

Abstract from the paper of inbreeding of Norwegian and Swedish Fjord horses

The paper is called :

Segment-based coancestry, additive relationship and genetic variance within and between the Norwegian and the Swedish Fjord horse populations.

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You can find the whole paper on the address below :

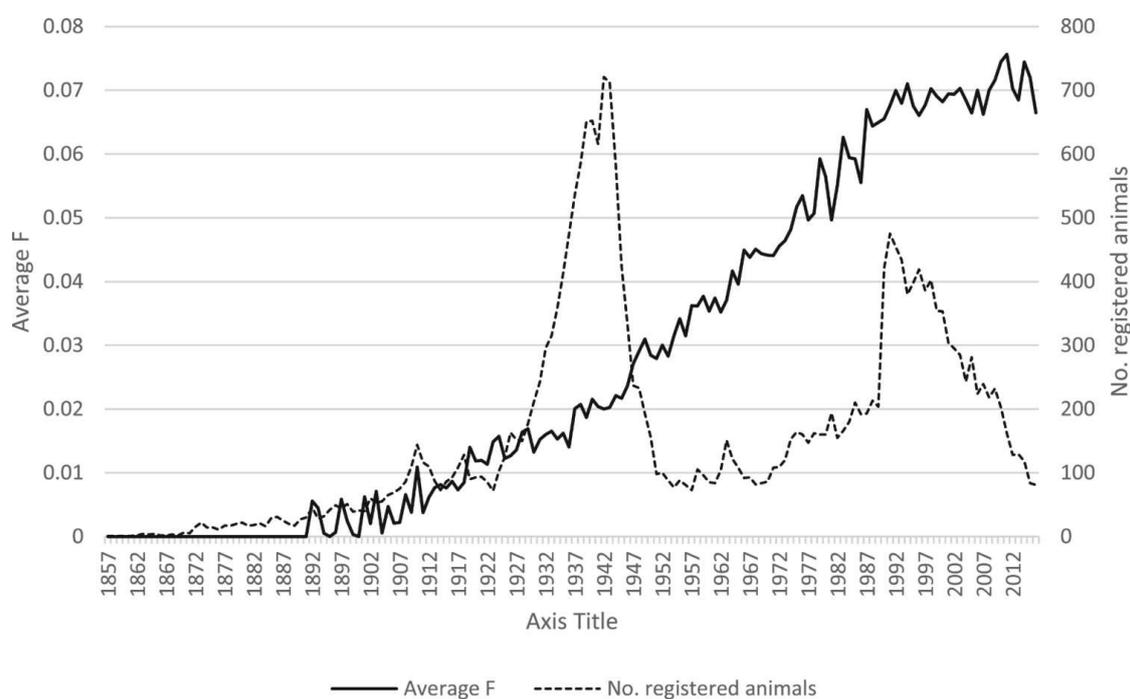
<https://www.tandfonline.com/doi/full/10.1080/09064702.2019.1711155>

The Fjord horse originates from Norway but forms a global population due to several small populations in foreign countries. There exists no information about the additive relationship and the genetic variance between these subpopulations. By collecting blood samples from Norwegian and Swedish Fjord horses, a sample of 311 Norwegian and 102 Swedish horses gave 485,918 SNPs available for analysis. Their inbreeding coefficients were calculated and compared to the pairwise coancestry and the shared genomic segments.

The study showed that coancestry from shared genomic segments can be used to estimate additive genetic relationship and genetic variation within and between the global populations of the Fjord horse.

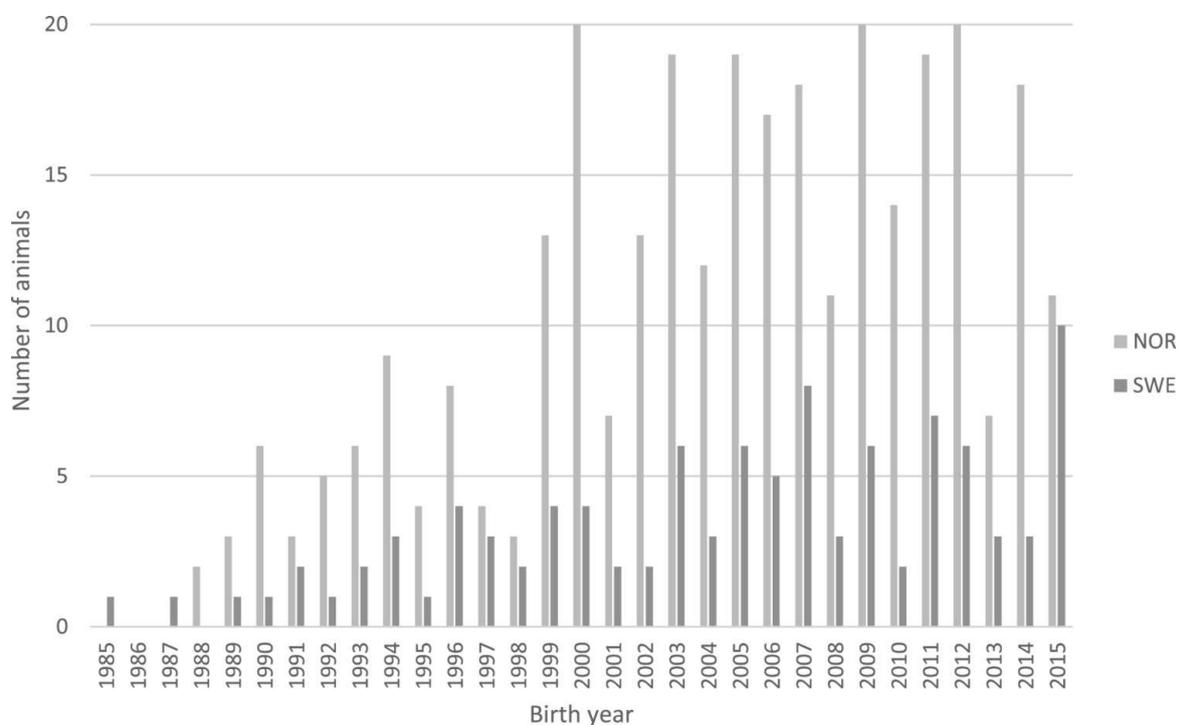
The Fjord horse population in Norway has had a steady increase in the average inbreeding coefficient since the start of the studbook in 1857 (Figure 1).

Figure 1. Average coefficient of inbreeding (F) per birth year and number of animals in the pedigree per birth year for the Norwegian Fjord horse population over the period 1857–2016.



In the period after 1990, the rate of inbreeding flattens out giving an average inbreeding of around 7%. Also, in the same period after 1990, the annual number of registered foals in Norway has been dropping quite drastically to below 100. The steep increase in the number of animals around 1990 was due to a shift in registration rules opening for all born horses to become registered, otherwise the population has been slowly built up after the major change in the production of horses after World War 2. In the Swedish Fjord horse studbook, too many individuals lacked information of birth year to be able to calculate the average inbreeding coefficient per year in a reliable way or displaying the number of foals registered per year. The birth years of the test animals contributing to genotyping data have a time span of 28 years in the Norwegian population and 31 years in the Swedish population (Figure 2).

Figure 2. The age distribution of the animals contributing with genotype data (recorded December 2015 to March 2016), shown through the number of animals born per year in the Norwegian (N = 311) and the Swedish Fjord horse populations (N = 102).



There is a natural decrease in the presence of the eldest birth years in both populations, and around 80% of the test animals are born in the period 1999–2016. However, except for some of the earliest years, all years were present in the test material of both populations. Due to practical and economic reasons regarding the collection of blood samples, there were over three times as many genotyped animals from the Norwegian population than from the Swedish (Table 1). Both populations had a complete generation equivalent (the average number of generations with known pedigree for individuals calculated with genomic data) as high as around 12, but the Norwegian population turned over generations faster, with a generation interval of 9.1 years, versus 11.6 years in Sweden (Table 1).

Table 1. Number of Norwegian (NOR) and Swedish (SWE) individuals passing the genotype tests (reference population) and their estimated complete generation equivalent and generation interval per population.

	Norway	Sweden
Number of animals	311	102
Number of generations in the data	12.7	11.6
Generation interval	9.1	11.6

Calculated from a subset of the genotyped horses (224 NOR and 103 SWE).

The inbreeding coefficients from the pedigree information were 7.7 % in the Norwegian population, and with the highest occurrence of individual inbreeding coefficient of 19%. Whereas the Swedish population had an average level of inbreeding from pedigree information of 5.2%. In both populations, the level of inbreeding from genomic calculations was more than twice than from pedigree, 14.1 in the Norwegian population and 11.9 in the Swedish population. This means that the normal used calculation of inbreeding based on known ancestors here called pedigree information seems to be too low. We know from earlier research that one loose pedigree information when horses are sold abroad or are imported. One cannot follow the relatives back to the day they left Norway. Missing pedigree information leads to that horses which are relatives is looked upon as totally unrelated.

The average genomic relationship between the Norwegian and Swedish population was 11.5 %.

The effective population size calculated from pedigree information with confidence limits was 71 (70-72) in the Norwegian population and 269 (259-279) in the Swedish population, in harmony with the high fraction of immigration in Sweden. The effective population size from genomic calculations was 63 (57-72) in the Norwegian population and 1136 (119-∞) in the Swedish population. The calculations of the effective population size based on genomic data in Sweden was not possible to estimate, it went towards infinity. The explanation for this is that the number of horses was too low and one needs about 250–300 horses to make the calculation possible. For both the Norwegian and Swedish horses together the effective population size based on genomic calculations were 87 (range: 77–100), somewhat increased compared to the estimate of the effective population size relative to the Norwegian alone.

Generally, the effective population size

(https://en.wikipedia.org/wiki/Effective_population_size) is a more robust and important way to estimate how the inbreeding will develop in a population. If the effective population size is less than 50 it is critical. Across the two examined populations, the effective population size was within the recommended size of 50–100, but with respect to the steadily reduced population size, it seems reasonable to recommend a future effective population size in a long-term perspective closer to or above 100.

When considering both populations, the effective population size increases to 87 (77–100) from the one for the Norwegian population. This indicates that combining the two populations adds genetic variation, which is an important result. Other Fjord horse populations probably possess additional genetic variation, for example, the population of Fjord horses in North America that has a Norwegian origin. Uniting the global population of the Fjord horse is a unique possibility to manage the genetic resources in a sustainable way for the future, and the use of genetic markers will be a powerful tool to both gain knowledge both about the relationship between the subpopulations, serving a basis for joint genetic evaluation, but also in management of the entire genetic variation across the subpopulations. At the same time, such a process represents a considerable political challenge, since there is currently no joint common breeding goal for the international Fjord horse, as not all countries follows the general goal in the hand book, likely because it is too general in practical breeding situations.

Conclusions:

1. The estimated inbreeding is the double using genetic methods, showing that the pedigree information in our populations are not complete.
2. Effective population size is low, but not critical.
3. Mixing our two population increases the effective population size compared to the Norwegian alone, from 63 to 87.
4. The genomic relationship between population are possible to calculate.
5. By sampling DNA from 250-300 horses one can be able to find the same result from any population.