Genetic diversity of the Faroe pony and the relationship to other breeds

SOFIA MIKKO¹, CARL-GUSTAF THULIN¹ & TRÓNDUR LEIVSSON²

¹Dept. of Animal Breeding & Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, and ²Breeders of Faroe Ponies, Tórshavn, Faroe Islands

E-mail: Sofia.Mikko@hgen.slu.se; Carl-Gustaf.Thulin@hgen.slu.se; tgl@post.olivant.fo





Background

SLU

Background

The Faroe ponies were presumably brought to the islands by Celtic or/and Scandinavian settlers after the settlement which occurred circa 500 - 800 AD, respectively The ancestors of these ponies are thus believed to be mainly Scandinavian and/or Celtic (i.e. from the British Isles) horses. Over the years some crossbreeding has taken place, and as late as in the 1960th there were only 4-5 purebred Faroe ponies left. In 1978 the association "Breeders of Faroe Ponies" started to register the remaining purebred ponies and organized a breeding program. Today the population counts to about 50 individuals. The degree of inbreeding is 0.22 and 0.21 for mares and stallions, respectively (1). There are however no signs of inbreeding depression in the present day population. Our main goal with this study was to estimate the amount of genetic variation. any population. Our main goal with this study was to estimate the amount of genetic variation within the Farce pony breed, and the genetic differentiation from other breeds. Finally, we wish to define the breeds that are most similar to the Farce pony.

Materials & Methods

A total of 1213 blood or hair samples were collected from 13 different breeds. Genomic DNA was extracted from blood using the QIAamp blood kit (2). A crude DNA-prep from hair was done by lysis of hair bulbs and proteinase K treatment. PCR was performed using the Equine Stockmarks kit (3). Genotyping was carried out on ABI310 or MegaBACE. Genetic molysis was reformed using the was carried out of ABSISIO or Meglacate. Genetic analysis was performed using the softwares Genepop on the Web 3.1c-3.4 (4), Genetix 3.3 (5), Population 1.2.28 (6), and Treeview (7). The P-values were corrected for multiple comparisons by a strict Bonferoni procedure (8).

Table 1. Summary of the results from the genetic analysis performed. *) F_{ST} values represent pairwist comparisons with the Faroe pony breed.

Breeds	No. of individuals	Heterozygosity		Mean no.	F *	-	HWE
		Exp.	Obs.	of alleles	F _{ST} *	Fis	dev.
Faroe pony	38	0.44	0.40	3.50	-	0.096	1
Dartmoor pony	11	0.62	0.74	4.25	0.333	-0.134	0
Fjord horse	51	0.65	0.63	5.83	0.260	0.040	0
Icelandic horse	230	0.67	0.68	7.50	0.176	-0.001	0
New Forest pony	18	0.74	0.73	6.25	0.239	0.039	0
Arabian thoroughbred	136	0.70	0.67	7.17	0.293	0.036	0
Shetland pony	214	0.65	0.63	6.92	0.256	0.043	1
Welsh pony	-10	0.68	0.69	5.00	0.335	0.038	0
English thoroughbred	386	0.67	0.67	5.92	0.291	0.001	0
Gotland pony	36	0.59	0.59	4.17	0.316	0.023	0
Shire horse	23	0.65	0.66	4.75	0.328	0.013	0
North Swedish horse	18	0.64	0.66	4.92	0.291	0.006	0
Connemara pony	42	0.74	0.75	6.42	0.221	-0.003	0

Abstract

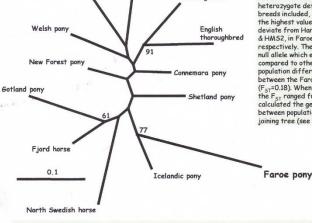
The Faroe pony is a unique breed of the Faroe Islands, that are situated in the North Atlantic. These horses were presumably brought to the islands by Celtic or/and Scandinavian settlers after the settlement which occurred circa 500 - 800 AD, respectively. The population has recently passed a bottleneck from where a few animals founded the present population. The genetic diversity of the Faroe pony population was investigated using 12 microsatellite loci. To evaluate the genetic status of this breed the results were compared with 12 other breeds. As expected from the bottleneck, few alleles were detected among Faroe ponies. When compared to other breeds, the lowest degree of population differentiation was estimated between the Faroe pony and the Icelandic pony (F_{ST} =0.18). When compared to the other breeds, the F_{ST} estimates ranged from 0.22 - 0.34. Thus, the Faroe pony appears to be a unique breed, with the Icelandic pony as the closest relative.



Results & Discussion

Among the 13 breeds included in this study the Faroe pony has the lowest level of heterozygosity (H₀h₀-0.40), as well as mean number of alleles (n=3.50). There is no overall heterozygote deficiency (F₁₅) for any of the breeds included, although the Faroe ponies show the highest value (F₁₅-0.096). Only two loci deviate from Hardy Weinberg equilibrium, HT610 &HMS2, in Faroe ponies and Shetland ponies, respectively. The locus HT610 contains a known null allele which explains this deviation. When compared to other breeds, the lowest degree of population differentiation was estimated between the Faroe pony and the Tcelandic pony between the Faroe pony and the Icelandic pony ($F_{\rm sT}$ =0.18). When compared to the other breeds, the $F_{\rm sT}$ ranged from 0.22 - 0.34. We also calculated the genetic distance (Nei's D_A) (9), between populations and constructed a neighbor joining tree (see Figure 1).

Figure 1. Neighbor joining tree with bootstrap values (50% minority consensus based on Nei's D, (9).



Conclusions

As a result of the recent population bottleneck the Faroe pony breed has a low degree of genetic variation.

thoroughbred

Our genetic analysis show no apparent signs of inbreeding, despite the low amount of genetic variation present in the Faroe pony breed.

Because of a successful breeding strategy which has aimed to include all available specimens, the present alleles are evenly distributed in the Faroe pony population.

The Faroe pony appears to be a unique breed, and the Icelandic pony seems to be the closest relative when studying these 12 genetic markers. To further evaluate these preliminary results, additional pony breeds, e.g.. Exmoor pony, will be included in our study.

References

Adalsteinsson, S. Personal communications. 1997
 QIAGEN GmbH, Germany.
 Applied Biosystems, Foster City, CA, USA

3) Applied Biosystems, Foster City, CA, USA
4) Roymond, M. & Rousset, F. (1995). 6ENEPOP (1.2): population genetics software for exact tests and ecumenicism. *Journal of Heredity* 86, 248-249. Current version 3.4, http://wbiomed.curtin.edu.au/genepop/
5) Belkhir K., Borsa P., Chikhi L., Raufaste N. & Bohnomme F. 1996-2004
6ENETIX 4.05, http://www.uiv-montp2.fr/-genetix/genetix/genetix/genetix.htm
6) Populations, 1.2.28 (12/5/2002) Copyright (C) 1999, Olivier Langella, CNRS
UPR9034, http://www.cnrs-gif.fr/pge/bioinfo/populations/index.php
7) Page, R. D. M. 1996. TREEVIEW: An application to display phylogenetic trees on personal computers. Computer Applications in the Biosciences 12: 357-358.
8) Rice, W.S. (1989). Analyzing tables of statistical tests. Evolution 43, 223-225.

9) Nei M, Tajima F, Tateno Y (1983). Accuracy of estimated phylogenetic trees from molecular data. II. Gene frequency data. *Journal of Molecular Evolution*