Short Communication

Estimation of effective population size by different methods for Czech endangered horse breeds based on genealogical information

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There are four Czech horse breeds: Silesian Noriker, Czech-Moravian Belgian, Old Kladruber (grey and black colour variety) and Hutsul included among the endangered breeds (Genetic Resources). These populations are currently closed to outside breeding. Effective population size is an important parameter used to assess genetic diversity for conservation program in these endangered breeds. Pedigree records for reference population, which included animals born in a 14-year period (from 1996 to 2010) were used for calculation. Realized effective population size was estimated from the individual rate in coancestry, from the individual increase in inbreeding and as effective population size based on population sex ratio. The values of effective population sizes were found low for all four analysed breeds. The results shown, that calculation based on population sex ratio gives overestimated values of effective population size. The approaches using either individual increase in inbreeding or individual increase in coancestry are more accurate and useful.

Keywords: effective population size, inbreeding, coancestry, endangered breeds

1   Introduction

Text, Small population bears the risk of reduction in genetic diversity. The objective of conservation breeding is to maintain genetic diversity in the population of farm animals. A reduction in genetic diversity is connected with the parameter of effective population size which is used to design the strategy for the conservation of endangered animal species. The Food and Agriculture Organization (FAO) classifies breeds into different categories according to the type of endangerment, e.g. whether population size increases, decreases or remains stable. Preservation of endangered species is one of the most important goals for the present biological science. Conservation programs are needed to preserve breeds in which a significant part of given species' genetic diversity still presents negative effects of inbreeding. Efficient implementation of management strategies for genetic conservation is required quantifying the contributions made to diversity. The effective population size is an important parameter in population genetics and indicates the genetic viability of populations. The determination of a strict critical level for effective population size is not straightforward and effective population size should be interpreted considering factors such as the method applied, animal species and the structure of population studied (Leroy et al., 2013). Increase in coancestry is slightly affected by population structure (Gutierrez et al., 2008) and the effective population size can be estimated from increase in coancestry instead of increase in inbreeding when dealing with structured population (Caballero, 1994).

The objective of present paper was to estimate effective population size with different approaches and select the most suitable one for breeding strategies planning of these endangered breeds.

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2   Material and methods

Pedigree files of four endangered horse populations: Silesian Noriker (SN), Czech-Moravia Belgian (CMB), Old Kladruber – grey and black variety (OKG and OKB) and Hutsul (H) were analysed. Pedigree analyses were performed using one reference population containing animals potentially contributing to the next generations. The reference population was defined as the entire active population of individuals (stallions and mares) born in the years of 1996-2010 and all effective population sizes were calculated only for these populations. A total of 498 animals of SN, 956 animals of CMB, 297 animals of OKG, 315 animals of OKB and 501 animals of H were included in the reference populations.

Three different approaches for effective population size calculation were compared.

The effective population size based on population sex ratio (Ne, Falconer and Mackay, 1996)

$$N_e = \frac{4N_s N_d}{N_s + N_d}$$

Where

Ns and Nd are number of sire and number of dam in the reference population.

The effective populations size calculated from individual increase in inbreeding (NeF) according to Gutiérez et al. (2009):

$$N_{eF} = \frac{1}{2\overline{\Delta F}}, \text{ where } \Delta F_i = 1 - \sqrt[t_i - 1]{1 - F_i},$$

where Fi is the inbreeding coefficient of individual i, ti is their equivalent complete generations (Maignel et al., 1996) and ΔF is increase in inbreeding.

The effective population size calculated from individual increase in coancestry (NeC) according to Cervantes et al. (2010):

$$N_{eC} = \frac{1}{2\overline{\Delta C_{ij}}}, \text{ where } \Delta C_{ij} = 1 - \sqrt[\frac{t_i + t_j}{2}]{1 - C_{ij}},$$

where ti and tj are equivalent complete generations (Maignel et al., 1996) of animals i and j, ΔCjk is increase in coancestry between any pair of individuals j and k and Cjk is the inbreeding of a descendent from both animals j and k.

3   Results and discussion

The average inbreeding coefficients are shown in Tab. 1. Only small differences were found between SN, CMB and H breeds, the average value of Fi for these breeds ranged from 4 % to 5 %. The average inbreeding coefficients were high in both colour variants of Old Kladruber horse. In other Old Spanish breeds, similar but somewhat lower inbreeding coefficients have been reported – 11 % (Zechner et al., 2002), 8 % (Valera et al., 2005) and 11 % (Vicente et al., 2012). The Fi coefficient of 7 % was also estimated in Spanish Arabian horses (Cervantes et al., 2008). Average inbreeding coefficient published for Polish Hutsul was similar with result of this study (0.04, Mackowski et al., 2015). High inbreeding and relatedness coefficients in the reference populations indicate a loss of genetic variability in all analysed breeds. The estimated effective population sizes for populations of endangered Czech horse breeds, calculated by different approaches are shown in Table 1. The effective population sizes based on individual increase in coancestry were lower than those obtained from calculation based on individual increase in inbreeding, excepting the Hutsul breed.

The effective population size estimated as NeF and NeC showed values in the range from 40 to 101. The estimated values of NeF were comparable for breed SN, CMB and lower for breed OKG, OKB and H than NeF estimated in the other horse breeds, including Lipizzaner horses (NeF = 117, Pjontek et al., 2012). All analysed breeds show values NeF higher than in the Lusitano breed (NeF = 41, Vicente et al., 2012). The effective population size estimated by Ne was strongly deviated from NeF and NeC, being in the range from 76 to 228. This overestimation is caused by expectation that sire and dam are unrelated. However this expectation does not apply, due to high coancestry between sire and dam in analysed breeds. A difference between NeC and NeF provides information about non-random mating of individuals in the analysed populations and a decrease in level of genetic diversity in future generations can be expected in relation to the parental combination. The NeF and NeC are asymptotically equivalent in an idealized population, the disagreement between these parameters

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mainly falls on their ability to assess the effect of preferential mating. In other words, the comparison between NeC and NeF would characterize the influence of preferential mating in the population (Cervantes et al., 2011). It is well known that many factors lead real populations to increases in inbreeding higher than those expected in the idealized population as a consequence of preferential mating (Falconer & Mackay 1996). However, increases in coancestry basically reflect the drift caused by the finite size of the population (Caballero 1994). Thus, discrepancies between increases in inbreeding and in coancestry can be interpreted as cryptic population subdivision (Cervantes et al., 2011). Minimum coancestry mating systems lead to lower increases in inbreeding than in coancestry that would be expected under random mating.

Table 1   Effective population size estimates (N_{eC}, N_{eF}, N_e), average coefficient of inbreeding (F_i) and equivalent complete generations (t)

	average F_i	N_{eC}	N_{eF}	N_e	t
SN	0.05	79,57	95.21	160.45	8.91
CMB	0.04	87,41	101.37	228.43	9.81
OKG	0.11	53,75	62.23	101.26	16.10
OKB	0.14	40,00	45.22	102.04	15.01
H	0.05	59,61	54.15	76.81	6.83

where SN – Silesian Noriker, CMB – Czech-Moravian Belgian, OKG – Old Kladruber (grey variety), OKB – Old Kladruber (black variety), H – Hutsul, Ne – effective population size based on sex ratio, NeF – effective population size from individual increase in inbreeding, NeC –effective population size from individual increase in coancestry

4   Conclusions

The results shown that calculation based only on rate of sex in mating population is inadequate and leads to overestimation of effective population size. However this method is commonly and frequently used by Czech breeders for conservation breeding strategy design as well as for the endangerment status determination in animal populations. The methods using either individual increase in inbreeding or individual increase in coancestry are more accurate and their practical implementation could be recommended.

Acknowledgments

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