

CONTRIBUTION OF DIFFERENT BREEDS TO LITHUANIAN RED CATTLE USING PEDIGREE INFORMATION WITH ONLY A FRACTION OF THE POPULATION ANALYZED

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Summary. With the aim to examine the genealogical structure and statement of Lithuanian Red dairy cattle open population pedigree analysis of two large breeding herds, consisting 2748 cows, was carried out. The data used in this study were obtained from the State Enterprise Agricultural Information and Rural Business Center and included pedigree records from three to five generations. Analyses were performed in R 2.11.1 and Excel 2003. High variability of genealogical structure was found within Lithuanian Red breed. 169 different genotypes were formed from 14 breeds, which were for many years used for the Lithuanian Red cattle improvement. It should be noted that the Lithuanian Red cattle for a long time have been bred as an open population. Only 1.09% of all analyzed cows were purebred Lithuanian Red. Cows, having 1/2 and more contribution of Lithuanian Red breed should be included into the conservation program. The results indicate that the Lithuanian Red breed is at the high risk of extinction and needs to be conserved.

Keywords: red cattle, pedigree, genotypes, open population.

ĮVAIRIŲ VEISLIŲ PROPORCIJOS LIETUVOS ŽALUOSIUOSE GALVIJUOSE PAGAL STAMBIŲ BANDŲ KARVIŲ KILMĖS ANALIZĘ

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Santrauka. Darbo tikslas buvo išanalizuoti Lietuvos žalujų galvijų atviros populiacijos genealogiją ir būklę. Išanalizuoti dviejų stambių žalujų galvijų veislinių bandų 2748 melžiamų karvių kilmės duomenys, skelbiami VĮ Žemės ūkio informacijos ir kaimo verslo centro veislinių gyvulių informacinės sistemos kilmės kortelėse. Rinkti ir analizuoti 3–5 kartų duomenys. Analizė atlikta naudojantis statistiniu paketu R 2.11.1 ir skaičiuokle „Excell 2003“. Lietuvos žalujų galvijų (dviejų bandų) genealogijoje rasti 169 keturiolikos veislių deriniai (genotipai), susidarę per ilgą laiką atvirų populiacijų veisimo metodu gerinant Lietuvos žaluosius galvius. Grynaveislės Lietuvos žalujų galvijų karvės iš visų analizuotųjų sudarė tik 1,09 proc. Taigi, norint išsaugoti Lietuvos žaluosius galvius kaip originalią veislę, reikėtų karves, turinčias 1/2 ir daugiau Lietuvos žalujų veislės dalį, traukti į veislės išsaugojimo programą.

Raktažodžiai: žalieji galvijai, kilmė, genotipai, atvira populiacija.

Introduction. Genetic variability can be studied through the estimation of the genetic variance of quantitative traits, the analysis of pedigree data and the description of visible genes and markers in the population. Demographic analysis allows describing the structure and dynamics of populations considered as a group of renewed individuals. Genetic analysis is interested in the evolution of the population's gene pool. Since the history of genes is fully linked to that of individuals, demography and population genetics are complementary matters. A complementary approach is to analyze the probabilities of gene origin (Gutiérrez et al., 2003).

The Lithuanian red cattle breed was developed in Lithuania by crossing local cattle with Danish Red livestock. In some places, Anglers, Swiss, Latvian Red, Swedish Red-and-White, and even Simmentals were used for crossbreeding. However, it was Danish Red livestock that played the major role in the development of the Lithuanian Red cattle breed. The foundation of the Lithuanian Red Cattle Society in 1924, as well as the appearance of herd books boosted the development of the

red breed. In 1951, the Lithuanian Red cattle were recognized as an independent breed (Petraitis, 1966; Razmaitė et al., 2007). During 1956-1962, for rapid improvement of the Lithuanian Red cattle and for creation of the new lines, the Danish Red, Estonian Red and Latvian Brown bulls have been imported (Petraitis, 1963; Banys, 1988). Since 1956, the extensive use of AI with Danish Red bulls has started on Lithuanian Red cows. Over the last 30 years, the sires of different Red breeds have been widely used. More and more breeding components were introduced from other countries and there has been a rapid increase in the proportion of imported genes in the Lithuanian Red dairy cattle population. Since 1984, the Red-and-White Holstein and Brown Swiss also the Danish Red bulls, having some portion of Red-and-White Holstein or Brown Swiss cattle breeds, were introduced for improvement of the Lithuanian Red (Darbutas and Oberauskas, 2004). Pedigree analysis is an important tool to describe genetic variability and its evolution across generations (Gutiérrez et al., 2003).

The objective of this study was to examine the contri-

butions from different dairy cattle breeds using pedigree analysis in large Lithuanian Red dairy cattle breeding herds, and the obtained results are used for detection of the statement of the Lithuanian Red open population.

Materials and methods. Within this study the Lithuanian Red population was defined as those individuals registered with a LŽ (Lithuanian Red) breed code in the database of breeding animals. The data used in this study were obtained from State Enterprise “Center of Agricultural and Rural Business Information” and included pedigree records from three to five generations. Two large breeding herds were under analysis and two data sets with pedigree records, one for each herd, respectively. Four data sets with production and reproductive records were formed. A total of 2748 cows and about 17800 pedigree records were included into the analysis. Pedigree of 1274

cows, born from 1988 to 2007 in Herd 1 and the same records of 1474 cows, born from 1983 to 2003 in Herd 2 were analyzed. Each cow has minimum 5 and maximum 8 records in the existing pedigree data sets. Analyzing pedigree data, the factor of “unknown pedigree” (NA) was not taken as a separate breed thus animals having 100 % of NA were considered as having independent genotype. The cows of both herds were divided into groups, according to the proportion of different breeds in their genotype. The experimental groups were formed on the basis of the proportion of Lithuanian Red breed genes in different composite genotypes. Statistical analyses were performed in R 2.11.1 and Excel 2003. Table 1 lists the all breeds, which were found in pedigree of the cows in the studied dairy herds, and the abbreviations used.

Table 1. **Description of abbreviations**

No.	Breed title	Abbreviation
1.	Lithuanian Red	LŽ
2.	Lithuanian Black-and-White	LJ
3.	Angler	AN
4.	Red Holstein	ŽH
5.	Holstein	H
6.	Swedish Red-and-White	ŠŽ
7.	Danish Black-and-White	DJ
8.	Danish Red	DŽ
9.	Ayrshire	AI
10.	Brown Swiss	ŠV
11.	Holand Red	OŽ
12.	Frensh Black-and-White	PJ
13.	Jersey	D
14.	Dutch Red-and-White	VŽ
15.	Pedigree unknown	NA

Results. The 45 different genotypes, formed from 11 breeds were found in Herd 1 (Fig.1) and 169 different genotypes, formed from 13 breeds were found in Herd 2 (Figure 2). However, there were many genotypes containing small number of animals in both herds. There were found 7 and 4 genotypes containing more than 50 cows, and only 3 and 1 genotype containing more than 100 cows in Herd 1 and Herd 2, respectively. In Herd 1, 11 genotypes have 30 and more cows (Figure 1). Seven largest groups contain from 59 to 347 animals. However, there were found 8 separate breed combinations having only one animal in each. Also, there are 3 genotypes which have only 4, 5 and 11 cows in each. Distribution of cows in genotypes and size of those genotypes in Herd 2 are shown in Figure 2. The distribution of genotypes in Herd 2 is quite different in comparison with Herd 1. In Herd 2, 9 genotypes have 30 and more cows (Figure 2). However, there were found 49 separate breed combinations having only one animal in each.

Cows in Herd 1 were daughters of 65 known breeding sires, which were used over past 19 years (3.42 average sires per year). Cows in Herd 2 were daughters of 95 known sires (4.75 average sire per year during the last 20 years) and of 198 sires with unknown pedigrees.

Even if the breeding herds were under analysis, there

were still many animals with unknown pedigrees. In Herd 2, most of the animals have some part (25% to 100%) of unknown pedigree (NA) and also 67.46% of found genotypes have NA in their structure. Animals with LŽ and ŽH are in pedigrees of 46.40% and 42.81% respectively. Table 2 shows the arrangement of animals in both herds, when the certain percentage of their pedigrees is unknown.

There were only 30 purebred Lithuanian Red cows and only in one herd. Few composite groups were formed on the basis of the proportion of Lithuanian Red breed having different 25%, 50% and 75% Lithuanian Red portions. The number and percentage of animals having different proportions of Lithuanian Red genes are shown in Table 3. The highest in range by number and percentage are animals with 25% of proportion of LŽ breed (32.46%). There is thus a difference between herds. While Herd 2 has most animals (33.45%) with gene proportion of 25%, Herd 1 has most cows (46.31%) with gene proportion of 50%. Also there is seen a big difference between herds in respect to cows with 75% gene proportion, Herd 1 has 17.03% of all cows and Herd 2 has only 1.56% of all cows. Lithuanian Red composite genotypes comprise 69.86% of the total studied genotypes in both herds.

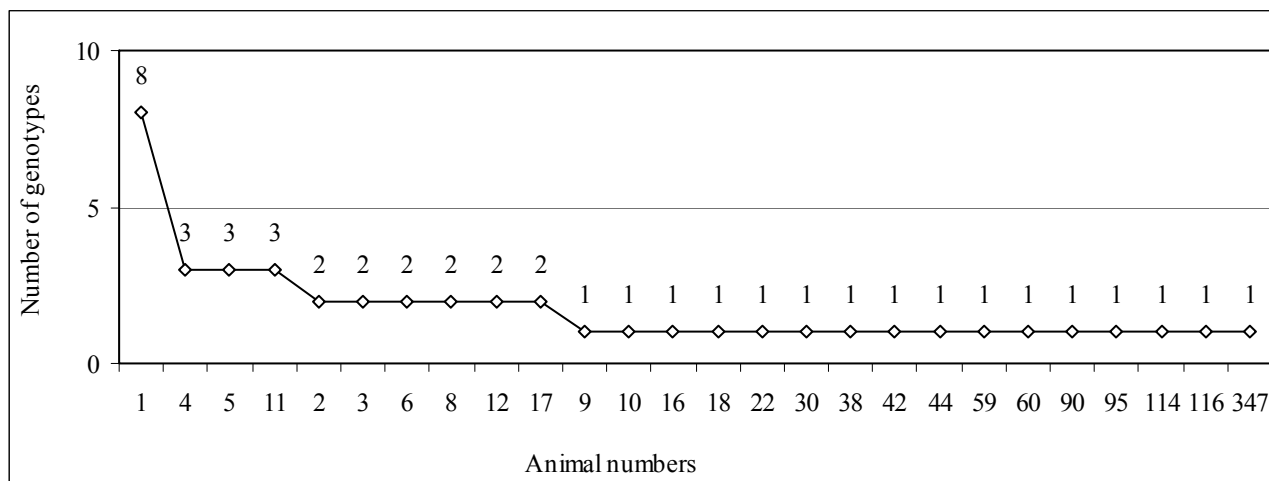


Figure 1. Number of genotypes by their size in Herd 1

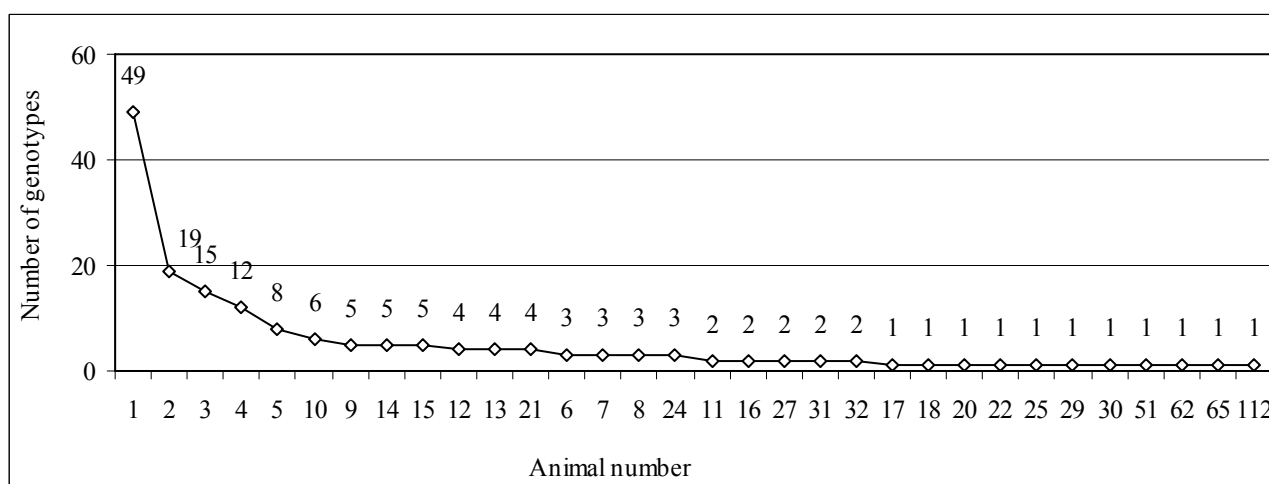


Figure 2. Number of genotypes by their size in Herd 2

Table 2. Cow pedigree completeness in the analyzed herds

Herd	Animals with full pedigree		Animals, when certain part (%) of pedigree is unknown							
			25		50		75		100	
	Number	%	Number	%	Number	%	Number	%	Number	%
Herd1	978	76.77	227	17.82	69	5.42	-	-	-	-
Herd2	392	26.59	539	36.57	428	29.04	56	3.80	112	7.60

Table 3. Cows, having different proportion of LŽ breed

The proportion of LŽ breed	Herd 1		Herd 2		Total in both herds	
	Number	%	Number	%	Number	%
25	399	31.32	493	33.45	892	32.46
50	590	46.31	168	11.40	758	27.58
75	217	17.03	23	1.56	240	8.73
100	30	2.03	-	-	30	1.09

In Herd 1, even 97.02% of animals have Lithuanian Red breeds portion in their pedigrees and 86.67% of found genotypes has Lithuanian Red (LŽ) breed (Table 4). The Danish Red (DŽ) (82.2% and 55.56%) is the second breed most common in pedigree and genotypes. The Holstein Red-and-White (ŽH) also is a quite common breed in Herd 1 (12.95% and 31.11%). Breeds and their

proportions found in the pedigree of cows in Herd 2 are shown in Table 5. In Herd 2, most animals have some portion (25% to 100%) of unknown pedigree and also 67.46% of found genotypes has NA in their structure. Animals with LŽ and ŽH are in pedigrees of 46.40% and 42.81% respectively.

Table 4. Breeds and their proportions found in the pedigree of cows in Herd 1

No.	Breeds found in pedigree	Proportion of breed in composite genotypes	Animals with different breed proportions		Genotypes	
			Number	%	Number	%
1.	LŽ	25-100	1236	97.02	39	86.67
2.	DŽ	25-75	1046	82.10	25	55.56
3.	NA	25-50	296	23.23	15	33.33
4.	AN	25-75	277	21.74	18	40.00
5.	ŽH	25-50	165	12.95	14	31.11
6.	H	25	49	3.85	3	6.67
7.	ŠŽ	25-50	28	2.20	7	15.56
8.	VŽ	25	9	0.71	2	4.44
9.	AI	25	7	0.55	3	6.67
10.	LJ	25	1	0.08	1	2.22
11.	DJ	25	1	0.08	1	2.22
12.	ŠV	25	1	0.08	1	2.22

Table 5. Breeds and their proportions found in the pedigree of cows in Herd 2

No.	Breeds found in pedigree	Proportion of breed in composite genotypes	Animals with different breed proportions		Genotypes	
			Number	%	Number	%
1.	NA	25-100	1135	77.00	114	67.46
2.	LŽ	25-75	684	46.40	85	50.30
3.	ŽH	25-75	631	42.81	66	39.05
4.	DŽ	25-75	527	35.75	70	41.42
5.	ŠŽ	25-75	346	23.47	36	21.30
6.	AN	25-75	254	17.23	53	31.36
7.	AI	25-75	139	9.43	27	15.98
8.	NA	100	112	7.60	-	-
9.	DJ	25-50	96	6.51	18	10.65
10.	H	25-50	83	5.63	24	14.20
11.	ŠV	25	40	2.71	5	2.96
12.	D	25-50	33	2.24	13	7.69
13.	OŽ	25-50	8	0.54	6	3.55
14.	VŽ	25-50	4	0.27	4	2.37
15.	PJ	25	3	0.20	3	1.78

Discussion and conclusion. Compared to the number of European dairy cattle breeds, there are only a few studies regarding the genetic structure of European local dairy cattle populations (Gutiérrez et al., 2003). Different authors analyzed population structures of different farm animal species in terms of census, generation interval, effective number of herds, pedigree completeness level, inbreeding coefficient, average relatedness, effective population size and effective number of founders, ancestors and founder herds (Roughsedge et al., 1999; Gutiérrez et al., 2003; Valera et al, 2005; Sorensen et al., 2005; Hamann and Distl, 2008; Cervantes et al, 2009; Teegen et al, 2009; Danchin-Burge et al., 2010). However, in this study due to incomplete pedigree records was impossible to trace founders, therefore on the basis of two large dairy herds only proportions of different breeds used for Lithuanian Red cattle improvement were analyzed. Previously, different studies have been done by Oberauskas and Juozaitienė (2004). These authors determined the variability in reproduction traits, milk, fat and protein

yield of the whole Lithuanian Red breed, in comparison with other Red breeds, assuming that all animals are purebred. Banys documented importations that occurred from Denmark in the last century and the early years of this century (Banys, 2004). However, greatest immigrations of different breeds were made during the last 30 years. Since 1984, the Lithuanian Red cows were started to improve by Holstein Red-and-White breed bulls, expecting that Holstein breed will improve production traits of the Lithuanian Red. Therefore in this study, the Lithuanian Red population was analyzed using pedigree information of red cows in large dairy herds. Pakėnas (1985) have noted that already in the middle of the 1990s artificial insemination was used on more than 90% of cows. An intensive use of semen of foreign bulls from many red breeds through AI has effected incorporation of these breeds into Lithuanian Red. It should be pointed out that Lithuanian Red cattle for a long time have been bred as an open population. In the present study a large number of different breed combinations (genotypes) was found.

Larger groups having different proportions of Lithuanian Red and breeds, which have had a higher impact in the formation of the Lithuanian Red breed, should be joined for further analysis. It should be noted, that the breeds, which have had the biggest impact for the Lithuanian Red, also were changing in their genetics over time. Since 1970, Denmark have sourced genetics from different red cattle breeds (US Brown Swiss and later from Red Holstein). In the 1990s, an import from Swedish Red and White started (Sorensen et al., 2005). It is difficult to distinguish between different types of the Danish Red.

Pedigree status of two large analyzed herds has shown that it is necessary to separate cows having certain part of Lithuanian Red breed and to conserve these Lithuanian Red genotypes. One of the two breeding farms in which the analysis has been performed was stated as participant in a Lithuanian Red conservation program. Thus it might be assumed that pedigree situation in other breeding herds would be very similar. However, this farm canceled the participation in conservation program; therefore the risk to the existence of the Lithuanian Red as original breed has increased. As the Lithuanian Red breed is at the high risk of extinction it needs to be conserved in another farm. Cows, having 1/2 and more contribution of the Lithuanian Red breed should be included into the conservation program (Razmaitė et al., 2006).

It can be concluded, that 14 breeds were found in the pedigrees of analyzed cows. It should be indicated that the Lithuanian Red cattle for a long time have been bred as an open population. 169 different combinations of genotypes were formed from the mentioned breeds and only 1.09 % of all analyzed cows were purebred Lithuanian Red. This small number of purebred animals indicates the importance of preservation of the breed. It repeatedly was shown, that cows having 1/2 and more contribution of Lithuanian Red breed should be included into the conservation program.

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