Evaluation Of Sustainable Mating Strategies In An Indigenous Swiss Horse Population

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Introduction

The Franches-Montagnes (FM) is the only indigenous Swiss horse breed. According to the FAO's criteria, the FM is considered as a breed with need to be monitored. Special efforts are taken for its maintenance. The FM breed developed at the end of the 19th century from local horses in the Jura region, with introgression of some Comtois mares, and some Anglo-Norman sires. During the 20th century the FM horse was introgressed with Warmblood and a few Coldblood breeds to satisfy transportation, agriculture and military need (Glowatzki-Mullis et al. (2006); Poncet et al. (2006)). Mechanical revolution shifted the FM from a work horse to a horse for leisure activities. This change in market demand, and consequently in breeding goals, may explain the introgression of lighter horse breeds like Warmbloods and even Arabians to the FM. However, in 1998, studbook policies changed and crossbreeding with other horse breeds was prohibited. The population is estimated to be about 21'000 animals with a total of about 2'500 foalings per year. Since the year 2006 breeding values for 43 different traits (conformation, riding and driving performance, coat colour) are estimated with a BLUP-multitrait-animal model. Due to its status as a closed population, special attention must be given to the increase in inbreeding and the maintenance of genetic variability.

The objective of this study was to develop an easy applicable management tool to optimize mating decisions in the Franches-Montagnes horse population. Therefore, the envisaged instrument should consider relationship between and breeding values of potential breeding animals. The instrument should allow and encourage breeders to mate animals with minimum relationship and breeding values above the population average. In this context Meuwissen (1997) and Meuwissen and Sonesson (1998) proposed the "optimum genetic contribution theory" (OGC) about ten years ago. Today a series of software packages exist implementing the idea of OGC-method. We evaluated different packages for their suitability, given the situation in the FM breed.

Material and methods

Data. For pedigree analysis we selected horses from the stud book with at least one registered progeny within the time span from 2003 to 2008. All together 16'402 horses were

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considered (5’863 dams and 258 sires and their ancestors). For the evaluation of the software packages only sires and dams with foalings in 2008 were taken into account (2’667 dams and 168 sires, respectively). Apart from the pedigree data we had access to genotype-data from 148 FM horses genotyped for the Illumina Equine SNP beadchip. Plink (Purcell et al. (2007)) was used to check the quality of these SNPs. After filtering, 40’012 SNPs and 146 individuals were left for the analysis. The estimation of effective population size (N_e), was performed with 142 FM horses (4 more horses had to be excluded because of their close relationship - sires - to other horses of the sample set). For the 142 horses pedigree information was available, totaling 5’359 individuals.

Analyses. Popular population parameters based on pedigree data were calculated using CFC (Sargolzaei et al. (2006)) and Endog (Gutiérrez and Goyache (2005)). Haploview (Barrett et al. (2005)) was used to estimate linkage disequilibrium (pair-wise r^2-values). N_e based on the mentioned SNP data was estimated applying the known relationship between r^2, N_e and the inter-genetic marker distance c between two loci under consideration. For the derivation of N_e the following equation which accounts for restricted sample size (n=2*sampled animals) was applied (Weir and Hill (1980)): $E(r^2)=(1/(1+4N_ec))+(1/n)$.

Results and discussion

The average relationship between selected horses (sires and dams from 2003 to 2008) was found 11.4%; the average relationship between all horses in the pedigree list was 6.8%. The mean inbreeding coefficient was found 5.2% for parents 2003-2008, and 3.8% for all horses in the pedigree (table 1). The average number of progeny per sire and year was ~15.

Table 1: Population parameters of the Franches-Montagnes horse breed

	all pedigree animals	parents 2003 - 2008
No. of animals	16‘402	6‘121
No. of inbred animals	14‘058	6‘116
Mean inbreeding coefficient	3.77 %	5.19 %
Mean inbreeding coefficient of inbreds	4.40 %	5.20 %
Maximum inbreeding coefficient	28.49 %	28.49 %
Minimum inbreeding coefficient	0.0000033	0.0000033
Mean relationship	6.80 %	11.37 %

The average generation interval for the sires and dams 2003 to 2008 (6’121 animals) varied between 7.5 and 9.5 years. These values slightly changed when considering all horses in the pedigree list (16’402 animals) and were found 7.7 and 12.6 years, respectively.

The effective population size for sires and dams 2003-2008 obtained from the log regression of (1-inbreeding) on the birth date was 90.48 and, when considering the whole pedigree list 83.63. The effective population size of sires and dams 2003-2008 computed via individual increase in inbreeding was 100.76. The pedigree based effective population size for the 142 genotyped horses, using the log of (1-inbreeding) on the birth date, was 86. The effective population size for the same horses, based on SNP data, was found 74 (one generation ago).

The relatively high inbreeding coefficient of 5.2% within the active breeding population and the effective population size of about 100, outline the need for continuous management of genetic diversity within the closed FM breed (Hasler et al. (2009)).

A series of software packages were evaluated in order to combine best the BLUP methodology with the optimal genetic contribution theory. None of these packages completely satisfied our needs. Finally, we looked for sires with highest breeding values and lowest average relationship to the dam population (figure 1): sires above and left of the brown lines. Those sires are thought to achieve a breeding gain, given a particular trait or a global index, while lowering the future increase in relationship within the breed. This methodology is practicable for every trait.

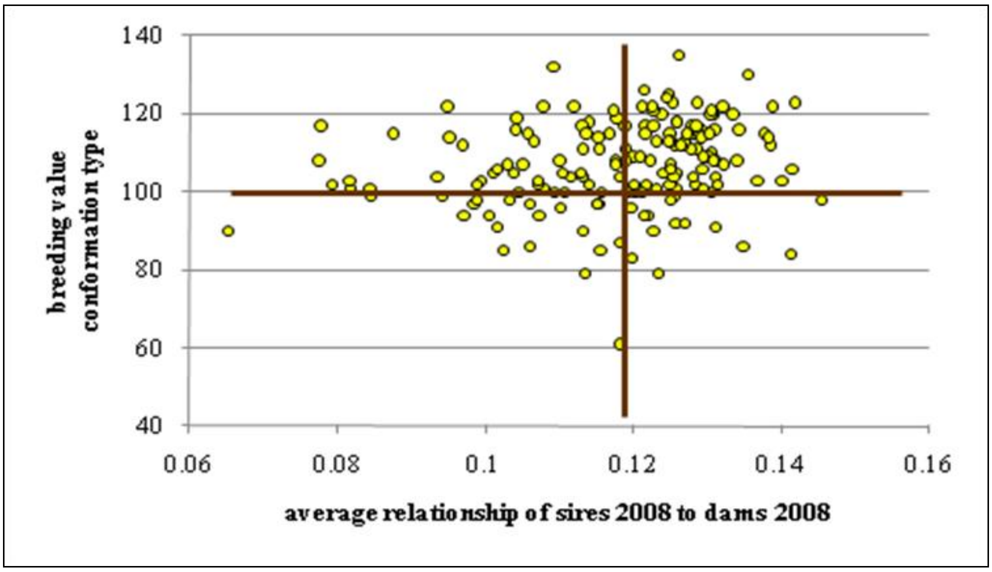

Figure 1: Average relationship of sires 2008 to dams 2008 and their breeding values for conformation type (horizontal brown line: breeding value 100 = population average, vertical brown line: average relationship 11.8% between sires and dams)

The software package EVA (Berg et al. (2009)) allowed the modeling under consideration of an optimum genetic contribution from parents to their offspring. Simulations were run to validate different scenarios. Results for three theoretical situations as well as for actual foaling data (year 2008) are shown in table 2.

Table 2: Mean inbreeding coefficients, mean average relationships and mean breeding values for the trait conformation type, performing three simulations and the foaling data from 2008 using the EVA software package

	Situation 1	Situation 2	Situation 3	Real 2008
	1‘000 progeny out of high related sires and dams	1‘000 progeny out of low related sires and dams	1‘000 (optimal) progeny out of 2‘667 dams	1’000 foalings randomly choosen out of 2’671 foalings (2008)
Inbreeding coefficient (%)	4.69	3.93	4.41	5.65
Relationship (%)	11.70	11.52	11.64	-
Average breeding value for conformation type	112.6	107.8	116.5	99.4

Conclusion

The maintenance of genetic variability within a population is important for the management of small, endangered livestock breeds. A management tool to optimize mating decisions in the Franches-Montagnes horse breed was developed. The study revealed, that optimization of matings is possible. The presented methodology is applicable for every livestock population. A prerequisite is the availability of quality pedigree data and if genetic gain is aspired, information on performance (e.g. breeding values). If performance data is lacking, optimized matings for the maintenance of genetic variability within a population can be achieved based on relationship only. The preliminary results we obtained from our SNP data are promising. Thus, in populations with no pedigree data available, SNPs might be a powerful tool for the monitoring of small livestock populations (Flury et al. (2010)).

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