

GENEALOGICAL ANALYSIS IN SMALL POPULATIONS: THE CASE OF FOUR SLOVAK BEEF CATTLE BREEDS

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ABSTRACT

The aim of the paper was to evaluate the genetic diversity in four beef cattle populations in Slovakia by the methods of pedigree analysis. The pedigree populations consisted of (reference populations in brackets) 481 (116) Blonde d'Aquitaine (BA) animals, 3,955 (1,772) Charolais (CH), 2,063 (786) Limousine (LI) and 916 (429) Simmental (SM). The highest inbreeding coefficient was in SM (3.87 %) and the lowest one in BA (0.33 %). Effective population size was computed via increase in inbreeding: 467.60 BA, 152.92 CH, 428.73 LI and 47.62 SM. The effective number of founders was 83, 233, 229 and 30 in BA, CH, LI and SM, respectively and the effective number of ancestors was 20, 72, 55, 13 in BA, CH, LI, SM, respectively. Contributions of animals to reference population were calculated. Unbalanced distribution of the most important ancestors within assessed populations was observed. The most significant genetic diversity loss was estimated in Simmental population.

Key words: beef cattle; diversity; genetic diversity; inbreeding

INTRODUCTION

Beef cattle breeding has not a long tradition in Slovakia. The very beginning of beef cattle breeding started in 70's of the last century, when some Hereford animals were imported to former Czechoslovakia. These herds were not successful and gradually disappeared. After 1990 few beef cattle breeds were imported to Slovakia (Charolais, Blonde d'Aquitaine, Limousine, Aberdeen Angus, Simmental, Piemontese, Highland, Galloway). The main goal of these imports was to create purebred populations and use these animals mainly in the program of suckling cows. In 1994 The Beef Cattle Breeders Association in Slovakia was established. This organization takes care about beef cattle development and it is responsible for breeding work and keeping of Herd Book as well. Slovak purebred beef cattle populations are small and their further development will depend on breeding programmes of each breed. The breeding strategies currently applied in cattle breeding are effective in genetic gain generating. Efforts to improve genetic

level of breed lead to use a few superior animals. This advancement usually increases a probability of generation of inbred animals (Verrier *et al.*, 1993). Therefore, it is very important to make breeding work purposefully because the long term survival of a population depends on the maintenance of sufficient genetic variation for individual fitness and population adaptability (Baumung and Sölkner, 2002). Maintaining of genetic diversity is a part of the goals in genetic management and evaluation of genetic diversity and knowing its level is the basis for effective genetic management of the breed. Genetic variability and its evaluation over time may be estimated from genealogical information. This methodology was used in more papers (Bozzi *et al.*, 2006, Cervantes *et al.*, 2009, Oravcová and Margetín, 2011, Kadlečík *et al.*, 2012). The trend in inbreeding is the most frequently used to quantify the rate of genetic drift (Gutiérrez *et al.*, 2003).

The goal of this paper was to evaluate genetic diversity of four beef cattle breeds on the basis of their pedigree information describing parameters of the probability of identity by descent and gene origin.

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MATERIAL AND METHODS

The analyzed pedigree populations consisted of (reference populations in brackets) 481 (116) Blonde d'Aquitaine (BA) animals; 3,955 (1,772) Charolais (CH); 2,063 (786) Limousine (LI) and 916 (429) Simmental (SM). Reference population (RP) set up heifers, cows and sires living in the year 2011. All animals were purebred and registered in Herd Books of The Beef Cattle Breeders Association in Slovakia. The analysis covered living sires (in insemination - AI and natural mating), as well as frozen genetic material deposited in reproduction centres. A total of 7,415 animals were registered. The number of animals according to each breed is presented in Table 1. The pedigree information was obtained from the database of The Beef Cattle Breeders Association in Slovakia. The software Endog v.4.8 (Gutiérrez and Goyache, 2005) was used for calculation of diversity parameters.

At first, the pedigree completeness according to MacCluer *et al.*, (1983) was evaluated. We used the index of pedigree completeness (PEC). $PEC = 2 C_{sire} C_{dam} / C_{sire} + C_{dam}$, where C_{sire} and C_{dam} are contributions from the paternal and maternal lines. $C = \frac{1}{d} \sum_{i=1}^d g_i$ where g_i is the proportion of known ancestors in generation i ; and d is the number of generations that are taken into account (Gutiérrez *et al.*, 2009).

The state of diversity was evaluated according to following parameters based on probability of identity by descent. The individual coefficient of inbreeding (F) reflects the probability that two individuals received two identical alleles by descent (Gutiérrez *et al.*, 2009). F value was computed according to algorithm of Meuwissen and Luo (1992). The average relatedness (AR) reflects the probability that an allele randomly chosen from the whole population in pedigree belongs to a given animal (Gutiérrez *et al.*, 2009). The individual increase in inbreeding (ΔF_i) was calculated by means of the classical formula $\Delta F_i = 1 - \sqrt[t-1]{1-F_i}$ where F_i is individual

coefficient of inbreeding and t is the equivalent complete generation (Gutiérrez *et al.*, 2009). We also calculated effective population size (Ne) defined as the number of breeding animals that would lead to actual increase in inbreeding if they contributed equally to the next generation (Gutiérrez *et al.*, 2009).

We assessed the parameters based on probability of gene origin, as well. Number of founders (f) where founder is animal with unknown genetic connections to other animals in pedigree except its own progeny (Lacy, 1989), was calculated. The effective number of founders (f_e) defined as the number of equally contributing founders that will produce the same genetic diversity as assessed in the population (Boichard *et al.*, 1997), was calculated as $f_e = 1 / \sum_{k=1}^f q_k^2$ where q_k is the probability of gene origin of the k ancestor. The effective number of ancestors (f_a) is the minimal number of ancestors necessary to explain the genetic diversity in the reference population (Boichard *et al.*, 1997), was calculated by formula $f_e = 1 / \sum_{j=1}^a q_j^2$ where q_j is the marginal contribution of an ancestor j .

RESULTS AND DISCUSSION

The number of sires operating in artificial insemination and natural mating is presented in Figure 1. The higher percentage of bulls in natural mating goes with the pasture system of beef cattle breeding.

The index of pedigree completeness (PEC) by the generations of ancestors for BA, CH, LI and SM is presented in Figures 2, 3, 4, 5, respectively. We can see that only BA and SM had 100 % completeness in the first generation of reference population. CH was very close to this level. Completeness had decreasing trend with increasing the number of generations. The lowest PEC through all generations was noted in LI. McParland *et al.*, (2007) presented higher values of pedigree completeness in Irish beef cattle breeds (Charolais, Limousine,

Table 1: Description of analyzed beef breeds

Population		BA		CH		LI		SM		Total	
RP	n	116		1772		786		429		3103	
	Sex	M	F	M	F	M	F	M	F	M	F
	n	71	45	707	1065	304	482	217	212	1273	2011
PP	n	481		3955		2063		916		7415	
	Sex	M	F	M	F	M	F	M	F	M	F
	n	229	252	1532	2423	808	1255	415	501	2984	4431

RP – reference population, PP – pedigree population, M – males, F – female

Simmental, Hereford and Angus). Very similar results to ours were presented by Bozzi *et al.*, (2003) on original Italian beef breeds (Chianina, Marchigiana, Romagnola and Maremmana).

The parameters of diversity based on probability of identity by descent are presented in Table 2. The highest inbreeding coefficient was in SM (3.87 %) and the lowest one in BA (0.33 %). The highest value of *F* was observed in SM (29.37 %). The highest average increase in inbreeding was in SM (1.05 %) as well. FAO (2007) states that average increase in inbreeding of one-half to one percent per generation is acceptable for maintaining of population. All observed populations are included in this range except SM. When we compare *AR* and *F* value, we can conclude that in the next periods an important growth of inbreeding may be expected. We calculated the effective population size via individual increase in inbreeding as well. The effective population size is an important parameter indicating the risk of population loss. The worst situation was observed in SM, where N_e was 47.62 individuals. The best situation was in BA

($N_e = 467.60$) and LI ($N_e = 428.73$). Gutiérrez *et al.*, (2003) presented diversity parameters of eight Spanish beef breeds with a local importance. They found out that all eight breeds are endangered ($N_e = 21 - 123$ individuals, increase in inbreeding by generation more than one percent in half of breeds).

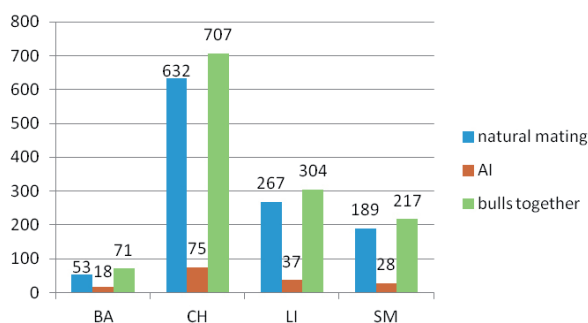


Fig. 1: Number of bulls operating in AI and natural mating (ZCHMP, 2011)

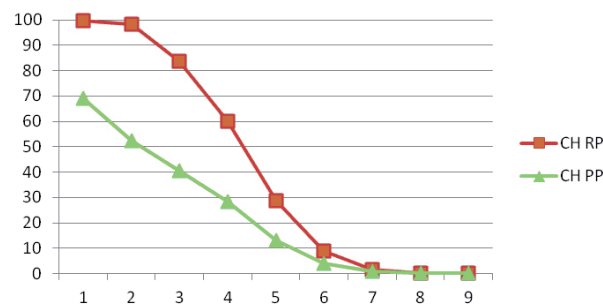


Fig. 3: Pedigree completeness by the generations of ancestors in CH

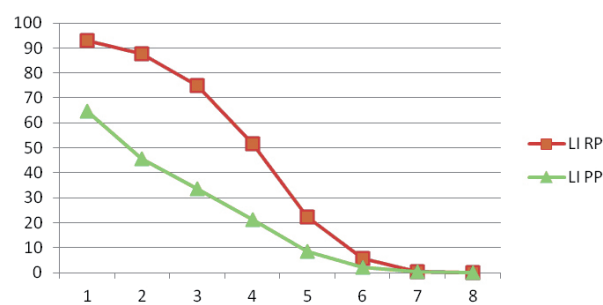


Fig. 4: Pedigree completeness by the generations of ancestors in LI

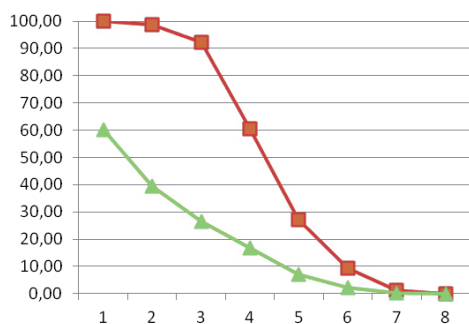


Fig. 2: Pedigree completeness by the generations of ancestors in BA

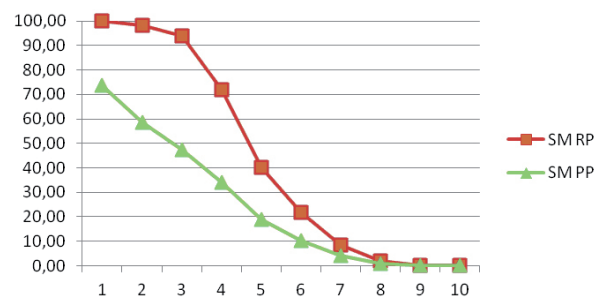


Fig. 5: Pedigree completeness by the generations of ancestors in SM

Table 2: Diversity parameters based on probability of identity by descent

Parameter	BA		CH		LI		SM		
	RP n=116	PP n=481	RP n=1.772	PP n=3.955	RP n=786	PP n=2.063	RP n=429	PP n=916	
F_i in %	\bar{x}	0.33	0.14	1.05	0.47	0.35	0.14	3.87	1.90
	s	1.05	0.97	3.10	2.14	1.54	1.01	5.19	4.17
	x_{\min}	0	0	0	0	0	0	0	0
	x_{\max}	7.03	12.50	25.10	25.10	25.00	25.00	29.37	29.37
AR in %	\bar{x}	2.58	1.25	1.00	0.55	1.14	0.62	6.65	3.53
	s	0.90	0.98	0.51	0.57	0.60	0.61	2.84	3.62
	x_{\min}	0.57	0.36	0.05	0.04	0.10	0.07	0.34	0.11
	x_{\max}	4.15	4.15	2.39	2.39	3.22	3.22	11.17	11.17
ΔF_i in %	\bar{x}	0.11	0.07	0.33	0.15	0.11	0.05	1.05	0.57
	s	0.33	0.71	1.17	0.80	0.51	0.37	1.46	1.56
	x_{\min}	0	0	0	0	0	0	0	0
	x_{\max}	2.00	12.50	16.31	16.31	8.36	8.52	13.65	25.00
N_e via ΔF_i	\bar{x}	467.60	-	152.92	-	428.73	-	47.62	-
	s	66.71	-	42.10	-	93.27	-	9.58	-

Table 3: Diversity parameters based on probability of identity by descent – inbred animals

Parameter	BA		CH		LI		SM		
	RP n=26	PP n=29	RP n=431	PP n=435	RP n=109	PP n=117	RP n=271	PP n=277	
F_i in %	\bar{x}	1.49	2.31	4.33	4.31	2.53	2.55	6.13	6.28
	s	1.81	3.32	5.04	5.02	3.41	3.45	5.37	5.49
	x_{\min}	0.05	0.05	0.04	0.04	0.15	0.10	0.39	0.39
	x_{\max}	7.03	12.50	25.10	25.10	25.00	25.00	29.37	29.37
AR in %	\bar{x}	3.21	3.02	1.33	1.33	1.70	1.68	8.38	8.26
	s	0.46	0.72	0.36	0.36	0.36	0.37	1.07	1.41
	x_{\min}	1.88	1.00	0.11	0.11	0.29	0.29	1.71	0.43
	x_{\max}	3.83	3.83	2.13	2.13	2.65	2.65	10.10	10.10
ΔF_i in %	\bar{x}	0.47	1.20	1.37	1.37	0.80	0.85	1.65	1.88
	s	0.56	2.69	2.06	2.05	1.17	1.34	1.53	2.37
	x_{\min}	0.01	0.01	0.01	0.01	0.04	0.02	0.12	0.12
	x_{\max}	2.00	12.50	16.31	16.31	8.36	8.52	13.65	25.00

The ratio of inbred animals in RP was 22.4 % in BA, 24.32 % in CH, 13.87 % in LI and 63.17 % in SM. The results of parameters based on probability of identity by descent of inbred animals are presented in Table 3.

The parameters based on probability of gene origin are presented in Table 4. We can see that f_e value was 83, 233, 229 and 30 in BA, CH, LI and SM, respectively. The f_a value was 20, 72, 55, 13 in BA, CH, LI, SM,

respectively. A disbalance between f_a and f_e indicates bottleneck occurrence in pedigrees of all breeds. The same situation was observed in eight Spanish beef cattle breeds by Gutiérrez *et al.*, (2003). A half of diversity was explained by lower number of ancestors in all breeds. McParland *et al.* (2006) presented very similar results in Irish beef cattle population. The f_a was 58, 82,

35 in CH, LI and SM, respectively. Bozzi *et al.*, (2003) presented higher values of parameters based on gene origin in Italian beef breeds but these populations were incomparably greater than ours.

The contributions of the five most important ancestors are presented in Table 5. We can see unbalanced distribution of the most important ancestors within

Table 4: Diversity parameters based on probability of gene origin

Parameter	BA		CH		LI		SM	
	RP	PP	RP	PP	RP	PP	RP	PP
Number of founders (f)	191	191	1225	1219	786	763	429	674
Effective number of founders (f_e)	83	136	233	381	229	324	30	58
Effective number of ancestors (f_a)	20	68	72	139	55	123	13	28
Number of ancestors contributing to population	51	135	562	877	373	555	87	171
Number of ancestors explaining 50 % of diversity	8	30	27	66	24	61	4	12

Table 5: Contributions of the most important ancestors to reference population

	Breed	Ancestors	sex	Marginal contributions	
				individual	cumulative
1	BA	BDV 051	♂	13.04	13.04
2		BDV 509	♂	9.48	22.52
3		BDV 081	♂	7.01	29.53
4		3291132274	♀	6.08	35.61
5		BDV 511	♂	6.04	41.65
1	CH	CHV 529	♂	4.83	4.83
2		CHV 161	♂	4.03	8.86
3		IL 000*	♂	4.02	12.88
4		CHV 241	♂	3.54	16.42
5		CHV 171	♂	2.87	19.29
1	LI	LIV 508	♂	7.48	7.48
2		ZLI 234	♂	4.91	12.39
3		ZLI 207	♂	4.06	16.45
4		ZLI 229	♂	3.66	20.11
5		LIV 525	♂	3.59	23.70
1	SM	SBV 041	♂	17.98	17.98
2		SIM 001	♂	12.84	30.82
3		SIM 002	♂	11.23	42.05
4		SBV 589	♂	8.00	50.05
5		921377	♀	5.64	55.69

* - the bull has not got Slovak state register (name:FONTENA, HB number: 8690100259)

assessed populations. The highest individual contribution was calculated in SM, where the sire SBV-041 (SWITZ HTF PANAMA RED) from USA had 17.98 %. The sire BDV-051 (DROP) from France was the most important ancestor in BA population with individual contribution of 13.04 %. The bull CHV-529 (CIKA-ET) born in Czech Republic was the most influential CH ancestor with contribution of 4.83 % what was the lowest top-

value among all breeds. The sire LIV-508 imported from France to Slovakia was the most important LI ancestor with individual contribution of 7.48 %. There were 2 cows in Top 5 ancestors in BA and SM. The trends of individual and cumulative contributions of 50 most important ancestors in BA, CH, LI and SM are presented in Figures 6, 7, 8 and 9, respectively.

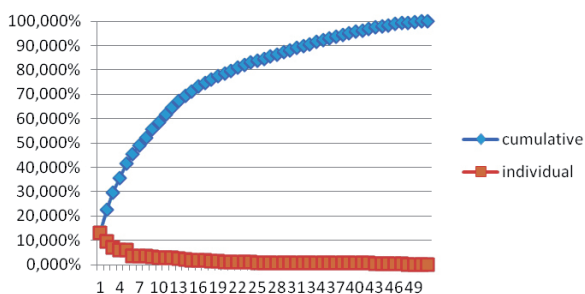


Fig. 6: Cumulative and individual contributions of the most important ancestors in BA

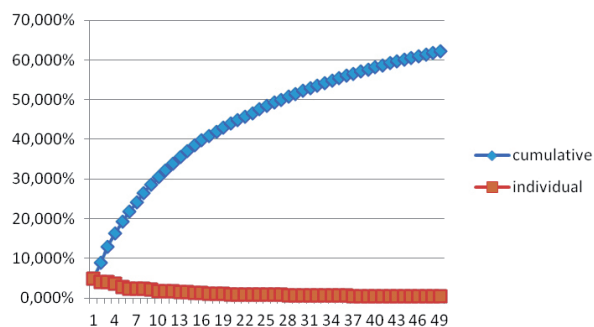


Fig. 7: Cumulative and individual contributions of the most important ancestors in CH

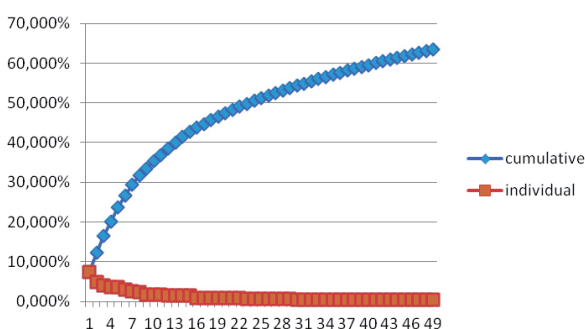


Fig. 8: Cumulative and individual contributions of the most important ancestors in LI

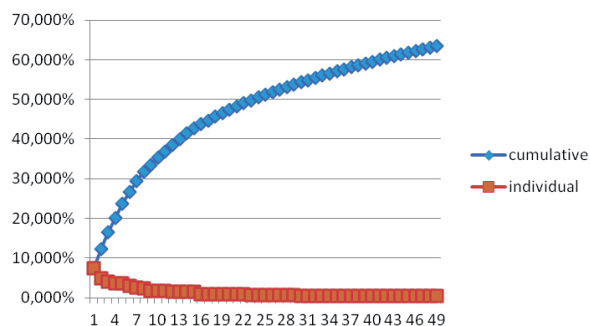


Fig. 9: Cumulative and individual contributions of the most important ancestors in SM

CONCLUSION

All populations assessed in this study are small and newly creating. They were based on imported animals (France, USA, Czech Republic, Hungary). The most significant genetic diversity loss can be observed in SM population. One of the most important factors reducing diversity in these populations is bottleneck effect and drift of genes. The reason for this state can be a disappearance of some important breeders and their animals which were the pioneers of beef cattle breeding in

Slovakia and unbalanced using of ancestors in reference populations. The level of inbreeding is not high except SM. The reduction of inbreeding should be based on optimization of mating programs and import of unrelated animals from abroad.

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