


Figure 1. Relationship of fat content and cholesterol amount in the milk of different breeds

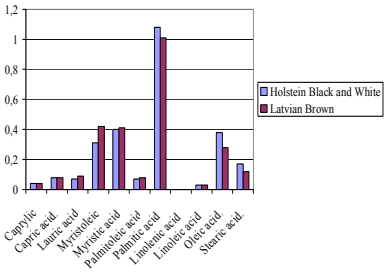


Figure 2. Composition of fatty acids in the milk of Latvian Brown, and Holstein Black and White dairy breeds

Comparison of milk fatty acids composition of Latvian Brown, and Holstein Black and White breed cows' milk is shown in Figure 2 (investigations by V. Sterna).

As it is seen in Figure 2, the concentration of linoleic acid in milk fat is very low, but there is no linolenic acid in milk fat. The presence of monounsaturated

fatty acid - oleic acid, in milk fat is positive. Unfortunately, milk fat contains undesirable saturated fatty acid - myristic acid.

**Pig recording in 2002**

Landrace breed sows form 48.5% in the pig breeds structure. The structure of sow breeds, developed in Latvia, is seen in Figure 3 (pig breeds recording data).

During testing, live weight gains per day of young sows (n=1582), improved by imported Landrace breed boars, were by 182 g higher and backfat tissue by 2.3 mm thinner than of these not improved.

Gilts with 75% Yorkshire breed genes were fast-growing, showing average live weight gain 780 g per day. Comparing fast-growing Yorkshire gilts with not improved gilts of Latvian White breed, the difference is 17 days, reaching 100 kg live weight by Yorkshire gilts before Latvian White. Backfat tissue thickness is by 2.2 mm less in Yorkshire gilts. Fast-growing genetic trend of the tested Yorkshire and Landrace breed gilts is seen in Figures 4 and 5 (pig recording data).

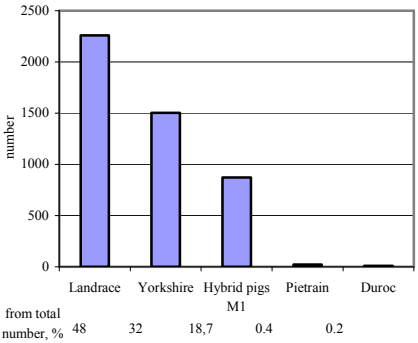


Fig. 3. The structure of pig breeds

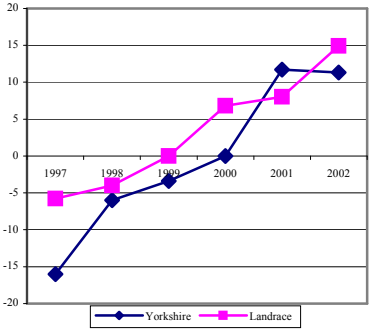


Fig. 4. Live weight genetic trend of sows, g/day

By crossing Latvian White (LW) sows with Pietrain boar progeny, the qualitative properties of production improved already in the first generation: backfat tissue layer thickness was decreased, *m. longissimus dorsi* loin eye area and this muscle was significantly increased as well as carcasses and qualitative meat peaces mass.

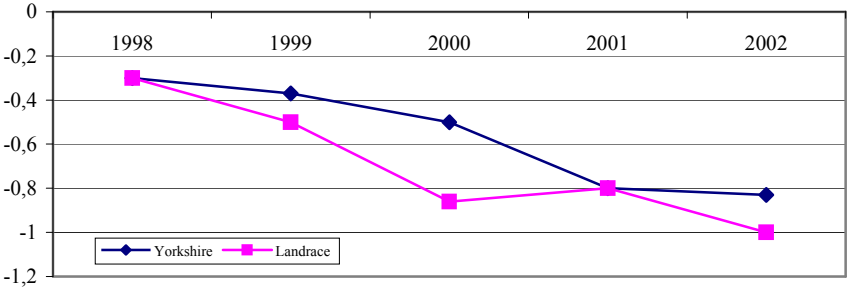


Fig. 5. Genetic trend of backfat thickness of sows, mm

Pigs, supplied to meat processing plants according to their origin, can be divided into three conditioned groups: 1) purposefully formed several breed crosses (49.5%); 2) occasional crosses without definite purpose (38.7%); 3) imported pigs and carcasses (11.8%) (Table 5) (investigations by R. Kaugers, E. Ramins).

Table 5. Carcasses and meat quality indices

| Measurements and analyses | Purposeful several stages crossing | | Indeterminate crossings | | Imported German Landrace | |
|---|---|---|---|---|---|---|
| | $\bar{x}$ | S $\bar{x}$ | $\bar{x}$ | S $\bar{x}$ | $\bar{x}$ | S $\bar{x}$ |
| Live weight, kg | 98.0±1.13 | 7.67 | 102.5±2.58 | 19.28 | 98.8±2.21 | 6.99 |
| Backfat thickness at 6-7 rib | 24.6±0.54 | 5.49 | 32.9±0.91 | 8.28 | 21.6±1.06 | 5.32 |
| *M.longissimus dorsi:* | | | | | | |
| *loin eye area, $cm^2$ | 45.8±1.41 | 10.85 | 35.2±0.73 | 6.44 | 39.2±1.29 | 4.28 |
| *chemical composition: | | | | | | |
| -protein, % | 20.8±0.15 | 1.04 | 20.02±0.17 | 1.28 | 21.2±0.32 | 1.02 |
| -fat, % | 2.29±0.17 | 1.12 | 3.61±0.20 | 1.48 | 2.01±0.19 | 0.59 |
| -oxyproline, g/kg | 1.29±0.08 | 0.55 | 1.14±0.07 | 0.50 | 1.16±0.07 | 0.21 |
| -tryptophane, g/kg | 3.83±0.06 | 0.41 | 3.19±0.12 | 0.87 | 4.28±0.06 | 0.21 |
| -ratio tryptophane / oxyproline | 2.9 | | 2.8 | | 3.7 | |

The highest backfat thickness was revealed to porkers from indeterminate occasional crossings and to those which origin base were Latvian White breed pigs. This difference of fat tissue thickness was significant ($p<0.001$) in

comparison with imported pigs as well as with pigs obtained in purposeful crossing.

The group of indeterminate crossings had the smallest loin eye area and *m. longissimus dorsi* mass ($p<0.05$-$0.001$), but the highest intramuscular fat content in muscle tissue ($p<0.001$). The highest oxyproline content was determined in the muscle tissue protein of pigs obtained in purposeful crossing, in comparison with both other groups, but this difference was not statistically significant ($p>0.05$). The best tryptophane/oxyproline ratio of imported pigs formed due to higher tryptophane content ($p<0.001$) but in pigs obtained by purposeful crossings, tryptophane content was essentially higher than in indeterminate crossings ($p<0.001$).

Animals obtained in purposeful crossing had by 10% more muscle tissue but almost 8% less fat tissue than indeterminate crossings (Figure 6) (investigations by R. Kaugers and E. Ramins). Bones and skin specific amount was lower in pigs with higher lean meat content in carcass.

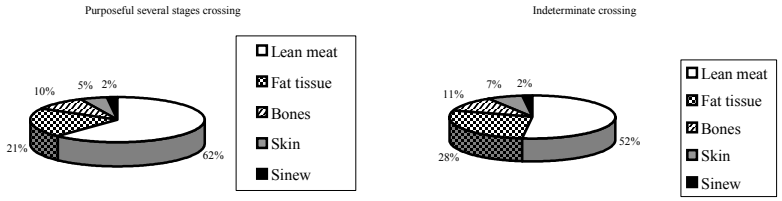


Figure 6. Distribution of the tested pigs according to realization weight groups

**Investigation of the meat quality of Latvia Blackhead sheep crosses**

The main goal was to investigate Latvian Blackhead breed sheep crossings with German Blackhead and Il-de-France breed rams' influence on progeny quality.

The average slaughter age was 9 to 10 months, average live weight before slaughter was 44.0 to 47.5 kg. Live weight gain of individual sheep from birth to slaughter varied from 120 to 226 grams, but that of groups in average from 136.7 to 154.3 grams. The obtained results, compared by groups, showed that live weight of lambs before slaughter did not differ significantly in the groups (Table 6) (investigations by D. Kairisa and J. Spruzs).

More valuable carcasses were obtained from both trial group animals, especially from Il-de-France breed ram progeny

Table 6. Growing intensity of lambs

| Investigated traits | Groups | | | |
|---|---|---|---|---|
| | 1st group ♀ Latvian Blackhead x ♂ Latvian Blackhead | 2nd group ♀ Latvian Blackhead x ♂ German Blackhead | 3rd group ♀ Latvian Blackhead x ♂ Il-de-France | 4th group ♀ Latvian Blackhead x ♂ Il-de-France (castrated ♂) |
| | Animals number | | | |
| | 10 | 10 | 7 | 4 |
| | $\bar{x} \pm s_{\bar{x}}$ | $\bar{x} \pm s_{\bar{x}}$ | $\bar{x} \pm s_{\bar{x}}$ | $\bar{x} \pm s_{\bar{x}}$ |
| Number at birth | 1.6±0.16 | 1.5±0.17 | 1.6±0.20 | 1.3±0.25 |
| Live weight at birth, kg | 3.77±0.026 | 3.82±0.039 | 3.74±0.029 | 3.75±0.029 |
| Age before slaughter, days | 308±16.84 | 318±17.38 | 278±25.77 | 293±30.67 |
| Live weight before slaughter, kg | 45.3±1.83 | 47.2±1.25 | 44.0±2.20 | 47.5±1.26 |
| Live weight gain per day from birth to slaughter, kg | 0.137±0.005 | 0.141±0.005 | 0.151±0.013 | 0.154±0.017 |

By using German Blackhead and Il-de-France breed rams for crossing with Latvian Blackhead breed sheep, the increase of muscle specific weight in lamb carcasses, very important for qualitative lamb meat production, has been achieved already. The work must be continued for obtaining and estimation of new early-maturing sheep crosses.

# CONCEPT OF SUSTAINABILITY IN DAIRY CATTLE BREEDING

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## Introduction

Sustainability in animal breeding and reproduction is defined as the extent to which animal breeding and reproduction contribute to maintenance and good care of animal genetic resources for the future generations (Merks, 2003). This definition has to be worked out by the breeders into applicable breeding goals and scenarios. Breeding goals have to be based on consumer and society demand and therefore contribute to sustainable farm animal production.

The average milk, fat and protein production per dairy cow per year has increased due to the increased use of high productive breeds. The increase in milk production is also a result of the European milk policy as due to the implementation of milk quota system in the European Union the number of cows has reduced. For a long time productivity has been the main selection criterion and type traits were used as selection criterion as indicators for functional traits. The term "functional traits" is used to summarise those characteristics that increase the efficiency not by higher output of products but by reduced costs of input. Major groups of traits belonging to this category are health, fertility, calving ease, efficiency of feed utilisation, and milkability (Groen et al., 1997). Economic value of milk, fat and protein production was first calculated for the Estonian cattle population in 1997 (Pärna and Saveli, 1997). Thereafter they were re-estimated and added economical values also of some functional traits (Pärna and Saveli, 1998; Pärna and Saveli, 2002; Pärna et al., 2003). Since 1997 the milk performance has risen more than by 1000 kg, but the fertility parameters and functional traits have deteriorated. The population size has decreased by 6%. During the last years the increase of product output per cow has lead to the deterioration of animal health and reproduction. This is the reason of reduced longevity. To avoid the negative tendencies many breeding organisations have changed their breeding goal, paying less attention to production and putting increased emphasis of functional traits.

A cattle breeding in Estonia has some prerequisites of sustainability. In Estonia there has been a long history of variety of breeds and breeding practices. Genetic material comes from all over the world, breeding is becoming more uniform, but in Estonia "everything is a little bit smaller" than in the rest of the world.

There are people within animal husbandry, food industry and animal breeding who are convinced that in Estonia there is substantial potential for dairy product differentiation, niche product and quality products. The growing interest of

tourists for unspoiled nature of Estonia should offer a lot of opportunities. In Estonia, dairy farming is the main source of income for agricultural holdings.

During the last years the main foreign investments have been made in the dairy industry. Food industry gives a quarter of the total industrial output, the dairy industry is the largest, accounted for 28% of the total food industry. Because of EU membership, Estonian dairy products have to compete with those of the other EU states in the EU internal market. Competition between local dairies has also tightened.

The paper aims to provide an introduction to sustainability in the context of the application of sustainability in dairy cattle breeding and reproduction.

**Development of the concept of sustainability**

Idea of sustainability has evolved over hundreds of years (Gamborg, Sandøe, 2003). Sustainability is a characteristic of states or processes which can be maintained with the right kind of management. In this very basic form the idea is to maintain renewable resources.

This idea was implemented in a more than 350-year old principle of *sustained yield*, described for the first time in connection with German forest and mining activities. Sustained yield was the regular periodic output that a forest could produce continuously at a given intensity of management without impairing the land's productivity. This use of the general idea of sustainability focused on the *continuous procurement* of goods from natural resources and connected demands for the *wise use* of resources for the sake of present and future generations. During the next 200 years the concept of sustained yield was concerned with maintaining output from a natural recourse. Much later the idea of sustainability developed in its contemporary wording, focused on nature *preservation*. Sustainability was no longer merely about preserving natural resources but about preserving biodiversity at large.

Given that some sort of wise use of resources is possible – what would be a fair *distribution* of natural resources between generations? Thus, the notion of sustainability now combined the idea of wise use of resources and other natural goods with the idea of a fair distribution over time. Over the past decade, with the notion of sustainability more and more issues have been *considered* – covering many matters, from a good working environment to profit for the farmer and animal welfare. These issues were included under umbrella ideas of maintaining and making wise use of resources as well as preserving natural values (Fig.1).

The now prevailing idea of sustainability seems to offer much. According to Gamborg and Sandøe (2003) it is indeed difficult *not* to be in favour of a development which : (i) allows industry to prosper, (ii) gives a sustained yield of high quality products, (iii) protects the natural environment, (iv) cater for the needs of future generations, (v) makes provisions for the needs of poor people,

and (vi) takes care of animal welfare, and so on. However, the problem now becomes one of balancing several potentially conflicting ideals – assuming of course that these ideals can be satisfactorily identified. Bromley put it in the wording as: sustainability is at once a fine idea and hopeless concept. It is good because it reminds us of the fate of future persons, it is hopeless because it begs for operational content (Bromley, 1998).

| | Key concept | Key aspect |
|---|---|---|
| Time ↓ | Sustainability / Sustained yield | Procurement of goods<br>Wise use of resources |
| | Sustainability / | Preservation of species and ecosystems<br>Distribution between generations, between rich and poor |
| | Sustainable development | Consideration of biodiversity, animal welfare, working environment, food safety, farmer profitability, … |

Figure 1. Diagram of selected aspects of sustainability, as the concept has developed over the past 350 years (Gamborg and Sandøe, 2003)

There are two solutions for the practical use of sustainability. According to the first, to surrender the concept of sustainability to decision makers and politicians, and according to the second, to create greater awareness about distributive justice and the value of nature. Due to the sharpened focus, sustainability has inevitably lost its role as an instantly recognisable denominator for all things "good" (Dubgaard et al., 1999; Gamborg and Sandøe 2003).

**Livestock as "capital"**

Farm animals are "used up" in the production process by becoming the final saleable product and so this capital must be replaced by subsequent units in order for production to continue; in other cases the animal "wears out" in the sense of it not being worthwhile continuing for a further lactation and it is culled (McInerney and Bennet, 2003). According to the above named attitude in both the above circumstances, the basic process of animal reproduction is the direct equivalent of maintaining the capital stock, and anything that slows the annual rate at which the breeding stock reproduces (reduced fertility, longer calving intervals) inherently threatens the resource base of the production system and its sustainability. In an economic sense, farm animal breeding and reproduction is the equivalent of capital maintenance and capital creation in the rest of economy. It is the key component underpinning the sustainability of the farm livestock industry as an economic process, and the major driver in its development over time to deliver greater level of output, more consistently and at lower cost (or with higher rates of return – yield- form the animals themselves). The relevance of identifying the role

of farm animals as directly analogous to the role of „capital“ in the generalised production processes in the economy is that we can utilise the principles and considerations associated with the capital resource in the economy theory to illuminate the role and requirements of farm animal breeding and reproduction in the economic sustainability of the livestock sector.

**Sustainability in the context of farm animal breeding and reproduction**

According to the Sustainable European Farm Animal Breeding and Reproduction (SEFABAR) survey product quality, diversity, acceptability, animal welfare and efficiency were listed by breeders as criteria that deserve attention in sustainable breeding schemes (Liinamo and Neeteson, 2001). No production can be sustainable unless it is economically viable. Efficiency of production and the ability to balance both short term and long term economic gain determine the final success of all and any breeding programs.

SEFABAR Thematic Network revealed the economic aspects of both livestock production and of farm animal breeding and reproduction which are of considerable importance to the future sustainable development of the European livestock industries. The main driving forces of change toward 2020 were identified as the profitability of livestock production within EU, food safety and consumer preferences, and the actual developments in breeding technology (McInerney and Bennet, 2003). Respondents to the SEFABAR survey scored on a scale from 0 to 10 the importance of different breeding and reproduction technologies in Europe toward 2020 (where 0 denotes “not at all important” and 10 denotes “extremely important”). Figure 2 summarises the main results.

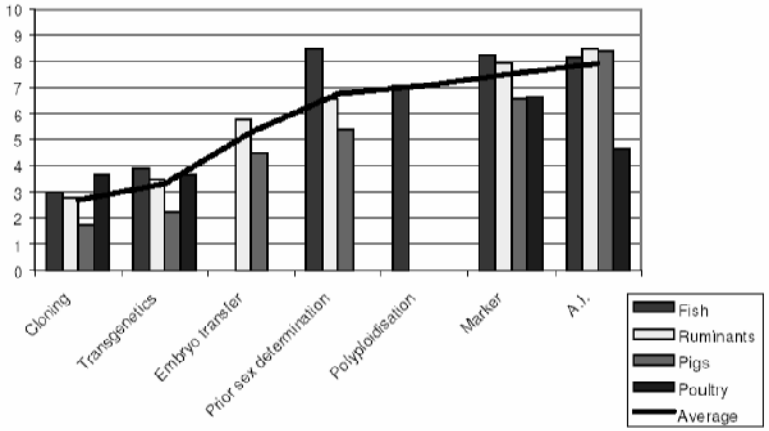


Figure 2. The importance of breeding/reproduction technologies (McInerney and Bennett, 2003)

Artificial insemination was considered an important technology for ruminants, pigs and fish (with scores of 8.5, 8.4 and 8.2 respectively) but not for poultry (4.7). The use of gene assisted selection was also considered important by fish (8.3) and ruminant (8.0) experts but less so by pig (6.6) and poultry (6.7) experts. Polyploidisation is relevant only for fish breeding but was given relatively high importance (7.1). Fish experts gave the highest importance of all to prior determination of sex (8.5) but it was considered less important by ruminant (6.6) and pig experts (5.4). Embryo transfer was rated of some importance by ruminant (5.8) experts but less so by pig experts (4.5). Perhaps surprisingly (at least given the prominence they receive in the media) both transgenetics and cloning received relatively low mean importance scores (around 1.8-3.9) for all species groups.

Clearly, consumer concerns about particular technologies, such as the use of transgenetics, may be an important determinant of what technologies are adopted and how those technologies are applied to livestock breeding and reproduction.

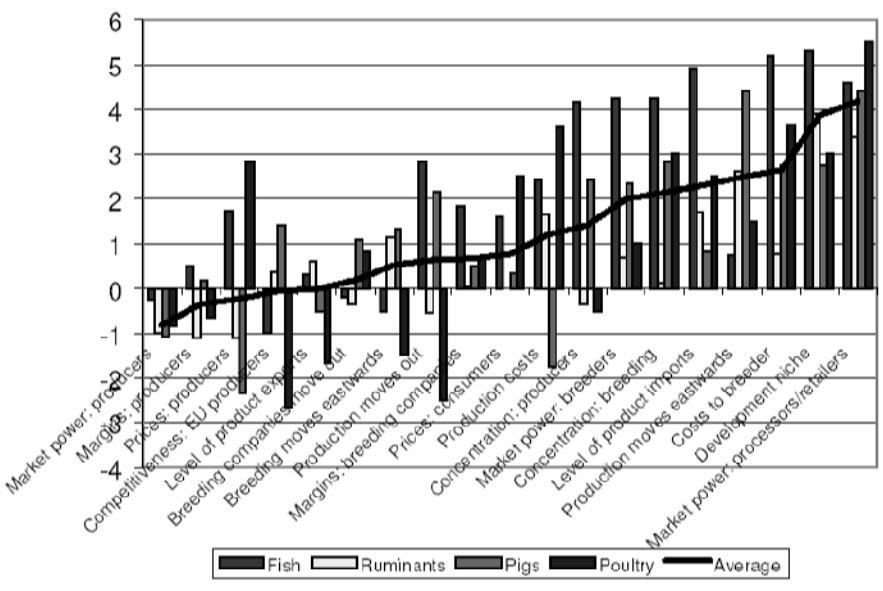


Figure 3. The magnitude of effects of changes in livestock breeding and reproduction (McInerney and Bennett, 2003)

To reveal changes in breeding and reproduction toward 2020 and their main impacts SEFABAR respondents to the expert survey were asked to score the

overall magnitude of effects of changes in livestock breeding and reproduction on three distinct areas (i) costs of production, prices and profits (ii) location of production and (iii) structural changes in the livestock breeding and production industries (McInerney, Bennet, 2003). SEFABAR respondents could score from -10 to +10, where zero would denote no effect, a negative score denotes a downward change and a positive score an upward effect. Figure 3 summarises the main results.

Overall, the largest upward changes were foreseen with respect to the market power of food retailers and processors (mainly due to the structure of the food/livestock industries) and the development of market niches (due to consumer demands). Downward changes identified were relatively very small, with the market power of producers, the margins of producers, the price received by producers and the competitiveness of EU producers all being seen as declining slightly (mainly due to policy and trade influences). Ruminant experts considered the largest upward changes to be the development of niche markets and the market power of retailers/processors with, again, small downward changes in the market power and margins of producers and producer prices.

The initial definition of animal breeding in the scientific literature as “the means available for improving the heredity of farm animals” (Lush, 1945) has changed into the more sophisticated definition by Ollivier (2000) “animal breeding may be seen as the optimal exploitation of the species' biological variation, under given constraints of reproductive capacity, using appropriate breeding value estimation tools”. The term “genetic improvement”, often considered as synonymous to “breeding”, also implies that something better is being looked for (Van Arendonk and Liinamo, 2003). Reproductive capacity of animals put a major constraint of any animal breeding operation. Reproductive techniques like artificial insemination and embryo transfer can be used to overcome these constraints. These techniques play an important role in the activities of the breeding organisations. In essence, the most basic effect of reproductive technologies is to increase fecundity. This means that fewer parents are needed to produce a given number of offspring. The application of reproductive techniques has had a major impact on the structure of breeding programs, the rate of genetic gain, and the dissemination of genetic gain in livestock production.

**Acknowledgement**

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# EFFECTS OF GENETIC SELECTION FOR PRODUCTIVITY ON DAIRY COW FERTILITY

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## Introduction

In most dairy cattle breeding programmes selection is mainly for high milk yield. Reports from several countries indicate that the fertility of the high producing dairy cow has deteriorated during the past 30 years, especially in the Holstein Friesian breed. This decline can be examplified in decrease in conception to 1st service by 0.45 % a year in the USA (Beam & Bulter, 1998), 1% a year in the UK (Royal et al., 2000), and 0.9 % a year in Ireland (Mee et al., 1999). A number of other reproductive parameters are altered in lactating dairy cows including expression of estrus, pregnancy loss, incidence of anovulation. In many countries icluding Estonia infertility has become the main reason for involuntary culling. The aim of the present paper is by compiling recent literature to give a short overview of the changes in the physiology of the dairy cow leading to subfertility, which have been caused by genetic selection. Selection strategies for improving fertility will also be discussed in brief.

## Undesirable side effects of selection for high milk production on fertility

Experiments comparing high and low genetic merit animals, also the estimated genetic correlations suggest that increasing genetic merit for yield reduces fertility. Genetic parameters predict a prolongation of the calving interval by 5 to 10 days per 1000 kg milk when selecting for yield alone (Pryce et al., 1998). Negative association between fertility and milk yield is partly due to a poorer energy balance and a lower condition score for high genetic merit cows. Selection indices may have favoured bulls whose daughters use body lipid in early life at the expense of production, health and fertility in later life. The dairy cow in early lactation has an endocrine profile characteristic of under-nutrition i.e. raised growth hormone (GH) coupled with reduced insulin-like growth factor I (IGF-I) and insulin. Selection for milk yield has increased blood concentrations of GH and decreased concentrations of insulin, IGF-I and glycose (Snijders et al., 2001). Thus, a dairy cow selected for high milk yield suffers from a more severe negative energy balance in the postpartum period because of the physiological state of the animal (undernutrition), which has been amplified by genetic selection. Negative energy balance can affect fertility both at the level of oocyte and of the embryo. Snijders et al. (2000) found that high genetic merit cows yielded oocytes of lower quality, resulting in fewer blastocysts, than medium genetic merit cows, and the ability of an oocyte to be fertilized and develop to the blastocyst stage *in vitro* was

affected by the body condition of the donor cow. Poor oocyte quality and poor early embryonic development may reflect a compromised state of follicular development in postpartum cattle. The concentration of IGF-I represents a possible signaling pathway whereby poor nutritional status can prevent the final stages of follicular maturation (Wathes et al., 2003). Dairy cattle that have been selected for milk production have longer postpartum intervals to first ovulation (Gong 2002). The longer interval to first ovulation reflects a compromised state of luteinizing hormone (LH) secretion necessary for ovarian follicular development and ovulation (Butler and Smith, 1989). Failure of early reinitiation of ovarian activity may result in fewer ovulatory cycles before insemination and thus result in lower conception rate and decreased fertility (Senatore et al., 1996). In a recent study Lucy et al (2003) by comparing dairy cattle selected for milk production with traditional 1964 dairy cattle demonstrated a greater incidence of anestrus and a greater incidence of long luteal phases in cows selected for milk production. Factors known to affect postpartum cows, such as negative energy balance, periparturient disorders and postpartum diseases, are known risk factors for delayed cyclicity and prolonged luteal phases (Opsomer et al., 2000). Early phases of luteolysis are modulated by estradiol (Okuda et al., 2002). Lucy (2003) has suggested that long luteal phases in dairy cattle selected for milk production may be the result of dominant follicles that are developmentally compromised and produce insufficient oestradiol to initiate the luteolytic cascade. Hooijer et al. (2001) estimated genetic correlation between cystic ovarian disease and 305-d milk production trait to be 0.345 in Dutch Black and White dairy cattle and concluded that ongoing selection for production will increase the incidence of cystic ovarian disease. Post-partum differnces in milk progesterone levels between groups of different genetic merit were observed by Veerkamp et al. (2000). Circulating progesterone levels are closely linked to early embryo development (Mann and Lamming 2001), which explains higher early embryonic mortality rate in high genetic merit cows. The incidence of twinning has also increased in modern dairy cattle because there are positive genetic correlations between the incidence of twins and amount of milk production (Kinsel et al., 1998). Inbreeding negatively affects reproductive traits in dairy cows but a “safe” level of inbreeding is poorly defined. In their analyses of Guernsey cattle, Hermas et al. (1987) concluded that every 1% increase in inbreeding led to a 0.17 increase in services per conception, a 2-d increase in days open, and a 3.3 percentage-unit decrease in conception rate. Present levels of inbreeding in US holsteins are approximately 5% and some have predicted that levels of inbreeding will be 10% by 2020 (Hansen, 2000). There is little published information available on genotype by environment interactions for health, fertility and longevity. Such evidence as exists (Pryce et al., 1999; Buckley et al., 2000) suggests that the

poorer fertility of the high genetic merit cows cannot be compensated by feeding higher levels of concentrate, but it is not known if particular bulls have more fertility problems in high or low input systems.

**Selection strategies to improve fertility**

Scandinavian breeding programmes have included non-production traits (fertility, mastitis resistance etc.) in addition to production traits in their selection indices for many years. Inclusion of reproduction and health traits into total merit indexes (TMI) has successfully contributed to maintained or improved results in these traits despite strongly increased production, however response in different breeds has been shown to be different (Philipsson and Lindhe, 2003). Despite the same type of TMI used in Swedish Red and White Breed (SRB) and Swedish Holstein (SLB) breeds the expected negative response in fertility from selection for increased production has been fully counteracted in SRB by the selection for total economic merit, while the fertility of SLB has declined steadily to reach a 6-8% lower level than previously. The same difference has been found between the red and the black and white breeds in the other nordic countries (Juga et al., 1999). The reason for the different trends has been suggested to be an effect of the 'holsteinisation' of the black and white populations, whereby bull sires have consistently been chosen from North America, where no daughter fertility information has been available (Philipsson and Lindhe, 2003). The Scandinavian experiences are unanimous, and prove the needs to develop national systems for genetic evaluation for female fertility and that relevant measures of fertility are chosen from all dairy populations. Several studies have demonstrated that crossbreeds compared favourably with purebred Holsteins in terms of profitability in a variety of environments. McAllister et al. (1994) compared Holstein pureline, an Ayrshire-based pureline, and 10 crossbred groups of these purelines and found that lifetime yields, lifetime milk value, and annualized discounted net returns of the Holstein x Ayrshire-based line F1 and an F1 x (F1 x F1) cross were not significantly different from those for the Holstein pureline. However, net reproductive rate for F1 females was 9% greater than that of contemporary Holsteins. Although there are large genetic differences within breeds, the use of other breeds might be desirable when another breed has a combination of characteristics which is rare within the commonly used breeds. For example the results of a five-year study performed in Ireland comparing different dairy cow breeds highlights the importance of breed / strain of dairy cow in the Irish grass-based seasonal calving system of milk production. Although the Holstein-Friesian produced the highest milk production, this increased milk production did not compensate financially for the reduced reproductive performance when compared to the Montebeliarde breed (Dillon and Veerkamp, 2001). Traditional measures of fertility (nonreturn rate, calving interval) have low heritability $h^2 < 0.05$, and

recording is often poor, hindering identification of genetically superior animals. An alternative approach is to use endocrine measurements of fertility such as interval to commencement of luteal activity (CLA), length of the first luteal phase (LUT1), and persistent corpus luteum type I (PCLI). The three endocrine fertility traits are of additive genetic nature ($h^2$ = 0.16 to 0.21, Darwash et al, 1997; Royal et al., 2002), $h^2$ = 0.17, and $h^2$ = 0.13, respectively (Royal et al., 2002), and they are free from management bias. The incorporation of CLA, LUT1 and PCLI into fertility index may offer the potential to improve the accuracy of breeding value prediction for fertility, thus allowing producers to make more informed selection decisions. Boettcher (2001) has suggested that the most definitive feature of the changes to be undergone in dairy cattle breeding will be general convergence. The dairy industry will succeed by blending harmoniously the best animals of each breed, the most important traits among many. Selection programmes will be designed to combine the economic interests of the industry with the nutritional needs and philosophical desires of the public.

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