

Faroese Horse: Population status & conservation possibilities

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Introduction

The Faroese horse (Føroysk Ross) is an integral part of agricultural history on the Faroe Islands. There is no unambiguous evidence of the origins of the Faroese Horse. It is believed, though, that the Faroese horse was brought to the islands by Celtic or/and Scandinavian settlers approximately 500-800 AD. Molecular genetic studies have indicated the closest genetic relationship with the Icelandic horse. Influences from Dartmoor and Exmoor ponies are also likely. Traditionally Faroese horses were kept free ranging in the mountains, and only gathered and brought to the villages when there was a need for transporting heavy goods. After finishing their duties, the horses were again turned out without supplemental feeding. This semi-domestic management contributed to the Faroese horse developing into a small, strong and feed efficient horse with a compact body and strong legs and hoofs, well adapted to the climate, terrain and vegetation. The population size of the Faroese horse was likely 600 to 800 individuals at its highest. Mechanisation of agriculture and heavy exportation of Faroese Horses to the British Isles as mining ponies resulted in a drastic decrease in population size. Currently a small population of Faroese horse exists on the Faroese Islands, which stems from a few horses born between the 1940s and 1960s. Today, the Faroese horse is used for recreational purposes. The objective of this study was to conduct a pedigree analysis of the current population of the Faroese horse, as well as to describe the possibilities for a sustainable management of the breed by using optimal contribution selection (OCS).



Data and statistical methods

Data were obtained from the Society for Faroese Horses (Felagið Føroysk Ross). The pedigree of horses born between 1917 and 2016 contained 178 individuals with information on the following:

- Identification of the individual
- Identification of the sire
- Identification of the dam
- Sex
- Birth year
- Name (when available)
- Status: alive or dead
- Availability for breeding

Due to the low numbers of animals recorded each year, biannual cohorts were formed for horses born in 1991 and onwards. Horses born between 1995 and 2014 were considered as breeding candidates. Additionally, individuals with known health or reproductive problems were excluded as breeding candidates. In the 1960s there were only 5 individuals alive (Figure 2.1). These were one stallion, born in 1962 (FR62101), and four mares born in 1946 (FR46102), 1952 (FR52106), 1956 (FR56102) and 1958 (FR58102), respectively. One of these mares (FR52106) is the dam of two of the others, both being the result of a sire-daughter mating (Figure 2.1). Thus essentially three stallions have a large contribution. A simplified pedigree of the genetic bottleneck is shown in Figure 2.1. Only one of the mares alive in the 1960s is unrelated to the other four individuals; the rest are related through one or more common ancestors. Between 2000 and 2016 a total of 92 foals were born, out of those 66 are currently alive. The current population comprises (December, 2016) 81 horses. For the full pedigree see Figure 2.2.

The pedigree was analysed with the software EVA (available at <http://www.nordgen.org>), ENDOG (available at https://pendientedemigracion.ucm.es/info/prodanim/html/JP_Web.htm#_Endog_3.0:_A) and Pedigree Viewer (available at <http://www-personal.une.edu.au/~bkinghor/pedigree.htm>).

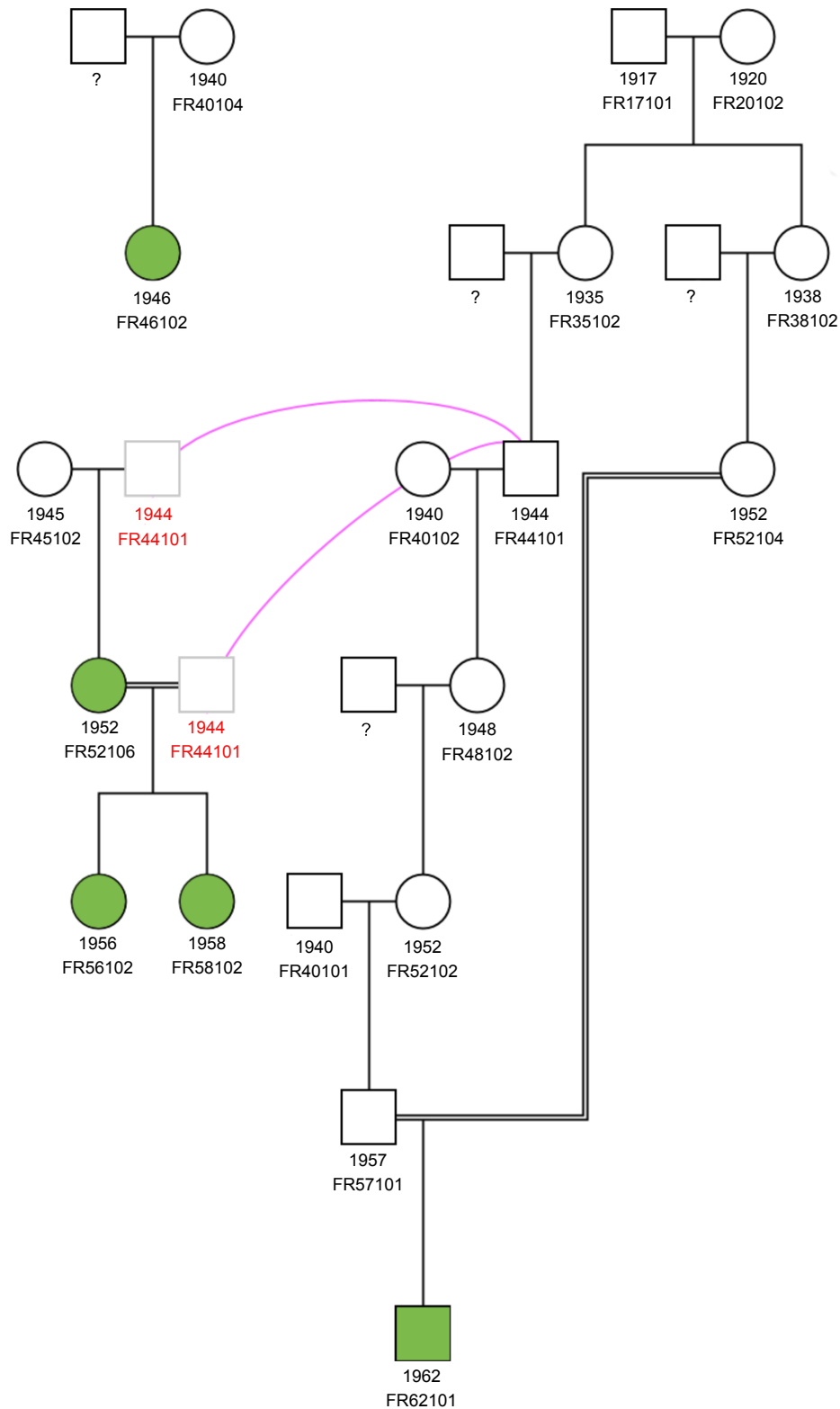


Figure 2.1: Pedigree for animals in bottleneck. Stallions are marked as squares and mares as circles, symbols with green filling are the five individuals alive in the 1960s.

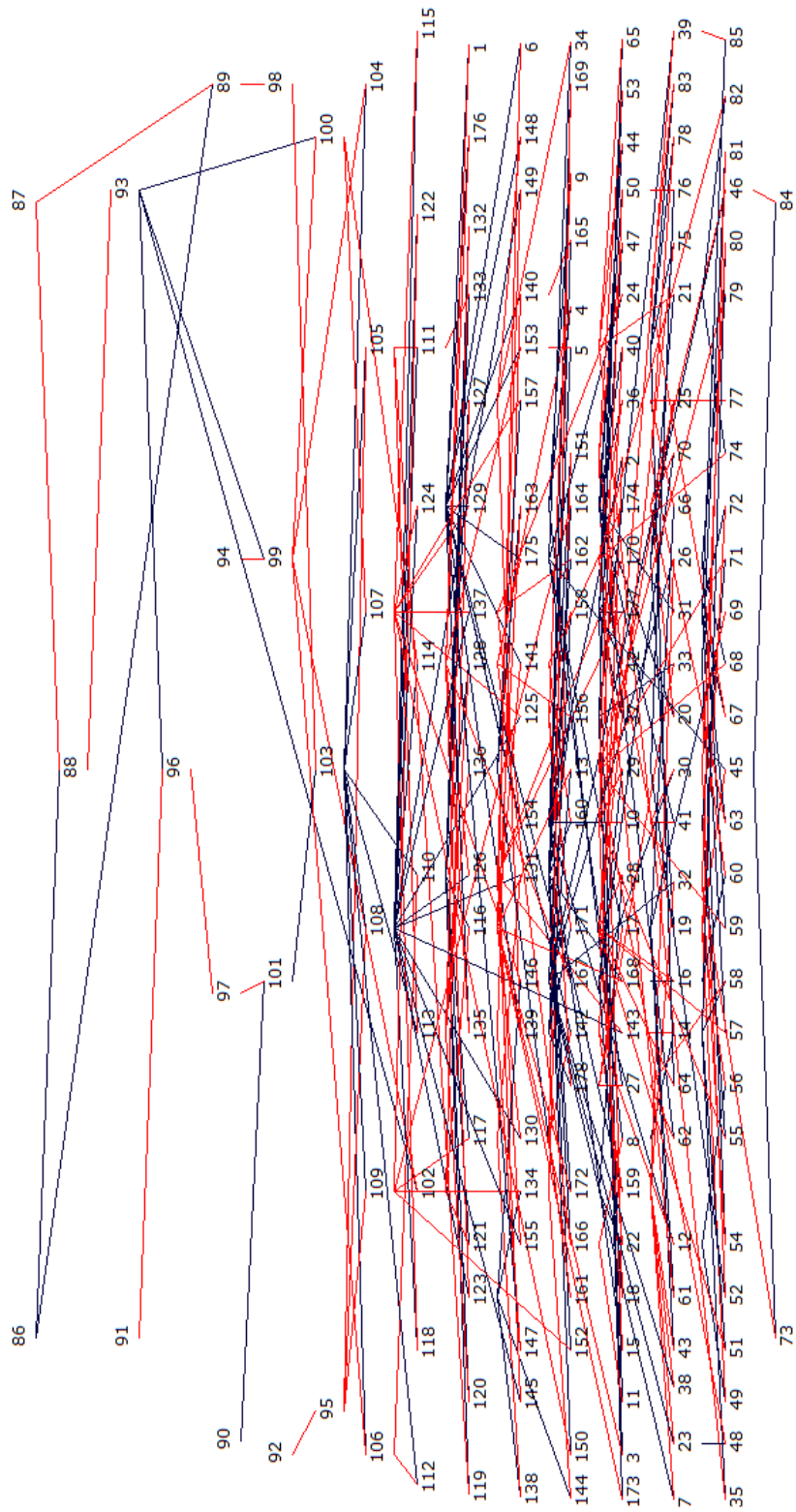


Figure 2.2: Full pedigree of the Faroese horse. Dark lines indicate stallions and red lines mares.



Results

3.1 Pedigree completeness

Pedigree completeness (PCI) is essentially a measure of the proportion of known ancestral combinations that could contribute to inbreeding. PCI can have values from zero to one. Low values of PCI indicate that little pedigree information is available for an individual. Low population level PCI will likely result in underestimation of inbreeding and overestimation of measures of genetic diversity. This is due to the fact that unknown relationships are treated as unrelatedness. For this study the pedigree completeness was computed five (PCI5), seven (PCI7) and ten (PCI10) generations back. Figure 3.1. shows the development in the pedigree completeness as a function of birth year between 1917 and 2016.

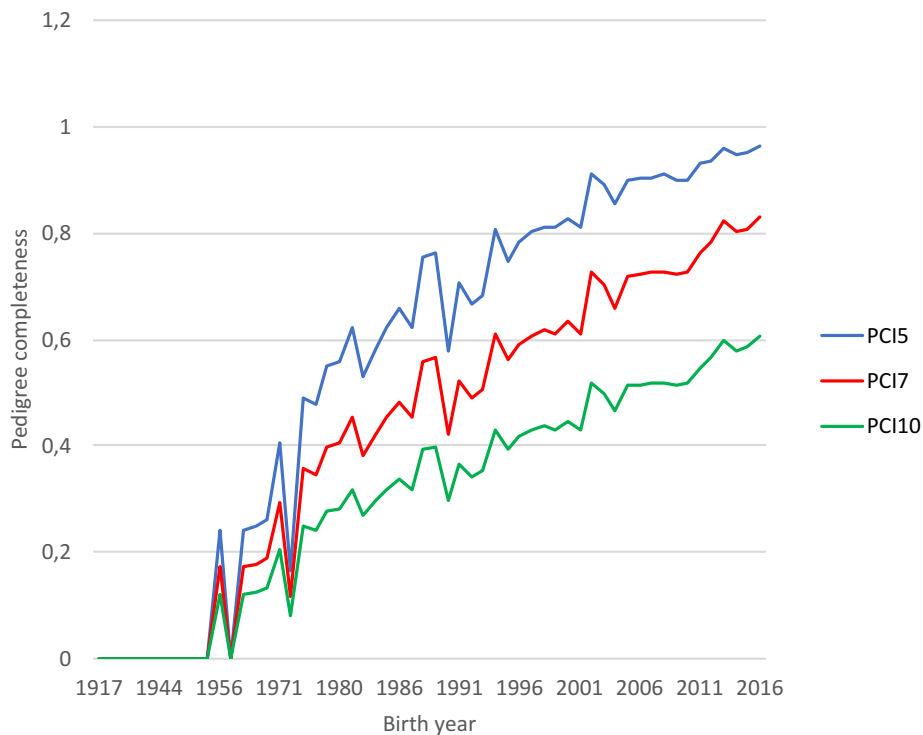


Figure 3.1: Pedigree completeness five (PCI5), seven (PCI7) and ten (PCI10) generations back over birth years.

The recorded pedigree is relatively limited, with even the most recent individuals having unknown ancestors in the last 5 generations. Pedigree completeness in the last cohort, foals born in 2016, was 0.96, 0.83 and 0.61 for PCI5, PCI7 and PCI10, respectively.

3.2 Inbreeding and effective population size

The base population (one or more unknown parents) comprises 10 individuals. The effective number of founders, ancestors, non-founders and founder genome equivalents were 9, 3, 1.7 and 1.4, respectively. For individuals born in 1980 and onwards the average age of females was 11.8 years and males 9.8 years, resulting in an average generation interval of 10.8 years. The mean inbreeding over the whole population history is 21.9 %, and that of the last cohort 2016 26.8 %. 22.48 % of the matings in the whole pedigree were between half-sibs (12.36 %), full-sibs (1.69 %) or between parent and offspring (8.43 %). The trend of average inbreeding over birth years is shown in Figure 3.2. Sire-daughter mating between two same

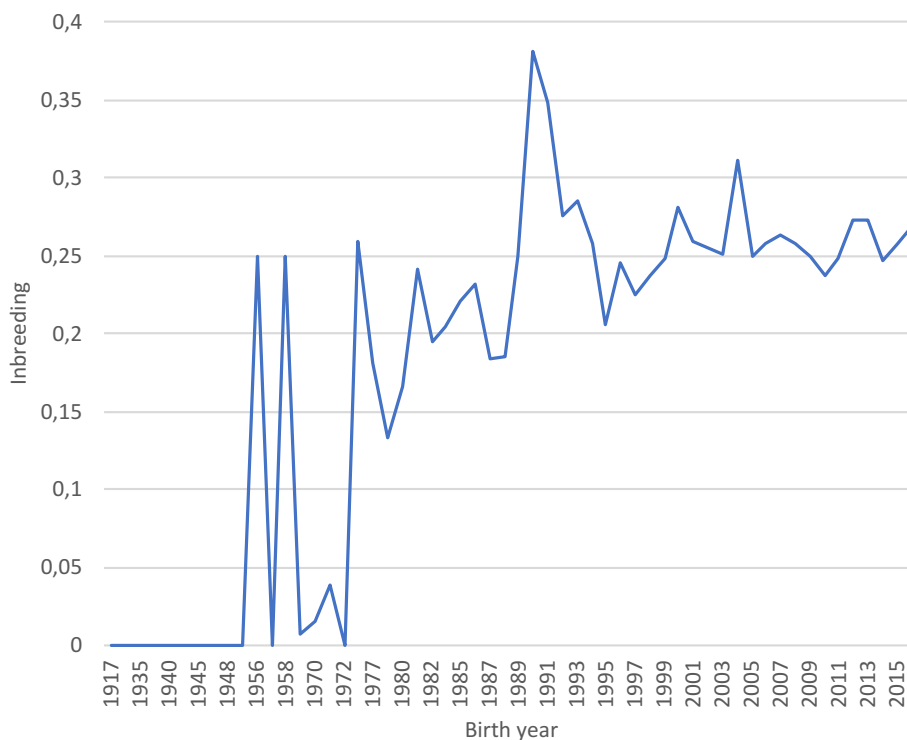


Figure 3.2: Average inbreeding over birth years 1917-2016.

individuals resulted in highly inbred individuals born in 1956 and 1958. There was a rapid increase in the level of inbreeding during the 1970s, with a more moderate increase from 1980 and onwards. Regression based methods estimated the effective population size (N_e) to be between 9 and 24. Methods that account for the whole population history, that is those based on the individual increases in inbreeding or co-ancestry, gave an N_e estimate of 8. N_e calculated from the increase in inbreeding since 1980 and a generation interval of 10.8 years was double of that. This reflects that although the average population size in the history of the breed has been very low there are signs that the rate of inbreeding in recent years has declined (Figure 3.3). This explains the increase in N_e .

The estimated N_e is critically low and significantly lower than the recommended 50 to 100, to ensure a viable and sustainable population.

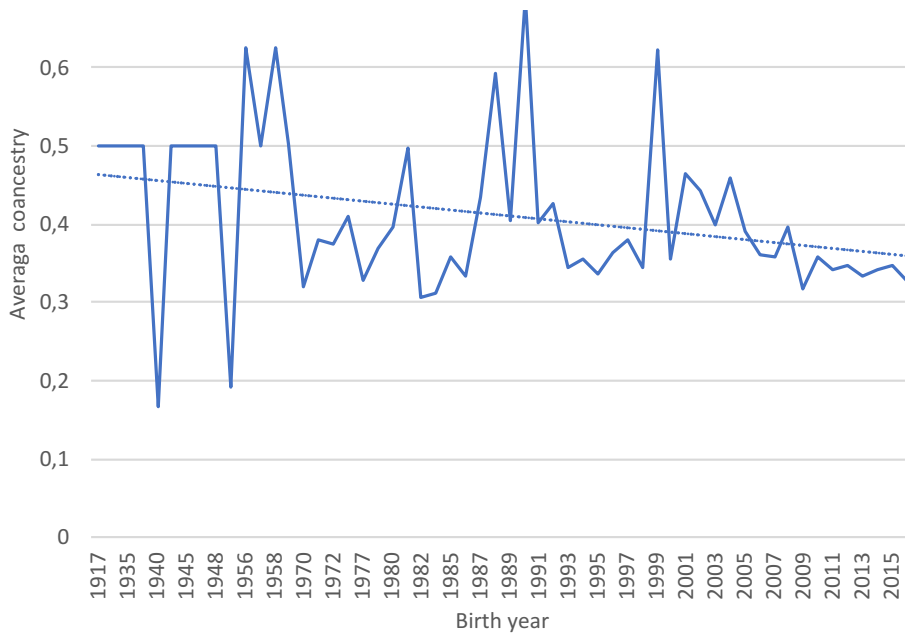


Figure 3.3: Average co-ancestry over birth years 1917-2016.

3.3 Mating strategy

A comparison of the expected inbreeding, based on the average co-ancestry among parents, and the realised inbreeding of individuals indicates that inbreeding has been intentionally avoided. In other words, lower inbreeding in the progeny (than expected with random mating) is a result of mating parents less related than on the average, see Figure 3.4. This is more pronounced in the recent years. This said, the same trend could be observed if matings that would result in inbred progeny fail and fewer offspring would be born from these matings.

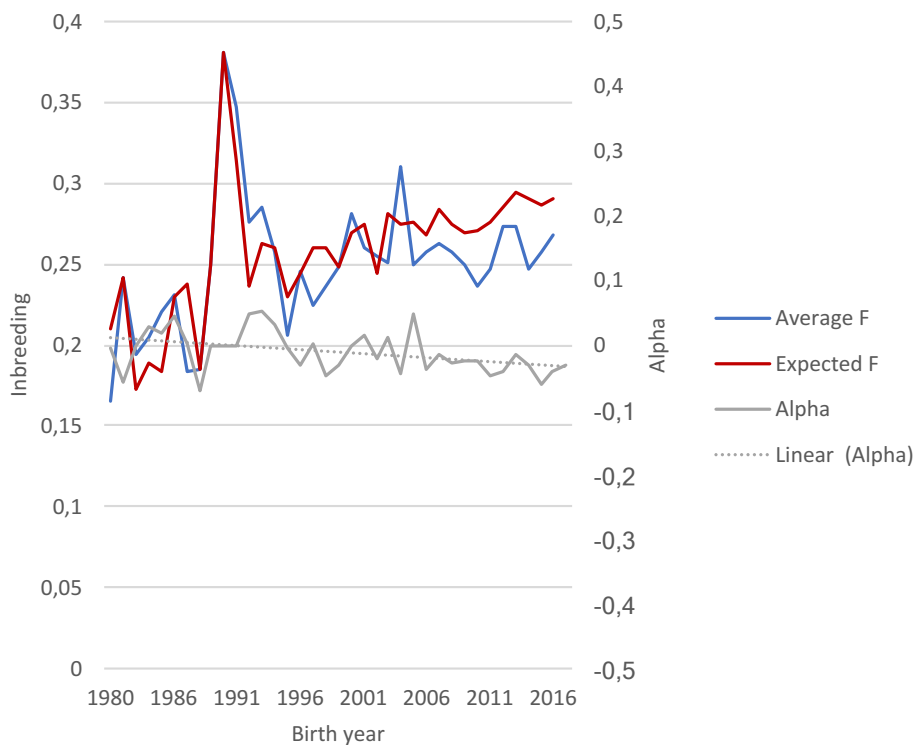


Figure 3.4: Expected and observed inbreeding and their deviation (alpha) between birth years 1980 and 2016.

3.4 Genetic contributions

The genetic contributions (proportion of alleles) from the five horses in the bottleneck are shown in Figure 3.5, for the period from 2005 to 2016. The sire, FR62101, has contributed 49 % of the alleles in the 72 individuals born in this period. The unrelated dam, FR46102, has contributed 25 %, and the other three related mares have contributed 16 % (FR56102), 15 % (FR52106) and 7 % (FR58102) respectively. This sums to more than 100 % as they are related and thus the genetic contributions are not independent. The sire (FR44101) of the three mares has a genetic contribution of 22 %.

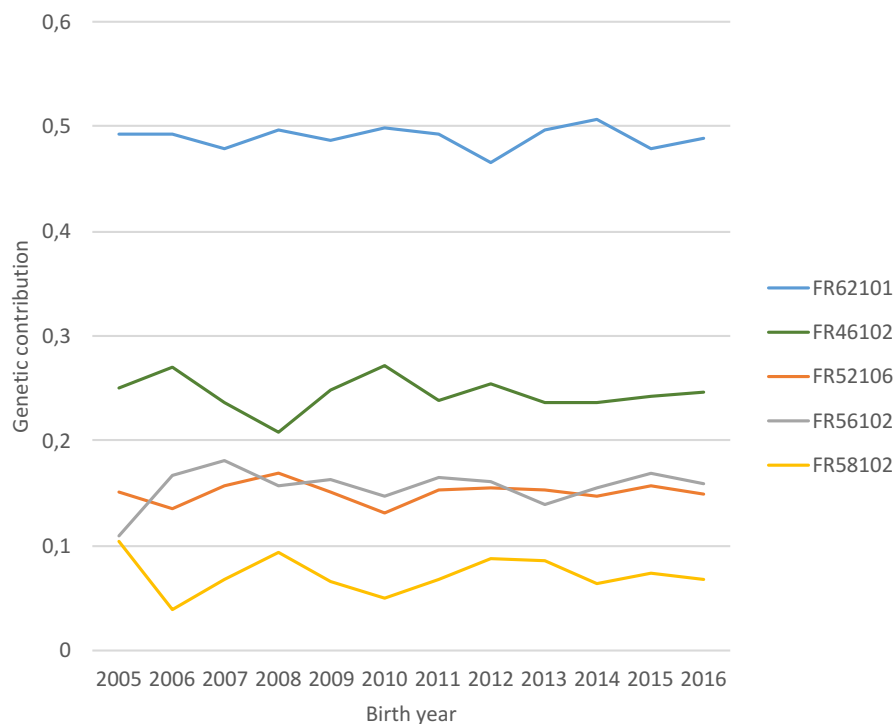


Figure 3.5: Genetic contributions of the five individuals in the bottleneck to foals born in the period from 2005 to 2016.

3.5 Optimal contribution selection

A total of 24 males and 28 females were considered available for breeding. In 2017 the selection candidates are on average 8.3 years old. The average age of males is 7.5 years (from 3 to 21) and for females 9.1 years (from 3 to 22). The average inbreeding coefficient of the candidates was 0.26. The average relationships between selection candidate males, males and females, and between females were 0.62, 0.59 and 0.62, respectively.

We assessed the impact of using optimal contribution in selection of breeders for the next cohort. From 6 to 12 matings were optimized in OCS analysis, with a constraint on the number of matings allowed for each stallion ranging from 1 to 4. In this case the optimization was done by minimizing the relatedness in the next cohort (conservation goal only).

Breeding scenarios of 6-12 matings, where males were mated with 1 to 4 females, were assessed relative to the average relationship (Figure 3.6), rate of inbreeding (Figure 3.7) and selected individuals (Table 3.1). Within a fixed number of matings the repetitive use of stallions resulted in the lowest level of average relationships, although differences between scenarios were very small and at maximum approximately 0.4 % unit (Figure 3.6). In an extremely small population, as is the case for the Faroese horse, an increase in the number of selected individuals necessarily results in the selection of more related individuals. The average relationship with random mating of candidates would have been 59.4 %, approximately 1 % unit larger than that realized by OCS.

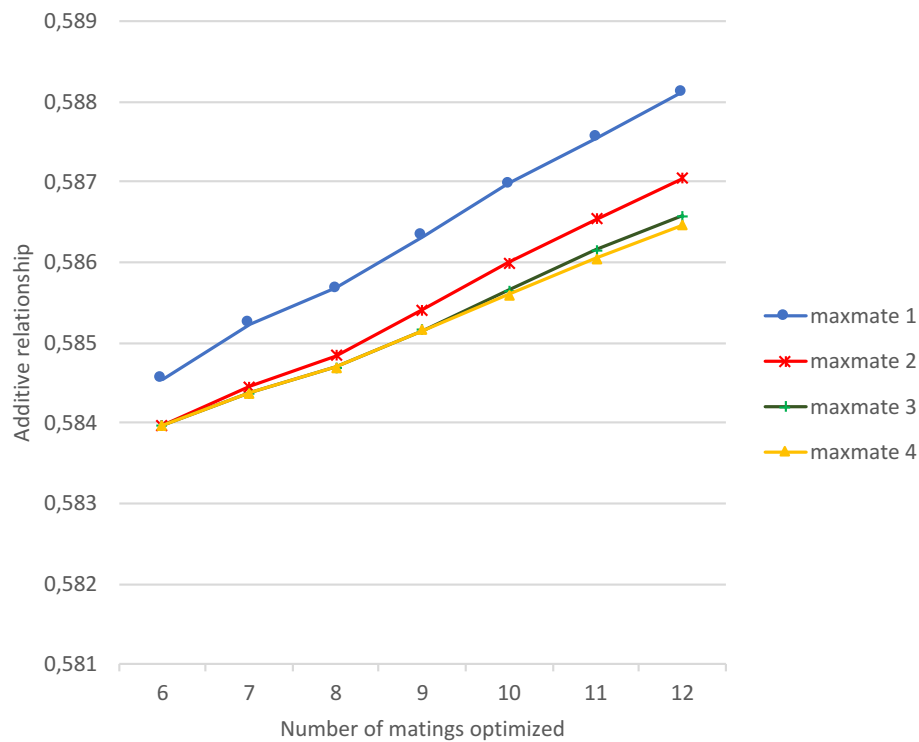


Figure 3.6: Average relationship of selected individuals in different breeding scenarios. Number of matings for each stallion was constrained to 1/2/3/4. A total of 6 to 12 matings were optimized. The points represent the lowest possible average relationship for a given number of matings and constraints on stallion use.

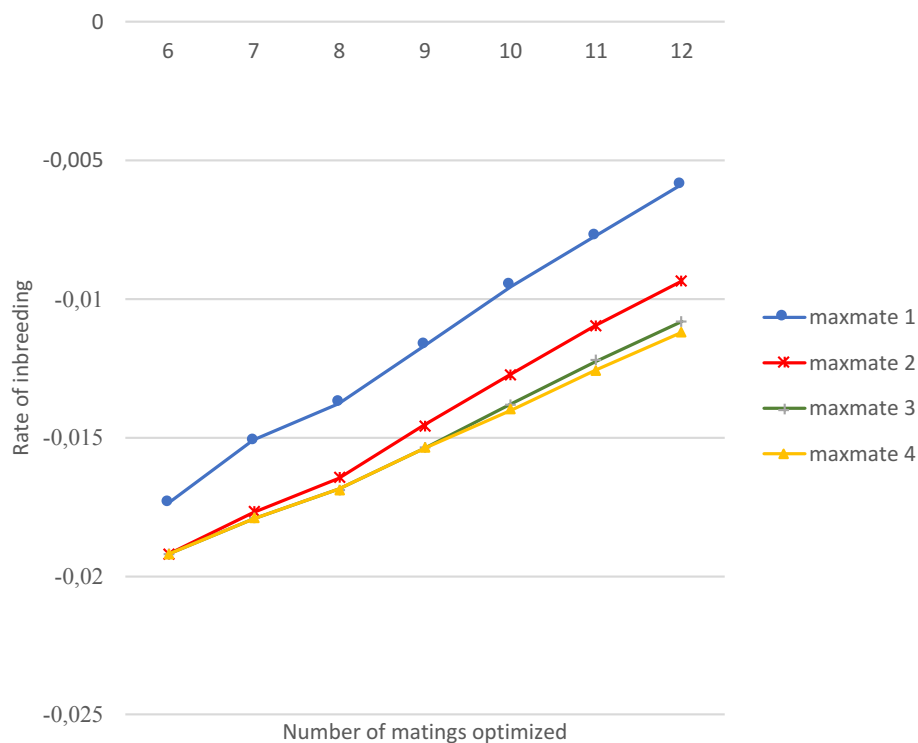


Figure 3.7: Rate of inbreeding with different selection scenarios. A total of 6 to 12 matings were optimized. The points represent the lowest possible rate of inbreeding for a given number of matings and constraints on stallion use.

A minimum 4 and a maximum 7 stallions were selected for breeding over all the scenarios allowing repetitive use of stallions. A subset of the same 7 stallions were selected in all scenarios (highlighted in Table 3.1).

The additive relationship of each of the selected males with all candidate males (0.60-0.62) and females (0.53-0.59) was equal or lower than the average amongst male candidates (0.62) or between male and female candidates (0.59). Additionally, the additive relationship of the selected stallions with the individuals born during the last two years (2015-2016) was lower than the average of all candidate males: 0.57 vs. 0.60. Similarly, the additive genetic relationship of the selected females with all candidate females (0.60) and males (0.57) was lower than that amongst female candidates (0.62) or between female and male candidates (0.59). The additive genetic relationship of the selected females with individuals in the last two cohorts was lower than that of all female candidates: 0.58 vs. 0.60.

Table 3.1: Breeding candidates with their relationships to all candidate males and females. Individuals selected in any of the scenarios are marked in red and individuals selected for all scenarios with 6-12 required matings and repetitive use of males (2-4) are highlighted.

	Name	Relationship with	
		males	females
Males			
	Bello	0.6009	0.5763
	Rani	0.6421	0.6263
	Grani	0.6166	0.5318
	Hugin	0.6019	0.5742
	Grafaksi	0.6357	0.5976
	Brusi	0.6130	0.5935
	Liggjas	0.6338	0.5849
	Prins	0.6250	0.5977
	Stormur	0.5822	0.6096
	Borr	0.6289	0.6086
	Neisti	0.6350	0.5812
	Sommer	0.6064	0.5736
	Glothi	0.6162	0.5722
	Njørður	0.6391	0.6140
	Askur	0.6357	0.5782
	Aegir	0.6162	0.5722
	Sleipnir	0.6327	0.6080
	Jallur2	0.6521	0.6150
	Froyur	0.6408	0.5840
	Meldur	0.6040	0.5919
	Mimir	0.6408	0.6229
	Garpur	0.6057	0.5890
	Munin	0.6306	0.5991
	Roði	0.6269	0.6113
Females			
	Gilja	0.6175	0.6165
	Disa	0.6230	0.6246
	Døgg	0.5859	0.6345
	Brynja	0.6230	0.6208
	Luna	0.6197	0.6454
	Skakka	0.6237	0.6307

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Name	Relationship with	
	males	females
Females		
Litla	0.5008	0.5734
Flykra	0.6334	0.6037
Odn	0.5739	0.6096
Chanel	0.5942	0.6285
Bestla	0.6341	0.6361
Mira	0.6137	0.6284
Disan	0.6050	0.6073
Freia	0.5147	0.5555
Ly	0.5895	0.5932
Fenja	0.6010	0.5852
Embla	0.6060	0.6236
Logn	0.5787	0.6213
Teiga	0.5230	0.5715
Saga	0.6194	0.6258
Joséfinna	0.6016	0.6157
Sól	0.6026	0.6308
Iris	0.5489	0.6036
Stjörnuskot	0.6010	0.6403
Heiða	0.6063	0.6258
Skessa	0.5882	0.6325
Daniella	0.5489	0.6036
Brim	0.6040	0.6327

Sustainable breeding of an extremely small and a priori highly inbred population is of great importance. Successful follow-up of mating schemes planned with OCS helps to avoid a rapid increase of inbreeding in the future generations. Therefore, whether an individual is eligible as a breeding candidate should be evaluated thoroughly relative to the health of the individual and possible previous experiences regarding fertility and mothering characters. This is to avoid that the planned mating will not be realized or does not result in viable progeny. Maximization of success is of high priority to be able to expand the census size.



Management recommendations

1. Strict control of inbreeding

Due to the small census size only individuals ensuring the maintenance of maximum genetic variation should be used for breeding. This is optimally done by minimising the rate of inbreeding. It is highly recommendable to use a computational tool to optimize the contributions of parents in the next cohort of foals. EVA is one such tool.

2. Expansion of census population size

The small census size sets a limit for constraining the future rate of inbreeding in the population. Initiatives to increase the population size is of great importance. Actions should be taken to increase the popularity of the breed both amongst private horse owners as well as promote the use of the breed for example in horse tourism. To increase the effective size of the breed it should be ensured that these horses will be considered as breeding candidates.

3. Recording of fitness related traits to detect recessive deleterious alleles

The current population can be traced back to five horses, four of them being related. This, as reflected in the high inbreeding coefficients, indicates considerable genetic drift, and potentially increased frequencies of recessive deleterious alleles. To counteract the effects of unfavourable allelic combinations and to support breeding of healthy well-functioning horses, registrations of mortality and disease are recommended. Additionally, to detect unsuccessful mating (no pregnancy/early abortion), information on breeding details, such as date(s) of mating and stallion used, should be registered.

4. Molecular genetic characterization

Molecular genetic characterization is recommendable for two reasons. First, additive genetic relationships between individuals may be assessed precisely. Consequently, individuals that are less related to the other breeding candidates may be recognized and prioritized in breeding due to their high conservational value. Second, molecular genetic information may be used for screening for known lethal recessives. This allows recognition of carriers of detrimental alleles and enables that their use as breeding animals may be restricted.