Pedigree Analysis of Slovak Holstein Cattle

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Abstract

The aim of the study was to evaluate the genetic diversity in Slovak Holstein cattle population by the methods of pedigree analysis. The 94,528 individuals (94,359 dams and 169 sires) born from 1997 to 2009 set up the analysed reference population. An average individual inbreeding intesity was 1.92 % (2.48 % in purebred cows and bulls), individual increase in inbreeding was 0.40 % (bulls 0.53 % and purebred cows 0.50 %). The average relatedness was 2.38 % (bulls 2.72 % and purebred cows 2.69 %). The effective population size computed via individual increase in inbreeding was 125.26 and 48.35 via regression on equivalent generations. The effective number of founders was 129, effective number of ancestors 48 and only 22 ancestors described 50 % of diversity. Obtained results point out the need to improve mating strategy as well as include maintaining of genetic diversity into breeding goals of breed development.

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

Table 1 Parameters based on identity by descent

Parameter		**Reference population**	**Cows**	**Bulls**	**Purebred cows**
Inbreeding coefficient (%)	$\overline{x}$	1.92	1.92	2.48	2.48
	s.d.	2.36	2.36	1.53	2.45
	x_{min}	0	0	0	0
	x_{max}	45.40	45.40	8.95	45.40
Averege relatedness (%)	$\overline{x}$	2.38	2.38	2.72	2.69
	s.d.	0.87	0.87	0.65	0.75
	x_{min}	0	0	0	0
	x_{max}	4.60	4.60	4.60	4.50
Increase in inbreeding (%)	$\overline{x}$	0.40	0.40	0.53	0.50
	s.d.	0.52	0.52	0.33	0.54
	x_{min}	0	0	0	0
	x_{max}	11.30	11.30	1.82	11.30

Table 2 Parameters based on gene origin

Parameter	**Reference population**
Number of founders	62,063
Effective number of founders	129
Effective number of ancestors	48
Number of ancestors explaining 50 % of diversity	22

Conclusion

The level of inbreeding and its increase is not high but in future it is necessary to minimalise mating of relative animals. However, **the most of the animals in RP are related**. The value of effective population size idicates **unbalanced using of very small number of sires**. From these results we can conclude that the **genetic diversity** of Holstein population in Slovakia **is reduced by more factors (inbreeding, bottlenecks).** Further reducing of diversity could lead to degradation of production and the other important traits.

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