SPARKS: One potential tool for Fjord population diversity and health

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Fjord breed diversity is an important topic for our closed breed. We need to consider the available tools for maintaining diversity, redistributing it, and minimizing loss over time. Many of the Fjord-specific articles I've read on this topic have highlighted the issues, but not really provided solutions or actionable guidance. The SPARKS is one of multiple tools that the Fjord breed could use to help reach population-level goals here in the USA and around the world.

SPARKS, Single Population Analysis and Records Keeping System, is a pedigree analysis system originally designed for conservation of small populations of endangered animals in zoos. When used in conjunction with GENES genetic analysis program, it can help breeders choose the optimal pairing of stallions and mares for the maintenance of genetic diversity, or reduced loss or redistribution of diversity, in the overall population. SPARKS was first designed for the Cleveland Bay Horse Society and brought about an improvement to the effective population size, from a non-viable level of 22 in 2004 to a red line of 50 in 2013, to 68 by 2018, and 241 by December 2021. It has also been used by the Suffolk Punch breed in recent years.

An effective population size depends on the breed-specific genetic diversity present, and is the minimum population size required to avoid loss of genetic variation. In 2015 and 2016, Fjord horses from Norway and Sweden were sampled genetically and pedigrees compiled for 12.6 generations (Norway) and 11.5 generations (Sweden) for comparison of reliability of these different methods of determining effective population size. The two methods suggested nearly equal effective population sizes for the Norwegian horses (63 from shared pedigree ancestry vs. 71 from shared genomic segments, and high precision for both), but quite different effective population sizes for the Swedish Fjords (269 vs 1136, with much less precision in the genomic estimate). The genomic data suggest a larger minimum breeding population size due to pedigree calculations being statistical estimates and not based on actual genetic recombination, and likely missing pedigree information that counts related individuals as unrelated. When the two countries data were combined for analysis, the authors suggest a minimum breeding population of 87 (range: 77-100), which indicates that combining the two populations adds genetic variation. Another study that investigated genomic relatedness among 21 Fjords (Peterson et al., 2013) had suggested an effective population size of 335. The more recent research involved 311 Fjords from Norway and 102 Fjords from Sweden, so the results and estimates are more reliable. Figure 1 gives

a sense of the coefficients of inbreeding (COI, denoted by F) calculated from that research and over time for the Norwegian and Swedish population combined.

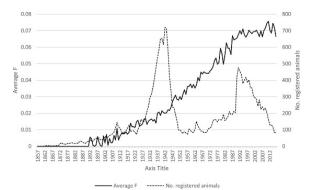


Figure 1. Norwegian and Swedish Fjord coefficients of inbreeding (F) and number of registered Fjords from 1857 to 2016. From Olsen et al. 2020.

Small populations can lose genetic diversity faster than large populations by virtue of random genetic drift. popular sire effects, maintenance of fewer stallions, fewer mares being bred, globalized availability of genetic material, and breeders choosing personal goals over population goals. The loss of genetic diversity manifests itself in reduced fertility, increased health problems, shorter lives, and impaired performance of horses. The Suffolk Punch breed in the UK has been experiencing fertility issues, and an unbalanced foal sex ratio of mostly colts born, as the population has become increasingly inbred. The Norwegian Horse Association in Norway is currently collecting hair samples to assess the prevalence of the sub-fertility gene in the Fjord population around the world due to the impacts this could have on an already small population.

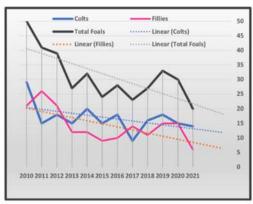


Figure 2. UK Suffolk Punch Annual Foal Gender Disparity for 2010-2021. From Hatch, E.A. 2021.

I've spoken with the director of the UC-Davis Veterinary Genetics Lab, where all of the NFHR Fjord DNA samples are tested for parentage verification, and the Lab doesn't currently have the ability to conduct the genomic relatedness assessments that were done for the Fjords in the Olsen et al. (2020) study. With funds, submitted samples and time, that testing service could be made available here in the USA.

In the meantime, and given the minimal differences between the pedigree- vs genomic-based coefficients of inbreeding for Norway Fjords in the Olsen et al. study (2020), the SPARKS and GENE approach could be helpful because it ranks all available stallions for their genetic diversity value as a breeding mate with every breeding mare in the population based on mean kinship values. Each mare gets a personalized list of stallions demarked by a traffic light rank of green (use for breeding), to red (don't use for breeding). The goal of these lists are to minimize losses of genetic diversity, and redistribute the diversity. The foundation of the breed is genetic diversity and breeders need to use the entire gene pool so that there is something contributed to each successive generation, made from the best mating choices available with the resources at hand. Even average Fjords have something to contribute.

Admittedly, this approach has some qualifiers and should not be the only tool in the toolbox for breeding pair selection. It says nothing about the quality of any individual Fjord for all of the other traits that are important to meeting the breed standard. Breeding great Fjords is luck, art and science, with recommendations such as SPARKS being a part of the science. Fjords have a larger population and are not as critical and the Cleveland Bay or UK Suffolk Punch, but the Fjord numbers currently being used for reproduction in the USA are near the minimum of the Norwegian effective population levels and not all genetic diversity is being carried forward in our current breeding approach, so employing more science as we

move forward can help preserve the diversity of Fjords for generations to come.

References:

- Cleveland Bay Horse Society of North America. Census of Horses.

 https://clevelandbay.org/wp/wpcontent/uploads/2021/12/CBHSNA16Dec2021census.p
 df . Accessed 5/1/2022.
- Cleveland Bay Horse Society. 2021. Guidance on the use of SPARKS Data Sheets.
- Dell, A. 2018. SPARKS Equine Breeders Seminar. Rare Breeds
 Survival Trust. Shared by Hatch, Y.A. 2021. Suffolk
 Punch Australia. http://suffolkpunchaustralia.com/wp-content/uploads/2018/10/RBST-Equine-Breeders-Seminar-2.pdf
- Grønntun, I. 2022. Conservation breeding in real life: Is conservation of different stallion and mare lines ensuring genetic diversity of the Norwegian Fjordhorse as a breed. Translated by Inger Helene Hagen Sira. Fjord Horse International, Nordfjordeid, N-6770, Norway.
 - https://www.fjordhorseinternational.org/FjHI/images/ Norway/2021/conservation_breeding.pdf
- Holmoy, I.H, et al. 2022. FeNomen: Fertility in national Norwegian horse breeds.

 https://www.fjordhorseinternational.org/FjHI/images/Norway/2021/FeNomen FHI.pdf
- Olsen, H.F., et al. 2020. Segment-based coancestry, additive relationship and genetic variance within and between the Norwegian and the Swedish Fjord horse populations, Animal Science, 69:118-126.
- Peterson, J.L. et al. 2013. Genetic diversity in the modern horse illustrated from genome-wide SNP data. PLOS One, 8:1-15.
- Hatch, E.Y. 2021. Suffolk Punch Australia. The Suffolk Punch
 Horse. Where are we now? May 2021 Part 2: More
 Rocks & Difficult Terrain
 https://suffolkpunchaustralia.com/thirteen-articles-on-the-status-of-the-suffolk-horse/where-are-we-now-may-2021-part-2-more-rocks-difficult-terrain/