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Short Communication

The most important sires in Pinzgau population

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The aim of this study was to calculate the inbreeding coefficients of the most used sires in population of Slovak Pinzgau and summarize milk production of theirs daughters as main criterion in present in selection of sires besides pedigree based level of inbreeding of future progeny. The runs of homozygosity (ROH) greater than 4 Mb cover on average 1.9% of genome, ROH >8 Mb cover 1.3% and ROH >16 Mb cover 0.4. Obtained results were compared to genealogical pedigree analysis; the observed inbreeding was higher than that expected based on pedigree data (0.16%), despite the fact that ROH >16 Mb representing recent inbreeding approximately three generations ago. The average milk performance of evaluated Slovak Pinzgau cows has been 5,259 kg of milk, 3.6% of protein and 3.85% of fat. These results are important for the management of the Pinzgau population in Slovakia due to more precise values of inbreeding obtained as well as knowledge about the ancient inbreeding which was not possible to estimate from the pedigree data.

Keywords: inbreeding, milk performance, runs of homozygosity, Slovak Pinzgau cattle

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1 Introduction

As a consequence of mating closely related individuals, inbreeding manifests itself phenotypically as a loss in general level of performance and fitness of the progeny (Charlesworth and Willis 2009; Bjelland et al., 2013). It leads to the loss of genetic variation within population and accumulation of recessive mutations, which may be associated with several lethal effects (Bjelland et al., 2013). Controlling the level of inbreeding in livestock populations is especially important, since only a subset of animals from the whole population is used for breeding. This enforces composition of well-designed mating plans which enable maintaining the level of relatedness possibly low.

When calculations are performed using incomplete pedigrees with low number of generations, inbreeding coefficients may be underestimated because some of the genealogical relationships between ancestors may not be included. Therefore, when calculating inbreeding coefficients, other sources of information would be beneficial, especially those derived from estimation of the genome autozygosity on the basis of molecular markers (Gurgul et al., 2016). By using high-density SNP markers, the level of inbreeding can be calculated on the basis of the analysis of runs of homozygosity (ROH) which are uninterrupted homozygous segments of the individual genome, which are polymorphic within population (Marras et al., 2014). By the evaluation of the genome portion in ROH segments, it is possible to calculate inbreeding estimates which have a large chance to include information about ancient relatedness (Ferenčaković et al., 2011). This information may be used to supplement pedigree-based estimates, or may be useful when no sufficiently reliable pedigree information is available.

Slovak Pinzgau is dual purpose Alpine cattle breed with good milk and beef performance. Breed is suitable for mountain regions with good longevity, fertility and adaptability on poor production conditions. In former times, Pinzgau cattle were among the most popular breeds in the Austro-Hungarian Empire. Unfortunately, it has lost its economic importance during the Second World War. Today, the population size is declining. Moreover, the breed is additionally threatened by continuous crossings and/or replacements with Red Holstein-Friesian cattle (Pavlík et al., 2014).

The aim of this study was to calculate the inbreeding coefficients of the most used sires in population of Slovak Pinzgau and summarized milk production of theirs daughters.

2 Material and methods

A total of 10 Pinzgau bulls, for which the information about their daughters' performance records was known (_n_ = 76), were genotyped with the use of BovineSNP50

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Table 1 Inbreeding coefficient based on runs of homozygosity (FROH) of Slovak Pinzgau bulls and milk performance of theirs daughters

Fathers	Birth year	F_{ROH4} (F_{ROH4_MAF})	F_{ROH8} (F_{ROH8_MAF})	F_{ROH16} (F_{ROH16_MAF})	n	Milk (kg)	Fat (%)	Fat (kg)	Protein (%)	Protein (kg)
NERO	2004	0.051 (0.045)	0.036 (0.031)	0.013 (0.013)	15	5444	3.79	206	3.68	200
LUTGO	1999	0.046 (0.043)	0.038 (0.036)	0.025 (0.018)	10	4702	3.81	179	3.76	177
LOLTEL	2000	0.024 (0.025)	0.017 (0.018)	0	5	5777	3.87	223	3.46	199
NOBTELO	2002	0.020 (0.020)	0.012 (0.012)	0.007 (0.007)	5	5406	3.87	208	3.51	190
GOELL	1997	0.021 (0.019)	0.013 (0.013)	0	3	5155	3.91	202	3.60	185
LUTLUX	2002	0.014 (0.015)	0.009 (0.010)	0	10	5414	4.01	217	3.68	199
LEMO	2000	0.010 (0.009)	0.004 (0.004)	0	3	5219	3.72	191	3.58	184
SAMFO-ET	1999	0.007 (0.007)	0	0	6	5042	4.06	204	3.54	178
GOMOL	1998	0.002 (0.002)	0	0	5	5493	3.70	203	3.68	201
CARLO	2005	0	0	0	14	4943	3.78	186	3.55	175

n – number of daughters per bull

BeadChip (Illumina, San Diego, CA, USA). SNPs were filtered to remove those with missing genomic positions or those located on sex chromosomes. Two types of quality control were performed aimed to calculate ROH using PLINK (Purcell et al., 2007) and SAS (SAS Institute Inc: SAS/STAT Software, 2011). 1) MAF quality control – by applying parameters --geno 0.1, --mind 0.1 and --maf 0.05, 42,371 SNPs left for the analysis with mean MAF of 0.265 ±0.140. 2) GC and GT Score quality control - dataset was filtered to remove SNPs with GeneCall score ≤0.7, GeneTrain score ≤0.4, SNPs with missing genotypes ratio >0.1 and animals with >10% of missing SNPs. Depending on the minimum length of ROH in which no heterozygote SNP was allowed (except for length >16 Mb, where 1 heterozygous call was allowed), we calculated ROH4, 8, 16 according to the size of ROH being 4, 8 and 16 Mb long. We also calculated molecular inbreeding coefficients based on ROH4, 8, 16 (F_{ROH4}, F_{ROH8} and F_{ROH16}). Pedigree data were analysed and inbreeding coefficients were calculated using ENDOG software (Gutiérrez et al., 2008).

3 Results and discussion

The inbreeding coefficients of 10 bulls and milk production of 76 cows were observed (Table 1). The ROH greater than 4 Mb cover on average 1.9% of genome ($F_{ROH4} = 0.0193$ and $F_{ROH4\_MAF} = 0.0185$), ROH >8 Mb cover 1.3% ($F_{ROH8} = 0.0130$ and $F_{ROH8\_MAF} = 0.0125$), ROH >16 Mb cover 0.4% ($F_{ROH16} = 0.0044$ and $F_{ROH16\_MAF} = 0.0038$). The total length of genome was taken to be 2 499 557kb. The observed inbreeding was higher than that expected based on pedigree data (F_{PED} = 0.16%), since only 3 equivalent generations in pedigree data was known. According to pedigree data only 2 animals have arisen by breeding of related animals (Lutgo – 0.78% and his son Lutlux – 0.78%), based on F_{ROH16} recent inbreeding (3 generations in the past) in 3 animals was observed (Lutgo, Nero, Nobtelo), whereas based on F_{ROH4} even 9 animals were inbred (ancient inbreeding; 12–13 generations in the past). The inbreeding coefficient based on ROH is more accurate when GeneCall and GeneTrain score are used in quality control step. Pruning SNPs that show low MAF can affect the results (Albrechtsen et al., 2010). Statistically significant positive correlation was obtained between recent inbreeding (F_{ROH16}) and percentage of protein in milk.

The smallest milk performance had the daughters of bull Lutgo (4,702 kg) with the highest recent inbreeding (F_{ROH16} = 2.5%) and second highest ancient inbreeding (F_{ROH4} = 4.6%). The second highest production of milk (5,493 kg) had cows with father Gomol (F_{ROH4} = 0.2%, F_{ROH16} = 0%). The highest milk performance had the daughters of Loltel with zero recent inbreeding and ancient inbreeding F_{ROH4} = 2.4%. The average milk performance of evaluated Slovak Pinzgau cows has been 5,259 kg of milk, 3.6% of protein and 3.85% of fat. According the Breeding Services of the Slovak Republic, s. e. (2014) the milk production in average was 4,530 kg of milk, 3.42% of proteins and 3.93% of fat in purebred animals and 4,332 kg of milk, 3.44% of proteins and 3.89% of fat in animals with more than 12.5% introgression of other breeds.

4 Conclusions

Performing analyses with ROH of different lengths here allows estimation of the distance of the current population from the base population, hence provides information on age of inbreeding. The observed inbreeding based on ROH was higher than that expected based on pedigree data (0.16%), despite the fact that ROH >16 Mb represents recent inbreeding approximately three generations ago.

The smallest milk performance was observed in group of daughters of the bull Lutgo (4702 kg) with the highest recent inbreeding ($F_{ROH16} = 2.5\%$), second highest ancient inbreeding ($F_{ROH4} = 4.6\%$) and pedigree inbreeding 0.78%. Statistically significant correlation was obtained between recent inbreeding and percentage of protein in milk. Controlling the level of inbreeding in livestock populations is especially important, since only a subset of animals from the whole population is used for breeding. This enforces composition of well-designed mating plans which enable maintaining the level of relatedness possibly low.

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