BALTIC ANIMAL BREEDING CONFERENCE

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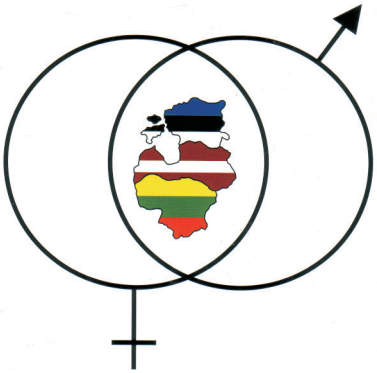

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FOREWORD

The annual Baltic Animal Breeding Conference starts its fifth round. Over the twelve years, the goal of this conference series has been to promote research on scientific aspects of breeding of different livestock breeds, conservation of genetic resources, and animal nutrition.

In the farm animal sector increasing attention has been paid to quality and safety of animal production, competitiveness of farm animal production, animal and human health, and sustainability of farmed livestock. Throughout the years, good collaboration has been developed between the researchers from the Baltic and other countries. The research is international. There are some new financing opportunities designed to support a wide range of participants: from universities, through public authorities to small enterprises and researchers from various countries. We expect that the Seventh Research Framework Programme will broaden perspectives for further extensive collaboration and increase synergy between related research areas.

We hope the 13th Baltic Animal Breeding Conference gives you an opportunity to exchange information and ideas and will facilitate further effective cooperation and mutual personal contacts.

On behalf of the Organizing Committee,

Prof. Haldja Viinalass

CONTENTS

GENETICS

INVESTIGATION OF BETA LACTOGLOBULIN GENE POLYMORPHISM IN GOATS BRED IN LITHUANIA

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Introduction

During the last ten years the number of goats has increased in Lithuania. The economic impact of the goat sector is not yet significant, but the potential of grazing these animals in less favourable conditions for farming has been recognized. According to Annual Report of Animal Recording (2006), six imported (Saanen, German White, German Mottled, Togenburg, Russian White, Czech White) and one local goat breed are found on goat farms. Traditionally, goat milk is more important than goat meat. Goat cheese is becoming more and more popular in Lithuania. The quality of goat milk for production of cheese depends not only on environmental conditions but also on genetic make up of goat. Some variants of goat milk caseins and lacto globulins are more favourable for cheese production than others. Genetic variants of goat milk caseins and whey components were published, and some of them have significant impact on milk quality (Grosclaude et al., 1994; 1997; Moioli et al., 1998). *The aim of this study* was to characterize polymorphism of beta lactoglobulin gene in goats bred on Lithuanian farms.

Materials and Methods

In the study 82 animals from four goat breeds were included. Hair root samples were collected from 23 Lithuanian Native, 21 Saanen, 20 Czech White, and 18 German White unrelated animals. DNA extraction from hair roots have been performed according to protocol obtained from Van Haeringen Laboratorium, Holland (personal contacts). The polymorphism of beta lactoglobulin genotypes has been identified by polymerase chain reaction (PCR) methodology. For PCR reaction beta lactoglobulin primers were used: forward 5ʻGTCACT TTCCCGTCCTGGGG-3 reverse 5ʻGGCCTTTCATGGTCTGGGTGACG-3ʻ

(Folch et al., 1994). DNA was amplified with 10 cycles (97°C 15s, 63°C 1 min, 72°C 1 min 30s) and 25 cycles (95°C 30s, 63°C 1 min, 72°C 1 min 30s) followed 5 min 72°C by GeneAmp PCR system 2700. The amplified DNA fragment was digested with *SmaI* restriction nuclease (MBI Fermentas, Lithuania; 10 units/20ml, overnight). After restriction the products were separated electrophoretically using 2% agarose gel 35 min at 100V. Visualization of the different beta lactoglobulin gene genetic variants was carried out after staining the gels with ethidium bromide, using UV light.

Results and Discussion

Beta lactoglobulin (ß-LG) is the major whey protein in the milk of ruminants. It is also found in the milk of other mammals, but is absent from the milk of rodents, lagomorphs, humans, and probably camels (Hambling et al., 1992). In ruminant milk, the native protein was found as a dimer with a molecular weight of 36.4 kDa corresponding to 162 amino acids. In most other species in which it has been found, ß-LG appears to be monomeric (Hambling et al., 1992). Under physiological conditions (pH 6.5), the protein presents a globular and compact structure and it tends to dissociate into monomers at low and high pH (below 3.5 and above 7.5). Beta-lactoglobulin was the first milk protein in which polymorphism was evidenced by electrophoresis of bovine milk samples (Ashaffenburg and Drewry, 1955).

In the goat species ß-LG protein was considered to be monomorphic, although protein variants with faster electrophoretic mobility have been reported by Russian authors (Stupiniskii and Il'Chenko, 1967). As far as coding region is concerned, no genetic variants are referred in ß-LG gene. Two polymorphic sites (a single nucleotide substitution and a 10–bp insertion) have been identified and characterized in Spanish and French breeds, and localized in the 3'-non coding region (exon7) of the gene (Pena et al., 1999). These polymorphisms are also observed in Italian breeds (Pappalardo et al., 2001). The goat beta-lactoglobulin gene was assigned by in situ hybridization to chromosome 11q28 (Hayes et al., 1993).

Table 1. Comparison of C and T allele frequencies of beta-lactoglobulin gene promotor in goats bred in Spain, Hungary and Lithuania

Breeds	**C**	**T**	**References**
Murciano Granadina (69)	0.86	0.14	Yahyaoui *et al*. (2000)
Canaria (42)	1.00	0.00	Yahyaoui *et* al. (2000)
Payoya (11)	0.73	0.27	Yahyaoui *et al*. (2000)
Malaguena (18)	0.75	0.25	Yahyaoui *et al*. (2000)
Saanen (20)	0.73	0.27	Yahyaoui *et al*. (2000)
Hungarian Milk (109)	0.88	0.12	Veress *et al*. (2004)
Lithuanian Native (23)	0.92	0.08	
Saanen bred in Lithuania (21)	0.75	0.25	
German White bred in Lithuania (18)	0.73	0.27	
Czech White bred in Lithuania (20)	0.78	0.22	

In our study beta lactoglobulin gene polymorphism in promoter region was investigated in goats bred in Lithuania - Lithuanian Native, Saanen, Czech White, and German White.

The following DNA restriction fragments were obtained for the *SmaI* polymorphism: PCR product 472, allele C produces four fragments 472, 181, 50, 7 bp, whereas allele T only three fragments 472, 231, 7 bp. Fragments 181 and 231 allow identification of C and T variants.

Up to date, 82 goats bred in Lithuania have been genotyped for beta-lactoglobulin promotor polymorphism, based on the method published by Yahyaoui *et al*. (2000). Allele frequencies for all 10 breeds are similar with the exception of Canaria breed where allele T is not found. The allele C was found most frequent in all tested breeds ranging from 0.73 to 1.00, in Lithuanian from 0.73 to 0.92. The highest frequency of C allele was found in Lithuanian Native goats. Allele frequencies in goats of Saanen breed bred in Lithuania and Spain do not differ (C allele frequency is 0.75 and 0.73, respectively) (Table 1). The influence of promoter polymorphism on beta lactoglobulin gene expression levels has to be evaluated.

Identification of beta-lactoglobulin gene genotypes as molecular markers for milk properties could be practiced in goat selection programs. The results of beta-lactoglobulin gene polymorphism can also be used in characterization of breeds, biodiversity and evolution studies.

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APPLICATION OF GALLIFORMES SPECIFIC MICROSATELLITE PRIMERS TO INVESTIGATION INTO GENETIC DIVERSITY OF CHICKENS, TURKEYS AND GUINEA FOWL

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Introduction

Assessment of the genetic structure of populations provide useful information for evaluation of the poultry genetic resources (Weigend and Romanov, 2001). Improvement of our insight into the mechanisms underlying genetic diversity may assist in the assessment of genetic variation within populations. When comparing DNA markers and protein polymorphisms in studying the genetic diversity of domestic animals, it can be seen that DNA markers display a greater variation than protein polymorphisms (Barker et al., 1997). Various types of DNA markers have been used for investigation of genetic diversity of domesticated bird species, including RFLP, RAPD, minisatellites and microsatellites (Vanhala et al., 1998; Zhou and Lamont, 1999; Sharma et al, 2001). There are several examples of diversity studies in poultry employing microsatellites. Vanhala et al. (1998) used nine microsatellite markers in the investigation of eight lines of chickens of a different genetic origin. Zhou and Lamont (1999) analyzed 23 highly inbred lines derived from White Leghorns and exotic breeds using 42 microsatellite loci. The first results of the European project on chicken biodiversity (AVIANDIV) were obtained from microsatellite typing in DNA pools of 51 diverse chicken breeds (Weigend and Romanov, 2001). Twenty four Chinese native duck breeds were studied to estimate genetic diversity and genetic structure using microsatellite markers (Li et al., 2006). Kayang et al. (2002) found that five primer pairs originally constructed for the Japanese quail (Table 1) enabled amplification of polymorphic DNA fragments in three species of Phasianidae (Japanese quail, chicken and guinea fowl) to be made. According to the data published in scientific literature, development history of breeds appears to have had an effect on their genetic structure (Li et al., 2006).

Our study is aimed at investigating genetic diversity of different domesticated galliformes species in order to detect genetic differences in the studied poultry populations influenced by breeding peculiarities. Thus, we have studied representatives of chicken layer lines, heavy meat-type turkey populations, and a flock of unselected guinea fowl.

Table 1. Profile of five Japanese quail microsatellite markers

Locus	Sequence (5′ - 3′)	Size range for Japanese quail (bp)	Annea-ling temp	Repeat array
GUJ 0017	F:AGAGAGATTAGAGGAGCTGC R:GGCACTAAAACCATCGAGAG	153 – 165	60	(CA)14
GUJ 0023	F:GAGAGGTACAGCAACACTTT R:GGTTTCTTTCTGGAGTGTCT	219 – 237	55	(CA)7TA(CA)11
GUJ 0063	F:GCTCAGGTTCTCAGCTGATG R:GGGAGAGATCAAGGGAACAG	242 - 250	55	(CA)7CT(CA)2CT(CA)7
GUJ 0084	F:ACTCCTCCTCTTTCTCCCTC R:TCCCGTCTCCCGATGTGTTT	159 – 165	55	(CA)10
GUJ 0086	F:AGCTGCCATATCTACTGCTC R:TGGCTTAGTGCTTTCAGAGG	197 - 207	55	(CA)19

Materials and Methods

Blood samples of pure lines of "Lohmann White LSL" hens (16 individuals), hybrids of heavy type turkeys of crosses BIG-6 and BUT-9 (12 individuals) and guinea fowl (36 individuals) from local breeder were obtained by means of venipuncture.

Samples of DNA were extracted by using proteinase K and salt-extraction method (Miller et al., 1988). Amplification of DNA fragments was carried out by means of microsatellite primers GUJ0017, GUJ0023, GUJOO63, GUJ0084 ir GUJ0086 (Kayang et al., 2002). The PCR has been performed in 25µl final volume containing the following: 20 ng of genomic DNA; 200 ng of a single primer; 0.75 unit of Taq DNA polymerase (MBI Fermentas, Lithuania) and 200µl each of dATP, dCTP, dGTP and dTTP. The reaction buffer contained 1.5 mM $MgCl_2$, 10 mM Tris-HCL pH 8.8 (at 20^0C), 50 mM KCL and 0.08% NP-40. Amplifications have been carried out in Ependorf Gradient Mastercycler (Eppendorf, Germany). Following the initial denaturation step at 95^0C for 2 min, the reaction was subject to 30 cycles of amplification denaturing at 94^0C (30 sec.), annealing at 53^0C (45 sec.), elongation at 72^0 C (45 sec.) and final elongation at 72^0C (5 min.).

Samples of the amplification products (15 µl) have been dissolved electrophoretically on 10% polyacrilamide gels in the TBE buffer for 4 hours. DNA fragments have been photographed, saved and analysed by means of MiniDoc^{TM} Documentation System (Herolab) and TotalLab V1.10 software.

Results

Interspecific differences have been detected for primer pair GUJ0023 (Table 2). Amplified DNA fractions were monomorphic and its size was about 500bp for all hens investigated. For turkeys amplified DNA fractions were also monomorphic and its size was about 700bp. By means of primer GUJ0023 we have amplified one polymorphic zone with two 150 and 160 bp fractions which could be evaluated as different alleles, for guinea fowl.

Table 2. Size of amplified DNA fractions for chickens, turkeys and guinea fowl

	GUJ0017	GUJ0023	GUJ0063	GUJ0084	GUJ0086
Chickens	100 bp 120 bp 130 bp	500 bp	210 bp 250 bp	260 bp 300 bp	–
Turkeys	110 bp 120 bp 130 bp 140 bp	700 bp	210 bp 250 bp	60 bp 90 bp 250 bp 280 bp 350 bp	–
Guinea fowl	160 bp 250 bp 270 bp 300 bp	150 bp 160 bp	170 bp 230 bp 250 bp	180 bp 200 bp 220 bp 300 bp 320 bp	210 bp 240 bp

Such interspecific differences between chickens and turkey were not detected for amplified DNA fractions obtained by using primer GUJ0063. 210 and 250 bp DNA fragments were characteristic of all individuals of both chicken and turkey species. Three fractions of similar size were amplified for guinea fowl using the same primer GUJ0063. This marker could be characterized as the most conservative one of all tested.

Primer pair GUJ0017 has been ascertained as a valuable tool for investigation of the intraspecies genetic variability of chickens, turkeys and guinea fowl as dominant marker, presumably.

Primer pair GUJ0084 was suitable for detection of interspecific differences, as well as for investigation of intraspecific genetic diversity among hens and turkeys. Homozygous and heterozygous individuals with 260 and 300 bp alleles were discovered in different chicken individuals. Two zones of amplified DNA fractions representing different loci were amplified for turkeys: 60 and 90 bp fractions were characteristic of both crosses, and 250, 280 and 350 bp were characteristic of BIG-6, and only one fraction of 280 bp was characteristic of BUT-9 turkeys. In addition, two polymorphic zones presumably representing

different loci with two and three alleles, respectively, were detected for guinea fowl confirming suitability of primer GUJ0084 for investigating genetic diversity of galliformes.

No optimal conditions of PCR were found for primer pair GUJ0086 and thus no DNA fractions were amplified successfully for chickens and turkeys during our investigation, while in guinea fowl one polymorphic zone with two alleles amplified using the same GUJ0086 primer was detected. It should be noted that the detected alleles were of a similar size as compared with the data obtained by Kayang et al. (2002) for Japanese quails and guinea fowls.

Conclusions

- It has been established that primer pairs GUJ0017 and GUJ0084 are suitable for the evaluation of intraspecific genetic diversity among chickens, turkeys and guinea fowls.
- GUJ0063 could be characterized as the most conservative marker among the tested primers and it is not suitable for the investigation of intraspecific genetic diversity.
- Optimal PCR conditions and two alleles were detected for guinea fowl only using primer pair GUJ0086.

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APPLICATION OF MICROSATELLITE PRIMERS FOR INVESTIGATION OF PEKING DUCKS HYBRID LINE

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Introduction

The evaluation of genetic changes is highly important in breeding researches, and organized breeding programs of various domestic birds and animals require the objective of evaluating candidates for selection, a mating design, and a way to validate the design through genetic improvement.

Domestic duck is an economically important poultry species and identification of genes that control the expression of economically important traits is also very important in breeding researches. Most traits of this category display a wide variation in expression and are controlled by numerous genes. In order to identify the genes that are associated with a particular trait, the predominant method uses evenly spaced deoxyribonucleic acid (DNA) markers to screen a population that exhibits phenotypic variation for the trait of interest (referred to as a resource of population). Analysing the association of various segregating alleles at any one marker locus with the trait value allows for the identification of regions in the genome known as quantitative trait loci influencing the given trait.

There are several examples of genetic diversity in domestic birds employing microsatellites. Isolation and characterisation of microsatellite genetic markers from Peking and Muscovy ducks has been done (Genet et al., 2003). Microsatellite markers available for domestic as well for wild waterfowl species have been presented (Buchholz et al., 1998; Maak et al., 2000). Genomic DNA of Mallard duck (Anas platyrhynchos) has been evaluated by using chicken and duck specific microsatellite primers (Slavėnaitė et al., 2004). Cross-species applicability of microsatellite markers for investigation of waterfowl genetic differentiation has been shown (Sruoga et al., 2006).

Despite availability of numerous data on genetic variability investigation of waterfowl and domestic birds by using microsatellites, the data on genetic variability of commercial hybrid line of Peking ducks (Cross TEMP–2) are insufficient. Thus the task of our work was to perform microsatellite – PCR analysis of genomic DNA of commercial hybrid line of Peking ducks (Cross TEMP–2) using chicken specific microsatellite primer corresponding to anonymous polymorphic DNA marker (ADL 231) and specific primers of Mallard duck (Anas platyrhynchos) (Molecular Ecology Notes DB search).

Materials and Methods

Blood samples from the commercial hybrid line of Peking ducks (Cross TEMP –2) were obtained by means of venipuncture. Samples of DNA were extracted by using rapid salt extraction method (Aljanabi et al., 1997). Amplification of DNA fragments was carried out by using specific microsatellite primers chicken-specific microsatellite primer corresponding to anonymous polymorphic DNA marker (ADL 231) and specific primers of Mallard duck (*Anas platyrhynchos*) (Molecular Ecology Notes DB search) in Eppendorf Gradient Mastercycler (Eppendorf, Germany). The data of primers identification are shown in Table 1. The final volume of polymerase chain reaction consists of 25µl. Reactions were initially denaturated for 3min at 94ºC, then 30 cycles of 94ºC for 1min, 43 to 58 for 1min and 72ºC for 1min with a final elongation step at 72ºC. Samples of amplification products (15µl) have been dissolved ellectrophoretically on 12% polyacrilamide gels by using tris EDTA – borate buffer and after stained in 0.5 µg/ml ethidium bromide. The electrophoresis was performed with constant voltage at 200V from 3 to 4 hours. PCR products were visualised in a UV transilluminator, also photographed and evaluated.

Results and Discussion

In our data PCR products appropriate size was resolved, suggesting that specific markers of Mallard duck (Anas platyrhynchos) APH21, APH24, APH25 and chicken specific microsatellite primer corresponding to anonymous polymorphic DNA marker (ADL 231) may be useful for examining genetic structure of the commercial hybrid line of Peking ducks (Cross TEMP–2). The number of amplified DNA fragments, detected with microsatellite markers, is presented in Table 2. The number of amplified DNA fragments differs according to the primer used from two to nine. The highest number of amplified DNA fragments of the cross TEMP–2 has been detected with APH25 primer pair and fluctuates from seven to nine. The primer pair APH 24 exhibits the lowest amount of DNA fragments (2-4) accordingly. The size of amplified fragments also differs from 50bp till 250bp according to the primer pair used exhibiting the shortest DNA fragments with APH21 and APH24 primer pairs (50bp), and the longest with APH25 (250bp) primer pair.

As homozygous and heterozygous individuals of species possessing different amount of alleles were detected with specific primer pairs, the above primers were detected as suitable tools for further investigation of intra-cross genetic variability of the commercial hybrid line of Peking ducks (Cross TEMP–2). The detection within cross genetic variation and increasing number of available markers provide an elementary and especially powerful tool for better understanding of population architecture related to the breeds and lines of ducks.

Both between and within breed genetic variations are important for the future viability of livestock. Continued genetic improvement of livestock is dependent on the fact that substantial genetic variation exists within individual breeds allowing them to respond to selection for different traits.

Conclusions

1. It has been established that primer pairs APH21, APH24, APH25, and ADL 31 are suitable for evaluation of genetic variability of the commercial hybrid line of Peking ducks (Cross TEMP –2).
2. Cross-species applicability of chicken specific microsatellite marker ADL 231 has been detected after amplification of DNA fragments of the commercial hybrid line of Peking ducks (Cross TEMP –2).

Table 1. Characteristics of species specific microsatellite primer pairs of various bird taxa

Taxon	Locus	Motif	Size (bp)	GenBank accession number
Anatidae	APH21	(CA)8	137	AJ515896
Anatidae	APH24	(CA)2TA(CA)9	147	AJ515899
Anatidae	APH25	(GA)9	167	AJ515900
Phasianidae	ADL231	(GT)12	136	G0 1651

Table 2. The number and size of amplified DNA fractions of commercial hybrid line of Peking ducks (Cross TEMP–2)

Genomic markers	Number of DNA fragments	Length of DNA fragments (bp)
APH21	6-8	50-200
APH24	4-2	50-180
APH25	7-9	60-250
ADL231	5-6	75-150

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PATERNITY CONTROL AND EXCLUSION PROBABILITIES OF FARM ANIMALS IN ESTONIA

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Introduction

In Estonia, the pedigree control of farm animals has been performed for nearly four decades. In animal breeding, the correct determination of relatedness and efficient control of pedigree registration is of great importance. In estimation of breeding values wrongly attributed sire information can be severely disruptive.

In dairy cattle populations the rate of pedigree errors is reported to be about 10% on average (Visscher et al., 2002; Sanders et al., 2006). Among randomly analyzed Estonian Holstein cows, the rate of pedigree errors was 6.4% ranging from 0.5 (wrongly declared dam) to 4.8% (wrong sire) in 2006.

It has been reported that wrong or missing sire information has an impact on the reliability of predicting merit and gain. Sanders and her colleagues (Sanders et al., 2006) have determined that the impact of wrong sire was even more harmful than missing sire information on response to selection.

At present, molecular genetic markers for individual identification have almost replaced the blood typing. Essential property of DNA-based markers is technical simplicity of individual genotyping, compared to blood typing. The introduced DNA typing needs neither labor-consuming production of specific antisera nor existing pedigree/family data to determine individual genotypes.

As the wrong parentage has an impact on the estimation of genetic evaluations, ICAR has defined minimum requirements for laboratories running cattle DNA analyses for breeding purposes to guarantee high quality standards

Comparability of data among the labs is guaranteed by comparison tests organized biannually by the International Society for Animal Genetics (ISAG). Since 2001, the Laboratory of Genetics of EMÜ has standardized DNA microsatellite data as a result of attending the ISAG tests.

Likewise, since 2001, when DNA typing as a method was applied, Estonian horse breeders have had the opportunity to genotype their horses. There are different rules set up by horse breeding organizations for genetic identification and parentage verification. In Estonia, however, all stallions used for breeding have to be genetically identified and their parentage has to be verified.

Pursuant to the Estonian Farm Animals Breeding Act, each year a breeders' association shall verify the correctness of the parentage data of at least one per cent of the horses and cattle entered in herd-books and animal breeding registers. The animals to be tested shall be selected at random.

The aim of our study was to determine the exclusion probabilities for wrongly declared parents for cattle and horses on the ground of data collected by our workgroup.

Material and Methods

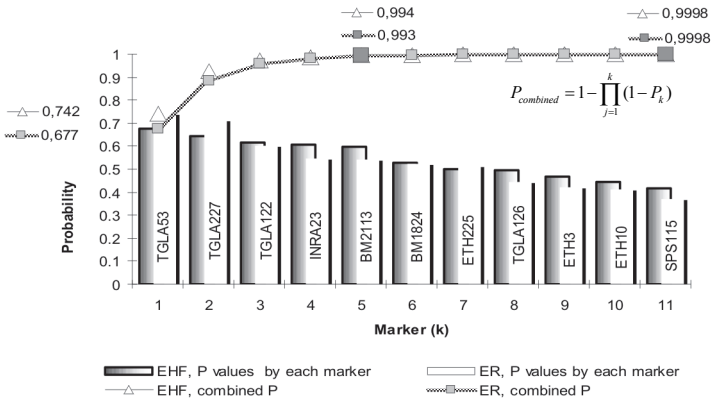
In the current study, data from 607 cattle genotyped by DNA microsatellites was used. Separately, Estonian Holstein (415) and Estonian Red cattle (67) were analyzed. Only representative individuals (114) of all Estonian dairy cattle breeds, Estonian Holstein (EHF), Estonian Red (ER), and Estonian Native (EN), were used in computing exclusion probabilities by blood groups (10 loci) which have been genetic markers employed for a long time. Blood groups were determined by hemolysis test, genotypic data were obtained after completing family analysis. Data on 50 Estonian horses, genotyped by microsatellites to carry out the analysis, were used. The horses were genotyped by 17 microsatellites, and cattle by 11 microsatellites that are commercially available in kits (StockMarks Paternity Kit, Applied Biosystems, USA). The number of detected alleles varied from 5 to 13 in horses, and from 7 to 22 in cattle per microsatellite locus. List of the markers is presented in Figure 1.

Allele frequencies and exclusion probabilities for each marker loci, each population, and combined exclusion probabilities over analyzed loci were estimated. The exclusion probabilities were calculated for more commonly occurred disputed paternity case: in practice, often two alleged parents and one offspring are given, where exclusion for wrongly identified sire (one parent) has to be confirmed by genetic analysis. The calculations were performed by Jamieson (Jamieson, 1994); itemized formulas could be found on web page http://www.isag.org.uk/ISAG/.

Results and Discussion

The exclusion probabilities ranged from 0.428 at SPS115 to 0.742 at TGLA53 by microsatellite loci for cattle breeds, and from 0.420 at HTG7 to 0.678 at ASB2 for horses. The combined exclusion probability was 0.99994 in total for 11 cattle microsatellite loci and 0.9999996 for 17 horse microsatellite loci. The exclusion probabilities varied by cattle breeds among microsatellites (Figure 1). The rate of exclusion probability was associated with the level of locus polymorphism. Our calculations revealed, that exclusion probabilities varied less in ER cattle and in horse population than in EHF cattle by single microsatellite loci. This could be explained by different number of studied individuals in different populations that influenced detected variability within population and at locus.

A



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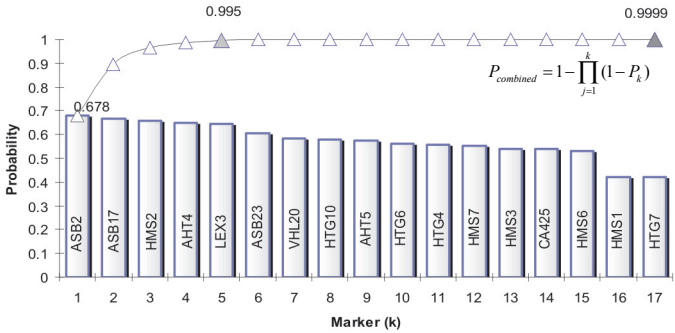

Figure 1. Exclusion probabilities by each marker, and effect of marker number (k) on combined exclusion probabilities in Estonian cattle (A) and horses (B)

Adding one marker locus at a time to calculation of the combined P value, the probability P>0.99 was reached after the fifth locus both in horses and cattle when each following marker was added to the combined probability by descending order of its value. Starting from the locus with the lowest P value (ascending order), the number of loci increased to seven and eight in EHF and ER cattle, respectively.

Even if the results showed that the high statistical power was reached already with 7 microsatellite loci irrespective of their single P value levels, it could not be sufficient for correct pedigree analysis. We have found genetic nonconformity between offspring and parental genotypes at one to seven microsatellite loci in cattle population. Out of wrong paternity cases, the genotypic discrepancy was discovered for the most part at TGLA227 and ETH225 (63.6 and 45.5%, respectively). The lowest effectiveness was found for ETH3, TGLA126, and INRA23 (18.2%); in some cases these loci played an important role, e.g. ETH3 locus occurred as one of two exclusive markers in paternity exclusion.

Our analyses showed that the DNA markers are as effective as the previously used blood groups in routine parentage testing. On the ground of analyzed data, collected from Estonian farm animal breeds, the wrongly attributed parentage of breeding animals could be excluded probabilistically on high rate.

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CATTLE

ANALYSIS OF MILK PRODUCTIVITY TRAITS STABILITY IN LATVIAN BROWN COWS

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Introduction

In Latvia, as of January 1, 2006, recording was performed in more than 11,785 dairy herds. More than 700 certified persons and 2000 persons having obtained certificate for carrying out recording in their own herds are engaged in recording activities. Accuracy in cow milk productivity recording is greatly due to performance quality of these persons. Regulations of the International Committee for Animal Recording envisage the inspection of recording activities to assess performance quality of these certified persons. In Latvia the inspection of recording is carried out by the State Breeding inspector within three days after the current control. Significant differences in data obtained in inspection and recording of cows are not permitted.

In different periods of time the cow milk productivity in Latvia and abroad has been widely investigated (Strautmanis, 1996; Paura, 1999; Huths, 1995). However, there is little research done in the variations of cow milk productivity within a short period of time under conditions of Latvia.

In the research, the main attention is paid to the analysis of the stability in cow milk productivity traits assessing the influence of particular physiological factors of an animal organism and that of environmental factors.

Material and Methods

The research was organized on the training and research farm of the Latvia University of Agriculture "Vecauce". The experiments were conducted for 30 days during pasture period within two years.

In the test group clinically healthy milking cows of different lactations were included. In the first and second research year 2211 and 1988 milk samples, respectively, were analyzed.

Research was started in pasture period in current cow milk recording day preparing milk samples and recording the obtained milk yield per cow in the research group. In milk samples analyzed in Milk-Testing Laboratory at Kurzeme Artificial Insemination Station, the content of fat, protein (%) was determined with *Milko-Skan 133B*.

The repeatability (r_w) was determined as intraclass correlation coefficient (Falconer; Mackay, 1996) by GLM:

$$y_{ijklmnopr} = \mu + \alpha_i + L_j + LF_k + IG_l + LFG_m + SE_n + G_o + PS_p + TM_r + e_{ijklmnopr}$$

where, $y_{ijklmnopr}$ - phenotypic value of animal jkmnopr trait;
μ - Average value of the general group;
α_i - random animal genetic effect (i=1-74 un i=1-66);
Fixed factors:
L_j - lactation (j=1–3); LF_k - lactation phase (k =1–3);
IG_l - milk yield group (l=1–3); LFG_m- interaction lactation, lactation phase, and milk yield group (m_1=16; m_2=14); SE_n - heating time (n =1–3);
G_o - pasture (o=1–3); PS_p - supplementary rough forage (p_1=1-7; p_2=1–5);
TM_r - interaction air temprerature and humidity (r_1=1–9; r_2 =1–8)
$e_{ijklmnopr}$ - residual influence factors.

Results

When analyzing research results we came to the conclusion that the values of the cow milk productivity traits could significantly vary within several days as influenced by physiological and environmental factors. When comparing the milk yield, fat and protein content obtained on the first research day (control) of the pasture period with lactation performance of the following three days we obtained difference which was expressed as percentages. Obtained results indicate that the milk productivity traits varied in a wide range (Figures 1−3).

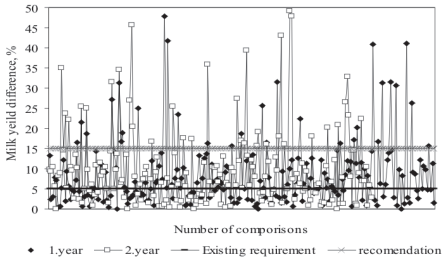

Fig. 1. Difference between milk yield on the day of control and next three days

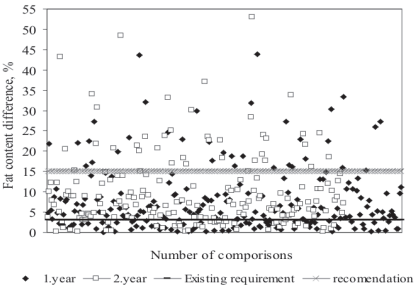

Fig. 2. Difference between fat content on the day of control and next three days

A 5% milk yield difference (Regulations of the Cabinet of Ministers) within three days after the control day in the first research year was observed for 41.5% cows and in the second research year it was observed only for 35.5% cows. Results obtained in two research years show that the milk yield deviation from the control day milk yield for individual cows could be significantly higher. Increasing the milk yield deviation up to 15% we see that in the first research

year 87.2% of cows, and in the second year 83.0% of cows fell into the suggested range of variations.

The difference in fat content within three days after the control day should be 3%. Research results proved that the fat content was the most variable milk productivity trait, therefore we suggested the maximum permissible difference in the fat content on the control day and within the following three days for individual cows within the range of 15%.

In the first research year 84.0% of cows of the research group corresponded to the suggested difference in the fat content, and in the following year – 79.0% of the research group cows, respectively.

Several foreign authors have reported that out of the milk composition components the highest short-time variations have been observed for the milk fat content, as this trait more than others is dependent on exogenic and endogenic factors (Rossow et al., 1990; Huths, 1995).

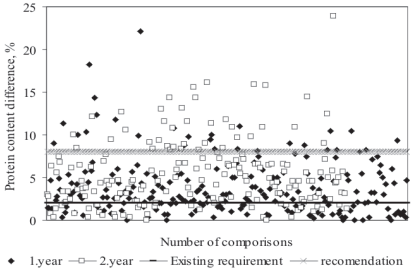

Fig. 3. Difference between fat content on the day of control and next three days

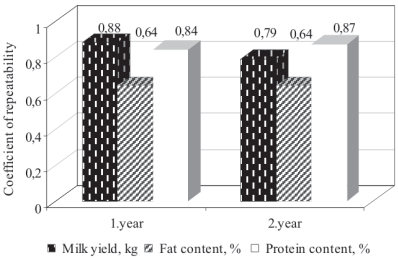

Fig. 4. Repeatability coefficient for three-day period

The suggested difference in the control day and the over-control content of protein in the Regulations is 2%. However, the investigations showed that even for the protein content such a small difference in the first research year was observed for 40% cows, but in the following year only for 24% cows. Therefore, we suggested increasing also the permissible difference of the protein content for individual cows up to 8%. The majority of the research group cows corresponded to such difference (92.2% and 83.0%) both in the first and second year of research.

According to our research, the stability of milk productivity traits in the first research year was lower than that in the second year.

Therefore, the values of the repeatability coefficient for the 30-day period were for the milk yield (r_w=0.84 and 0.73) and protein content (r_w=0.72 and 0.73). In both research years we obtained the highest values of the repeatability

coefficient for milk yield and protein content, but the lowest for the fat content (r_w=0.50 and 0.32).

Similarly, the repeatability coefficient of the studied milk productivity traits was calculated for a three day period (Figure 4).

The highest value of the repeatability coefficient was for the milk yield (r_w=0.88 and 0.79), but the lowest – for the fat content (r_w=0.64). It was found that if the milk productivity trait had high variation, the repeatability was lower. So the traits having higher values of the repeatability coefficient are more stable; these traits are less influenced by environmental factors (Paura, 2002; Jonkus, 2004).

Conclusions and Proposals

The highest values of the repeatability coefficient for the milk productivity traits were observed for the milk yield r_w=0.73 to 0.88. The fat content was less stable with the lowest coefficient of repeatability (r_w=0.32 to 0.64). Within three days after the control day the stability of milk productivity trait was higher than that in 30 days.

Considering traditional cow keeping and feeding practice in Latvia, for individually estimated cows it is advisable to determine the possible deviation in control day and the following three days milk yield and fat content up to 15%, and in protein content up to 8%, but in the herd average milk yield and fat content up to 10% and in protein content up to 5%.

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INFLUENCE OF MILKING CHARACTERISTICS OF COWS ON THE MILK PRODUCTION AND SOMATIC CELL COUNT IN MILK

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Introduction

Milk production and milk flow characteristics are important economic factors in dairy practice. Both are used for animal selection (Miller et al., 1976; Bruckmaier et al., 1995), animal breeding, and monitoring udder health (Duda, 1995; Naumann et al., 1998). Recent knowledge shows the importance of recording not only the udder milk flow, but also the flow of milk in different quarters for faster progress in development of milking technology (Mačuhova et al., 2003).

The measures of milk flow are also important in studying physiological responses of dairy animals to milking (Marnet and McKusick, 2001) or indicating the efficiency of milk ejection (Tančin and Bruckmaier, 2001).

In most studies the analysis of milk flow was based on an udder or a half udder level (Rogers and Spencer, 1991; Slettbakk et al. 1995), although there is a considerable variability in milk flow profiles between the quarters of an udder (Wellnitz et al., 1999; Weiss et al., 2003).

The milk flow from different quarters can also be quite different. One gland might have longer milking time and lower milk flow rates, while another gland of the same udder might need a shorter milking time with higher milk flow rates, where the difference probably indicates some kind of disturbances in the udder (Svennersten-Sjaunja, 2004).

The aim of this study was to estimate milking characteristics of cows' different udder quarters and somatic cell count in milk.

Keywords: Cows, udder morphological index, milking speed, udder quarter, somatic cells.

Materials and Methods

The investigation was carried out in 2006–2007 on a dairy farm of Lithuanian Veterinary Academy. Monthly milking control of cows during lactation months 2-6 were performed on Black and White cows. Lactation, milkability traits and milk quality indicators were studied: milking time (min.), milking speed (kg/min.), milk yield (kg), somatic cell count test day (SCC, $x10^3$/ml). The tested cows' somatic cell count in milk (SCC) was determined at the State Laboratory

'Pieno tyrimai'. Morphological index of udder was evaluated for 99 cows, which were milked using quarter udder machinery - УРВ – 1.

Statistical analysis (mean - $\overline{X}$, standard error - m_x, standard deviation - Sd, variation coefficient - Cv, Pearson correlation coefficient - r) was carried out using "R 1.8.1" package (http://www.r-project.org/).

Results and Discussion

The average index of udders of investigated cows was 44.57%. The milk yield in the front quarters was 5.2 kg and in the rear quarters 8.4 kg ($p<0.05$). The maximal differences between the milk yield in different udder quarters was 13.1%. The data is shown in Table 1.

Table 1. Milk yield in different udder quarters

Trait	Milk, kg	Milk yield,%				Udder index,%	Uneven,%
		Front quarters		Rear quarters			
		Right	Left	Right	Left		
$\overline{X}$	12.47	21.38	23.19	27.12	28.30	44.57	13.10
$\pm m_x$	0.26	0.52	0.60	0.62	0.49	0.75	0.80
Sd	2.55	5.17	5.94	6.17	4.91	7.47	7.98
Cv	20.43	24.19	25.61	22.76	17.35	16.76	60.92

The process of milking different quarters of udders varied from 5.34 (right front quarter) to 6.28 (left rear quarter). The maximal differences between the milking time of different udder quarters was 1.76%. The data is shown in Table 2.

Table 2. Milking time and milking speed in different udder quarters

Trait	Front quarters		Rear quarters		All quarters	Uneven,%
	Right	Left	Right	Left		
Milking time, min.						
$\overline{X}$	5.34	5.75	5.95	6.28	6.65	1.76
$\pm m_x$	0.17	0.20	0.15	0.17	0.20	0.13
Sd	1.72	1.99	1.51	1.68	1.99	1.25
Cv	32.17	34.58	25.43	26.82	29.93	71.02
Milking speed, kg/min.						
$\overline{X}$	0.53	0.52	0.58	0.59	1.98	0.24
$\pm m_x$	0.02	0.02	0.02	0.02	0.05	0.02
Sd	0.18	0.18	0.17	0.19	0.54	0.17
Cv	34.08	34.25	28.50	32.89	27.31	71.47

The least speed of milking (0.52 kg/min.) was tested in the left front and most right rear udder quarters (0.59 kg/min.) ($p<0.05$). Similar results were also determined by Weiss et al. (2004) and Tančin et al. (2006).

Table 3. Correlations of milk yield and somatic cell counts with udder index and milking features

Trait	Milk yield, kg	Somatic cell counts
Milk yield, kg	-	-0.044
Udder index,%	0.303**	0.099
Milk yield uneven	-0.216*	0.021
Milking time, min	0.184	0.012
Milking time uneven	0.021	0.051
Milking speed kg/min	0.515**	-0.057
Milking speed uneven	0.074	0.001

* - $p<0.05$, ** $p<0.001$

A positive significant correlation was observed between milk yield and udder index ($r=0.303$; $p<0.01$), milk yield uneven ($r=0.216$; $p<0.05$), and also milking speed ($r=0.515$; $p<0.01$).

Negative correlations were observed between somatic cell count and milk yield ($r=-0.044$), and also with milking speed ($r=- 0.057$).

A negative correlation (–0.12) between milk yield and SCC was also determined by Nauman et al. (1998), though Rupp et al. (1999) determined a less positive correlation between these traits (0.007). Bahr et al. (1995) found that a slower milking speed can be used to explain a SCC decrease, however, until then investigators had stated positive correlations between milking speed and SCC. Luttinen et al. (1997) determined a higher negative correlation between milkability traits and SCC (–0.11 – 0.29).

However, information about udder quarters milking features is highly important and must be used in dairy cattle selection.

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EFFECTS OF SUPPLEMENTAL YEAST CULTURE ON GROWTH CHARACTERISTICS IN CALVES

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Introduction

Influences of yeast (*Saccharomyces cerevisiae)* culture supplementation on health, intake, growth and production traits have been studied in most ruminants. However, results are somewhat inconsistent throughout the literature, partially because of confounding effects of nutrient digestibility and diet composition, level of yeast culture inclusion, and source of yeast culture product tested (Williams *et al.*, 1991, Galvão *et al.*, 2005). Only a few studies have used pre-ruminant and pre-weaning dairy calves (Cole *et al*., 1992; Seymour *et al.*, 1995, Kumar *et al.*, 1997; Lesmeister *et al.*, 2004). When live yeast (Quigley *et al*., 1992; Cole *et al.*, 1992; Lesmeister *et al*., 2004; Keyser *et al*., 2007) was included in calf diets at levels between 0.75%, 1.13%, 1.0%, 1.5%, and 2.0%, dry matter intake (DMI), average daily gain (ADG), rumen epithelial growth, rumen ammonia, ruminal lactic acid production, and ruminal propionate were either decreased or not affected. However, yeast culture has increased feed efficiency (FE), daily gain, ruminal pH, total ruminal VFA concentration when included in calf diets (Kumar *et al*., 1997; Lesmeister *et al.*, 2004). Williams *et al*. (1991) suggested that calf diet supplementation with yeast culture may increase ruminal pH regulation via reduced lactic acid production and rumen epithelial growth.

Regulation of ruminal pH and reduced lactic acid production are of interest in rumen development research because of the effect of these parameters on intake, health and parakeratosis (Bull *et al.*, 1965). Furthermore, increased butyrate production, decreased lactic acid production, and subsequently, increased ruminal pH may synergistically influence calf rumen development (Sander *et al.*, 1959; Sutton *et al*., 1963; Heinrichs and Lesmeister, 2005). However, the effect of supplemental yeast culture on rumen development has not been determined. Lesmeister *et al.* (2004) suggested that the addition of yeast culture in a dairy calf starter enhances dry matter intake and growth and slightly improves rumen development in dairy calves. It is hypothesised that yeast (*Saccharomyces cerivisiae*) culture inclusion in a calf starter would aid rumen development and calf growth. Therefore, this trial was conducted to determine the effects of supplemental yeast culture in a dairy calf starter on feed intake, structural growth, and production.

Materials and methods

Twenty calves were separated from their dams shortly after birth, randomly assigned by sex to a treatment, blocked by birth date and placed on experiment at 5 d of age. Calves were maintained on the study until 65 d of age. Growth parameter measurements were conducted monthly. The calves were weighed at 5, 35 and 65 d of age. Starter, hay and milk replacer intake were measured daily. Treatments consisted of a texturized calf starter containing 0% (control), or 2% (2YC) supplemental yeast culture as a percentage of starter DM. Calves were housed in a naturally ventilated barn and kept in individual pens. All calves received colostrum and dams received milk twice a day. Calves received a 18.6% CP, 15.6% fat, and 16.9 MJ/kg DM milk replacer containing 50% whole milk powder, 3% dried skimmed milk powder and 47% dried whey powder; and vitamin premix from 5 d of age until weaning. Milk replacer was provided in 2 equal feedings at 10% of body weight (BW) at the first month and 5% of BW at the second month of age. Texturized calf starter and hay were offered *ad libidum*, and intake was measured daily, beginning when calves were placed on the study. Water was provided free choice.

Experimental results were processed in a computer using a spreadsheet programme MS Excel. Variation statistics was used. Arithmetical means and standard deviation of the studied parameters were calculated. Significance of a difference between means was compared by T-test.

Starter and the other feeds samples analyzed for the content of DM, crude protein, crude ash, crude fibre, crude fat and minerals (AOAC, 2005). For determining crude ash concentration, samples were reduced to ashes in a furnace at 550°C for 6 hours. Crude protein was analysed by the Kjeldahl method with the Kjeldec 2300 analyser (FOSS Tecator Technology), crude fat using a Tecator Soxtec System 2043 and crude fibre using a Tecator 1042 Hydrolyzing Unit System. The concentration of NDF and ADF in the samples was determined with a fibre analyser ANKOM 200 (Van Soest *et al*., 1991). Calf starter ingredient and nutrient composition are presented in Tables 1 and 2, respectively. By design, nutrient composition was similar between treatments with the exception of yeast culture content.

Table 1. Ingredient composition of texturized calf starter containing 0 (control) and 2% (2YC) supplemental yeast culture

Ingredients,% DM	Control	2YC
Soya extracted meal	23	23
Oats	17	17
Maize	13	13
Barley	13	13
Wheat	11	11
Wheat bran	10	8
Linseed cake	6	6
Wizan	3.3	3.3
Limestone	1.5	1.5
Monocalcium phosphate	1	1
Magnesium sulphate	0.5	0.5
Salt	0.5	0.5
Premix	0.2	0.2
Yeast culture	0	2

Table 2. Nutrient composition of textured calf starter containing 0 (control) and 2% supplemental yeast culture, on a dry matter basis

Items	Control	2YC
Dry matter,%	88.8	88.5
Crude ash,%	10.5	7.6
Crude protein,%	23.1	22.5
Crude fibre,%	9.0	9.0
NDF,%	21.9	22.0
ADF,%	8.8	8.8
Crude fat,%	4.8	4.8
N-free extractives,%	52.6	56.1
Metabolisable protein, g/kg	115	117
Metabolisable energy, MJ/kg	13.2	13.5
Ca, g/kg	20.4	14.6
P, g/kg	10.2	8.4
Saccharomyces cerevisiae CBS 493.94, CFU/kg	0	4000

Results and discussion

Table 3 presents least squares means for initial, in the middle, and final BW; ADG, and DMI, metabolisable energy(MEI) and protein (MP) intake. Values for ADG, DMI are presented the first, the second and overall periods. Initial and final

BW, therefore, daily gain and DMI, MEI and MPI were not significantly different between treatments. For 1 kg weight gain in the 1st period, the control group used 3.15 kg DM and 2YC group 4.04 kg; in the 2nd period the amounts were 2.33 kg and 2.25 kg, respectively. It was not significantly influenced by yeast supplementation in the starter ration. In the first period, the amount of MP for 1 kg weight gain for the calves of the control group was 396 g MP and for those of the 2YC group 513 g – difference was statistically significant ($P<0.05$).

Table 3. Pre-weaning least square mean for intake and BW of Holstein calves receiving 0 (control) and 2% supplemental yeast culture in a calf starter.

Items		Control	2YC
BW, kg			
Initial, 5 d	$\bar{x}$	49.27	49.16
	s	3.8	5.5
35 d	$\bar{x}$	60.78	59.61
	s	6.7	5.5
Final, 65 d	$\bar{x}$	90.59	90.60
	s	5.3	5.3
Daily gain, g/d			
6 to 35 d	$\bar{x}$	396	302
	s	157	132
36 to 65 d	$\bar{x}$	983	1034
	s	220	126
6 to 65 d	$\bar{x}$	689	701
	s	71	75
DMI, kg/d			
6 to 35 d		1.25	1.22
36 to 65 d		2.29	2.33
Metabolisable energy intake, MJ/d			
6 to 35 d		17.4	17.2
36 to 65 d		29.6	30.4
Metabolisable protein intake, g/d			
6 to 35 d		157	155
36 to 65 d		263	269

In the 2nd month, difference between the groups was not significant – 267 g and 260 g, respectively. In the 1st month, for 1 kg daily gain 43.9 MJ was used by the control group and 56.9 MJ by 2YC group; in the 2nd month 30.1 MJ and 29.4 MJ was used, respectively. Results for DMI from the current study partially

support the findings of Lesmeister *et al.* (2004), who found numerically increased starter and total DMI prior to pre-weaning and weaning. Conversely, significantly higher starter and total DMI for calves receiving 2YC starter post-weaning and overall in the current study are in contrast to the results of Quigley *et al.* (1992), who indicated a significant decrease in DMI post-weaning and overall with supplemental yeast culture. However, the yeast culture content for 2YC starter was greater by a factor of 10 in the current study in comparison with that incorporated in the Quigley *et al.* (1992) study. In addition, others have found decreased DMI when brewer's yeast (Seymour *et al.*, 1995) or live yeast (Wagner *et al.*, 1990) was added to calf diets.

Although there were no statistically significant differences between average daily gain in the 1st and 2nd months and thoughout the experiment, it should be admitted that in the 2nd month the daily gain of the 2YC calves was by 51 g higher than that of the control group (P=0.739).

Average daily gain during the first month for calves receiving the control and 2YC starter overall were lower than predicted by the model. However, actual the second month ADG was higher for all treatments than predicted by the NRC (2001) model.

Conclusion

Supplemental live yeast culture in the calf starter did not increase dry matter intake of the calves in the two first months of life. In the second month of life yeast supplementation slightly increased the daily gain of 2YC group and improved the usage of metabolisable protein, as compared to the control group. The results revealed that supplemental yeast culture did not have any positive results before calves begin to ruminate.

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INVESTIGATION OF FACTORS AFFECTING PRODUCTIVE LIFE OF DAIRY COWS

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Introduction

In dairy production, longevity is a highly important trait, considerably affecting overall profitability. With increased longevity, the average production of the herd increases: a great proportion of culling decisions are based on production, and the proportion of mature cows that produce more milk than young cows, is increased (Allaire and Gibson, 1992; VanRaden and Wiggans, 1995).

However, it is very hard to achieve genetic improvement of longevity traits because of their low heritability. Heritability estimates range from 0.03 to 0.20 (Van Doormaal *et al*., 1985; Jairath *et al*., 1998; Ducrocq, 2002; Roxstrom *et al.*, 2003; Sewalem *et al.*, 2005). Moreover, it takes time until an animal or its relatives leave their respective herds before a direct measurement of longevity. Therefore, for carrying out selection in dairy cattle, the length of productive life of cows, measured as the number of days or months between first calving and culling, is used.

The objective of this study was to investigate the relative importance of genetic, management and other parameters to productive life performance of dairy cows.

Keywords: cows, Black and White breed, productive life.

Material and methods

The data included 232140 records of Black-and-White cow population in 30076 herds for 11 years.

The statistical investigation was performed during 2006-2007 in the Lithuanian Veterinary Academy.

To study the factors affecting productive life of cows, statistical method of the ANOVA test was used. Statistical analysis (mean - $\bar{x}$, standard deviation - Sd) was carried out using “R 1.8.1” package (http://www.r-project.org/).

Results and discussions

Productive life of cows was measured as the total number of months in milk. The analysis revealed that the average productive life of Black and White cows was 31.2 months. The data is provided in Table 1.

Table 1. Productive life of cows

Productive life	No. of cows	X	Sd	m_x
Productive life of all cows	232140	31.12	24.71	0.051
Productive life of live cows	113987	33.88	24.66	0.073
Productive life of dead cows	118153	28.45	24.46	0.071

The estimated effect of genetic factors on productive life of cows showed that it is difficult to improve the productive life of cows genetically. According to the results of the study, mother had no influence on the productive life of cows. The results presented in the Table 2 demonstrate that the use of animal models for genetic evaluation of productive life is not expendable. The impact of father on the productive life (21.45%) and maternal grandsire (5.85%) shows that for genetic evaluation it is recommendable to implement the sire-maternal grandsire model.

Table 2. Influence of genetic factors on the productive life of cows (%)

Factor	No. of class	Influence%
Father	1995	21.45 ***
Mother	102683	0
Maternal grandsire (Father of mother)	2731	5.85***
Breed	8	9.20***

***p < 0.001

Table 3. Influence of genetic factors on the productive life of cows (%)

Factor	No. of class	Influence%
Herd	30076	24.75 ***
Year	11	54.58 ***
Season	2	0.02 ***
Herd*Year*Season	99582	64.38 ***
Age at the first calving	23	3.41 ***
Average milk yield	39318	45.78 ***
Average milk fat and milk protein production	6699	17.06 ***
Live or dead animal	2	28.18 ***
Period of lactation	8	33.04 ***
Herd size	306	14.37 ***
Change of the herd size	537	12.19 ***
Average herd milk yield	12025	23.01 ***
Average herd milk fat and milk protein production	3036	16.30 ***

***P < 0.001

Table 3 reveals significant effect of the fixed, non-genetic factors on the productive life of cows ($p<0.001$).

Several studies have shown that the length of productive life is correlated with milk production. The length of productive life is also influenced by production traits, and through voluntary culling of cows by insufficient milk yield (Short, 1992; Weigel *et al.*, 1998, Rogers *et al.*, 1999).

Average milk yield production of cows affected the productive life of Black and White cow population in Lithuania by 45.78% and the average herd milk yield – by 23.01% ($p<0.001$).

In Lithuania, the average herd size is very small and the use of herd-year-season effects for productive life of cows (64.38%; $p<0.001$) might be problematic; thus alternative ways with regard to culling must be evaluated.

Changes in management and size of herd also affect productive life of cows by 12.19 to 14.37% ($p<0.001$).

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PCR-SEXING, GENOTYPING AND VIABILITY OF BOVINE PREIMPLANTATION EMBRYOS AFTER FREEZING-THAWING AND BIOPSY

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Introduction

Bovine embryo transfer is considered to be of great significance in animal reproduction biotechnology. It influences the use of the genetic potential of high producing cows and cattle reproduction results. Natural breeding of animals results in sex differentiation at a rate of 1:1. Transplantation of sex-identified embryos results in lower raising expenses for desirable offspring, and a lower number of recipient cows is required.

The latest achievements in the field of molecular biology, especially the development and application of polymerase chain reaction (PCR) for amplification of sex-specific DNA sequences and other loci of breeding value, has opened new ways of bovine embryo sex determination and genotyping by collection of only several blastomeres [1, 2, 6].

Embryo genotyping technologies applied to animal breeding have the important role in increasing the impact of superior genotypes in the population [3].

One of the main problems in embryo genotyping is very small amount of DNA available, i.e. 1 or 2 cells (the lowest level of reaction sensitivity), because only a few blastomeres can be collected from the embryo [1, 4, 5, 8].

Our previous studies indicated that successful sex determination of bovine embryos can be achieved using several blastomeres, by detection of male-specific Y-chromosomal DNA using the PCR and by PCR-amplified ZFX/ZFY loci. The first method resulted in 92.6% and the second in 82.2% successful sex determinations [7].

In our sex determination experiment, k-casein loci were additionally PCR-amplified. This amplification was less successful, and k-casein loci were determined in 74.1% of analysed samples [7]. The method of biopsy had a direct influence on the amplification of the K-casein gene loci: efficiency was 37.5% after suction and after cutting – 86.7%.

A larger embryo biopsy reduces its viability and, hence embryo genotyping becomes meaningless.

The objectives of this study were to assess the feasibility of performing blastomere biopsies by cutting and by suction on bovine embryos after freezing-thawing and to determine the effects of biopsy on postthaw embryo development

in vitro and *in vivo*.

Material and Methods

Embryo recovery. Healthy cows of the Lithuanian Black-and-White breed, of 4 to 12 years of age and 500-650 kg of weight were selected as donor cows. To induce superovulation, donor cows were treated with 2500 I.U. Folligon *(Internet, Holland)* at days 9-12 of the estrous cycle. In 56 hours, donor cows were treated with 250 μg of Cloprostenol *(Oestrophan, Czech Republic)* to induce luteolysis of the yellow body. Seven days after artificial insemination, embryos were recovered using standard non-surgical procedures. The uterine horns were flushed with Dulbecco's phosphate buffered saline (DPBS) *(Jurievets, Russia)* containing 1% foetal bovine serum (FBS) *(Biochemical Institute, Lithuania)*. The embryos were collected from the flushing medium, rinsed several times and held in DPBS with 20% FBS.

Embryo microsurgery. Late morulae or blastocysts of excellent or good quality were selected for biopsy. Simplified micromanipulators of our own design were used. Biopsy was carried out in two ways, i.e. either by suction (embryos were fixed with a holding pipette, bevelled micropipette was pushed through the zona pellucida and several blastomeres were removed by gentle suction) or by cutting (embryos were fixed with a holding pippette and biopsies were obtained by cutting the embryo with a microrazor blade).

Freezing and thawing of embryos. Embryos were frozen using controlled freezing regime by M. Renard (1985). Embryos were prepared for freezing according to four step protocols using 1.4M glycerol as cryoprotectant. Embryos were frozen in straws. Freezing regime in "Minicool": temperature decreased at a rate of 5°C/min from +20°C to -7°C, 120 sec stabilization, seeding and temperature decrease at 0.3°C /min until -35°C, 15 min stabilization, and immersion into liquid nitrogen. The straws were thawed for 12 seconds in a 37°C water bath.

Assessment of embryo viability after biopsy. Embryo viability after freezing-thawing and biopsy was evaluated by cultivation *in vitro* in DPBS with 20% FBS at 38.5°C or in TCM-199 with 20% FBS at 38.5°C in 5% C02 atmosphere for 48 hours.

Embryo viability after freezing-thawing and biopsy was evaluated by embryo transfer to recipient cows and the pregnancy rate.

Estrus of recipient cows was synchronized by administration of 250 p.g of Cloprostenol at days 9-12 of the estrous cycle. Only recipients with *corpus luteum* of good quality on the day of embryo transfer were used. A non-surgical method of embryo transfer was applied. Pregnancy was determined in 60 days.

PCR-sexing and genotyping of bovine embryos Embryo sex determination

was achieved by two methods: 1) detection of male-specific repetitive Y-chromosomal DNA sequences after PCR amplification with primers BRY1 and BRY2; 2) amplification the ZFX/ZFY loci with outer ZFX/Y1 ZFX/Y2 and inner ZFX/Y3; ZFX/Y4 primers. The kappa-casein gene loci were PCR amplified with primers KCN1 and KCN2**.**

The x^2-test was used to compare differences between groups. Values are presented as least squares means and are considered statistically not significant if not marked otherwise.

Results and Discussion

The study was conducted to determine the effect of biopsy performed after freezing-thawing on embryo viability. At the first stage of the experiment, embryo viability after freezing-thawing and biopsy, were evaluated by cultivation *in vitro* (Table 1).

Table 1. Effect of biopsy after freezing-thawing on bovine embryo viability evaluated by development *in vitro*

Cultivation time, h	Experimental I		Experimental II		Control	
	Cutting (total)		Suction (total)		No.	%
	No.	%	No.	%		
0	20	100.0	20	100.0	20	100.0
12	13	65.0	15	75.0	14	70.0
24	12	60.0	11	55.0	12	60.0
36	8	40.0	10	50.0	10	50.0
48	5	25.0[a]	8	40.0[b]	9	45.0[b]

[a,b]$P < 0.05$.

In vitro embryo cultivation indicated that biopsy by cutting had a greater negative influence on embryo viability (development amounted to 25.0%) than biopsy by suction (development amounted to 40.0%; $P < 0.05$; Table 1).

Embryos at blastula stage were more susceptible to cutting and suction than at morula stage (Fig. 1). After freezing-thawing, cutting or suction and 48-hour cultivation, 20.0% and 30.0% of blastula reached blastula stage and successfully hatched from ZP, respectively.

Morula like blastula after freezing-thawing were more susceptible to cutting than to suction: after 48-hour cultivation developed, respectively, 30.0% and 50.0% morula.

The method of biopsy carried our on postthaw embryos had a direct influence on subsequent development: biopsy by cutting lowered development of embryos in vitro by 15.0% in comparison with biopsy by suction.

At the second stage of experiment embryo viability after freezing-thawing and biopsy by suction were evaluated after transfer to recipient by pregnancy rate.

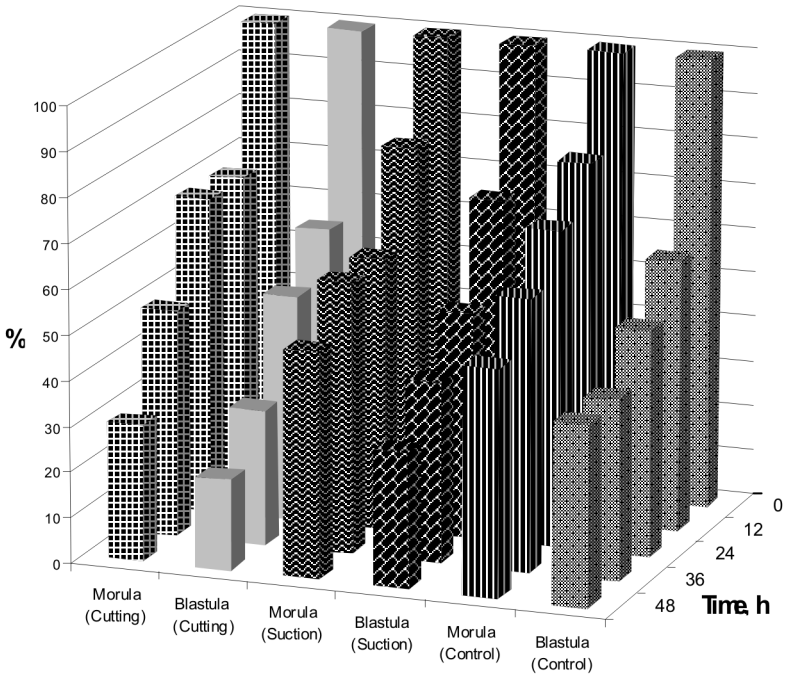

Figure 1. Effect of biopsy after freezing-thawing on bovine embryo viability evaluated by development *in vitro*

The transfers of 28 embryos that were biopsied by suction after thawing resulted in 9 pregnancies (32.1%; Table 2). It has been noted that the pregnancy rate for these embryos had decreased by 15.0% compared with the pregnancy rate after transfers of intact embryos, when 17 embryo transfers resulted 8 pregnancies (47.1%; $P > 0.05$).

The stage of embryonic development had influence on pregnancy results: 14 morula and 14 blastula after freezing-thawing, suction and transfer to recipients resulted, respectively, in 4 (28.6%) and 5 (35.7%) pregnancies ($P > 0.05$).

The results demonstrate that bovine embryos after freezing-thawing can tolerate biopsy by suction and proceed to advanced stages of development and resulted in pregnancies similar rate as control-intact embryos.

Table 2. Effect of biopsy on embryo viability evaluated by pregnancy rate and carried out with embryos at different stages of development after freezing-thawing

Stage of embryonic development	Experimental group			Control group		
	No. of embryos transferred	Cows pregnant		No. of embryos transferred	Cows pregnant	
		No.	%		No.	%
Morula	14	4	28,6[a]	7	3	42,9[a]
Blastula	14	5	35,7[a]	10	5	50[a]
Total	28	9	32,1[a]	17	8	47,1[a]

[a,a]$P > 0.05$.

It creates prerequisite for embryo genotyping and selection according to breeding value at the embryonic stage.

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EFFECT OF DIETARY FAT SOURCES ON MILK AND CHEESE FATTY ACID COMPOSITION

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Introduction

The objective of altering milk fatty acid composition is to improve beneficial health properties of consumer-oriented milk and milk products. Beneficial fatty acids in milk fat are n-3 polyunsaturated fatty acids and conjugated linoleic acid (CLA).

Polyunsaturated n-3 fatty acids reduce risk of cardiovascular diseases (Simopoulos, 1991). Health benefits of CLA mainly based on animal studies, include anti-carcinogenic, anti-atherogenic, anti-obesity, anti-diabetic and immunomodulatory functions as reviewed by Bessa *et al.* (2000) and Collomb *et al.* (2006).

The content of CLA and n-3 fatty acid in milk fat can be mostly increased by the addition of polyunsaturated fatty acids to the cows diet (Donovan *et al*., 2000; Shingfield *et al*., 2006; Bu *et al*., 2007).

The objective of the production experiments was to explain the effect of combined feeding of various fat-rich cakes of Estonian local oil cultures (fat sources) on fatty acid composition of milk fat, milk renneting properties and fatty acid composition of cheese prepared from the milk.

Material and Methods

Two experiments with Estonian Holstein cows (n=108) were conducted. Duration of the preliminary period was 2 weeks and that of experimental period 4 days. In both experiments the cows were fed *ad libitum* total mixed ration (TMR) containing 50% legume silage to which high-moisture grain, maize meal, mineral feed and 3 different oil cakes as fat sources had been added. In Experiment 1, three different fat sources were combined on the basis of their crude fat content in dry matter: 50%, 25% and 25%; and 33.3%, 33.3% and 33.3%, respectively in Experiment 2. Lactating cows were divided into two feeding groups considering that the diet of the first half of lactation was fed from 5 to 270 days in milk and the diet of the 2nd half of lactation from 271 days in milk up to the end of lactation. The diet used in both experiments for the 1st half of lactation contained 11.4 MJ kg^{-1}metabolisable energy, 15.7% crude protein and 5.3% crude fat; for the diet of the 2nd half of lactation the values were 10.6 MJ kg^{-1}, 14.6% and 4.3%, respectively. Fat originating from fat sources formed 50% of the total crude fat content in the diet of the 1st half of lactation and 35% in the diet of the 2nd half of lactation.

The chemical compositions of feeds were determined by the methods accepted by the EU (AOAC, 2005). The calculation of metabolizable energy content was based on

the instruction of calculating energy content of feeds compiled by Ü. Oll and S. Tölp (1997).

In the pre-experimental period and in Experiments 1 and 2, a representative milk sample was taken from a cooling tank. One part of the sample was preserved with Bronopol® while the other part was frozen. The preserved milk samples were analysed for chemical composition in the Estonian Animal Recording Centre; pH value and milk renneting properties (renneting time and curd firmness) according to Kübarsepp *et al.* (2005) were determined in the milk quality laboratory of the Institute of Veterinary Medicine and Animal Sciences of the Estonian University of Life Sciences. The frozen milk samples were analysed for milk fatty acid composition.

For cheese preparation, 10 litres milk was taken from the milk tank in the pre-experimental period and on the last day of both experiment. Edam-type cheese was prepared with FT20-MkII cheese vat. The cheese was packed in film, matured at 12°C for 5-6 weeks and analysed for fatty acid composition.

For determining the composition of fatty acids in milk and cheese fat, the fat was extracted according to international standard ISO 14156 / IDF 172:2001. Fatty acid methyl esters were prepared according to the method proposed by Christie (1982) and Chouinard *et al*. (1999); the fatty acid profile was analysed with *Agilent 6890* gas chromatograph.

Results and Discussion

Co-effect of feeding dairy cows different fat sources was revealed in milk production as well as in milk composition (Table 1). In Experiment 1 milk production remained at the same level as it was in the pre-experimental period while in Experiment 2 it increased by 1.7 kg. The mixture of fatty acids used in Experiment 1 depressed the synthesis of milk fat by 0.45 percentage units; the mixture used in Experiment 2 decreased it by 0.48 percentage units. Milk protein content remained at the same level

Table 1. Effect of fat source on milk production and composition

Traits	Pre-experimental period	Experiment 1	Experiment 2
Milk yield, kg/day	22.3	21.7	24.0
Fat,%	4.44	3.99	3.96
Protein,%	3.51	3.50	3.38
Lactose,%	4.82	4.81	4.83
pH	6.61	6.65	6.64
RCT, min[1]	10.34	10.55	9.51
E_{30}, mm[2]	31.61	31.22	29.03

[1]RCT – rennet coagulation time; [2]E_{30} – curd firmness 30 min after rennet addition

in Experiment 1 while in Experiment 2 it was depressed by 0.13 percentage units. Milk fat depression accompanying diets containing unsaturated fatty acids has been described also by Griinari *et al.* (1998) and Shingfield *et al.* (2006). Combined feeding of different fat sources had no effect on milk renneting properties or on pH value.

Identified fatty acids and their isomers formed over 97% of total fatty acids in analysed milk and cheese fat samples. In Table 2 the data are grouped according to the most important fatty acids.

Table 2. Effect of fat source on milk fatty acid composition, g/100g total fatty acids

Fatty acid	Pre-experimental period		Experiment 1		Experiment 2	
	Milk	Cheese	Milk	Cheese	Milk	Cheese
$C_{4:0}$	3.95	3.19	3.97	3.88	4.11	3.82
$C_6 \ldots C_{11}$	5.39	5.04	5.81	5.76	5.46	5.01
$C_{12} \ldots C_{17}$	41.21	42.89	38.01	38.05	35.00	34.62
$C_{16:0}$	27.24	27.75	22.56	22.65	21.08	20.89
$C_{18:0}$	12.06	12.46	12.05	12.21	12.97	12.85
$C_{18:1}$, *t*-6...*t*-10	1.77	1.77	2.27	2.25	2.29	2.21
$C_{18:1}$, *t*-11	2.05	2.03	2.78	2.75	2.71	2.59
$C_{18:1}$, *c*-9	24.22	24.77	23.74	23.77	24.80	23.44
$C_{18:2}$, n-6	1.70	1.71	1.71	1.79	1.67	1.65
$C_{18:3}$, n-3	0.46	0.47	0.57	0.56	0.63	0.64
CLA[1]	0.86	0.86	1.14	1.11	1.04	1.01
$C_{18:2}$ n-6 / $C_{18:3}$ n-3	3.70	3.64	3.00	3.20	2.65	2.58
Σ n-6[2]	2.94	2.78	3.09	3.15	3.30	3.03
Σ n-3[3]	0.67	0.70	1.01	1.02	1.22	1.29
Σ n-6 / Σ n-3	4.41	3.94	3.05	3.09	2.70	2.34
Saturated[4]	60.49	60.31	57.82	57.83	55.85	54.53
Monounsaturated[5]	32.25	32.80	33.56	33.58	34.61	32.91
Polyunsaturated[6]	4.85	4.65	5.86	5.95	6.43	6.11

[1] $C_{18:2\ c\text{-}9,\ t\text{-}11}$, $C_{18:2\ t\text{-}10,\ c\text{-}12}$

[2] $C_{18:2\ n\text{-}6}$, $C_{18:2\ t\text{-}9,\ t\text{-}12}$, $C_{18:2\ c\text{-}9,\ t12}$, $C_{18:2\ t\text{-}9,\ c12}$, $C_{18:3\ n\text{-}6}$, $C_{20:2\ n\text{-}6}$, $C_{20:3\ n\text{-}6}$, $C_{20:4\ n\text{-}6}$, $C_{22:2\ n\text{-}6}$, $C_{22:4\ n\text{-}6}$

[3] $C_{18:2\ t\text{-}11,\ C15}$, $C_{18:3\ n\text{-}3}$, $C_{20:3\ n\text{-}3}$, $C_{20:5\ n\text{-}3\ (EPA)}$, $C_{22:5\ n\text{-}3}$, $C_{22:6\ n\text{-}3}$

[4] $C_{4:0}$, $C_{6:0}$, $C_{8:0}$, $C_{10:0}$, $C_{11:0}$, $C_{12:0}$, $C_{14:0}$, $C_{15,0}$, $C_{16:0}$, $C_{17:0}$, $C_{18:0}$, $C_{19:0}$, $C_{20:0}$ $C_{21:0}$, $C_{22:0}$

[5] $C_{10:1\ c\text{-}9}$, $C_{14:1\ c\text{-}9}$, $C_{15:1\ c\text{-}10}$, $C_{16:1\ t\text{-}9}$, $C_{16:1\ c\text{-}9}$, $C_{17:1\ c\text{-}10}$, $C_{18:1\ t\text{-}6\ldots t\text{-}11}$, $C_{18:1\ c\text{-}9}$, $C_{18:1\ c\text{-}11}$, $C_{20:1\ c\text{-}8}$, $C_{20:1\ c\text{-}11}$, $C_{22:1\ c\text{-}13}$, $C_{24:1\ c\text{-}15}$

[6] $C_{18:2\ n\text{-}6}$, $C_{18:2\ t\text{-}9,\ c\text{-}12}$, $C_{18:2\ t\text{-}9,\ t\text{-}12}$, $C_{18:2\ t\text{-}9,\ c\text{-}13}$, $C_{18:2\ c\text{-}9,\ t\text{-}11\ (CLA)}$, $C_{18:2\ c\text{-}9,\ t\text{-}12}$, $C_{18:2\ t\text{-}10,\ c\text{-}12\ (CLA)}$, $C_{18:2\ t\text{-}11,\ c\text{-}15}$, $C_{18:3\ n\text{-}3}$, $C_{18:3\ n\text{-}6}$, $C_{20:2\ n\text{-}6}$, $C_{20:3\ n\text{-}6}$, $C_{20:4\ n\text{-}6}$, $C_{20:3\ n\text{-}3}$, $C_{20:5\ n\text{-}3\ (EPA)}$, $C_{22:2\ n\text{-}6}$, $C_{22:4\ n\text{-}6}$, $C_{22:5\ n\text{-}3}$, $C_{22:6\ n\text{-}3}$

Heat treated rapeseed cake (fat content 10%) used in Estonia is the main source of dietary bypass protein and ruminally inactive fat is a widely used energy feed for high productive cows – due to that the milk fat of the pre-experimental period can be partly regarded as modified. Thus we compare the co-effect of different dietary sources versus a traditional feeding scheme that is not typically used in other countries.

No significant changes occurred in the content of short-chain fatty acids (C4 and C6 …C11) of milk fat. However, decrease in the content of medium-chain fatty acids (C12…C17) was observed, especially in Experiment 2 where the proportion of fat sources 2 and 3 was increased and the proportion of fat source 1 decreased.

The experimental feeds decreased the content of saturated fatty acids and increased the content of polyunsaturated fatty acids. The content of CLA and n3 fatty acids showed a significant increase both in milk- and cheese fat.

Processing of milk to cheese appears to have no effect on the final content of fatty acids in cheese. The same result has been shown by Ryhänen *et al.* (2005).

Conclusions

Combined feeding of oil cakes which are being used in Estonia can improve beneficial health effects of milk fat – by decreasing the content of medium-chain saturated fatty acids and by increasing the content of n3 fatty acids and CLA in milk fat.

Acknowledgment

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FACTORS INCREASING MILK PRODUCTIVITY IN ESTONIA

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Introduction

Thirty years ago, the Estonian Research Institute of Animal Breeding and Veterinary Science arranged a feeding trial with the cows of the Estonian Holstein (Black-and-White) breed at the Piistaoja (former Vändra) Experimental Station (Metsaalt, 1985). The trial involved ten healthy Holstein cows with high body weight and good parentage, who had finished their 2nd lactation. In the 2nd lactation, the 305-day productivity of the test cows was 5,600 kg milk and 224 kg milk fat (4.0%). The trial was carried out during the dry period. The feed ration was changed, taking into use high-quality feeds, balancing the protein to carbohydrate ratio, and feeding the cows *ad libitum* during lactation.

Taking into consideration the transition from the 2nd lactation to the 3rd, and from twice-daily milking to thrice-daily milking, the productivity data would have been 6,700-270-4.0. The actual yield, however, was 9,700-428-4.4%, i.e. 3,000 kg milk and 160 kg milk fat more than expected, whereas the milk fat content increased by 0.4% as well.

Piistaoja herd was one of the best herds of that time and, based on performance data, the average genetic potential of Estonian cows for milk productivity can be presumed to have been over 6,000 kg. Unfortunately, however, their experience was not put into practice. Thus, the recorded average yield was only a little over 3,500 kg. After regaining independence in Estonia, the productivity rapidly dropped to the level of 1970, and only in the late 1990s the production capacity started to increase again.

3,000 kg was exceeded	in 1966: 3,030 kg – 111 kg milk fat;
4,000 kg was exceeded in 20 yrs	in 1986: 4,104 kg – 164 kg milk fat;
5,000 kg was exceeded in 14 yrs	in 2000: 4,960 kg – 213 kg milk fat.

During the mid 1990s, experts from foreign companies organised trips for Estonian dairy farmers to the USA, Denmark, the Netherlands, and Germany. By that time, many of the farmers had already visited Finland and Sweden. Almost everywhere loose keeping of dairy cows, often a cold loose-housing system, was applied. Moreover, cows were fed total mixed ration *ad libitum,* or silage and concentrates at the electronically controlled automatic manger feeders. Although Estonian cattle breeders were convinced of the appropriateness of the systems applied abroad, they could not afford to use these more proven methods themselves due to lack of finances. Low procurement prices of milk (*ca* 55% from expenses in 1998/1999) bankrupted and indebted several farms.

However, due to foreign investments, the reconstruction of former large-scale farms was started. Valuable experience was gained in the most severe winter conditions. Since nutritionists conducted additional research and explained the advantages of ensilage, large numbers of rolling machines for baled silage were purchased. Bank loans were used for building new uninsulated loose housing cowsheds for dairy cattle.

Since 2000, the yearly increase in milk productivity has been 317 kg. According to the results of several studies, the average breeding success for increasing milk productivity is usually claimed to be 150 kg, i.e. a half of the increase.

6,000 kg was exceeded in 4 yrs in 2004: 6,055 kg – 259 kg milk fat;

+862 kg was exceeded in 2 yrs in 2006: 6,862 kg – 286 kg milk fat.

In the Netherlands, for example, over ten years (1984-1994) the milk protein yield increased by 45 kg, of which 91% or 41 kg was the result of breeding work (Veepro Holland, December 1997). From 1990 to 1994, the milk protein yield of Estonian Holsteins increased by 30 kg, whereas only 15% or 4.5 kg was due to breeding work. The results for Estonian Red breed were even worse.

Materials and Methods

The current analysis is based on the animal recording data registered in 2006 (Results…, 2007).

Since November 2006, breeding value estimation for production traits has been carried out simultaneously for Estonian Holstein cattle and Estonian Red cattle, using the BLUP random regression test day animal model (RRTDM).

SPAV as a production index is a relative breeding value with mean of 100 and SD of 12 points, combining breeding values of milk, fat and protein quantity by relative economic weights of 0:1:4 and 0:1:6 for EHF and ER, respectively.

In August 2002, the first Danish type cold loose housing dairy cattle shed was opened in Torma POÜ, and another, of the American type, in Põlva POÜ in September 2002. Later on both facilities were expanded. In 2006, the above two farms held the first positions among the dairy farms of the size category of over 100 cows: 1. Põlva POÜ – 11,145 kg and 3. Torma POÜ 9,632 kg. In 2004 - 2006, several cattle houses were reconstructed and new facilities built for 29,000 dairy cows (27% of the total population) in Estonia.

In 2006, milk production per cow increased by 353 kg, i.e. only 138 kg remained unachievable from the goal of 7,000 kg, which was largely due to the hot and dry summer (Table 1). On 14 dairy farms the average milk production exceeded 9,000 kg. The productivity of the Estonian Native cattle slightly dropped, while the cows of the Estonian Red breed surpassed them in milk protein content. The Estonian Native cattle are still being kept on smaller farms

which mostly use old-fashioned feeding facilities. Moreover, the restrictions set for breeding of endangered breeds usually decrease their genetic potential, particularly regarding the milk fat and protein content.

Table 1. Milk production in 2006

Breed	No. of cows	%	Milk, kg	Fat,%	Protein,%	F+P, kg
ER	23 348	25.6	6338	4.31	3.44	491
EH	72 894	73.7	7069	4.13	3.32	527
EN	544	0.5	4394	4.56	3.40	350
Other	161	0.2	4008	4.17	3.35	302
	98 947	100	6862	4.17	3.35	516

The average production data prove the effectiveness of the change in the farm technology. While several countries have experienced that the smaller farmsteads show higher productivity, compared with the large-scale units, the situation is completely different in Estonia. For example, up to 6,300 kg milk on the average was obtained on the cattle-sheds with up to 300 cow places, and more than 6,900 kg on larger farms.

A problem exists with the production level of adult cows (3rd and later calving), which does not exceed the productivity of the 2nd lactation cows, while their share in the herd comprises 46% (Table 2).

Table 2. Milk production (%) during different lactations

	Breed	No of cows	Lactations (%)	
			2nd : 1st	3th : 1st
Estonia	All breeds	82 908	+11	+11
Põlula	All breeds	72	+16	+ 9
Tartu Agro	ER	64	+20	+37
	EH	56	+26	+46
Põlva Agro	EH	160	+22	+33

Each age group consists of cows with different genetic capacity, and presumably the older groups include more cows of lower genetic potential. The results of a trial, conducted on Põlula Farm where cows were still kept tethered and pipeline milking system was in use, revealed 550 kg reduction in milk yield of the cows having calved three times. The drop in production was apparently related to health problems, as the genetic value cannot change. The diseases of reproductive organs and udder tend to affect the cows at a very early age. Loose-house keeping and parlour milking will hopefully improve the situation, as the

production of 3rd lactation cows is constantly increasing on several farms (e.g. Tartu Agro and Põlva Agro).

Another major problem is related to the fact that often heifers with moderate breeding values are being used for replacements in foundation herds, which was revealed comparing pedigree indexes by birth years of heifers with the relevant data of the replacement heifers.

Furthermore, several problems are associated with reproduction issues. The delayed first service is one of those. According to scientific research, the ovarian function of high producing cows is estimated not to recur before the 3rd lactation month.

Based on the estimation of genetic parameters, the breeding value for milk productivity of cows has constantly increased over ten years (Figures 1 and 2). The graphs of both trends are rather similar, although genetic trend for SPAV is calculated on a basis of milk fat and protein production, excluding the milk production. Consequently, in case of the stable fat and protein content in milk, the total dry matter production is primarily influenced by milk quantity.

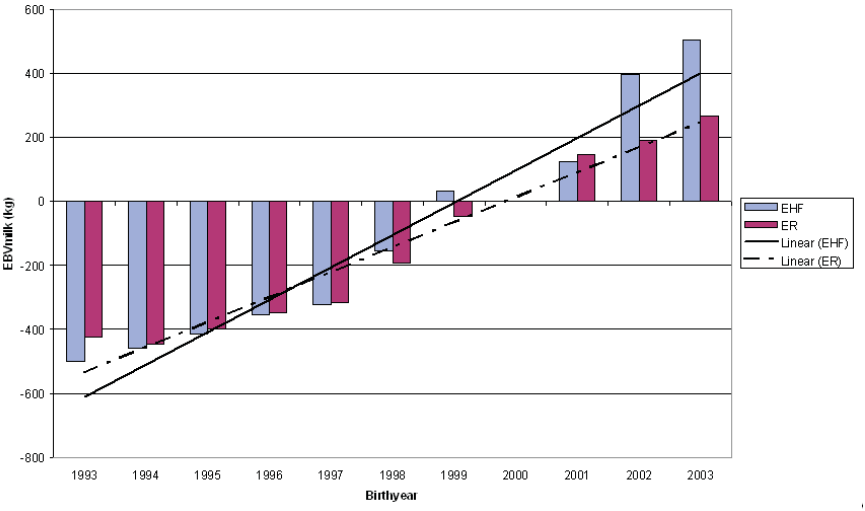

Figure 1. Genetic trend for milk yield by breed

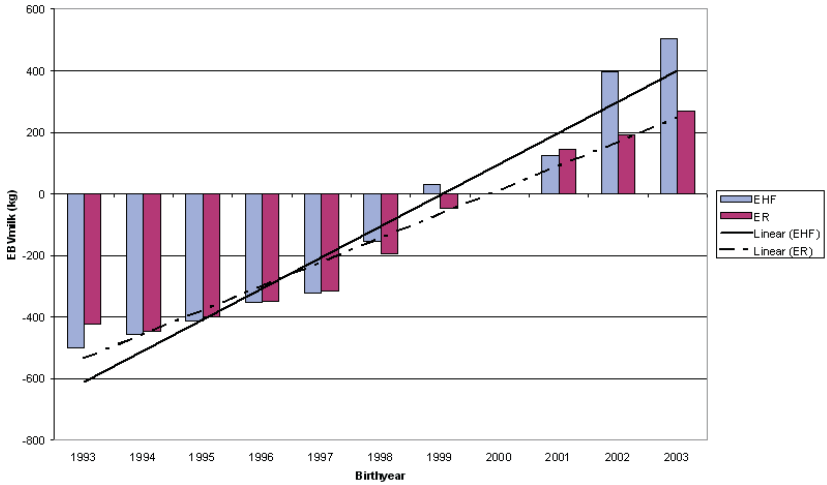

Figure 2. Genetic trend for SPAV by breed

Since 2003, the EBV of Estonian Holstein cows has shown markedly faster increase, compared with the Estonian Red, even though the protein content of the milk of the ER cows has continuously been increasing.

Table 3. Phenotypic and genetic change over 10 years in production traits of cows (birth years 1993 and 2003)

Trait	Estonian Red			Estonian Holstein		
	Change	EBV		Change	EBV	
	kg	kg	%	kg	kg	%
Milk	+2628	+699	27	+2899	+1015	35
Fat	+ 117	+ 21	18	+ 111	+ 28	25
Protein	+ 98	+ 22	22	+ 104	+ 30	29

Genetic evaluation reveals faster improvement in the Estonian Holstein breed -- 316 kg increase in milk and 15 kg increase in milk dry matter production. We foresee further increase in the role of genetic factors in improving our dairy herds.

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ECONOMIC EFFICIENCY OF MILK PRODUCTION IN ESTONIA

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Introduction

In the farming business the knowledge about the economic principles behind the milk production and a business-like approach to farming is important if you want to remain competitive in the long run. High costs and poor profitability will make it difficult to expand or even just survive.

Reproductive performance is one of the major factors influencing the profitability of a dairy herd. Reproductive performance affects the amount of milk produced per cow per day of herd life, breeding costs, rates of voluntary and involuntary culling, and the rate of genetic progress for traits of economic importance. The actual breeding efficiency obtained within any dairy herd is highly influenced by the care and attention provided by the manager, inseminators, and others involved with herd health and feed supply (Plaizier et al., 1997)

A significant objective of a profit-making dairy farmer is maximization of total farm income (Renkema et al., 1979). The decisions about breeding and replacement play an important role in the management of a dairy herd. Maximizing farm profits requires optimizing reproduction and replacement decisions (DeLorenzo et al., 1992). To improve expected future profits on the dairy farm, culling decisions should be based on economic principles rather than on biological considerations (Lehenbauer et al., 1998). Economic analysis of the replacement decision should include the prospect of the cow's future performance as well as that of the probable replacement (Groenendaal et al., 2004)

Materials and Methods

According to experimental design, five test groups were formed from different breeds: 1) Estonian Native (EN), 2) Estonian Red (ER), 3) Red Holstein (RHF), 4) Estonian (SPAV up to 112) Holstein (EHF), 5) Estonian (average relative breeding value for milk production index SPAV above 112) Holstein (EHFt). Current investigation data from years 2000-2005 were used. On the experimental farm a total mixed ration (TMR) was used, distributed by feed mixer to ensure constant feed availability. The animals of all the test groups were kept in similar conditions and fed mixed feeds *ad libitum*. One milking operator milked cows three times a day.

The milk production data of 5 years of the Põlula Experimental Farm were obtained from database of the Animal Recording Centre. Economical analysis

involves data from cows with three calvings – i.e. with two calving intervals. Based on the above data, it was possible to find out cost effectiveness of cows with different levels of fertility.

Results

Over the past 15 years, the proportion of dairy breeds has been changed remarkably. In 1990 the dairy herd was comprised of two equal parts of Estonian Red and Holstein breeds, but currently the Holstein breed covers three-quarters of dairy herd population.

Proportion of breeds

Breed/year	1990	2000	2005
• Estonian Red	49.1	29.3	26.5
• Estonian Holstein	50.7	70.3	73.0
• Estonian Native	0.2	0.4	0.5

Milk production has increased from 4,000 kg per cow/year in 1986 to 6,862 kg per cow/year in 2006, respectively. Primary reasons are the use of a total mixed ration, and introduction of free-stall barns. The Estonian Holsteins have higher milk production: +681 kg compared with Estonian Red, and +2,675 kg compared with Estonian Native breed.

The analysis of test holdings (*Farm Accountancy Data Network* – FADN**,** Aamisepp, 2007) studied the competitive ability and sustainability of minor and major agricultural producers, and whether investment grants were allocated to producers who needed them most. When producers were grouped by incomes from agricultural production, it turned out that lower turnover concurred with the relative importance of subsidies within incomes. For example, the subsidies formed 57.4% of incomes in the group where revenue from sale was up to 100,000 EEK, and only 10.1% in the group with the highest income. The analysis of investments showed that producers with lower incomes had adequate amount of resources neither to purchase capital assets nor to receive investment grants, while 92% of producers with higher incomes invested to capital assets and 16% of producers of this group received investment subsidies.

Results obtained on test farm (Figure 1) showed that 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. Total production of milk fat and protein was the highest in EHF group and in EHFt group. 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.

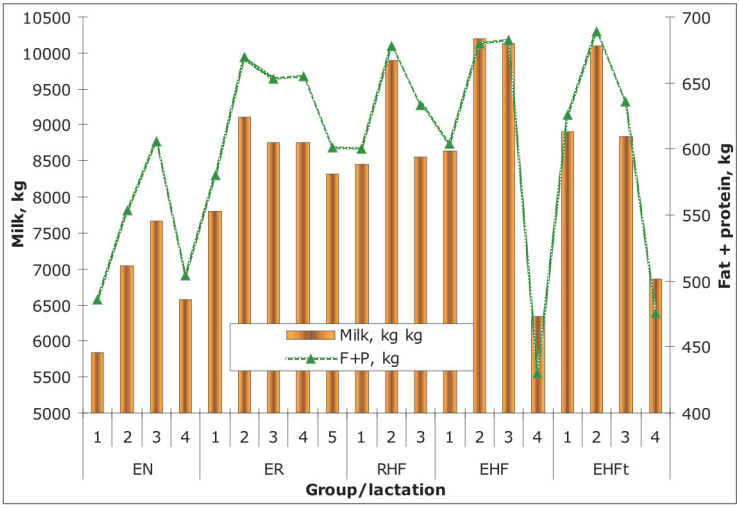

Figure 1. Milk production of the test groups by lactations

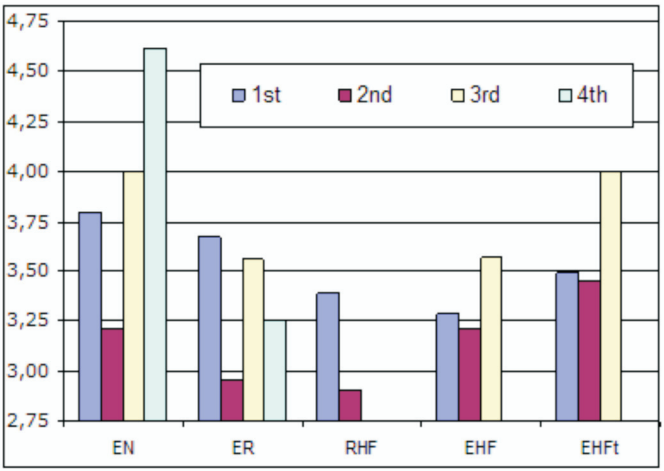

Figure 2. The effect of lactation on milk production costs

Milk production costs were the highest in the EK group and the lowest in the EHF group (Figure 2). That formed the level of the total costs. The lowest production costs were observed in 2nd lactation and highest in 3rdand 4th lactation. The average total costs of the experiment farm were 3.68 EEK per kg milk. Total costs ranged between 2.95 EEK and 4.61 EEK.

Procurement price was 3.87 EEK. However, income and intensive production do not assure profits, because milk production costs are not included in herd reproduction costs. Feeding costs constituted 62% and labour costs 9% of total costs.

Summary

Regarding expedience of feeding, the ratio was highly concentrated. The required energy ratio was achieved by feeding different cereals, protein feeds and herbal oils. The aim is to keep dry matter content per unit of metabolizable energy 12 MJ per kilo, which is close to what is recommended for feeding of high yielding cows in the Netherlands, Germany and Denmark, but 0.5 MJ lower than preferred in the United States.

Estonian Black-and-White Holsteins were superior in milk productivity to Red-and-White Holsteins, which were better than Estonian Red and Estonian Native cows. The milk production efficiency of high-producing cows was better (3.34–3.41 EEK/kg vs. 3.57–3.87 EEK/kg) despite their lower fertility. As to the functional traits, the fertility is the major factor to guarantee sustainable dairy herd production.

Acknowledgements

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PIGS

EVALUTION OF PROTEIN CONTENT IN PIG DIETS

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Abstract. Two groups (control and experimental) of pigs were used; each group included 20 animals, similar by age, sex, live weight and origin. Influence of protein content was studied during the fattening period. Two kinds of feeds were used. The control group animals of 50-80 kg live weight were fed mixed feed with 16.1% crude protein and 0.72% lysine; those of 80-100 kg live weight received diet with 13.7% protein and 0.72% lysine. The diet of the experimental group pigs with 50-100 kg live weight, contained 14% protein, 0.75% lysine, and 0.45% methionine+cystine throughout the experiment. Evaluating the increase of pigs' live weight during the experiment, it is seen that the diets containing 14% protein decreased the live weight, but differences were not significant. Feed consumption per 1 kg live weight gain was also a little lower in the experimental group. 14% protein content in pig diets did not have significant effect on indices of "muscle-eye" area and fat thickness, except the amount of lean ($p< 0.05$). Morphological composition of the carcass showed no considerable differences among groups. Economical calculations of the research showed that 14% protein in pig diets decreased the feeding costs.
Key words: protein, diets, amino acids, pig.

Introduction

Usually protein supply is based on the table values for the total content of amino acids in feedstuffs, while the content as well as the digestibility of amino acids may vary significantly (Jondreville *et. al*., 1995). Present practical pig feeding in different countries relies on recommendations based on empirically determined relationships between common analyse values of amino acids and observed performance when feeding typical rations in the specific country. This may often lead to suboptimal feeding, particularly when lot of alternative feedstuffs are being used. Protein evaluation of feeds, based on their crude protein content that is calculated from total nitrogen (N) by multiplying it with the conversion factor 6.25, usually leads to a significant overestimation of the protein by 30% (Boisen, 1998).

The aim of this paper is to give a zootechnical and economical evaluation of protein content in pig diets and its effect on pig performance.

Material and methods

Two groups (control and experimental) of pigs were used, each group included 20 animals, similar by age, sex, live weight and origin. The pigs were

grouped after separation, according to the principle of fair similarity. Each animal had his own number. Influence of protein content was studied during the fattening period. Two kinds of feeds were used (Table 1).

Table 1. Scheme of the experiment

Indices	Basic feed and additives	
Live weight, kg	50-80	80-100
Control group	Mixed feed with 16.1% protein content	Mixed feed with 13.7% protein content
Experimental group	Mixed feed with 14% protein + 0.18% synthetic lysine content	

According to a previously prepared recipe, it contained wheat, barley, soybean meal, lysine and vitamin/mineral premix. To check the nutrition quality, chemical analyses of feeds were done at the LUA scientific laboratory of agronomical analyses using the following methods: the content of dry matter was determined by drying the samples at 105°C; crude protein by using the BUCHI Kjeldahe Line B-324 device; and the content of crude fibre by the Weende method (ISO 5498 Animal feeding stuffs).

Dietary content of ME was calculated on the basis of the composition of the diets (MJ, kg-1) and the content of amino acids was calculated using table values.

Animals were fed in groups ad libitum. The feed was given from an automatic feeding equipment in groups. The needed amount was calculated beforehand by weighing the feed to be filled in the equipment and by recording the amount daily in the data registration list. Before starting and at the end of experiments the live weight of each animal was individually recorded by weighing animals. Basing on the weighing results, the following indices were calculated and compared: average live weight gain per day (g), and feed consumption for obtaining 1 kg live weight gain (kg).

The “muscle-eye” area (cm2) of live pigs was measured across the last rib (6 cm from midline), also the backfat thickness was measured (mm). Control test was done weighing pigs individually and measuring the indices using the Renco lean-meter (Pedigree standard documents, 1999).

In order to clarify the effect of protein content on the carcass traits, control slaughters were carried out. The carcass was evaluated by comparing the ham weight (kg), “muscle-eye” area (cm2), the amount of lean meat (%) and fat thickness (mm).

Estimation of economical data was carried out by recording the amount and value of the consumed feed and additives, the obtained live weight gain and meat marketing prices. Numerical values of all results obtained during experiments

were biometrically processed. Statistical analyses were done using the MS Excel mathematical programme (ANOVA) – calculating arithmetical means, standard errors, standard deviations and dispersions.

For comparison of the obtained results, the F-test – to compare dispersions of two clusters, and T-test – to compare arithmetical mean of two clusters, were used.

Results

The analyses of the basic feed for pigs showed that energy concentration, calculated per kg of feed dry matter, was sufficient – from 12.5 to 12.8 MJ. Protein requirement is very important for pigs, in our experiment the content of crude protein in feed dry matter was 13.7-16.1%, that of lysine 0.72-0.75% and methionine+cystine 0.45%. Although pigs' requirement for biologically full-value protein is greater than that of ruminants, under practical conditions the setting and control of amino acids is limited only by the sum of lysine and methionine+cystine. That was ensured for experimental group pigs in right relationships with 13.7-14% protein content in diets. Formulating pig diets, it must be considered that feed protein should satisfy the requirements for all essential amino acids at the lowest obtainable protein level (Boisen, 1997, 1998).

Evaluating the increase of pigs' live weight during the experiment, it was revealed that it was decreased by lower protein content, yet differences were not significant (Table 2). Feed consumption per 1 kg live weight gain was also a little lower in the experimental group.

Table 2. Growth of intensity (n = 20)

Indices	Control group	Experimental group
Average initial weight, kg	51.4 ± 2.60	52.5 ± 0.57
Average live weight at the end of the experiment, kg	96.6 ± 1.47	96.2 ± 0.95
Average daily live weight gain, g	794.0 ± 0.02	745.0 ± 0.01
Feed consumption per 1 kg live weight gain, kg	3.41	3.36

Low protein content (13.7-14%) in pig diets did not lead to significant changes of indices of "muscle-eye" area and fat thickness, except the amount of lean ($p < 0.05$) (Table 3). Morphological composition of the carcass showed no considerable differences among the groups.

Economical calculations of the research show that lower protein content in pig diets decreased feed cost by Ls 1.67 per pig and protein consumption was lower by 33 g (Table 4).

Table 3. Meat quality (n = 20)

Group	Live weight, kg	"Muscle- eye" area, cm^2	Amount of lean,%	Fat thickness, mm
Control	96.5 ± 1.47	47.8 ± 0.98	51.6 ± 0.54	18.5 ± 0.49
Experimental	95.2 ± 0.96	49.3 ± 0.98	53.9 ± 0.70*	18.1± 0.63

* $p < 0.05$

Table 4. Economical estimation

Indices	Control group	Experimental group
Feed consumption per 1 kg live weight, kg	3.39	3.35
Consumption of ME per 1 kg live weight gain, MJ	42.0	41.8
Consumption of crude protein per 1 kg live weight gain, g	509	476
Feed cost per pig in the experiment, Ls	14.61	12.94

Conclusions

Growth performance and feed consumption of pigs were not significantly affected by dietary protein level as pigs were fed at the lowest dietary protein level (13.7-14%). Pork quality was better in the experimental group. Backfat thickness of the pigs belonging to that group was about 0.4 mm smaller and lean meat by 2.3% larger as compared to these of the control group pigs. Economical calculations show also benefit in feed cost: for the experimental groups it was by Ls 1.67 per pig cheaper than for the control groups pigs.

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GENETIC TREND OF THE LEANNESS OF PUREBRED PIGS IN LITHUANIA AND ITS RELATION WITH OTHER CARCASS TRAITS

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Introduction

Meatiness of pigs is depending on numerous factors. Breed is one of them (De Vries and Kanis, 1994; Somelar *et al*., 2000; Klimienė and Klimas, 2001; Klimas *et al.*, 2006). At different periods of pig weight, fat and lean tissue deposition varies for different pig breeds (Kolstad, 2000). However, backfat thickness is an indicator of pig leanness, because lower backfat thickness means higher lean meat content. Also it has been shown (Vege *et al*., 2000; Veide, 2002; Tänavots *et al*., 2002; Klimienė and Klimas, 2005) that the correlation coefficient for these traits is highly negative (r=–0.6 to – 0.9). According to the data of previous investigations (Климас, 1990), fattening pigs up to 130 kg decreases relative lean meat content in carcass by 2-3% on average, and the amount of fat with a skin increases by 2.6-4.5% compared with pigs of 100 kg weight. Accumulation of subcutaneous fat (backfat) is becoming especially intensive when pigs are fattened more than up to 130 kg (Джяугис, Штанкялис, 1988). The tendency is valid for pigs of all breeds.

With increasing demands for lean pork meat, selection of pigs in Lithuania is developed namely by this trend. According to half carcass length, backfat thickness, loin lean area and weight of ham of progeny, fattened at a control fattening station and slaughtered in average weight 95 kg, selection of boars and sows is carried out in the breeding centres. Besides that, since 1996, breeding progeny in the breeding centres of Lithuania has been selected for backfat thickness and lean meat percentage determined by *in vivo* with ultrasonic apparatus *Piglog 105* (phenotypical evaluation).

Pig breeds in Lithuania are classified into three groups:

- maternal breed – Lithuanian native, Lithuanian White, Large White/Yorkshire;
- intermediate breed – Landrace;
- paternal breed – Duroc, Pietrain, Hampshire and their hybrids with Landrace pigs.

The objectives of this study were to carry out comparative evaluation of the lean meat percentage obtained by *Piglog 105,* and its genetic trend for purebred pigs bred at the breeding centres; and to determine relationship between lean meat content and other carcass traits of slaughter pigs.

Material and methods

The analysis of the ultrasonically measured lean meat percentage data for purebred Lithuanian White (LW), Large White (La.W), Yorkshire (Y), Landrace (L), Duroc (D) and Pietrain (P) pigs was carried out on the basis of the data for the years 2000-2006 supplied by the State Pig Breeding Station. The number of tested purebred pigs in the breeding centres of the country is presented in Table 1. Breeding progeny was evaluated for the lean meat content at 85-110 kg live weight.

The lean meat percentage was determined with Piglog *105* by measuring the backfat thickness (mm) on live pigs at two points (Piglog 105 User's Guide, 1991):

1) between the 3rd and 4th vertebrae of the loins and 7 cm sideways from the middle dorsal line (FAT-1);

2) 10 cm from the last rib towards the cranial part and 7 cm sideways from the middle dorsal line (FAT-2). The thickness of the *musculus longissimus dorsi* (mm) was also measured at this point.

After the control slaughter, relationship (r) between muscularity of dominating pig breeds (Lithuanian White, Large White/Yorkshire, Landrace), Duroc and Pietrain, and other carcass traits as half carcass length, backfat thickness and loin lean area was defined according to the accepted methodology (Saikevičius, 2003). Lean meat percentage of slaughtered pigs was determined with apparatus "Fat-o-meater" (FOM). The number of tested pig carcasses at the slaughterhouse of the State Pig Breeding Station is presented in Table 2.

The data were processed biometrically (Tucker, 2003). The difference was considered significant when $P<0.05$.

Results and discussion

According to the *Piglog 105* measurements (Table 1), in 2006 at the breeding centres of the country the average lean meat percentage of Lithuanian White pigs was 56.9%, that of Yorkshire 58.0%, Large White 58.5%, Landrace 58.8%, Pietrain 59.4% and Duroc 59.5%.

If compared with the data for 2000, the leanness of Lithuanian White pigs in 2006 has increased by 6.9% ($P<0.001$), that of Large White and Landrace, respectively by 2.2 and 2.5% ($P<0.01$), Duroc by 1.6% ($P<0.05$), Yorkshire by 0.2%; and lean tissue deposition in Pietrain pigs decreased by 0.6% (Table 1 and Fig. 1). Higher genetic trend of the leanness of Lithuanian White pig breed has been influenced by immigration of English Large White boars.

Table 1. Data for lean meat content in pigs of different breeds measured by Piglog 105

Item	Year				Comparison (±) 2006/2000
	2000	2002	2004	2006	
Lithuanian White (LW)					
No. of pigs	1939	2320	1790	1846	x
Lean meat %	50.0	51.9	56.7	56.9	+6.9***
Large White (La.W)					
No. of pigs	416	335	550	1285	x
Lean meat %	56.3	58.1	58.4	58.5	+2.2**
Yorkshire (Y)					
No. of pigs	1348	1371	1386	1351	x
Lean meat %	57.8	57.8	57.6	58.0	+0.2
Landrace (L)					
No. of pigs	1479	1726	3779	3218	x
Lean meat %	56.3	57.6	58.1	58.8	+2.5**
Duroc (D)					
No. of pigs	60	59	106	43	x
Lean meat %	57.9	59.7	59.1	59.5	+1.6*
Pietrain (P)					
No. of pigs	223	153	104	66	x
Lean meat %	60.0	58.5	58.7	59.4	-0.6

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

Carrying out selection of pigs according to several productivity traits, it is necessary to know their interrelation. Analyzing correlation between muscularity of the investigated pigs (Table 2) and other carcass traits, it was defined that the less is thickness of backfat, the bigger the content of lean meat in carcass is (r= from –0.50 to –0.83). Positive correlation between loin lean area and lean meat content in carcass (r=from 0.43 to 0.55) has been defined. The correlation coefficient between half carcass length and lean meat percentage was not equal, depending on pig breed. This coefficient was positive for Lithuanian White, Large White/Yorkshire and Landrace (r= from 0.18 to 0.54) – the longer is half carcass, the higher lean meat content in carcass is. Negative correlation between the mentioned meatiness traits was indicated for Duroc (r= –0.13) and Pietrain (r= –0.11). Thus, for Duroc and Pietrain this tendency was not valid. Pigs of the latter breeds are shorter, however distinguishing by high muscularity.

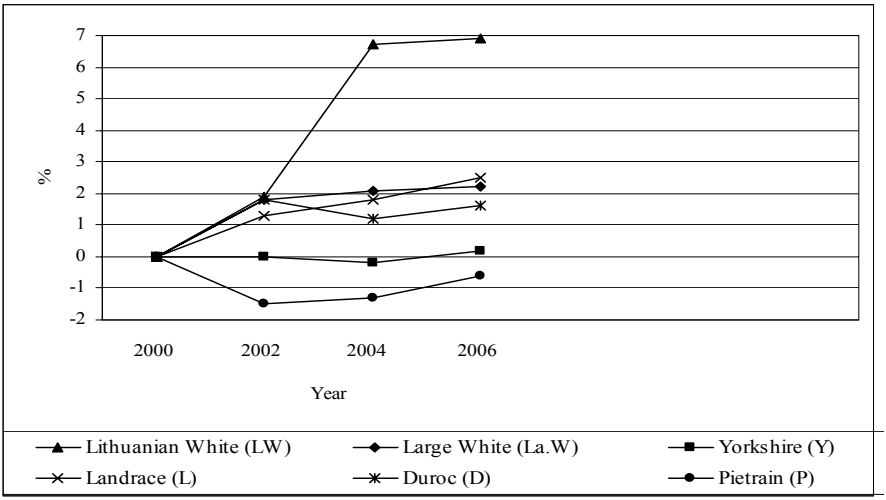

Figure 1. Genetic trend of leanness in the pig breeding centres

Table 2. Correlation (r) between lean meat content and other carcass traits of pigs

Item	Lithuanian White	Large White/ Yorkshire	Landrace	Duroc	Pietrain
No. of pigs	38	42	34	15	12
Half carcass length, cm – lean meat content in carcass,%	0.18	0.43	0.54	-0.13	-0.11
Average backfat thickness, mm – lean meat con-tent in carcass,%	-0.50	-0.51	-0.48	-0.83	-0.76
Loin lean area, cm^2 – lean meat content in car-cass,%	0.43	0.43	0.53	0.55	0.52

Conclusions

According to the *Piglog 105* data gained in 2006, the average lean meat percentage of purebred pigs in the breeding centres of Lithuania ranged from 56.9% (Lithuanian White) to 59.5% (Duroc).

During the observed period (2000-2006) genetic trend of the muscularity of the pigs ranged from 6.9% (Lithuanian White) to –0.6% (Pietrain). By their leanness, Lithuanian Whites are becoming comparable to Yorkshires and Large Whites bred in the country.

Depending on pig breed, the correlation coefficient between half carcass length and lean meat content ranged from –0.13 to 0.54. Consequently, for improvement of leanness the half carcass length should not be used as the main selection indication of pigs.

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PERFORMANCE TRAITS OF DIFFERENT GENERATIONS OF ENGLISH LARGE WHITE PIGS

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Introduction

By the end of 2005, at Lithuanian breeding centres about 26% of all purebred pigs were Lithuanian White, 29% – Large White (Yorkshire), 42% – Landrace and 3% – Lithuanian native pigs (gene pool), Duroc and Pietrain (Saikevičienė *et al*., 2005). Recently, the number of foreign pig breeds imported into Lithuania has increased, especially of pigs that in their origin countries have been selected for lower backfat and higher lean meat content. Animals imported from other countries get into different environmental conditions (climate, feeding, housing) and strive to survive. It is supposed that reproductive, fattening and meatiness traits (phenotype) of pigs depend on environmental conditions even up to 60%, and only up to 40% depend on genotype (Close, 1970; Curtis, 1983; Verhagen, 1987; Cameron, 1993; Diekman *et al*., 1994; Verstegen *et al.,* 1994; Lynch and Walsh, 1998; Hoste, 2003). Therefore, after changing environmental conditions, productivity of animals is often getting worse. This is related to the natural resistance of organism against unfavourable influences. If new conditions are very different from the earlier ones, adaptation can last even through several generations. During this period weaker animals die and only those adapted normally to new conditions survive. Adaptation, like reproduction, is directed towards survival. Provided the environmental conditions are favourable, all the processes may even have an improving effect on the animals. However, if more energy has to be spent on survival, performance dramatically falls down, especially that of highly productive animals. Thus, adaptation of pigs under new environmental conditions should be investigated. Besides that, the course of adaptation depends on the breed and individual features: type of nervous system, stress-resistance and age (Терьмяева, 1988; Мейснер, 1991; Смирнов, 1991; Cameron, 1993; Hoste, 2003; Kriauzienė *et al.*, 2005).

The purpose of this work was to investigate changes of the reproductive traits, fattening performance and meatiness of English Large White pig's breed in their adaptation process.

Material and methods

Decisions about the adaptation of English Large Whites were made when analysing changes in productivity data of the imported pigs and offspring born in the Rabikiai breeding centre of the stock company "Krekenava" (Panevėžys district). Various breeding records for the years 2000–2005 have been studied:

pedigree certificate of imported progeny, sow farrowing and offspring records, control fattening and slaughter data.

In March 2000, the Rabikiai breeding centre brought from Ireland 5-7 months old gilts from 9 families (Molla, Fanna, Katalina, Haura, Kumara, Raula, Coleena, Dakla, Jiena), and boars of 4 lines (Vikingas, Baras, Fildmarshalas, Bikas), belonging to English Large White breed. Currently, three families (Coleena, Dakla, Jiena) are extinct already. All gilts (sows) in this breeding centre are inseminated. Microclimate in stables is regulated by computerized equipment. In premises for sires temperature is kept at the level of 16-18°C, in premises for pedigreed gilts at 20^0C, and in premises for piglets it is up to 26°C. Relative humidity is 70%. The number of pedigreed gilts kept in stalls is up to 16-18. Sawdust litter is used. Pigs are fed full-value compound feed produced in stock company "Krekenava feed". One kg feed assigned for pedigreed gilts contains

13 MJ metabolizable energy and 15.5% protein; for lactating sows 13.2 MJ and 18%, respectively; for farrowing sows 12 MJ and 14.3%, respectively; and for sucking piglets 13.7 MJ and 20.8%, respectively. Feeding is computerised. Reproductive traits – litter size, number of piglets at 21 days of age and survival rate – of primiparous sows of the imported and born and raised in this breeding centre, English Large Whites of the first (F_1) and second (F_2) generation (n=72, 24 primiparous sows in each group) have been analyzed, as well as fattening performance and meatiness traits of delivered F_1 (n=30), F_2 (n=55) and F_3 (n=54) progeny.

Therefore, fattening performance and meatiness traits of the offspring of 139 F_1 – F_3 generations of English Large Whites, born in Rabikiai breeding centre, were evaluated in control fattening stables of State Pig Breeding Station, according to accepted methodology (Saikevičius, 2003). During the control fattening, keeping and feeding conditions were equal for all groups. Pigs were fed with special dry compound feed KRET - KOM58-1404, containing 1.1 feed units, 13.84 MJ metabolizable energy and 16.0% proteins per kg.

The investigation data were processed using statistical package Statistics for Windows version 6.0 (StatSoft, 2001) and following the basic guide to the statistical analysis of biological data by Tucker (2003). The difference was considered significant when $P<0.05$.

Results and discussion

The results of reproductive traits of different generation English Large White sows are presented in Table 1. Litter size of primiparous sows and the number of piglets at 21 days of age was statistically not significantly different after environmental conditions changed for the English Large Whites imported and born and raised in Rabikiai breeding centre. However depending on adaptation to

new conditions, the rate of piglet losses was declining. Preserving of offspring of the second generation (F2) English Large Whites, compared to the imported and F1 sows, improved by 9.3% ($p<0.01$) and 5.8% ($p<0.05$), respectively.

Table 1. Reproductive performance of primiparous sows of English Large White breed

Item	Imported pigs	Pigs born and raised in Lithuania	
		F_1 generation	F_2 generation
No. of sows	24	24	24
Litter size	10.4±0.3	10.3±0.1	9.9±0.1
No. of piglets at 21 days of age	8.9±0.2	9.2±0.2	9.4±0.1
Survival rate %	86.1±1.8	89.6±1.5	95.4±1.2

Table 2. Control fattening and meatiness traits of English Large White breed offspring

Item		Offspring born in Lithuania		
		F_1 generation	F_2 generation	F_3 generation
No. of pigs		30	55	54
Age at 100 kg weight, d.		192±2	189±3	182±1
Daily gain, g		711±10	824±11	780±11
Conversion per kg gain:	Compound feed, kg	2.81±0.04	2.94±0.03	2.91±0.04
	Metabolizable energy, MJ	38.89±0.55	40.69±0.42	40.27±0.55
Half carcass length, cm		96.3±0.4	97.9±0.3	98.8±0.2
Backfat thickness:	At 6-7 rib, mm	19.3±0.6	17.8±0.5	19.9±0.5
	At last rib, mm	16.9±0.6	15.1±0.5	16.4±0.4
Loin lean area, cm^2		38.8±0.4	37.3±0.3	39.8±0.5
Ham weight, kg		11.6±0.1	11.5±0.1	11.7±0.1
Lean meat % (*Piglog 105* data)		57.5±0.3	56.7±0.2	56.7±0.3

According to evaluation data analysis of the control fattening and carcass for English Large Whites progeny born in Rabikiai breeding centre (Table 2), faster growth of progeny of this breed was indicated beginning from the second generation (F_2). Average daily gain for F_2 and F_3 progeny was respectively by 15.9% ($p<0.001$) and 9.7% ($p<0.01$) higher than that of F_1 progeny. Though difference was not significant, starting with F_2 generation the decrease of muscularity by 0.8% can be noticed.

Therefore, tendencies of changing productivity indicators for English Large Whites are opposite, compared to these of Swedish Yorkshires, born in Lithuania

(Klimienė and Klimas, 2006). More variable changes of reproductive traits and fattening performance during adaptation have been determined for pigs of Swedish Yorkshire breed.

Conclusions

New environmental conditions did not have negative influence on the adaptation of pigs of English Large White breed.

Due to adaptation to new environmental conditions, the rate of piglet losses of English Large White breed born in Lithuania was lower, compared to that of the imported primiparous sows.

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HERITABILITY AND GENETIC CORRELATIONS COEFFICIENTS OF LITHUANIAN WHITE PIGS

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Introduction

Pig husbandry has a very important role in agriculture. In the world, in Europe as well as in Lithuania consumption of pork is prevailing over other meat types – it is nutrient, tastes good and is a quite cheap product.

Nowadays in Lithuania we have already a fixed pig breeding system comprising of 43 breeding farms in which besides Lithuanian White pigs also Large White, Landrace, Duroc and Petrain breeds are bred. In 1996, phenotypic evaluation of lean meat was started by ultrasound instrument "Piglog-105". In 2002, the uniform SEUROP system running in European economical zone was introduced in Lithuania, giving guarantees to pig breeders to get payment according to the quality of pig carcass. BLUP method for genetic evaluation of Lithuanian White, Large White (Yorkshire) and Landrace pigs had been implemented in Lithuania since 2003.

Objective of the research was to evaluate genetic correlations and heritability coefficients in herd "Berka" and the whole Lithuanian White pig population.

Keywords: Lithuanian White pig breed, production, genetics correlation, heritability coefficient.

Materials and Methods

This scientific research was carried out from 2001 to 2006 at the largest Lithuanian White pig breeding farm "Berka", but also at the State Pig Breeding Station and Lithuanian Veterinary Academy.

Research data have been evaluated statistically (arithmetic means - $\bar{x}$, standard error - Sx) by programme "R". For estimation of genetic correlation (r_g) and heritability (h^2), coefficients for pig production traits PEST and VCE packages (Groeneveld E., 1998) were used. The mixed linear model was used for genetic evaluation of the following production traits determined in control fattening and slaughtering station: daily gain, g; feed consumption, kg; fat thickness in point F2, mm.

$Y_{ijkln} = \mu + Litter_i + L_j + SMS_k + ANIMAL_l + e_{ijkln}$

$Litter_i$ – litter from which animal originated, random effect;

L_j – sex, fixed effect (gilts and castrates);

SMS_k – station_year_season, random effect (season was determined as year season on the base of date slaughter);

$ANIMAL_l$ – additive genetic effect of animal (random effect);

e_{ijkln}– random error.

The following statistical model was used for genetic evaluation of the production traits determined on farm (total daily gain in g and animal lean meat%):

$Y_{ijkln} = \mu + Litter_i + L_j + \bar{U}MS_k + ANIMAL_l + e_{ijkln,}$

$\bar{U}MS_k$ - farm_year_season, fixed effect (season was determined as year season on the base of "Piglog-105" measuring data).

For analysis of fat thickness the model was supplemented with regression of slaughter weight (SV_m):

$Y_{ijklnm} = \mu + Litter_i + L_j + \bar{U}MS_k + SV_m + ANIMAL_l + e_{ijklnm.}$

Rates indices were statistically significant when differences between indices and measurement data 1.96xSE were higher than 0.

Results and discussions

Coefficients of genetic correlation (r_g) and heritability (h^2) had been estimated for 8285 animals of "Berka" farm.

Table 1. Heritability (diagonal) and genetic correlation (above diagonal) coefficients of Lithuanian White pigs on farm "Berka"

Traits	Daily gain g (station)	Feed consumption kg (station)	Fat thickness at point F2 Mm (station)	Daily gain, g (farm)	Lean meat % (farm)
Daily gain g (station)	**0.118***	0.821***	-0.839***	0.865***	0.648***
Feed consumption kg (station)		**0.160****	0.934***	0.590***	-0.851***
Fat thickness at point F2mm (station)			**0.447*****	0.486***	-0.956***
Daily gain, g (farm)				**0.214*****	0.209**
Lean meat% (farm)					**0.381*****

Statistical reliability *p<0.05; **p<0.01; ***p<0.001

The results in Table 1 reveal that the largest heritability coefficients were determined for fat thickness at point F2 (0.447 p<0.001) and lean meat (0.381, p<0.001). They matched well with the results gained by Chen *et al*. (2001).

Table 2. Heritability (diagonal) and genetic correlation coefficients (above diagonal) of Lithuanian White pig population

Traits	Daily gain g (station)	Feed consumption kg (station)	Fat thickness at point F2 mm (station)	Daily gain, g (farm)	Lean meat % (farm)
Daily gain g (station)	**0.583*****	0.693***	0.148**	0.302***	0.098**
Feed consumption kg (station)		**0.305*****	0.078*	0.288***	0.305***
Fat thickness at point F2mm (station)			**0.163*****	0.147***	0.163***
Daily gain, g (farm)				**0.110****	0.110**
Lean meat% (farm)					**0.292*****

Statistical reliability *p<0.05; **p<0.01; ***p<0.001

It was determined that some heritability coefficients got on the farm differ from the coefficients of the whole Lithuanian White pig population (Table 2). Daily gain (station test) had high heritability coefficient in the whole Lithuanian White pig population (0.583), but was found to be low (0.118) on farm "Berka". Heritability of fat thickness at point F2 was low in the whole Lithuanian White pig population (0.163), but high (0.447; p<0.001) on the farm. Heritability of lean meat% was higher on farm "Berka" (0.381; p<0.001) in comparison with the whole Lithuanian White pig population (0.292).

In the studies the estimated heritability coefficient for the feed consumption on the farm (0.160; p<0.01) and in Lithuanian White pig population (0.305; p<0.001) shows the possibilities of effective pig selection according to this trait. By other authors (Cameron and Curran 1995; Binadel and Ducos, 1996; Clutter and Brascamp, 1998; Tribout *et al*., 1998; Remeikiene, 2001) the estimated heritability for the feed consumption was between 0.18 and 0.61.

Statistically significant genetic correlations were determined between the main production traits on farm "Berka" (Table 1) and in the whole Lithuanian White pig population (Table 2). Very close negative relation was determined between pigs' lean meat and feed consumption - r_g = -0.851 (p<0.001) on farm "Berka", while in the whole Lithuanian White pig population the correlation was positive (0.305; p<0.001). Genetic correlation between daily gain on the farm and at the pig station in "Berka" was 0.865 (p<0.001); in Lithuanian White pig population it was 0.302 (p<0.001).

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INFLUENCE OF DIFFERENT GENOTYPE ON ASSOCIATIONS AMONG PORK QUALITY PARAMETERS

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Introduction

For many years the major objective of swine husbandry was to increase the lean:fat ratio of carcasses. More recently an increasing amount of emphasis has been placed on improving pork quality traits. Meat quality concepts include eating- and technological quality, meat functionality, nutritional value, safety and diversity. The advantage of wild boar meat over pork has been shown by Žmijewski et al. (2001), Marchiori et al. (2003), but the population of wild boar is limited and therefore some meat may be derived from wild boar and domestic pig crosses. Pork quality traits are often truly composite traits, being influenced by different factors (Huff-Lonergan et al., 2002), and thus relationships among biochemical measurements and processing characteristics must be known. The objective of this study was to determine phenotypic associations between specific biochemical and physical characteristics to obtain understanding of how different proportion of wild boar changes associations of specific traits influencing pork quality.

Material and Methods

Animals used were male hybrids from Lithuanian indigenous wattle x wild boar intercross (1/2 WB genotype) and their backcross (Lithuanian indigenous wattle x wild boar) x Lithuanian indigenous wattle (1/4 WB genotype). The study included material from nineteen 1/4WB and twenty 1/2WB genotype hybrids. The hybrids were reared indoors from birth to slaughter consuming twice a day the same standard concentrate feed with a small amount of grass in summer and beet and apples in autumn**.** Animals were slaughtered when they reached approximately 90 kg weight**.** Cooling loss was measured as difference between warm and cold carcass weight in percentage of warm carcass weight. Technological meat quality and chemical composition were measured on the samples of *M. longissimus dorsi* (LD). Thawing loss and processing yield were measured on *M. semimembranosus* (SM). All samples of SM were deep frozen for five days. To determine processing yield, muscles SM were weighed at each step of the process whereupon the yields were calculated as yield difference between initial weight and weight after smoking (Hullberg and Lundström, 2004). The samples of LD were analysed in duplicate for meat chemical content. Crude protein was analysed by the Kjeldahl method using the Kjeltec system 1002 apparatus (Foss-Tecator AB); crude ash and ether extract after hydrolysis of intramuscular fat were determined according to standard

methods described in the Official Methods of Analysis of the Association of Official Analytical Chemists (AOAC 1990). Meat pH was determined using Knick pH-766 meter (Germany). Colour intensity – by the method with Khornsi's modification using a spectrophotometer СФ-46 (Russia) and water holding capacity of LD was determined by the method of Grau and Hamm as described in the methodological guidelines (Misik, 1978). Cooking losses were estimated by weighing before and after cooking and thawing loss as weight difference of initial and defrosted SM, described by Heyer et al. (2004). Associations between traits were determined by calculating Pearson's correlation. Calculations were performed using MINITAB release 14.20. Significance was determined at $P<0.05$, but differences of $0.05 \leq P<0.10$ would be considered as trends.

Results and Discussion

There were no statistically significant effects of genotype on chemical composition and technological meat quality (unpublished data). There were high significant negative correlations between carcass weight and cooling loss for both groups (Table 1). Cooling loss of carcasses from 1/2WB hybrids was higher than that from 1/4 WB hybrids and correlation between these traits was higher for 1/2WB hybrids. Müller et al. (2000) have reported that carcass cooling loss was higher in wild boar than in Meishan and Pietrain and differed largely in the F_1 and F_2 generations, and these results are consistent with our study. There were high positive significant correlations for both groups between dry mater and protein and fat. Moderate negative correlations between cooling loss and dry matter and protein tended to be significant ($P=0.067$ and $P=0.08$, respectively) for 1/2 WB hybrids, but there were no significant correlations between these traits for 1/4 WB hybrids. Water holding capacity for 1/2 WB hybrids was negatively correlated with cooking loss ($P<0.01$), but positively with pH and intramuscular fat ($P<0.05$). These data indicate that in this study pork from hybrids with a higher proportion of wild boar and with higher water holding capacity had lower cooking loss but higher fat content and pH. Suzuki et al. (2005) have found negative correlation between water holding capacity of the fresh meat and fat for selected Durocs. Like for domestic pigs, in this study the correlation between water holding capacity and fat for 1/4 WB genotype was negative but it was low and statistically insignificant. Water holding capacity for 1/4 WB hybrids was insignificantly but also negatively correlated with cooking loss, whereas insignificant moderate correlation between water holding capacity and pH was positive. The negative correlation observed between pH and cooking loss for ½ WB hybrids ($P<0.001$) indicated that meat with lower pH tended to be evaluated as having high cooking loss, but for 1/4 WB hybrids this association was very low and statistically insignificant.

Table 1. Pearson's correlation coefficients among carcass and meat quality traits. Correlation coefficients of 1/2 WB hybrids are above the diagonal, and correlation coefficients of 1/4 WB hybrids are below the diagonal

	Carcass weight	Cooling loss	Thawing loss	Water holding capacity	Cooking loss	Dry matter	Protein	Fat	Colour	pH	Processing yield
CW		**-.695**[2]	.225	.155	.124	**.496**[1]	.371	.314	-.003	-.234	-.147
CoolL	**-.470**[1]		.142	-.048	-.258	**-.454**	**-.430**	-.196	.237	.330	.316
ThL	.445	.025		-.227	.410	.327	**.491**	-.116	.457	**-.627**[1]	**-.553**[1]
WHC	-.470	-.134	.262		**-.599**[2]	.249	-.092	**.477**[1]	-.324	**.484**[1]	.392
CookL	.434	.114	-.252	-.210		.032	.205	-.194	.258	**-.808**[3]	**-.659**[1]
DM	.045	.024	-.149	.089	.327		**.680**[2]	**.553**[1]	.142	-.360	-.025
P	.025	-.333	-.110	.294	-.175	**.620**[2]		-.225	.080	-.396	-.440
F	-.010	.290	-.094	-.192	.567	**.613**[2]	-.239		.074	-.018	.484
C	.324	-.133	**.631**	-.130	-.222	**-.486**[1]	-.171	**-443**		-.381	-.116
pH	-.157	.217	**-.634**	.369	-.049	-.138	.061	-.243	.091		**.518**
ProcY	-.558	.368	**-791**[1]	.044	.132	-.01	-.128	.108	**-.853**[2]	.491	

Coefficients in bold: 0.05≤P<0.10.
Bold: [1]P<0.05 [2]P<0.01; [3]P<0.001.

For 1/4 WB hybrids colour negatively correlated with dry matter (P<0.05) and tended to correlate (P=0.07) negatively with intramuscular fat, but for 1/2 WB hybrids associations between these traits were low and positive. These results showed that pork from 1/4 WB genotype having higher IMF is lighter in colour and this is in agreement with the findings of Suzuki et al. (2005) who have reported about correlations among meat quality traits of selected Duroc, but associations between these traits for 1/2 WB hybrids were different compared with those for domestic pigs. Thawing loss negatively correlated with pH for 1/2 WB hybrids (P<0.05) and tended (P=0.07) to correlate for 1/4 WB hybrids. For both groups processing yield correlated negatively with thawing loss (P<0.05). Moderate positive correlation coefficients between processing yield and pH were estimated but this correlation tended (P=0.07) to be significant only for 1/2 WB hybrids.

Implications

Pearson's correlations obtained herein indicated that introgression of different proportion of wild boar into Lithuanian indigenous pigs has changed phenotypic associations between specific pork characteristics**.**

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EFFECT OF CARCASS WEIGHT AND LENGTHS ON MEATINESS TRAITS OF YOUNG BOARS

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Introduction

To estimate value of pigs, control testing stations were established in Estonia in 1927. Since 1929, the price of pig carcasses has been based on carcass weight and value. Ultrasonic measurement of fat thickness was utilized first time in 1961. This technique was widely used from 1994 in farms and slaughterhouses. In 1995, the crossbreeding program Marble Pork of the Estonian Pig Breeding Association was introduced, targeted at measuring carcass traits of progeny of top boars in slaughterhouses (EPBA, 2005).

The objective of this study was to study the effect of carcass weight and lengths on meatiness traits of young boars.

Material and Methods

Estonian Landrace (EL), Estonian Large White (EY), Pietrain (Pi) and Hampshire x Pi young boars from four top breeding farms were included in study to predict meatiness traits both from live animal and carcass measurements.

Meat traits in live pigs were measured by ultrasonic equipment Piglog 105: 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).

A total of 202 pigs were slaughtered in four slaughterhouses during 2006. Average age at slaughter was 172 days and carcass weight 72.6 kg (Table 1). Carcasses were divided lengthways into halves and hanged into monorail along back leg. Weight and lean meat percentage were recorded with Ultra-FOM 300, prior to chilling of carcasses, in a cooling chamber. 24 hours after slaughtering, carcass measurements were taken by meat technologist of the Estonian Pig Breeding Association. Measuring tape was used to determine backfat thickness at four points in one half of carcasses (Figure 1). Two carcass lengths were fixed.

Lean meat percentages of carcasses were calculated using two point method (ZP-method). For that purpose, fat thickness on thinner point above *m. glutaeus medius* (S), and distance between anterior part of *m. glutaeus medius* and upper edge of vertebrate spine (F) were measured.

$$ZP\% = 47{,}978 + (26{,}0429 \times \frac{S}{F}) + (4{,}5154 \times \sqrt{F}) - (2{,}5018 \times \lg S) - (8{,}4212 \sqrt{S})$$

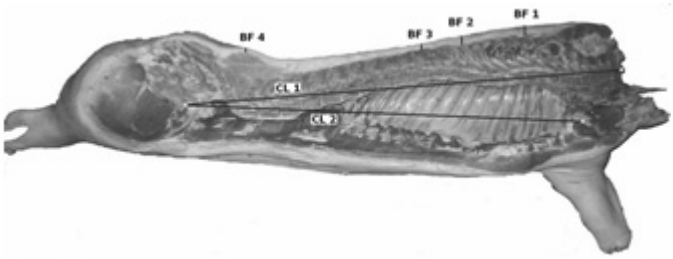

Figure 1. Measuring points of backfat thickness and carcass lengths. Backfat thickness was measured: BF 1 – thicker spot on shoulder; BF 2 – above between 6^{th}-7^{th} rib; BF 3 – thinner spot in dorsum; BF 4 – from the higher spot of *gluteus medius*. Carcass length: CL 1 – from cranial edge of first neck segment to anterior edge of the *symphysis pubis*; CL 2 – from *symphysis* of rib on the sternum to anterior edge of the *symphysis pubis*.

Right halves of carcasses were divided between 13th and 14th ribs, and the digital photo was taken from opened loin eye and rest of fat above it. PC program Scan Star was used to measure loin eye area, fat area, and two fat thicknesses (Figure 2).

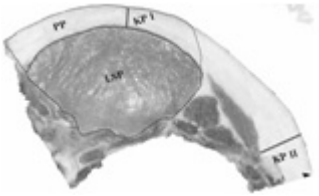

Figure 2. Traits measured by PC program Scan Star. LSP – loin eye area, PP – fat area, KP I – fat thickness at thinnest point, KP II – fat thickness above *serratus dorsalis* (Scan Star, 2007).

Loin eye area (LSP) : fat area (PP) ratio is expressed by meatiness index (MI).

$$MI = \frac{PP(cm^2)}{LSP(cm^2)}$$

Carcass weight and lengths were divided into classes to estimate their effect on meatiness traits. Carcass weight classes were <65, 65-69, 70-74, 75-79, 80-85, and >85 kg. Carcass length 1 classes were <95, 95-99, 100-105, and >105 cm; and carcass length 2 classes <80, 80-84, 85-90, and >90 cm.

A least square analysis of variance using GLM of SAS (SAS, 1999) was performed to evaluate carcass measurements for sources of variation. The model included fixed effects of breed, year of evaluation, and slaughterhouse.

$$Y_{ijklmn} = \mu + B_i + E_j + W_k + L_l + M_m + e_{ijklmn}$$

Y = dependent variable; B_i = breed (n = 1-4); E_i = season of evaluation (n = 1-4); W_k = carcass weight class (n = 1-6); L_l = carcass length 1 class (n=1-4); M_m = carcass length 2 class (n=1-4); e_{ijklmn} = random residual effect.

Table 1. General statistics of carcass measurements (n=202)

Traits	Mean	Std. dev.	Min.	Max.
Slaughter age, days	172.18	10.65	148.00	200.00
Carcass weight, kg	72.59	7.58	53.70	92.70
Carcass length 1, cm	100.78	5.16	84.00	116.00
Carcass length 1, cm	84.35	4.25	72.00	99.00
Ruler				
BF 1, mm	24.75	3.66	10.00	35.00
BF 2, mm	16.80	3.57	8.00	28.00
BF 3, mm	13.01	3.12	6.00	24.00
BF 4, mm	9.29	1.41	5.00	14.00
Avg BF 1-4, mm	15.96	2.51	8.75	23.25
Avg BF 1-3, mm	16.95	2.49	9.00	23.67
Scan Star				
KP I, mm	7.86	2.53	4.00	18.00
KP II, mm	15.87	4.53	5.00	27.00
Fat area, cm^2	12.69	2.82	7.50	22.10
Loin eye area, cm^2	49.44	6.20	36.00	68.50
MI	0.26	0.06	0.15	0.42
Piglog 105				
X1, mm	9.41	2.33	6.00	16.00
X3, mm	9.95	2.18	6.00	17.00
X2, mm	57.16	5.29	43.00	72.00
Lean meat%				
Piglog 105,%	64.29	1.82	58.96	67.68
ZP,%	61.80	1.56	57.30	65.90
Ultra-FOM 300,%	61.82	1.64	56.50	65.90

Levels of significances are expressed conventionally: a, b, c, d – least square means within each effect with one letter in common do not differ significantly; *** - P<0.001, ** - P<0.01, * - P<0.05. Pearson product-moment correlation (PROC CORR) coefficients were used to analyse relationship between carcass measurements (SAS, 1999).

Results and Discussion

Carcasses were evaluated by three procedures**.**

Ruler. Pig carcasses lighter than 65 kg had significantly thinner backfat than carcasses over 65 kg, except in backfat 1 and 4, where significant difference was observed in heavier carcasses. Backfat thicknesses were uniform at the weight from 65 to 79 kg, but increased significantly in heavier carcasses. Fat was distributed evenly at all four points measured.

Table 2. Effect of carcass weight on meatiness traits

Traits	Carcass weight, kg					
	<65	65-69	70-74	75-79	80-85	>85
n	29	45	59	33	25	11
Ruler						
BF 1, mm	23.50^{a}	25.11^{ab}	25.42^{b}	25.69^{b}	26.72^{bc}	28.37^{c}
BF 2, mm	14.83^{a}	16.91^{b}	17.63^{b}	18.28^{bc}	19.83^{c}	22.40^{d}
BF 3, mm	11.14^{a}	12.70^{b}	13.19^{b}	13.81^{b}	15.47^{c}	17.05^{c}
BF 4, mm	8.58^{a}	9.00^{a}	9.09^{a}	9.31^{ab}	9.80^{bc}	10.54^{c}
Avg BF 1-4, mm	14.51^{a}	15.93^{b}	16.33^{b}	16.77^{b}	17.95^{c}	19.59^{d}
Avg BF 1-3, mm	15.64^{a}	17.01^{b}	17.38^{b}	17.76^{bc}	18.78^{c}	20.44^{d}
Scan Star						
KP I, mm	6.35^{a}	6.66^{a}	8.37^{b}	7.22^{a}	8.60^{b}	10.50^{c}
KP II, mm	10.88^{a}	13.89^{b}	13.64^{b}	14.66^{bc}	16.46^{cd}	18.87^{d}
Fat area, cm^2	10.31^{a}	11.66^{b}	12.72^{c}	12.46^{bc}	14.42^{d}	16.79^{e}
Loin eye area, cm^2	46.45^{a}	48.83^{ab}	49.70^{b}	51.31^{bc}	52.72^{c}	53.75^{c}
MI	0.225^{a}	0.242^{ab}	0.259^{bc}	0.245^{ab}	0.276^{c}	0.318^{d}
Piglog 105						
X1, mm	8.41^{a}	9.24^{ab}	9.62^{b}	10.07^{bc}	11.03^{cd}	12.56^{d}
X3, mm	9.03^{a}	9.61^{ab}	10.19^{bc}	10.41^{bc}	10.82^{c}	13.38^{d}
X2, mm	59.24^{a}	59.72^{a}	60.28^{a}	61.50^{ab}	61.72^{ab}	63.29^{b}
Lean meat%						
Piglog 105,%	65.36^{a}	64.87^{ab}	64.53^{ab}	64.46^{ab}	63.99^{b}	62.37^{c}
ZP,%	62.19^{ab}	62.23^{a}	61.97^{ab}	62.03^{a}	61.72^{ab}	60.94^{b}
Ultra-FOM 300,%	62.25^{ab}	62.41^{a}	61.77^{abc}	62.38^{a}	61.49^{bc}	60.79^{c}

ScanStar. Fat thickness at the thinnest point (KP I) was 6.35-10.50 mm, and above *serratus dorsalis* (KP II) 10.88-18.87 mm, measured using PC software ScanStar. Fat thickness was uniform at the weight up to 79 kg, but it increased significantly along with further weight increase. Since fat thickness is related to fat area, similar difference was found regarding this trait. Loin eye area increased

constantly in each carcass weight class, while growth rate did not vary significantly in weight classes of 65-69, 70-74 and 75-79 kg. Meatiness index showed a significantly better loin and fat area relationship in <65 and 65-69 kg classes, while pigs over 85 kg had a significantly higher (0.318) meatiness index value, compared with other classes.

Table 3. Effect of carcass lengths on meatiness traits

Traits	Carcass length 1, cm				Carcass length 2, cm			
	<94	95-99	100-104	>105	<79	80-84	85-89	>90
n	25	40	96	41	27	72	82	21
Ruler								
BF 1, mm	25.23^{a}	26.33^{a}	26.06^{a}	25.57^{a}	26.83^{a}	26.20^{a}	25.30^{a}	24.88^{a}
BF 2, mm	18.72^{a}	18.83^{a}	18.44^{a}	17.26^{a}	19.84^{a}	18.35^{a}	17.18^{a}	17.88^{a}
BF 3, mm	15.16^{a}	13.41^{a}	13.67^{a}	13.33^{a}	14.21^{a}	14.32^{a}	13.77^{a}	13.28^{a}
BF 4, mm	9.66^{a}	9.16^{a}	9.58^{a}	9.15^{a}	9.58^{a}	9.46^{a}	9.12^{a}	9.40^{a}
Avg BF 1-4, mm	17.19^{a}	16.93^{a}	16.94^{a}	16.33^{a}	17.61^{a}	17.08^{a}	16.34^{a}	16.36^{a}
Avg BF 1-3, mm	17.87^{a}	18.11^{a}	18.03^{a}	17.33^{a}	18.75^{a}	18.00^{a}	17.20^{a}	17.38^{a}
ScanStar								
KP I, mm	9.04^{a}	7.96^{a}	7.67^{a}	7.14^{a}	6.81^{a}	8.58^{a}	8.23^{a}	8.18^{a}
KP II, mm	16.05^{ab}	15.90^{a}	14.23^{ab}	12.77^{b}	14.83^{a}	14.11^{a}	14.57^{a}	15.42^{a}
Loin eye area, cm^2	50.51^{ab}	48.25^{a}	50.46^{ab}	52.62^{b}	48.59^{a}	50.34^{a}	50.90^{a}	52.01^{a}
Fat area, cm^2	14.45^{a}	12.23^{b}	12.85^{ab}	12.72^{ab}	12.00^{a}	13.89^{a}	12.99^{a}	13.29^{a}
MI	0.287^{a}	0.255^{a}	0.257^{a}	0.245^{a}	0.254^{ab}	0.278^{a}	0.257^{b}	0.255^{ab}
Piglog 105								
X1, mm	9.66^{a}	10.56^{a}	10.38^{a}	10.02^{a}	10.95^{a}	10.14^{a}	9.79^{a}	9.75^{a}
X3, mm	9.82^{a}	10.89^{a}	10.81^{a}	10.78^{a}	12.10^{a}	10.55^{ab}	9.95^{b}	9.70^{b}
X2, mm	61.25^{a}	60.24^{a}	60.21^{a}	62.13^{a}	61.22^{a}	61.06^{a}	60.55^{a}	61.00^{a}
Lean meat%								
ZP,%	61.46^{a}	61.91^{a}	61.73^{a}	62.28^{a}	63.24^{a}	64.30^{a}	64.65^{a}	64.86^{a}
Piglog 105,%	64.86^{a}	63.88^{a}	63.97^{a}	64.35^{a}	61.59^{a}	61.62^{a}	62.11^{a}	62.06^{a}
Ultra-FOM 300,%	61.22^{a}	61.99^{a}	61.78^{a}	62.40^{a}	61.92^{a}	61.55^{a}	62.04^{a}	61.88^{a}

Piglog 105. Backfat measuremets carried out using Piglog 105 showed that lighter pigs (<65 kg) had significantly thinner fat compared with heavier (>85 kg) pigs. Backfat was relatively even in weight classes 65-69, 70-74 and 75-79. Diameter of *longissimus dorsi* was only 2.48 mm longer in the class 80-85 kg compared with lighter carcasses (<65 kg). However, major increase was found in carcasses over 85

kg weight, where diameter of *longissimus dorsi* was significantly bigger, compared with <65, 65-69 and 70-74 kg classes.

Lean meat% measured by using three different methods showed that heavier carcasses had lower lean meat percentage. The biggest difference in lean meat percentage between the lightest and heavier carcass classes was recorded with Piglog 105 (2.99%), while it was almost two times lower using ZP-method and Ultra-FOM 300 (1.25% and 1.46%, respectively). Piglog 105 showed also higher lean meat percentage, whereas ZP-method and Ultra FOM 300 had similar results. Lean meat percentage did not differ significantly between classes <65, 65-69, 70-74, and 75-79 kg.

Carcass lengths did not have a significant effect on fat thickness, except for carcass length 1, where significant difference in fat thickness 2, measured with ScanStar, was found between classes 95-99 and >105. Significantly thinner fat in carcass length 2 was also registered in classes 85-89 and >90, compared with class <79. Although significant difference in fat thickness was not found between carcass classes, a slight trend, that longer carcasses had thinner fat, could still be noticed.

With the ScanStar system we recorded the most significant differences between carcass length classes. As for carcass length 1, the loin eye area was 4.37 cm^2 larger in class >105 cm, compared with class 95-99 cm. On the other hand, the fat area was significantly larger in class <94 cm, compared with class 95-99 cm.

Carcass length had no major effect on lean meat percentage.

Conclusions

Lighter pig carcasses had thinner fat, while the loin eye records were also smaller. Meatiness traits changed slightly, being between 65 and 79 kg. However, lighter and heavier carcasses showed major changes. Lighter carcasses were leaner and therefore it is not justified to fatten pigs heavier, as shorter fattening time is more effective and leaner carcasses more valuable. Since the carcass price is based on its weight, farmers should find a balance between these two controversial traits.

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OTHER SPECIES

ANALYSIS OF GROWTH RATE INDICES FOR DAUGHTERS OF BROOD RAMS OF DIFFERENT ORIGIN

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Abstract

The research has been carried out on peasants' farm "Mežkalēji" in Platone village of Jelgava region. The farm is one of the largest farms raising breed sheep in Latvia. During the recent five years, for coupling of sheep mothers, brood-rams of the Latvian dark-heads as well as the German blackheads brought from Europe and the Estonian blackface are used.

During the research it was clarified that the largest live weight in all control periods was shown by the ewes that had been included in the 4th research group (LT x IT x OF). Thus, at the age of 100 days, the average live weight of ewes from the given group was 25.9 kg, which was in comparison with the control group (LT) by 3.7 kg, with the 2nd research group (LT x LT x VM) by 4.8 kg, and with the 3rd research group (LT x VM) by 2.6 kg higher. In all variants the difference was significant. A significantly higher live weight was also registered with 365 days old ewes as well as at commencing the coupling.

Key words: rams and mothers belonging breed, live weight augmentation, live weight at days.

Introduction

In the sheep-breeding branch of Latvian agriculture, great changes have occurred. Wool production as well as the direction of the basic production is being taken over by mutton production [6]. Currently, sheep breeders work on improving indices of mutton productiveness. One of the most rapid ways to attain this target is industrial hybridization, which improves such vitally significant features as viability of lambs, quality of growth rate, the carcass itself and the mutton [7]. Opportunities to produce mutton are defined not only by the provision of the technological conditions of production, but also by the genetically conditioned adequacy of the raised animals to produce a corresponding type of animals. Productivity of ewes, viability of lambs and peculiarities of growth, properties of lamb carcasses and other features are also genetically conditioned. As such, they can differ in different kindred groups (breeds and their structural units) and, thus, become as features of selection used in the selection to perfect the genetic material.

For improving mutton productiveness of the Latvian dark-heads, sheep breeds such as the Texel, the German blackheads and Il-de-Francs are used which leave a positive effect on the early ripening of lambs [6; 7; 8].

Aim of the research: to carry out analysis of growth rate indices for daughters of brood rams of different origin.

Materials and methods

The research has been carried out on the peasants´ farm "Mežkalēji" in the Platone Village of the Jelgava Region, which is one of the largest farms specializing in raising the Latvian dark-head sheep breed. To improve indices of mutton productiveness, for coupling of ewes the purebred rams of Il-de-Francs and the German blackheads were used as well as a ram of the Estonian dark-heads with 50 % blood admixture of the Oxford breed.

In the 2005/2006 monitoring year, there were 104 ewes with the average live weight of 61.9 kg on the farm, which corresponded to the requirements of the breed [4; 5]. The economic indices of the farm are greatly influenced by fertility of the ewes and rearing of the lambs. In 2005/2006, fertility of the ewes was 156%. The average live weight obtained per a 100-days-old ewe reached 32.4 kg.

The research was carried out according to the scheme presented in Table 1.

Table 1. Trial scheme

Trial groups	n	Blood of the subordinated in trial	
		mother belonging breed	rams belonging breed
1. Control	56	LT	LT
2. Trial	24	LT	LT x VM
3. Trial	10	LT	VM
4. Trial	19	LT	IT x OX

LT - Latvian darkhead; VM - German blackhead; IT – Estonian blackface; OX – Oxford Down

During the research, the following features of growth rate were recorded and analysed:

1. birth weight, kg;
2. live weight at 100 days, kg;
3. live weight at 365 days, kg;
4. live weight at 1.5 years, kg.

Data are processed using Microsoft Excel for Windows 2000 [1] and SPSS 8.0 programme package [2; 3]. Significance of difference in traits is designated using two levels of significance: *$p<0.05$ and **$p<0.01$.

Results and discussion

To clarify the effect the used broods have left on the production of daughters and rearing features; all female-type sheep were registered and weighed. The obtained average results are given in Table 2.

Table 2. The different origin of rams' birth rate indices for daughters

Trial indications	Groups							
	1. control		2. trial		3. trial		4. trial	
	$\bar{x}$	$\pm s_{\bar{x}}$	$\bar{x}$	$\pm s_{\bar{x}}$	$\bar{x}$	$\pm s_{\bar{x}}$	$\bar{x}$	$\pm s_{\bar{x}}$
Number at birth	1.68*	±0.06	1.63	±0.10	1.20*	±0.13	2.16*	±0.12
Birth weight, kg	3.7*	±0.04	3.7	±0.04	3.9*	±0.07	3.4*	±0.10

* The mean difference is significant at the 0.05 level.

Studying the results shown in Table 2, we can make a conclusion that the sheep included in the 4th group of the research were basically born as twins or even triples which, in turn, can explain the reduced live weight of the given group at birth. The highest live weight of units was obtained from the 3rd group of research, from the German blackhead breed ram. However, the obtained results revealed that sheep in this group arrived with a higher live weight, which confirms conclusions published in the scientific literature that a negative correlation exists between the number of lambs at birth and the live weight at birth.

For the analysis of the growth rate of sheep, the live weight at the age of 100 and 365 days was selected as well as at starting of coupling. The obtained results are presented in Table 3.

Table 3. The different origin of rams' growth rate indices for daughters

Trial indications	Groups							
	1. control		2. trial		3. trial		4. trial	
	$\bar{x}$	$\pm s_{\bar{x}}$	$\bar{x}$	$\pm s_{\bar{x}}$	$\bar{x}$	$\pm s_{\bar{x}}$	$\bar{x}$	$\pm s_{\bar{x}}$
Live weight at 100 days, kg	22.2	±0.48*	21.1	±0.68	23.3	±1.80	25.9	±1.01*
Live weight at 365 days, kg	50.9	±1.12	47.7	±1.31	46.8	±2.29	54.1	±1.19
Live weight at 1.5 years, kg	59.8	±0.90*	57.3	±1.12	59.6	±1.78	66.2	±1.33*

* The mean difference is significant at the 0.05 level.

As shown by the results, the highest live weight in all control periods was registered with the sheep included in the 4th research group which had been obtained from the Estonian blackface ram with 50 % blood admixture from the Oxford breed. Thus, 100-days-old sheep of the given group had the average live weight of 25.9 kg, which was in comparison with the control group by 3.7 kg higher, with the 2nd research group by 4.8 kg, and with the 3rd research group by 2.6 kg higher. In all variants, the difference is essential. Significantly higher live weight was shown by 365-days-old sheep of this group as well as at the beginning of coupling. Daughters of the German blackheads (3rd research group), although they were born with a higher live weight, did not distinguish with a high growth rate during raring. As shown by the obtained results, 365-days-old sheep of this group had a lower live weight, i.e. 46.8 kg as compared to all groups, although at weaning they showed the second highest live weight, i.e. 23.3 kg.

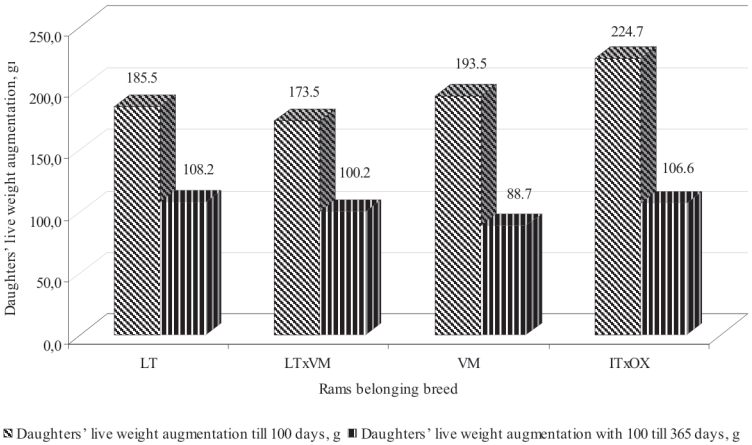

Figure 1. Different origin of rams' daughters' live weight augmentation over different periods, g

From Figure 1 it can be seen that the sheep of the control group, from their birth to the age of 100 days, reached the increase of diurnal live weight of 185.5 g which was by 8 g less than that of the sheep from the 3rd group and by 39.2 g less than that of the sheep from the 4th group ($p<0.05$*). This can be explained by the fact that animals of the German blackheads and the Oxford breeds belong to the mutton type, which is characterized by more rapid early ripening. The sheep showed the highest increase of the diurnal live weight within the period from 100

to 365 days from the 1st control group – 108 g. However, significant differences between the research groups were not observed.

Conclusions

1. During the research it was clarified that using the brood-ram of the Estonian blackface with 50 % blood admixture of the Oxford breed, sheep (4th group) were obtained, which basically were born as twins or triples. The average live weight of the sheep from this breed was 25.9 kg, which in comparison with the control group (LT) was by 3.7 kg higher. In all variants the difference was significant. The sheep gave significantly higher live weight from the 4th research group also at the age of 365 days, as well as at the beginning of coupling.
2. Daughters of the German blackhead brood rams (3rd group), although born with a higher live weight, did not distinguish during rearing with a high growth rate. As shown by the results, at the age of 365 days sheep of this group had the lowest live weight of 46.8 kg, compared to all groups, although at weaning they gave the second highest live weight, i.e. 23.3 kg.
3. Daughters of the Latvian dark-head brood ram, from their birth to the age of 100 days, reached 185.5 g diurnal increase of live weight which was by 8 g lower than that of the 3rd group and by 39.2 g lower than that of the sheep from the 4th research group ($p<0.05$*). It might be explained by the fact that the Latvian dark-head breed belongs to the wool- mutton breed, but the German blackheads and the Oxford breed belong to the mutton type.
4. We can make a conclusion that in equal keeping and feeding conditions the best growth rate was shown by the sheep obtained from the Estonian blackface ram with 50 % blood admixture of the Oxford breed.

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EFFICIENCY OF PEAS IN THE DIETS OF TURKEYS BIG-6

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Introduction

The greatest part of protein feeds for poultry, i.e. soybean and sunflower oil-meals, fish meal, maize, are imported from abroad. However, these feeds, as judged by experience, are not always of the best quality, yet quite expensive.

Comparatively large amounts of protein rich ingredients for feed manufacture are produced on the farms of Lithuania. These are peas, lupins, field beans and rape. These feed ingredients are cheaper than soybean oil-meal, the most widespread ingredient in poultry feeding (Morkūnas, 2002).

The efficiency of legume-grain feeds in the diets of poultry has been studied by foreign and Lithuanian authors only episodically.

Crude protein content on a dry matter basis in the peas grown in Lithuania accounts for 22.5-23.9%, and that of digestible protein in 15% wet grain accounts for 16.4-17.5% (Dovydaitis 1998). Different authors indicate different levels of peas to be used in broiler chicken feeds. Lithuanian authors (Morkūnas et al., 1999a, Morkūnas et al., 1999b, Vaitiekūnas et al., 1999) assume that the optimum content of peas in broiler feeds is 16%, while German authors indicate 30% (Kluge et al., 1998).

There were attempts to use peas in the diets for turkey poults (Savage et al., 1986). Turkey poults were offered diets containing 25% peas until 16 weeks of age. Later the level of peas in the diet was increased and accounted for 55% at the finishing stage.

Nutrient digestibility of peas has been also studied (Gruhn et al., 1990). The digestibilities of the organic matter, protein, fat and nitrogen free extracts of Grapis peas were 66.9, 78.5, 48.7 and 70.3%, respectively. Metabolizable energy was 2844 kcal/kg (Savage et al., 1986).

Peas contain digestion inhibitors such as trypsin inhibitors, hemagglutinins, tannins. It can be found in the literature, that digestion inhibiting factors have no effect on the performance of birds provided the level of peas in the diet does not exceed 30%.

Until 8 weeks of age, turkey poults are very sensitive to the environmental and feeding conditions, and thus, it is important to know the effects of different amounts of peas in the diets on turkeys of different ages (Janušonis et al., 2003).

Material and Methods

Heavy hybrid turkeys of BIG-6 cross were used in the study to determine the efficiency of peas in the turkeys diets and to find the most effective levels of protein content in the diets of turkey to poults till 20 weeks of age.

Due to the fact that male and female turkeys were housed separately, the turkeys were allotted into two control (one comprising male, another female birds) and six experimental groups of 12 birds each of which three groups were male and the other three female. Experimental design is shown below.

Experimental design

Age, wk	Protein content of feed, %	Control group	Group 1	Group 2	Group 3
		Soybean oil – meal,%	Pea content in the diet, %		
0 – 4	27 – 28	44.0	10	15	20
5 – 8	23 – 24	33.0	15	20	25
9 – 12	18 – 19	25.0	20	25	30
13 – 16	17	20.0	40	40	40
17 - 20	17	20.0	40	40	40

Results and Discussion

Control weighing of birds indicated (Table 1) that at the age of 12 weeks male turkeys in Group 1 weighed 350 g less, and those in Group 3 1330g more, compared with the control group.

Table 1. Weight of broiler turkeys, g

Age,wk	Control group		Group 1		Group 2		Group 3	
	♂	♀	♂	♀	♂	♀	♂	♀
4	971	900	999	900	1102	954	1200	1030
8	3890	2980	3640	3010	3950	3320	4560	3590
12	7980	5510	7630	5610	8000	5210	9140	6840
16	11900	7825	12310	8560	12470	8750	12971	8938
20	16063	11095	16070	11100	16150	11137	16540	11256

At this age, female turkeys had the lowest and the highest weights in Group 2 (5210 g) and Group 3 (6840g), respectively.

At 16 weeks of age, control male turkeys had the lowest weight of 11900g, and the weight of the birds in three experimental groups increased from 410 to 1071g.

Control females at this age weighed from 735 to 1113g less in comparison with the experimental females in three groups. The highest weight at the age of 16 weeks was reached by the males (12971g) and females (8938g) in Group 3.

At slaughter, i.e. at 20 weeks of age, the weights of the control and Group 1 turkeys became equal, while the male and female turkeys in Group 2 and 3 weighed 87-477 and 42-161g, respectively, more than the birds in the control group.

At the age of 20 weeks, the highest weights were determined for the males and females of experimental Group 3, 16540 and 11256g respectively.

In 16 weeks, the lowest food consumption was found in male and female Group 3, 13.86 and 10.77 kg, respectively, and that was by 8.6 and 6.5% lower compared with the control group. Female turkeys in experimental Group 1 and male turkeys in Group 3 had the lowest food consumption during the whole experimental period. The food consumption was, 8.38 and 5.11%, respectively, lower than that in the control group turkeys.

Table 2. Results from digestion trials

Item	Groups							
	Control group		Group 1		Group 2		Group 3	
	♂	♀	♂	♀	♂	♀	♂	♀
Daily food intake, kg	0.67	0.52	0.67	0.53	0.63	0.60	0.62	0.50
Dry matter retention, %	71.78	69.35	67.53	68.88	74.17	71.39	74.97	69.24
Fat retention, %	71.70	68.67	67.84	68.21	74.76	71.14	75.09	69.33
Energy retention, %	70.29	71.35	68.85	68.68	69.92	69.74	79.25	77.46
Nitrogen retention, %	57.25	55.39	47.94	50.65	60.21	54.66	58.59	53.48
Protein retention, %	90.27	94.78	91.98	92.89	93.55	94.28	93.75	92.67

Digestion trials (Table 2) indicated that increasing levels of peas in the diets led to better fat assimilation by 0.66-2.47 and 0.33-3.39%, respectively, in comparison with the birds of the control group.

Energy assimilation was 6.11% higher in male Group 3 compared with the control group. Protein digestibility by experimental female turkeys fed pea supplemented diets was higher from 1.71 to 3.48% in comparison with the control group.

Conclusions

1. The best growth performance was determined for turkeys fed diets containing 15% of peas instead of part of soybean oil-meal with the further increase of the amount of peas up to 40% with no soybean oil-meal usage. At the age of 20 weeks, male turkeys of this group weighed 16.5 kg, females 11.25 kg, but the data was not statistically significant compared with the control group.

2. Food consumption /kg gain was 3.9 and 4.7 kg, respectively, for males and females in the control group, while in the experimental Group 3 males consumed 3.4 and females 4.2 kg per kg gain.

3. The recommended amounts of peas to the diets according in this study are as follows: 15% from 0 to 4 weeks of age, 20% from 5 to 8 weeks of age, 30% from 9 to 12 weeks of age, 40% from 13 to 20 weeks of age, with no usage of soybean oil-meal.

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EFFECTS OF BLOOD INFUSION FROM OTHER BREEDS ON THE PHENOTYPE AND GENOTYPE OF THE ŽEMAITUKAI HORSE BREED

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Introduction

The Žemaitukai is a Lithuanian horse breed that is one of the oldest in Europe. From 19th to 21st centuries the breed was on the verge of extinction for even four times. Now the breed is recognized as internationally watched. The Žemaitukai is a universal pony type horse used for work, driving, tourism, children pastime, hippotherapy and sports. Their height at withers is from 128 to 142 cm, chest girth from 154 to 187 cm, cannon bone girth from 17 to 19 cm and weight from 360 to 420 kg [14].

A special selection programme is applied for the Žemaitukai breed conservation. This programme embraces two breeding methods: pure breeding by a circular mating scheme and blood infusion for the development of the new stallion lines [4; 5].

Žemaitukai horses produced by pure breeding account for 85.2% of the population, while 14.8% are the representatives of newly developed lines. After selection, the latter should make up no more than 10% of the population. The development of the new lines is one of the composite measured for breed preservation; however, this can serve the breed only after long, consecutive and thorough work. Irresponsible crossing might destroy the breed earlier than the consequences of harmful incest.

The development of the new lines of the Žemaitukai horse breed has been carried on at Vilnius Stud since 1994 and at the LVA Institute of Animal Science since 1999. Several mares from the existing five mare families were chosen for pairing with large-type Žemaitukai, Arab and native Estonian stallions in order to ascertain the founders of the new lines. The founders of the new lines at the LVA Institute of Animal Science are large type Žemaitukai and native Estonian stallions, while the founders at Vilnius Stud are two Arab horses.

The preservation of the old and valuable Žemaitukai breed is a very responsible process and, therefore, beside strict selection, scientific research is also required to indicate the effects of blood immigration on the unique nature of the Žemaitukai. The studies have shown [1, 3, 6, 13] that by the genetic structure the Žemaitukai horses are different not only from Lithuanian breeds – Lithuanian Heavy draft and large-type Žemaitukai – but also have a very rare allele T in ES genetic system [3] what confirms the existence of the exceptionally unique genome of this breed.

Material and Methods

Žemaitukai horses of the newly developed lines are evaluated and selected according to the evaluation rules for the Žemaitukai horse breed approved by the State Animal Breeding Supervision Service under the auspices the Ministry of Agriculture of the Republic of Lithuania in 2002 [15]. The progeny are selected by the breed standard – a model Žemaitukai horse and the set of traits as pedigree, body conformation and constitution, typicalness, body measurements, character, movements, progeny quality and working ability.

The blood in Žemaitukai horses was analysed at the Blood Typing Laboratory in the LIAS. The pedigree and blood samples were collected from 171 horses.

Standard blood typing methods were used. Blood groups were classified according to seven genetic systems: EAA, EAC, EAD, EAK, EAP, EAQ and EAU, and tested by agglutination and hemolysis reactions [11, 12]. 20 to 25 reagents test-serums were used for these reactions. The standard protein electrophoresis method in polyacrilamide gel (PAGE) was used for the analysis of blood protein polymorphism of the Žemaitukai [2]. This method leads to the identification of five genetic systems of blood protein: transferrin (Tf), postalbumin (Xk), protein binding vitamin D (Gc), albumin (Al) and esterase (Es). The following alleles were determined in the above systems: D, F, H, M, O, R in Tf system; F, K, S in Xk system; F, S in Gc system; A, B in Al system and F, I, S in Es system. Genetically most different are the systems of transferrins, albumins and esterase; therefore, further genetic analysis of blood protein was carried out in these systems. Allele frequency P and degree of homozygosity Ca for the blood groups (EAA, EAD and EAQ) and serum proteins (Tf, Al, and Es) were computed for the genetic evaluation and comparison of stallion lines [7, 8, 9, 10].

Results and Discussion

The genealogical structure of the Žemaitukai breed comprises 142 horses of the Erelis[3] line, 73 horses of the Astūras line and 38 progeny of the newly developed lines that account for 14.8% of the Žemaitukai population.

The evaluation analysis of the stallions certified for breeding indicated that the stallions from the old Erelis line received the highest score, i.e. on the average 85.4 points on a 100-point scale. The stallions from the Astūras line scored 84.9 points, while as for the stallions from the newly developed lines, stallions from the Arab line, Estonian native Torgel line and large-type Žemaitukai line scored, respectively, 83.7, 82.25 and 77 points (Table 1). Table 1 show that stallions from the old Erelis line are distinguished by their pedigree and body measurements and the total evaluation in general. Stallions from the Astūras line that was developed in the seventh decade of 20th C. are distinguished by their typicalness as regards the breed. Newly developed lines are distinguished by good body conformation and constitution as well as by movements (Arab line), desirable character and body measurements (large-type

Žemaitukai line), body measurements and type (Torgel line).

Table 1. Average scores for the stallion certified for breeding

Mean of traits						
Pedigree	Typical-ness	Body measurements	Body confor-mation	Character	Movements	Total
Erelis line (n=17)						
8.8±0.1	17.0±0.5	8.8±0.3	26.4±0.4	9.2±0.2	15.7±0.5	85.4±0.8
Astūras line (n=6)						
8.7±0.2	17.5±0.3	8.1±0.3	26.0±0.6	9.0±0.4	15.3±0.8	84.9±1.3
Arab line (n=2)						
8.0±1.0	16.0±0.0	7.0±2.0	27.25±1.2	9.5±0.5	16.0±0.0	83.7±1.8
Torgel line (Estonian native; n=2)						
8.0±0.0	17.0±0.0	9.0±0.0	25.25±0.8	8.0±2.0	15±1.0	82.25±2.2
Large type Žemaitukai line (n=2)						
7.0±1.0	11.0±5.0	9.0±1.0	25.0±0.0	10±0.0	15±1.0	77±6.0

Differences for the main body measurements, i.e. height at withers, chest girth and cannon bone girth, between the Erelis line stallions and the remaining ones have been calculated.

Erelis and Astūras line stallions were similar in their height and cannon bone girth, yet there was a significant difference ($P<0.025$) for the chest girth that was higher for the Erelis line stallions. Arab line stallions were higher than those of the Erelis line ($P<0.001$). A significant difference was found for the chest girth between the large-type Žemaitukai and Erelis line stallions ($P<0.001$). Torgel line stallions differed from Erelis line stallions in higher height at withers ($P<0.001$) and higher cannon bone girth ($P<0.01$).

The differences in body measurements between purebred mares and the mares with 1/2 and 1/4 blood immigration showed, that the height ($P<0.001$) and chest girth ($P<0.025$) of the mares with Arab blood were significantly higher than the corresponding parameters of purebred mares. However, their body measurements met the requirements for the model Žemaitukai horse. There were no other significant differences between the mares from different lines.

Genetic analysis of blood group alleles of the Žemaitukai horse indicated that allele A^{ad} in EAA genetic system is typical of all Žemaitukai progeny and ranges from 0.3112 (Erelis line) to 0.4630 (newly developed lines).

In the genetic system EAD, the most typical allele was D^{dghm} with the frequency from 0.3333 (new lines) to 0.4239 (Astūras line).

Blood protein polymorphism studies and data analysis indicated that allele AA of the Al system was most typical of the Astūras line progeny (0.7174), less typical of the

Erelis line progeny (0.6122) and little typical of the progeny of the new lines (0.3704). Allele AB (0.5185) was typical of the new line progeny and allele BB was characteristic only of the new line progeny (0.1111).

In Es system allele FI could be distinguished with the frequency from 0.2593 (new lines) to 0.5 (Astūras line). This allele was typical of all Žemaitukai horses.

Allele FS was more typical of Astūras line progeny (0.2174) and allele IS (0.2593) – of new line progeny.

The genetic system of transferrins was distinguished by high number (10) of alleles, but the most typical of the Žemaitukai horses was allele DF (0.3333-0.3878). Allele OR was very rare: its frequency in the Erelis line progeny was only 0.0102, while the new line progeny did not have this allele at all.

Alleles OO and RR was also rare. New and Astūras line horses did not possess them at all and only traces (0.0102) were found in the Erelis line.

Allele DO was more typical of the Astūras line (0.1739) and less typical of the new lines (0.1481). This was not typical of the Erelis line (0.0816).

The calculated degree of homozygosity Ca (%) indicated that the new lines had least homozygosity (Ca=32.42%), while Astūras line had the highest homozygosity (Ca=36.14%), Ca in Erelis line equalled 33.96%.

The presented data showed that there was not much difference between the Žemaitukai lines according to the blood group systems. All lines could be characterized by the same genetic systems and alleles: A^{ad} allele in EAA, A^{dghm} allele in EAD and Q^{c} allele in EAQ systems.

More significant differences between the lines were found in blood protein polymorphic systems. Alleles AB and BB in the albumin system and allele IS (0.2593) in ES system were typical only of the new line progeny. In the transferring system, the horses were devoid of alleles OR, OO and RR.

Comparative genetic analysis of the new lines will be involved in further genetic blood studies.

Conclusions

1. The evaluation analysis of the stallions certified for breeding indicated that the stallions of the new lines are distinguished by good body conformation and constitution as well as by movements (Arab line), desirable character and body measurements (large-type Žemaitukai line), body measurements and type (Torgel line).
2. Comparison of the body measurements of stallions and mares from different lines indicated that the newly developed lines meet the standard requirements of the breeds.
3. Genetic analysis of the lines indicated differences in blood protein polymorphism, i.e. alleles AB and BB in albumin system and alleles IS in Es system were found to be typical of only new lines.

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FATTY ACID CONTENT OF GOAT MILK FROM THE ESTONIAN LOCAL GOAT

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Introduction

The importance of goat husbandry is modest in Estonia. However, the goat population has increased and duplicated during the last ten years from 1700 goats in 1997 to 3400 goats in 2007. Although goat husbandry has low economic importance as regards the national income, it provides employment for a large number of rural families living in small holdings in Estonia. Most breeders keep small non-commercial herds for home consumption of milk, cheese and meat or for hobby purposes, with the exception of a few commercial milk producers. Estonian local breed of goat is the only goat breed and it is spread all over the country. The usual colour is white, but they are also found grey, brown or black or various shades or combinations of these colours. Usually they are shorthaired and horned animals. Estonian local goats are kept primarily for milk production. The main product of goat farming - raw milk - is consumed in an unprocessed form within farms, but in limited quantities it is converted into several milk products, for example soft cheese and yoghurt.

The biochemical facts of the unique qualities of goat milk are just barely known and little exploited.

Goats have unique differences in product biochemistry from sheep and cattle, which support the contention of many unique qualities of dairy goats products for human nutrition. Mammalian 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 of heart disease. An increase in the consumption of products with high saturated fatty acid content is associated with a rise in cardiovascular diseases, while the intake of PUFA has been associated with the decrease of cholesterol and due to that less heart problems. Especially important among polyunsaturated fatty acids are essential omega-3 fatty acids. Alpha-linolenic acid C18:3n3) is required in the diet, because humans cannot produce it (Piirsalu, 2004). 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 (PUFA) reduces the content of cholesterol in plasma low density lipoproteins (Ashes J.R. et al, 1997). Some authors (Jenness, 1980) have reported that average goat milk fat differs from average cow milk fat being higher in butyric (C4:0), caproic (C6:0), caprylic (C8:0), capric (C10:0), lauric (C12, myristic (C14:0), palmitic (C16:0), linoleic (C18:0). Medium chain triglycerides (C6-C14) are actually predominant in goat milk. Capric, caprylic and medium chain triglycerides have become established as medical treatment in the case of many clinical disorders, like intestinal resection, epilepsy, cystic fibrosis, premature infant feeding, coronary by pass, because of their unique metabolic ability to provide direct energy and because of their actions of lowering serum cholesterol (Alferez et al., 2001). Recently more beneficial fat, conjugated linoleic acid (CLA), has been identified as a potent anticarcinogen and is primarily provided to the human diet by dairy products (Pfeuffer, 2000), but it has not been studied much in goat milk yet. Monounsaturated (MUFA), polyunsaturated fatty acids (PUFA) and medium chain triglycerides are all known to be beneficial for human health, especially for cardiovascular condition (Haenlein, 2004), but trans-C18:1 fatty acid is undesirable.

The aim of this study was to investigate the fatty acid content of goat milk from the Estonian Local Goat and to get more information about fatty acid profiles in goat milk.

Material and methods

The study was carried out in March 2007 on Merike Bakhoff's Goat farm, Pärnumaa, with nine Estonian local lactating goats. Goats were selected for similar pedigree, age (3-4 years) and lactating month (mostly 3.-6. month) and body weight (average 50 kg). The diet included 1.6 kg hay (ME-8.0 MJ/kg, 39.2 g DP) and 0.35 kg compound feed (ME- 11.2 MJ, 78 g DP) and 0.5 kg potatoes (ME-2.7 MJ/kg, 12.2 g DP). Experimental goats ate per day 1.75 kg DM, 17.2 7 MJ of ME and 92 g of DP. Fatty acid content of each goat milk sample was analysed by the Laboratory of Feeding Department, using gas chromatography.

Results

Fatty acid profiles of goat milk is given in table 1. The total saturated fatty acid (SFA) content in goat milk fat was 73,5%, total MUFA content was 18.6% and total PUFA content was 3.4% from all lipids. Goat milk from the Estonian Local goats was a source of conjugated linoleic acid (CLA) and its content was an average of 0.35 %. The cis 9, trans-11 CLA is thought to have anticarcinogenic properties and makes up approximately 97 % of the total CLA. Some authors have reported that cis 9, trans-11 CLA forms approximately 75 to 85% of the

CLA in the milk fat of cows (Piperova et al, 2004) and 78 to 89% of the CLA in the milk fat of sheep (Antongiovanni et al, 2004). So, cis 9, trans-11 CLA, constituted 97 % of the total CLA. The content of another CLA isomer in goat fat, trans -10, cis 12 CLA which may have detrimental effects on human health (Wahle et al., 2004) was marginal, only 0.01% of total fats.

Saturated fatty acid content of goat milk is given in table 2.

Table 1. Fatty acid profiles of goat milk, n=9

Fatty acid	% of lipids	Standard deviation, s
Saturated (SFA)	73.53	3.72
Monounsaturated (MUFA)	18.60	2.49
Polyunsaturated (PUFA)	3.40	0.68
Conjugated Linoleic Acid (CLA)	0.35	0.06
in which 18:2 cis-9 trans-11	0.34	0.07
n 6	1.59	0.28
n 3	0.92	0.23
In which 18:3n 3 (linolenic)	0.64	0.18
n6/n3	1.74	0.26
n6 LCPUFA	0.33	0.11
n3 LCPUFA	0.28	0.07
n6 LCPUFA/n3 LCPUFA	1.19	0.22

Table 2. Saturated fatty acid content of goat milk, n=9

Fatty acid	% of lipids	Standard deviation, s
C 4:0	2.96	0.26
C 6:0	2.67	0.28
C 8:0	2.74	0.36
C 10:0	10.43	1.44
C 11:0	0.15	0.03
C 12:0	5.14	0.89
C 14:0	12.07	1.36
C 15:0	1.43	0.30
C 16:0	27.08	2.21
C 17:0	0.85	0.18
C 18:0	7.38	1.38
C 19:0	0.16	0.03
C 20:0	0.29	0.09
C 21:0	0.07	0.01
C 22:0	0.12	0.06

Our data showed that goat milk is a source of low (C4:0) and medium chain triglycerides (C6-14). Their content in goat milk was 2.96 and 33.2%. Those fatty acids are known because of their unique metabolic ability to provide direct energy instead of being deposited in tissues. Desirable fatty acids, like capric (C10:0) and caprylic, (C8:0) content in goat milk fat was respectively 10.4 and 2.7% of the total lipids.

Table 3. Monounsaturated fatty acid content of goat milk, n=9

Fatty acid	% of lipids	Standard deviation, s
C 10:1cis-9	0.26	0.06
C 14:1cis-9	0.18	0.07
C 15:1cis-10	0.35	0.09
C 16:1trans-9	0.05	0.01
C 16:1cis-9	0.73	0.16
C 17:1cis-10	0,37	0,07
C 18:1trans-6-8	0,09	0,02
C 18:1trans-9	0,12	0,02
C 18:1trans-10	0,07	0,02
C 18:1trans-11	0,63	0,14
C 18:1cis-9	15.17	2.17
C 18:1cis-11	0.45	0.08
C 20:1cis-8	0.03	0.03
C 20:1cis-11	0.07	0.01
C 24:1	0.04	0.02

Table 3 presents data about monounsaturated fatty acid content of goat milk. 15 different isomers were established among monounsaturated fatty acids and only one of them, C18:1 cis-9, makes up approximately 81% of the total MUFA in the milk fat of goats. Other monounsaturated fatty acids had uniformly low content (less than 1 %). Analyses revealed a large number of different trans-C18:1 fatty acids and other branched-chain fatty acids, which lend characteristic flavours to dairy foods (Alonso et al., 1999), but the content of those undesirable fats were low.

Omega-3 fatty acid content is given in table 4. The total omega-3 fatty acids contained 0.92 % of total lipids. As it was declared earlier that intake of PUFA has been associated with the decrease of cholesterol in the blood. Alpha-linolenic acid C18:3n3) is required in the diet, because humans cannot produce it. Even alpha-linolenic acid contributes to preventing atherosclerosis in humans (Kris-

Etherton and Yu, 1997). The amount of alpha-linolenic acid in goat milk fat was 0.64 % and its relative importance was 69% of the total omega-3 fatty acids. Thus goat milk is a dietary source of alpha-linolenic acid as well. The concentrations of eicosapentaenoic acid (C20:5 n3) and docosahexaenoic acid (C22:6n3) were low (0.08 and 0.06 % respectively), as is typical in the milk ruminant species, but still higher than it was reported by Nudda, et al. (2006).

Table 4. Omega-3 fatty acid content of goat milk, n=9

Fatty acid	% of lipids	Standard deviation, s
C18:3n3	0.64	0.18
C20:5n3	0.08	0.02
C22:5n3	0.15	0.04
C22:6n3	0.06	0.02
Total omega 3	0.92	0.23

Conclusions

Studies showed that goat milk fat has specific desirable healthy features for humans. Goat milk and goat products are the main dietary source of conjugated linoleic acid (CLA), polyunsaturated fatty acids (PUFA), especially alpha-linolenic acid, which humans cannot produce, and medium chain triglycerides (C6-14).

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HORSE GENETIC RESOURCE ANALYSIS IN LATVIA

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Introduction

Horse breeding has been a long-standing agricultural sector in Latvia, especially developed before the World War II. There is one horse breed considered as a national breed – Latvian horse, which was developed in 1937 – with two types: sport type and carriage type.

In the last two decades the main breeders' attention has been paid to the development of the sport type according to the market demand. As a result, the number of carriage type horses has been recently constantly decreasing. Due to that, the qualities of the type: steadiness, placability, trust to humans, great operational capability, have been gradually disappearing. These qualities are essential using horses in tourism, hippo therapy and as a school horses. To maintain the gene pool diversity, it is important to preserve these qualities as specific to horses of local origin.

Attention has been paid to carriage type horses again after Latvia accepted the convention on preserving biological diversity signed in Rio de Janeiro. In 2004, realization of "Latvian breed horse carriage type breeding programme for 2004 – 2009" was started.

The research is accomplished to analyze the situation characterizing horse genetic resources in Latvia. It covers the whole horse genetic resource population in Latvia, and includes the analysis of genealogical lines and congenial groups, age and regional distribution.

Material and methods

Horse genetic resource data was acquired in Latvian Breed Horses Association and Latvian Horse Breeders' Society. The data were registered for 42 breeding stallions and 303 mares as genetic resource individuals older than 3 years of age (in total 345 horses). Data for individuals younger than 3 years was not summarized, as their evaluation methods are different. Genetic resource of the horses was evaluated by certificated experts. The evaluation included pedigree, typicality, measurements, exterior and performance.

Latvian breed carriage type horses' pedigree and their relevance to stallion lines and related groups remaining in the breed were clarified and the number of individuals belonging to each of it determined. The mares' and stallions' age and regional distribution analysis was done. The relevance to stallion lines and related groups was identified by state studbook.

Results

The great majority of stallions included in genetic resources, represented Spēkonis Lsb 100 line as well as various Western European breed lines (mostly Hanoverian and Holstein) (Fig 1).

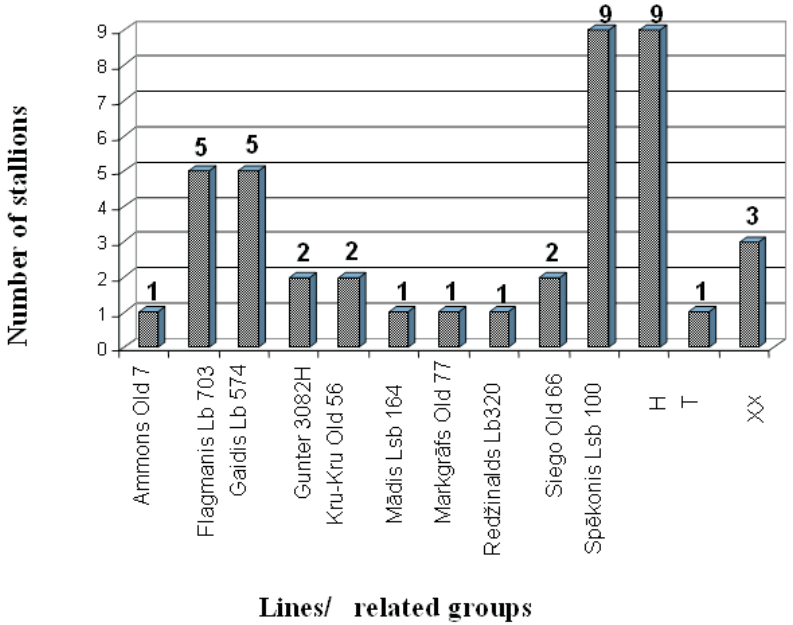

Figure 1. Pedigree and number of genetic resource stallions

Sufficient number of stallions represented Flagmanis Lb 703 and Gaidis Lb 574 lines. Five stallion lines and related groups – Ammon Old 7, Mādis Lsb 164, Markgrāfs Old 77, Redžinalds Lb 320 and those of Trakener breed origin had only one stallion in each of them.

As to mares, results showed similar tendency – most of them belonged to Western European breed lines (61 mares) and Spēkonis Lsb 100 line (47 mares) (Fig 2).

Sufficient number of mares represents Flagmanis Lb 703 and Gaidis Lb 574 lines, as well as Thoroughbred origin and Gunters 3082 H lines.

Unfortunately only few mares represent such old lines as Gotenfirsts Lsb 220, Juveels Old 49, Banko Old 51 and Kru – Kru Old 56. The Goldengel 3561 Old Stb-related group is represented by one mare only.

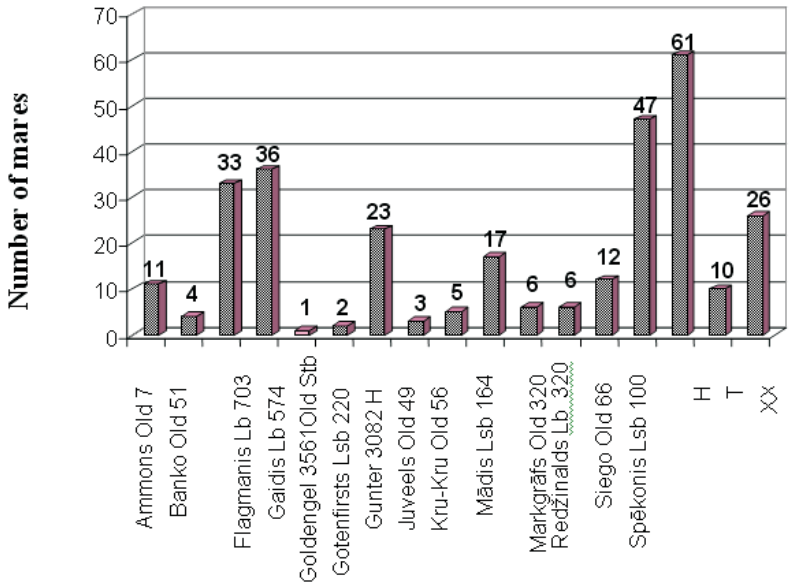

Figure 2. Pedigree and number of genetic resource mares

The results showed a tendency – if the particular line was represented by sufficient number of stallions, it was the same with mares as well. Some lines have remained only in "mothers" (there is no stallions) - Banko Old 51, Goldengel 3561 Old Stb, Gotenfirsts Lsb 220 and Juveels Old 49. These lines can be considered as endangered and close to extinction. The same refers to lines and related groups with only one or two stallions – Ammon Old 7, Gunters 3082 H, Kru – Kru Old 56, Mādis Lsb 164, Markgrāfs Old 77, Redžinalds Lb 320 and Siego Old 66.

The mean age of genetic resource stallions exceeds 13 varying between 3 and 27. Comparatively large number of stallions is at the age from 3 to 8 and from 17 to 21 (Fig 3). Five stallions are older than 22.

The average age of mares is 12. Most mares are at the age from 3 to 12 and significant number is at the age from 13 to 18.

The data indicate that most genetic resource mares are in breeding age, which is the primary condition to include them in the breeding programme. Mares older than 19 (40 individuals in total) are included in condition they can get impregnated and give tenacious descendants within three years.

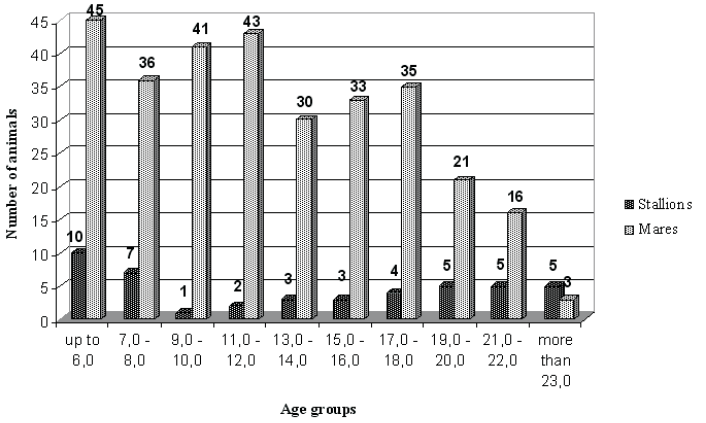

Figure 3. The age of genetic resource horses

According to regional distribution in the country, the smallest number of horses is located in Dienvidlatgale, Austrumlatgale, Dienvidkurzeme and Ziemeļkurzeme regions (Fig. 4). In Ziemeļkurzeme region no stallions are registered.

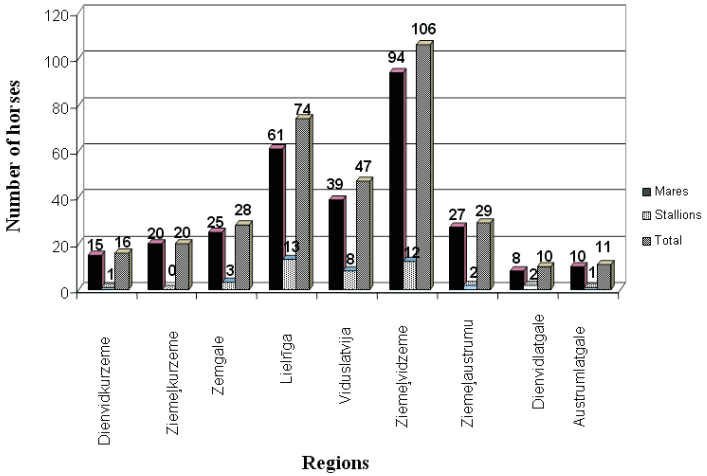

Figure 4. Regional distribution of horse genetic resources

Most stallions and mares are located in Ziemeļvidzeme region, mainly in districts of Valmiera, Cēsis and Limbaži. Sufficient numbers of genetic resource horses are located in Lielrīga and Viduslatvija regions mainly in Riga and Madona districts.

Conclusions

1. Great attention has to be paid to preservation and continuation of lines and related groups with only one stallion registered. This concerns Ammon Old 7, Mādis Lsb 164, Markgrāfs Old 77, Redžinalds Lb 320 lines and the related groups.
2. It is necessary to motivate Latvia breed carriage type horse breeding in regions with no or small number of individuals registered.

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CHANGES IN POPULATION SIZE OF LITHUANIAN HEAVY DRAUGHT HORSES

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Introduction

Until the middle of the 19th century, when the three-field system of agriculture was prevailing in Lithuania, mostly small horses of the Zemaitukai breed that could survive on pastures and meadow hay were raised. The second half of the 19th century witnessed intensification of agricultural production and small height and weight of the Zemaitukai became an obstacle. Thus, ways for local horse enlargement have been searched. Large heavy type horses gradually started to replace the dominating Zemaitukai. Enlargement was also promoted by the demand for heavy draft horses and high export price. In the first half of the 20th century the development of local heavy type horses was mostly influenced by their improvement with heavy draft horses. Thus, local Zemaitukai horses became the foundation for the Lithuanian heavy draft horse breed in the 1970's. In the last decade of the 20th century, horse breeding experienced depression due to political and agricultural reforms, and the native Lithuanian horse breeds started disappearing. Currently, Lithuanian heavy draft horses are recognized as breeds under preservation. All available genetic potential of horses should be used to widen the heterozygosity of the Lithuanian Heavy Draught horse breed. Therefore, the aim of our investigation was to evaluate the changes in genealogical structure of the breeding animals chosen for the development of the breed in order to stop the disappearing of the genealogical structure of the Lithuanian Heavy Draught breed.

Material and methods

Our study was based on the material of breed monitoring and status analysis. Data have been analysed during 1991-2006. In the study the population size was expressed as the total number of individuals of a breed alive at a time, the total number of animals of breeding age and the effective population size (Gandi, 1999). The effective population size was expressed as N_e (FAO, 1999; Wright, 1931). The generation interval for males (Lm) was defined as the average age of the male parents at the birth of their replacement. The definition for females (Lf) was similarly defined. The generation interval for population was as follows:
L = (Lm+LF)/2 (FAO, 1996). The pedigree of Lithuanian Heavy Draught horse males (M) and females (F) was analysed on the basis of state studbooks and stud documentation.

Results and discussions

In 2006, there were 600 registered Lithuanian Heavy Draught horses, including 27 stallions and 220 covering mares. Effective population size for Lithuanian Heavy Draught horses was 115 in 2001 and 101 in 2006. Therefore, the survival of the population is uncertain. In 2001, implementation of the special breeding programme of the local horse breeds in studs had stabilized reproduction of Lithuanian Heavy Draught population, but the number of foals compiled just 50% of all breeding mares (Fig.1).

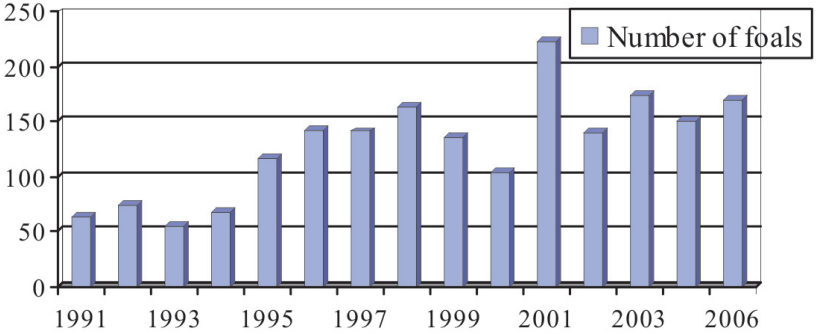

Figure1. Numbers of foals of the Lithuanian Heavy Draught horses in 1991-2006

A great number of Lithuanian Heavy Draught horses are exported: 5500 horses were exported for meat in 2006.

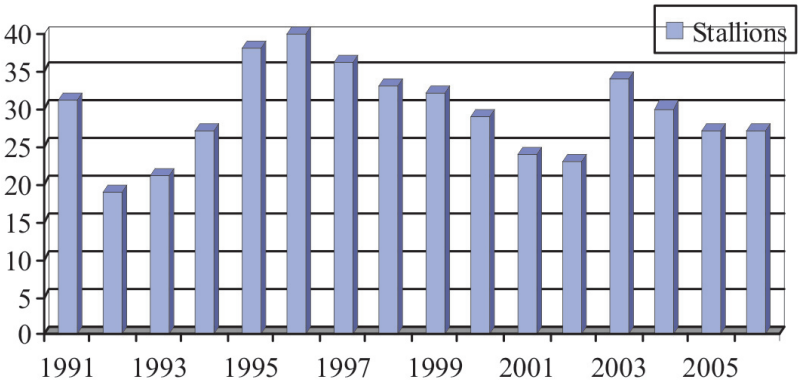

Figure 2. Numbers of stallions of the Lithuanian Heavy Draught breed used for breeding

In recent years, the numbers of stallions (Fig.2), mares and breeding herds are stable, but the number of stallion lines is decreasing ominously.

Lithuanian Heavy Draught horse breed was confirmed as an independent one with 12 lines in 1963.

Genealogical analysis of Lithuanian Heavy Draught stallion progeny (Fig. 3) indicated that three stallion lines and one new genealogical group of Gandras 0697 may be found. Distribution analysis of the lines and related groups shows that the biggest number of stallions (51.8%) and mares (46.5%) belongs to the Marsas 01252 line. The next biggest line is that of Gandras 0697 with 40.7% of stallions and 38.5% of mares belong to this line. Distribution analysis of Marsas 01252 and Gandras 0697 lines was similar in 2001 (Jeninas, Razmaite, 2001). The number of the progeny from the other lines is very small and still decreasing. There is only one stallion from Vikras 72 and Bijūnas 0150 line. The genealogical group of Gandras 0697 line horses may be regarded as a separate and individual line. The stallions of this line are of a desirable type and body conformation. The selected typical stallions will be included in the general programme for Lithuanian Heavy Draught horse breeding. It is suggested to breed the horses by a circular mating scheme, thus preserving their genealogical structure.

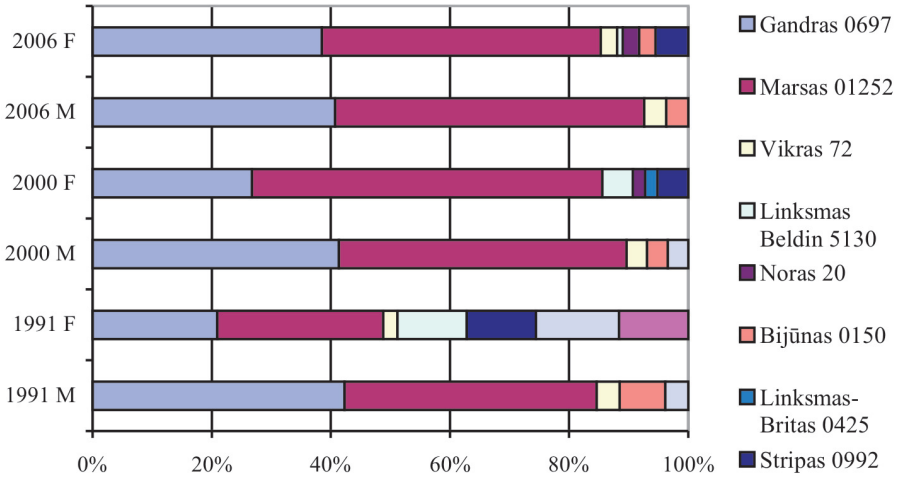

Figure 3. Genealogical structure of Lithuanian Heavy Draught horse in 1991-2006

The Lithuanian Heavy Draught Horse population has a generation interval (L) of 10 years. The generation interval is a measure of how long it takes to replenish the asset of parents. The generation interval for Lithuania Heavy Draught males

(11.2 years) / females (8.8 years) is the average age of the male (or female) parents at the birth of their straight-bred replacement. Since 2001, the breed conservation programme has been carried out, i.e. a son replaces a sire and a daughter replaces a dam. Sex ratio of Lithuanian Heavy Draught horses is 1:8. The generation interval is 11.2 years and each year two young sires enter the breeding cycle. The number of sires per generation will be 22.4. It follows that an extension of the generation interval leads to the use of more sires, if the same number of young sires enter the breeding cycle each year. Thus a prolonged generation interval can increase the effective population size. If carried out correctly, this strategy confers negligible genetic loss over an extended period of time, yet we have practical problems – not all animals breed equally well in different lines and families, and some do not produce good quality progeny with their selected partners.

Conclusions

There are four stallion lines of Lithuanian Heavy Draught horses, two of them on the verge of extinction. Therefore active conservation in-situ and ex-situ actions are needed.

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REVIEW

THE MAIN DIRECTIONS OF LATVIAN VETERINARY MEDICINE AND ANIMAL PRODUCTION DEVELOPMENT

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Abstract

To ensure Latvia consumers, milk production must be increased from 810.3 thousand tons in 2005 up to 1025.0 thousand tons in 2013. It is mainly based on the increase of cows' milk yield productivity. Analogically, production of beef, pork, poultry meat and eggs should be increased. Dynamics of increasing production will ensure Latvian population with these products. The second important factor that should be considered is production quality. Researchers of the Research Institute "Sigra" have carried out wide range of investigations to determine and recommend quality criteria for the animal food products: production safety, non-pollution and healthy. For this purpose, investigations are being carried out on determination of biochemical, microbiological and other risk factors. Conclusions have enabled producers to receive recommendations for correct animal selection, welfare and health preconditions. Simultaneously, strong and weak sides of research development and possible threats on animal husbandry and veterinary medicine are determined; methodological solutions for near and distant future development are given.

Key words: animal products, quantity and quality, research, future development.

Introduction

Analysing the situation in animal production from 2001 to 2006, prognosis was made for its development on the basis of investigations and analyses that were carried out in the Research Institute of Biotechnology and Veterinary Medicine "Sigra", other institutes of collaboration and Central Statistical Bureau. Besides, Internet sources and materials from the Ministry of Agriculture and Rural Support Service were used.

For elaboration, quantitative and qualitative methods were used: grouping, synthesis, analysis and logical construction as well as statistical mathematics and widely used expert methods.

Results

Climatic conditions are suitable for dairy farming and beef production in Latvia. Forage is the main and cheapest feedstuff in cattle diets. High forage consumption is a base for obtaining profitable animal products. Milk production is considered priority branch of agriculture. Payment for the quality of milk that is

sold for processing has reached a high level. The main milk quality evaluation criteria are feed and its quality, animal welfare and dairy cow productivity indices as average milk yield of a cow, the amount of protein and fat, milk biochemical and microbiological evaluation data.

Milk production, consumption indices and development prognoses are shown in Table 1.

Table 1. Milk production and direction of development

Indices	Years					
	2001	2003	2005	2006*	2009*	2013*
Dairy cows, thsd	209	186	185	182	~186	~186
Milk yield, thsd t	848.0	785.7	810.3	815.1	~930.0	~1025.0
Milk and milk products consumption, thsd t	828.1	767.7	670.6	675	~735.0	~760.0
Average milk yield from cow per year, kg	4 763	4261	4364	4492	~5000.0	~5500.0

Source: RI "Sigra" calculations according to Central Statistical Bureau of Latvia and Rural Support Service data; *experts' evaluations and data for specification

Beef breeding is a new branch that allows many-sided development of Latvian countryside, nature and environmental requirements. Higher production gives better possibilities in EU market with higher prices. Many new breeds are being developed. Qualitative and competitive beef can be obtained from all beef cattle breeds and crosses developed in Latvia. Production obtained from crosses is cheaper than that from purebred animals. Beef production by private farms develops by extensive farming because funds for intensive farming are lacking. The main criteria for beef and pork evaluation are widely known: EUROP for beef and SEUROP for pork systems that characterize carcass weight and its ratio to fat tissue. For scientific evaluation of meat quality and for determining the best breeds or their crosses, we carried out additional analyses of muscle protein, amino acids, under skin and intramuscular fat cholesterol and polyunsaturated fatty acid content in beef. At present, the most reared Latvian pure breeds are Charolais, Hereford, Limousin and Angus. There are extensive breeds as Highlands and Galloway, too. Prognoses for beef production, consumption and development are shown in Table 2.

Comparing the year 2005 to 2001 it can be seen that beef and veal production in Latvia has increased by 7.4% in Latvia. This can be explained by the fact that realization of cows and calves has decreased while realization of bulls has increased by 12.3%. This tendency can be regarded positively as beef cattle breeding have begun developing in Latvia.

Table 2. Beef production and direction of development

Indices	Years					
	2001	2003	2005	2006*	2009*	2013*
Cattle, thsd	385	378	385.2	377.0	~390	~400
Produced beef and veal (carcass mass), thsd t	19.0	21.2	20.4	20.7	~23.0	~24.0
Beef and veal consumption, thsd t	24.5	27.3	23.5	24.0	~24.5	~25.5

Source: RI "Sigra" calculations according to Central Statistical Bureau of Latvia and Rural Support Service data; *experts' evaluations and data for specification

Due to selection work and improvement of feeding quality, the amount of lean meat in pigs' carcasses has increased and therefore pigs are slaughtered with bigger carcasses. Pork production, processing indices and development prognoses are included in Table 3.

Table 3. Pork production and direction of development.

Indices	Years					
	2001	2003	2005	2006*	2009*	2013
No. of pigs, thsd	429.0	444.0	428.0	417.0	~530.0	~590.0
Produced pork (carcass mass), thsd t	31.6	36.9	38.6	37.8	~40.0	~42.5
Pork consumption, thsd t	49.4	66.2	73.2	74.3	~75.5	~78.0

Source: RI "Sigra" calculations according to Central Statistical Bureau of Latvia and Rural Support Service data; *experts' evaluations and data for specification

At present, the situation is not favourable for producers in pig farming branch: low purchase prices, high feed (grain) prices, big amount of imported pork in market and processing enterprises. All these conditions together have determined that the number of pigs at the end of 2006 formed 98.3% of that at the corresponding period in 2005. Pork production in 2006 has decreased by 2.6% in comparison with that in 2005.

The amount of produced milk and meat, and the quality are determined by animals' genetic potential, feeding and health.

Poultry farming branch has old traditions in Latvia: different poultry species as hen, geese, ducks, turkeys etc. were kept at each private farm. Currently, poultry keeping has two production directions: big, specialized poultry farming enterprises with intensive production, and small private farms that produce for a limited range of consumers. Small private farms keep poultry according to the

requirements of both conventional and organic farming systems. The main poultry products in Latvia are poultry meat and eggs. Mainly meat breed crosses are grown for poultry obtaining meat: Hibro-G, Ross 308, Cobb etc. For obtaining eggs, layer crosses are kept: Lohmann Brown (mainly), Hisex Brown, ISA Brown etc. Poultry meat production, processing indices and prognoses are included in Table 4.

Table 4. Poultry meat production and direction of development.

Indices	Years					
	2001	2003	2005	2006*	2009*	2013*
No. of poultry, thsd	3621.0	4003.0	4092.0	4488.1	~4450.0	~4900.0
Poultry meat production, thsd t	8.9	12.4	17.2	20.6	~18.5	~21.5
Poultry meat consumption, thsd t	28.6	38.3	44.9	45.0	~46.0	~48.5

Source: RI "Sigra" calculations according to Central Statistical Bureau of Latvia and Rural Support Service data; *experts' evaluations and data for specification

In 2006, the number of poultry increased by 19.8% and poultry meat production by 9.7% in comparison with 2005.

The main goal of sheep breeding in Latvia is to develop a stable sheep-breeding and processing branch that is able to produce qualitative and competitive meat and wool for the internal and external market. It is very important to preserve genetic diversity, develop qualitative breeds and promote processing and realization of goat products in the goat farming branch. According to scientific investigations, the main values of goat milk are its medical properties, easily utilized protein in the human digestive tract as well as the ratio of amino acids, fatty acids, minerals, vitamins and ferments, which is corresponding to the requirement of the human organism.

Horse breeding has old traditions in Latvia. The most appropriate are Latvian breed sport and carriage horses, developed from local horses by utilizing their good properties as endurance, good feed utilization ability, and good-nature. This breed was supplemented with the best properties of other breeds. Other horses reared in Latvia are Hanovere, Holstein and Trakene breeds. Internal market is very narrow due to small demand for saddle-horses and racehorses as well as for workhorses.

Latvian sound environment and decreased arable land area as well as natural meadows and bushes, wood clearings with rich nectar plant areas are suitable for the development of bee-keeping branch.

Currently, non-traditional branches of agriculture are being developing in Latvia. Quail rearing is one of them. Quails are kept for obtaining eggs and meat. In Latvia there are 15 ostrich-keeping farms; breeding work as well as meat and egg production takes place in 5 farms, rural tourism is developed at 10 farms.

In rabbit breeding rapid changes have taken place and varied products are obtained. All most popular meat rabbit breeds are developed in Latvia. Rabbits also serve as aesthetic object in rural tourism.

Deer gardens are developed in Latvia as well. Deer breeding is connected with rural tourism, hunting, and selection work, and partly with high quality meat production.

Breeding of fur-bearing animals is developed in 37 farms.

In Latvia climate conditions are suitable for animal production, the local feed base is sufficient, there are old traditions, animal keeping technologies are being improved – thus animal production plays a significant role in the total value obtained in agricultural branch. At present, selection work in animal husbandry is based on selection programmes, state support to selection activities and purchasing of qualitative breeding material. Due to production modernization in many farms, significant research potential is created for further development of animal husbandry in Latvia.

For successful animal production development, weak sides must be taken into account. Latvian unstable climatic conditions endanger production of qualitative feed in sufficient amounts. Large-scale farming development is prevented by great number of small farms; also only 50% of animals are under recording. Production effectiveness and the quality of products are not sufficient. Low labour productivity and comparatively small wages in animal production promote labour power flowing away from farms for better salaries. Shortage of branch specialists is observed. State support to animal husbandry is not sufficiently connected with increasing branch production efficiency and long-time state support programme for animal husbandry development is lacking. Prices stability is not ensured. Still high milk production expresses. The amount of organic farming production is low. Support for scientific investigations in animal husbandry is still not sufficient.

The main investigation directions must consider the following: production of non-polluted, safe and healthy food of animal origin; scientific motivation; knowing of risk factors and their prevention possibilities; investigation of raw materials and production “chain”; improvement of the genetic potential of productive animals; healthy development; feed preparation, increasing of feeding value, new feed-stuffs, elaboration and application of progressive methods in animal feeding; investigation of the development possibilities of non-traditional animal production.

The main current directions of veterinary medicine activities are as follows: the quality of animal origin food; control of factors influencing safety and animal welfare; treatment of diseases; improving prevention in herds. Risk factors in agricultural production, animal origin food included, must be considered critical as unstable links which react to unfavourable environmental conditions can cause deviations in physiological processes of plants or animals and have unfavourable effect on the quality of products. Products offered to consumer must be safe and prevent the possibility of dysfunctions after using the product. Non-polluted food does not contain chemical, toxic, mycological, physical etc. components or does not cause a short time or remaining activity. It optimally takes part in metabolistic processes ensuring as well as stabilizing these processes and improves health.

According to the investigations we consider that improvement of the activities of veterinary services (state, private) should be carried out. Work on prevention of infectious (incl. zoonosis) and non-infectious diseases must be continued. Simultaneously, control over the safety of food products must be improved. Attention should be paid to the necessity of monitoring the risk factors in agriculture, elaboration of new prevention and treatment measures of non-infectious and infectious (incl. zoonosis) diseases; also to scientifically motivated methods applied in utilization of wastes after processing of animal food products. It is very important to determine, evaluate and manage with the existing relationship between the needs of consumers and the structure of the offered food products, quantity and quality.

Considerations expressed in this article have been obtained in the investigations carried out by the group of researchers who elaborated the project "Latvian animal production and veterinary medicine scientific and practical development strategy". Investigation issues, analyses and future insight can be used in the work of ministries, private farmers, several institutions, associations, advisers and specialists.

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