Pedigree Analysis of Holstein Bulls in Slovakia

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Abstract

The aim of the study was to evaluate the genetic diversity in Holstein bulls population in Slovakia by the methods of pedigree analysis. The population was represented by the bulls with reserve of frozen semen doses in AI centers. Whole reference population consisted of 169 bulls born from 1997 to 2009. For calculation of diversity parameters the program Endog v.4.8 (Gutiérrez, Goyache, 2005) was used. An average maximal number of generations traced was 9.35, 3.06 complete generations and equivalent number of generations traced was 5.71. An average coefficient of inbreeding was 2.48%, individual increase in inbreeding was 0.53% and average relatedness was 2.72%. The 167 bulls from 169 were inbred (98.82%). An average number of offsprings per bull was 107.70 with maximal number 1,641 offsprings. The effective population size computed via individual increase in inbreeding was 94.50. The effective number of founders was 88, effective number of ancestors 31 and only 13 ancestors described 50% of diversity. From these results we can conclude that the diversity of Holstein bulls is reduced by more factors (inbreeding, high relatedness, bottlenecks). Obtained results point out the need to use new outbred bull lines for mating cows.

Key words: genetic diversity, Holstein, inbreeding, pedigree analysis, relatedness

1. Introduction

Holstein cattle is the most common cattle breed in Slovakia. It is widespread in most of dairy herds. At present we can see a deterioration of some very important traits like fertility, health and longevity. One reason of this situation is an inbreeding depression as a result of genetic diversity reduction.

Genetic diversity within populations is necessary for adaptive capacity and avoidance of inbreeding depression on the long term [1]. The assessment of the within-population genetic variability, population structure and gene flow is necessary during the implementation of selection programs to establish an appropriate management of the genetic stock in order to enlarge genetic basis for selection. In this respect genealogical tools are important to describe these subjects [2].

Despite being a numerically large breed, inbreeding of Holstein populations is increasing and becoming a concern in many countries [3]. For dairy cattle populations, inbreeding is expected to increase as a result of several changing breeding practices: high intensity of selection, use of reproductive techniques, more accurate genetic evaluations, and global ranking of sires [4].

The objective of our study was to evaluate the genetic diversity in Holstein bulls population in Slovakia by the methods of pedigree analysis.

2. Materials and methods

The analysis was performed in population of 169 Holstein purebred bulls born from 1997 to 2009. These bulls had a reserve of frozen semen in AI centers and they were registered in herd book of Slovak Holstein Association. The bulls originated

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from Slovakia, USA, Canada, Czech Republic, The Netherlands, Denmark, Germany and France. These animals set up a reference population (RP). There were 1,543 animals in the whole pedigree file. All pedigree information was obtained from the database of The Breeding Services of Slovak Republic, Department Žilina. The program Endog v.4.8 (Gutiérrez, Goyache, 2005) was used for computing of genetic diversity parameters.

First step of our analysis was to rate the pedigree completeness according to following parameters:

- Number of complete generations traced, defined as the number of generations separating the offspring from the furthest generation of ancestors where both ancestors are known [5].
- Maximal number of generations traced, defined as the number of generations separating the offspring from the furthest known ancestor [5].
- Equivalent number of generations traced, defined as the sum over all known ancestors in all found generations [5].
- The index of pedigree completeness (*PEC*) according to MacCluer et al. (1983). $PEC = \dfrac{2\,C_{sire}\,C_{dam}}{C_{sire} + C_{dam}}$, where C_{sire} and C_{dam} are contributions from the paternal and maternal lines.

The genetic diversity was evaluated according to these parameters:

- The individual coefficient of inbreeding (F_i), defined as the probability that two individuals received two identical alleles by descent [6].
- The individual increase in inbreeding (ΔF_i), calculated as the difference of inbreeding coefficient of individual i and its parents [3].
- The average relatedness coefficient (*AR*), defined as the probability that an allele randomly chosen from the whole population in the pedigree belongs to a given animal [6].
- The number of founders (*f*), where founder is defined as animal with unknown genetic connections to other animals in pedigree except its own progeny [7].
- The effective number of founders (f_e), defined as the number of equally contributing founders that will produce

the same genetic diversity as in the assessed population [8].
- The effective number of ancestors (f_a), defined as the minimal number of ancestors necessary to explain the genetic diversity in the reference population [8].
- The number of ancestors explaining 50 % of genetic diversity.

The diversity between sire genealogical lines was also evaluated. There were 60 lines in RP but only 15 lines were represented by more than 3 bulls. We computed the average pairwise coancestry coefficient (f_{ij}) between individuals of two subpopulations, *i* and *j*, of a given metapopulation including all N_i x N_j pairs [6]. The subpopulations were represented by genealogical lines having more than 3 bulls. Lines represented by less than 3 bulls were included into common subpopulation. We also computed founder genome equivalents (f_g) for each genealogical line. Founder genome equivalent is the theoretically expected number of founders that would be required to provide the level of genetic diversity observed in the living population if the founders were all equally represented and had lost no alleles [9].

3. Results and discussion

The pedigree completeness of the file was satisfying. The first and second generations were completely known. An average maximal number of generations traced was 9.35±1.26, number of complete generations traced was 3.06±0.52 and equivalent number of generations traced was 5.71±0.68. PEC in RP according to MacCluer et al. (1983) is shown in Figure 1.
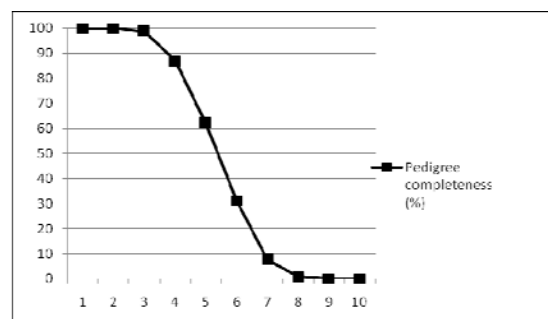

Figure 1. Pedigree completeness in RP

Obtained results of pedigree completeness are comparable with those published by Baumung and Sölkner [10] in Austrian Pinzgau and Maignel et

al. [5] in French Normande. The lower level of completeness was observed in Slovak Pinzgau population by Kadlečík et al. [11].

The paramaters of diversity are presented in Table 1.

Table 1. Parametres of genetic diversity

Parameter		Reference population	Inbred sires (n=167)
Individual inbreeding coefficient (%)	$\bar{x}$	2.48	2.51
	s.dev.	1.53	1.52
Average relatedness (%)	$\bar{x}$	2.72	2.74
	s.dev.	0.65	0.61
Individual increase in inbreeding (%)	$\bar{x}$	0.53	0.53
	s.dev.	0.33	0.32
Number of founders	n	562	-
Effective number of founders	n	88	-
Effective number of ancestors	n	31	-
Number of ancestors explaining 50 % of diversity	n	13	-

An average individual coefficient of inbreeding was 2.48% (max.8.95%), average relatedness was 2.72% (max. 4.60%) and average increase in inbreeding was 0.53% (max.1.82%). Average number of offsprings per bull was 107.7 with maximal value 1,641 offsprings. The 167 bull from 169 were inbred (98.82%). High ratio of inbred sires limits the assambling of mating plans. In inbred sires, we found out these results: F_i=2.51%, AR=2.74% and ΔF_i=0.53%. The average relatedness was higher in observed population than average inbreeding coefficient. We can predict an increase of inbreeding in future. The total number of founders was 562 in RP, effective number of founders was 88 and effective number of ancestors was 31. The 13 ancestors explained a half of genetic diversity. The effective population size computed via individual increase in inbreeding was 94.50.

Higher inbreeding coefficients were presented by Sørensen et al. [12] in Danish Holstein (3.4%), Kaerney et al. [3] in British Holstein (bulls 3.06%) and Wiggans et al. [13] in US Holstein (aproximately 6%). Maignel et al. [5] found out higher increase in inbreeding in population of French Holstein (1.09%). Effective population size was 46 in that case. Similar results were computed in French Normande and Brown Swiss. The same author computed f_e 140 and f_a 43 in French Holstein, but this parameters were computed for whole population (bulls and cows together). Very similar results were presented by Baumung and Sölkner [10] in population of Austrian Pinzgau cattle. F_i was 2.09%, ΔF_i was

0.66% and effective population size was 76. Pinzgau cattle is considered as endangered breed. There were 60 sire genealogical lines in RP. Only 15 lines were represented by more than 3 sires. The highest number of bulls was in BELLWOOD genealogical line (n=15). The lines with less then 3 bulls were included into common group named Other lines. The highest F_i had bull named MOZART (sire line Lucky Leo-included into other lines). Its inbreeding coefficient was 8.95%. There were 8 bulls with F_i value higher than 5 %. The average pairwise coancestry coefficients between genealogical lines are presented in Table 2. There are f_{ij} between 15 most important lines and the other lines (less than 3 bulls in line). The highest coancestry was in EMORY line (24.52%). The highest pair coancestry was between lines EMORY and PRELUDE (f_{ij}=5.51%). The lowest pair coancestry was computed between lines EMORY and LABELLE (f_{ij}=0.51%).

We also computed founder genome equivalents in RP. The highest f_g was in group named OTHER LINES (included 60 bulls from 45 lines with less than 3 bulls in it). Its value was 20.333. The founder genome equivalent in line LUKE (represented by 12 bulls) was 5.6472 what was the highest value from the lines represented by more than 3 bulls.

Hagger [14] presented analysis of founder genome equivalents in population of Brown cattle in Switzerland. The average f_g for Original Braunvieh was 16.1 and for Brownswiss 12.5 in whole populations.

Table 2. Average pairwise coancestry coefficients within (diagonal) and between (under diagonal) sire lines

F_{ij}	15	1	2	11	9	4	5	6	16	8	10	12	13	14	7	3
15	2.46															
1	1.68	11.72														
2	1.64	2.77	10.07													
11	2.32	2.00	2.01	16.85												
9	1.83	2.46	4.16	2.43	18.38											
4	2.13	1.72	1.79	5.51	2.47	24.52										
5	1.26	0.97	0.64	1.77	0.72	1.76	20.75									
6	1.90	2.59	2.68	2.52	2.33	2.44	1.17	15.53								
16	1.80	2.06	2.09	2.42	2.34	2.00	1.24	2.26	8.85							
8	1.77	2.14	1.60	2.79	1.74	1.77	1.12	2.62	2.37	21.67						
10	1.69	1.70	2.38	1.58	3.91	1.99	0.68	2.12	1.91	1.61	13.26					
12	1.38	1.40	0.80	1.96	0.89	1.05	1.46	1.32	1.58	1.79	0.69	18.67				
13	2.03	1.86	1.85	3.70	1.93	2.31	2.14	2.53	2.18	2.55	2.05	1.62	12.67			
14	2.12	3.45	1.97	3.07	2.25	2.20	1.32	2.24	2.47	2.24	3.67	2.18	3.08	24.12		
7	1.10	0.82	1.00	0.67	0.96	0.51	0.61	0.55	0.79	0.68	0.85	1.18	1.00	1.04	22.97	
3	1.69	2.37	3.82	1.98	3.84	1.65	0.65	2.40	2.24	1.90	2.53	1.42	1.76	3.06	1.14	17.52

Genealogical lines: 1-BESNE, 2-BELLWOOD, 3-ELTON, 4-EMORY, 5-FABER, 6-FORMATION, 7-LABELLE, 8-LUKAS, 9-MANFRED, 10-MOUNTAIN, 11-PRELUDE, 12-STOLLBERG, 13-STORM, 14-WINCHESTER, 15-OTHER LINES, 16-LUKE

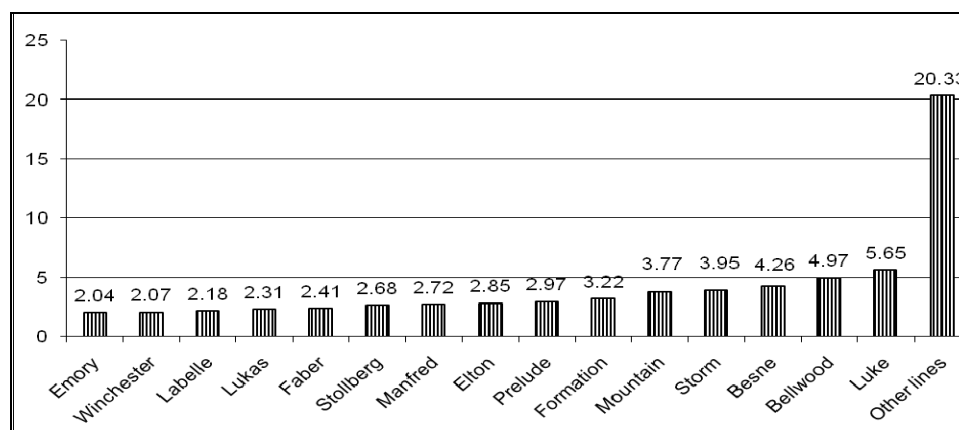The average founder genome equivalents by sire genealogical lines are presented in Figure 2.

Figure 2. Founder genome equivalents by sire genealogical lines

4. Conclusions

The results of this study indicate some important processes in population. The diversity of Holstein bulls is reduced by more factors (inbreeding, high relatedness, intensive selection). The level of inbreeding is not high but the ratio of inbred individuals is very high. The results of genealogical lines analysis can be used for managing of breeding and mating program. The coancestry between lines could be used for reduction of inbreeding. Obtained results point out the need to use new outbred bull lines for mating cows.

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