
Characterisation of cattle breeds in Baltic countries by genetic markers

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The genetic characterisation of breed is necessary to estimate the genetic variation within and between breeds and their uniqueness, to assess temporal changes that help breeders to develop sustainable breeding and conservation strategies.

The aim of this study was to estimate the genetic variation and the temporal changes in intra- and interbreed EAB allele variation of Baltic countries' red (Estonian Red, Lithuanian Red and Latvian Brown) cattle breeds in the situation of inextensive breeding and to describe the genetic diversity of Lithuanian, Latvian and Estonian native cattle breeds on the basis of classical genetic markers.

Key words: allele, cattle, gene frequencies, genetic similarity

INTRODUCTION

In the last decade, the tools for individual and for population characterisation have become more numerous. Discrete traits for individual characterisation range from long used phenotypic traits to individual base type in DNA sequence. Markers are widely used in the search for genes affecting diseases and traits of economical interest. The heritable units are transmitted from parent to offspring with a random choice. The use of these heritable units – genetic markers – in a population structure study make it possible to measure genetic diversity by gene frequencies and heterozygosity, and to measure the amount of introduced genes in crossbreed populations. According to Pirchner (1983) genetic markers are appropriate tools for the study of relationship between breeds and for breed development. [1].

The local breeds are well adapted to the local environmental conditions where they have been raised and selected, to available feeds and are resistant to diseases.

There are three cattle breeds in Estonia (Estonian Holstein, Estonian Red, and Estonian Native), three in Latvia (Latvian Brown, Latvian Black and

White, and Latvian Blue) and four in Lithuania (Lithuanian Black and White, Lithuanian Red, Lithuanian Light Grey, and Lithuanian White Back).

MATERIAL AND METHODS

The material consists of data on 1399 Estonian Red (ER) females and 314 Estonian Native cattle (EN) born in 1990–1998, typed at the Genetics Laboratory of Institute of Animal Science of Estonian Agricultural University; 1635 Lithuanian Red (LR) cattle tested in 1992–1998, and 104 Lithuanian Light Grey (LLG), 84 Lithuanian White Back (LWB) cattle typed at the Blood Typing Laboratory of Lithuanian Institute of Animal Science, and Latvian Brown (LaB) cattle tested in 1997–1998 and 23 Latvian Blue (LB) cattle typed in 1996–1999 at the Blood Typing Laboratory of Artificial Insemination and Stock Breeding Station Joint-stock Company in Sigulda. Only purebred EN cattle were included in this study. Upgraded cattle with relative Western-Finn cattle breed were considered as purebreds.

Hemolytic tests were made according to the commonly used methods. The erythrocyte antigen B locus (EAB) alleles were determined by family analyses.

The degree of homozygosity (C_a), the number of effective alleles (N_a) of populations, number of effective

tive alleles (N_a) of population, the genetic identity and distances between populations were computed by conventional methods described by Maijala and Lindström [2], Rendel [3], Matousek [4], Nei [5] and Zhivotovski and Mashurov [6].

The χ^2 test by Zhivotovski and Mashurov [6] was used for estimating the probability of differences between two populations concerning frequency (p) of alleles.

RESULTS AND DISCUSSION

The characteristic blood group alleles and the degrees of homozygosity of the compared cattle breeds are shown in Table 1. Data on single unknown allelic frequency of the Latvian Brown are displayed without values. The gene pool of different red populations

displayed the similarity by prevalent alleles of the marker locus. Alleles b, B_2O_1 , $B_2O_1Y_2D^1$, $B_1P^1I_1OQA^1E^1Q^1$, Q^1 and Y_2Y^1 , $OQJ^1K^1O^1$ and $B_1Y_2A^1G^1P^1Q^1G^{11}$ were found in Danish Red cows in the 60 s and in Angler's, as well as Estonian Red, Lithuanian Red and Latvian Brown breeds.

The degree of homozygosity in Baltic cattle breeds ranged from 5.4% in Lithuanian Red to 11.6% in small Latvian Blue cattle breed. By the EAB locus the number of effective alleles in Estonian Red population was 19 (allelic frequencies ranged from 0.013 to 0.128). There are 7 effective alleles attributed to the "old" Danish gene pool [7]. In the population of Lithuanian Red cattle the number of effective alleles was 14 with occurrence more than 0.01. The most frequent allele was b (frequency 0.139). The number of determined foreign genes introduced

Table 1. A comparison of Baltic cattle breeds by prevalent EAB allele frequencies

EAB allele	Estonian Red (ER) (n = 1399)	Lithuanian Red (LR) (n = 1635)	Latvian Brown (LaB) (Декче, 1981) (n = 1822)	Danish Red (Ibrahim and Larsen, 1966) (n = 1226)	Angler (Ökva <i>et al.</i> , 1989) (n = 242)	Lithuanian Light Grey (LLG) (n = 104)	Lithuanian White Back (LWB) (n = 84)	Latvian Blue (LB) (n = 23)	Estonian Native (EN) (n = 314)
I_2						0.139*	0.149*		0.097*
b	0.121*	0.139*	0.262*	0.129*	0.11*	0.139*	0.095*	0.174*	
B_2O	0.128*	0.145*	0.124*	0.148*	0.11*			0.174*	
Y_2Y^1	0.053**	0.106*	0.131*	0.187*	0.074*			0.043**	
$B_2O_1Y_2D^1$	0.058**	0.084*	0.170*	0.176*	0.008				
B_1P^1	0.045**	0.095*	0.039**	0.086*	0.074*				
$OQJ^1K^1O^1$	0.032	0.051**	0.029	0.034**	0.056**	0.062**		0.174*	
$I_1OQA^1E^1Q^1$	0.05**	0.044**	0.006	0.043**	0.041**				
Q^1	0.067**	0.014		0.042**	0.066**				
$B_1G_2KE^1F_2$									0.196*
$G_2Y_2E^1Q^1$	0.015	0.007			0.002	0.058**	0.083*		
$Y_2D^1G^1$									0.155*
$B_1Y_2A^1G^1P^1Q^1G^{11}$	0.009	0.014	0.076*	0.022	0.008			0.087*	
$B_1P^1Y_2G^1$	0.009	0.042**			0.089				
$D^1(F^1)G^1O^1$						0.053**	0.059**		
$Y_2G^1G^{11}$									0.104*
$G_3O_1T_1Y_2F_1$	0.051**	0.018							
$I_2Y_2E^1$								0.087*	
$I_1QE^1_2Q^1$						0.014	0.066**		
Y_2Q^1									0.075*
G^{11}	0.013	0.01			0.048**				
$I_2G^1Q^1$									0.07**
Sum	0.651	0.769	0.837	0.867	0.686	0.465	0.452	0.739	0.697
Ca (%)	5.4	7.4	X	12.0	5.8	6.0	6.0	11.6	10.2
N_a	19	14	X	8	17	17	17	9	10

X – unknown. * Most frequent alleles ($p \geq 0.075$); ** Medium frequent alleles (0.04–0.074).

into LR population was relatively smaller, especially that of the Holstein genes.

The most frequent EAB alleles typical of the Latvian Brown were b, B₂O₁Y₂D', Y₂Y', B₂O₁, B₂O₁Y₂D', B₁Y₂A'₂E'₃G'P'Q'G'', and B₁P' [8]. During 1997–1998, among the Latvian Brown cattle the total of 80 EAB alleles were established. The frequency of these typical Latvian Brown EAB alleles has diminished. The frequency of O₂J'₂K'O', introduced by Holsteins has increased. The frequency of EAB alleles considering the erythrocyte antigen G₂ has increased as well, showing an increase of the importance of Holsteins.

Statistically significant differences between alleles b, BG₂O₁, I₁E'G'G'' and I₁OQA'E''Q' frequencies in Estonian Red and “old” Danish Red breed data were not found. Statistically significant differences between alleles b, B₂O₁, B₁P', I₁OQA'E'Q' and O(Q)J'K'O' in Lithuanian Red and “old” Danish Red breed data were not found, either. The occurrence of alleles b and B₂O₁ has been stably high in “old” Danish, present Lithuanian and Estonian Red populations (0.129, 0.139, 0.121 and 0.148, 0.145, 0.128, respectively). The occurrence of allele I₁OQA'E'Q' was low in all of them (0.049, 0.044 and 0.05, respectively). A statistically significant difference was found in the occurrence of characteristic Danish Red allele B₂O₁Y₂D' (frequency 0.176 in Danish Red previously) and Y₂Y' (0.187) compared with the present data in our breeds. The high frequency of these alleles was mentioned by Ökva et al. [9] as well. At present, the occurrence of allele B₂O₁Y₂D' is rarer in Estonian Red than among Lithuanian Red cattle (0.058 and 0.084); Y₂Y' appeared with the frequency 0.053 and 0.106, respectively. The position of allele B₁P' among ranked effective alleles in Lithuanian Red was higher than that of Estonian Red cattle gene pool (0.095 and 0.045, respectively). The intrabreed occurrence of alleles BG₂O₁ and B₁Y₂A'G'P'Q'G'' was rare both in Estonian and in Lithuanian cattle population. Allele Q' (as D16 in Danish presumable) was more frequent in Estonian Red cattle population having been influenced by Angler breed.

The genetic identity between Estonian Red and Lithuanian Red populations was 0.899 (Table 2). By comparing these populations temporarily with the “old” Danish data, it was found that at present the Lithuanian Red population differs less than Estonian Red population. The immigration of foreign genes into the Estonian cattle population has been more extensive than that detected in Lithuanian Red cattle gene pool. The genetic distance between Danish and Estonian Red populations was 0.215, while it was only 0.093 between Lithuanian Red breed at present and “old” Danish Red cattle in the 60 s. The results obtained were similar to the data pub-

Table 2. The degree of genetic identity (I_{EAB}) and distances (D_{EAB}) between Estonian, Lithuanian and the “old” Danish Red breed gene pools by EAB markers

	I _{EAB}	D _{EAB}
Danish Red* – Estonian Red	0.807	0.215
Danish Red* – Lithuanian Red	0.911	0.093
Estonian Red – Lithuanian Red	0.899	0.107

* Data by Ibrahim and Larsen [7].

lished by Mashurov et al. [10]. They found by comparing erythrocyte antigens that the difference was smallest between Lithuanian Red and Latvian Brown and between Lithuanian Red and Angler breed (genetic distance D = 0.127–0.128); the greatest difference was found between Estonian Red (D = 0.160) and Danish Red (D = 0.148) cattle breeds. They suggested that the largest genetic distance between Lithuanian Red and Estonian Red cattle breeds referred to the originality of the genetic structure of Estonian Red breed.

It was found that the temporal intrabreed changes were bigger. Comparing genetical monitoring data on Lithuanian Red breed in 1988 [11] and 1998, the genetic distance (D_{EAB}) was 0.332, and the value of this characteristic was 0.583 when gene pool data of 1967 [12] were compared with those of 1998 (coefficient of genetic identity I_{EAB} was 0.718 and 0.558, respectively.). The Estonian Red cattle breed differed temporarily less. By comparing the current data with the data published by Jõgi [13], the genetic distance established over 30 years ago was 0.249, gene pool change over a 10-year interval displayed the genetic distance 0.086 (I_{EAB} = 0.780 and 0.917, respectively.).

Small native cattle populations have an original allelic constitution and differ in common allele frequencies. It was found that in Lithuanian native cattle some EAB alleles are characteristic only of Lithuanian Light Grey (LLG) and some of Lithuanian White Back (LWB) cattle breed. Alleles BO₁Y₂D'Y', B₂G₂Y₂, BGO₁Y₂A'₂O', GO₁T₁Y₂, G₂O₂ were determined in LLG and those BY₂A'₂G'P'Q'G'', GO₂Y₂, I₂Q', G'G'' only in LWB. A total of 48 and 42 EAB alleles were determined for LLG and LWB cattle, respectively. The alleles that had not been determined in Lithuanian Black-and-White and Lithuanian Red cattle were found in LLG or LWB these, are the following: BGT₁B', BY₂G'Y', B₂QT₂B'B'', G₂TD'G'B'', BY₂QT₂G'P'B', T₂I'Q'B'. The degree of homozygosity was 6.0%% for both Lithuanian native cattle breeds [14].

The frequent alleles of the Latvian Brown breed are b, B₂O₁, O(Q)J'K'O', BY₂A'G'P'Q'G'', Y₂Y'. According to Deksne [8], alleles B₂O₁ and Y₂Y' had

been typical of the Latvian Brown breed as well until unrelated red breed bulls were started to be used in selection.

Alleles characteristic of Estonian Native are $I_2G^1Q^1$, $B_1G_2KE^1F^1_2$, $O_1E^1G^1$, $Y_2D^1G^1$, Y_2Q^1 . Of these alleles, Y_2Q^1 and $I_2G^1Q^1$ were introduced with Western Finncattle after genetic monitoring in 1977. In Estonian Native population including graded cattle, the degree of homozygosity diminished from 9.7 in 1977 to 7.4% in 1995 [15]. In the current study the degree of homozygosity for Estonian Native purebred population was estimated to be 10.2%.

CONCLUSIONS

The analysed gene pools of red cattle populations in Baltic countries displayed similarity with Danish Red breed by EAB locus temporally. No statistically significant differences were found between allele frequencies identical in Estonian and "old" Danish data, as well as between identical alleles in Lithuanian and "old" Danish data.

The locus most heterogeneous by EAB was the Estonian Red cattle breed. Fractions of immigrated Holstein and Brown Swiss genes totalled to 0.117 and 0.091 by marker genes among effective alleles of the population. Allele Q^1 reflected the influence of Angler genes in Estonian and $B_1P_1Y_2G^1$ in Lithuanian Red cattle population. During 1997–1998, among the Latvian Brown cattle totally 80 EAB alleles were established. The most frequent alleles were the following: B_2O_1 , $B_2O_1Y_2D^1$, Y_2Y^1 and B_1P^1 . The frequency of typical Latvian Brown EAB alleles diminished and the frequency of allele $B_1P_1Y_2G^1$ and $O_2J^1K^1O^1$ increased.

The Lithuanian and Estonian Red cattle are genetically related by $I_{EAB} = 0.899$. The Estonian Red has changed less than Lithuanian Red breed. The coefficients of genetic identity were 0.917 and 0.780 ($D_{EAB} = 0.086$ and 0.248) in Estonian Red and 0.718 and 0.558 ($D_{EAB} = 0.332$ and 0.583) in Lithuanian Red over 10 and 30 years, respectively.

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BALTIJOS ŠALIŲ GALVIJŲ CHARAKTERISTIKA PAGAL GENETINIUS MARKERIUS

S a n t r a u k a

Pasaulyje yra apie 500 skirtingų galvijų veislių, tačiau jos sparčiai kinta ir artimiausioje ateityje gali likti mažiau nei 20 skirtingų galvijų veislių.

Genetiniai tyrimai būtini, kad būtų galima nustatyti veislių retumą, pokyčius, genetines variacijas tarp veislių ir veislių ribose.

Šiame darbe nagrinėtos Estijos, Latvijos, Lietuvos, Danijos žaliųjų, Anglių, Lietuvos šėmųjų, Lietuvos baltungarių, Latvijos šėmųjų, Estijos vietinių galvijų veislių genetinės variacijos ir jų pokyčiai, skaičiuotas homozigotiškumo laipsnis, efektyvių alelių skaičius, genetinis skirtumas ir panašumas tarp minėtų veislių.

Homozigotiškumo laipsnis Baltijos šalių galvijų veislėse svyruoja nuo 5,4% iki 11,6%.

Genetinis panašumas tarp Estijos ir Lietuvos žaliųjų galvijų buvo $I_{EAB} = 0,899$. Genetinis skirtumas tarp Estijos ir Danijos žaliųjų – $D_{EAB} = 0,215$, kai tuo tarpu tarp Lietuvos ir Danijos žaliųjų – tik $D_{EAB} = 0,093$.