POPULATION GENOMICS ANALYSIS REPORT

P2026-03 V2.0

FAROE ISLANDS – ATLANTIC SALMON AND TROUT

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Version changes:	• Added background information on samples, lakes and rivers and stocking history, provided during meetings held 14.4.2026 & 16.4 2026. • More in-depth interpretations of genomic relationship matrices and genetic structuring. • Provided recommendations for further stock-enhancement work in the summary.
Objective:	To use genome-wide DNA (SNP) markers to investigate population genomic structuring and quantify genetic diversity in Atlantic salmon and brown trout populations in the Faroe Islands. Also to compare Faroese Atlantic salmon to populations in Island and farmed Norwegian salmon to identify potential genetic admixture.
Client:	Føroya Silaveidifelag
Client's reference:	Føroya Trout and Salmon DNA analysis nr.1
Background:	Atlantic salmon (*Salmo salar*) in the Faroe Islands originate from Icelandic stock introduced in the 1960s, primarily from the Elliðaár river system. Since then, supportive breeding programs have been used to maintain and enhance populations. However, such programs can lead to increased relatedness and inbreeding if not carefully managed. In parallel, trout (*Salmo trutta*) populations in the Faroe Islands represent naturally structured systems, with potential variation in connectivity and isolation among water bodies. The aim of this study was to: 1. Assess the genetic structure of Faroese salmon relative to Icelandic and farmed Norwegian populations

	2. Evaluate relatedness, inbreeding, and diversity within Faroese salmon 3. Characterise population structure and diversity in Faroese trout

SAMPLE INFORMATION

Summary of provided sample information

POPULATION	POP abbreviation	Country	Number of samples	Sampling year/Cohort	Species	Sample material
Leynar/Saksun	*FI-*	*Faroe Islands*	*157*		*Salmon*	*Fin biopsy*
Saksun	*FI-*	*Faroe Islands*	*17*		*Trout*	*Fin biopsy*
Leynar	FI-	Faroe	69		Salmon	Fin
Leynar	FI-	Faroe	33		Trout	Fin
Sandá	FI-	Faroe	14		Trout	Fin
Dalsá	FI-	Faroe	14		Trout	Fin
Hoydalsá	FI-	Faroe	12		Trout	Fin
Dalá	FI-	Faroe	14		Trout	Fin
Niðara vatn	FI-	Faroe	24		Trout	Fin
Stórá- Slavik	FI-	Faroe	11		Trout	Fin
Leitisvatn	FI-	Faroe	11		Trout	Fin
Áin norðuri við	FI-	Faroe	2		Trout	Fin
Hviltkinnavatn	FI-	Faroe	1		Trout	Fin
Leynar/Saksun	FI-	Faroe	157		Salmon	Fin
Elliðaár	IS-2017	Iceland	16	2017	Salmon	Genotype
Elliðaár	IS-2020	Iceland	100	2020	Salmon	Genotype
Eystri-Rangá	IS-2019	Iceland	89	2019	Salmon	Genotype
aquaculture	NO-FARM	Norway	83	Aquaculture 2022-2025	Salmon	Genotype

SUMMARY OF RESULTS

This study used DNA markers to investigate how Atlantic salmon and brown trout populations in the Faroe Islands are related, how much genetic diversity they have, and whether there are signs of inbreeding.

- Moderate levels of genetic structure were observed between Faroese cohorts of Atlantic salmon Icelandic and Norwegian farmed populations, with greater levels of genetic similarity in comparisons of Faroese and Icelandic cohorts.
- The farmed Norwegian salmon form their own genetic clade based on the genomic relationship matrix, indicating no recent levels of genetic introgression with Faroese salmon.
- Within the Faroese salmon population, clusters of close family groups could be observed and some individuals show signs of inbreeding, although there are many individuals with low signs of inbreeding.
- The overall genetic diversity in the Faroese samples is sufficiently high to be maintained with careful breeding management.
- Trout populations show strong natural structuring with lake populations genetically distinct from sea-trout populations.
- Lower levels of genetic diversity were observed in individuals from lake populationspotentially vulnerable.

These results show that genetic tools can directly support breeding decisions to maintain healthy and sustainable fish populations.

Recommendation for further work with stock improvement in the Faroese salmon populations:

The integration of genomic relatedness and inbreeding information for potential broodstock provides a practical framework for breeding management. Specifically, avoiding matings between closely related individuals (e.g. full siblings) and prioritising individuals with lower genomic inbreeding coefficients would help to reduce the accumulation of inbreeding over time. In addition, balancing parental contributions across cohorts could further enhance effective population size and maintain long-term genetic diversity.

KEY CONCEPTS AND TERMINOLOGY WITH INTERPRETATION

- SNP (Single Nucleotide Polymorphism):

(SNP, pronounced "snip") is a common type of genetic variation where a single nucleotide (A, T, C, or G) in the DNA sequence differs between individuals. SNPs act as biological markers for tracking genetic traits, diseases, and ancestry, representing the most frequent form of genome

- **PCA (Principal Component Analysis):**

A data reduction method used to summarise complex genetic data and reveal patterns of variation among individuals. It transforms the dataset into a small number of axes (principal components) that explain the main sources of variation

  - Individuals that cluster together on a PCA plot are genetically similar

- Separation between clusters indicates genetic differences between populations

- **FST (Fixation indices):**

A measure of how genetically different populations are.

- Values near 0 → populations are genetically very similar
- Values ~0.05–0.15 → moderate genetic differentiation
- Values >0.1 → clear genetic structuring between populations
- Values approaching 1 → populations are highly genetically distinct

- **GRM (Genomic Relationship Matrix):**

Principal component analysis (PCA) in this study was based on a genomic relationship matrix (GRM), which quantifies genetic similarity using allele frequencies across the genome. Because GRM is influenced by allele frequencies, it is particularly well suited for detecting broad-scale population structure.

- High values = closely related
- Low/negative values = unrelated

- **IBD (Identity-by-Descent):**

Identity-by-descent (IBD) analyses identify genome segments shared due to recent common ancestry and are therefore useful for detecting and quantifying shared genetic ancestry and close family relationships such as parent–offspring or full siblings.

- **ROH (Runs of Homozygosity):**

Continuous genomic regions of identical DNA indicating inbreeding

- Longer/more ROH = more inbreeding
- FROH – estimation of inbreeding from ROH

KEY BACKGROUND INFORMATION

Faroes Island salmon are a stocked salmon population with sources originating from iceland and fiskaaling (H.Haitun pers com).

Icelandic salmon provided in this study are from samples taken in the river Elliðaár in two cohorts, and Eystri-Rangá and provided by MFRI in Iceland. No information on the sampling of these samples is known to the author of this study.

Norwegian farmed salmon used in this study are confirmed escapee salmon from Norwegian aquaculture farms sampled in 6 escapee investigations.

No Farmed salmon from the Faroe Islands or Iceland are included in this study

See the following pages for detailed methods and results

Part 1: Broad Population structure of Atlantic salmon

Population Structure

Population structure analyses revealed clear genetic differentiation among Faroese, Icelandic, and Norwegian farmed salmon. Principal component analysis (PCA) showed strong separation between these major groups, with Norwegian farmed salmon forming a distinct and tightly clustered group along PC1, indicating substantial genetic divergence from both Faroese and Icelandic populations (Figure 1). Within the Icelandic samples, individuals from Elliðaár (2017 and 2020) and Eystri-Rangá (2019) formed overlapping but distinguishable clusters, indicating moderate structuring among Icelandic populations. Faroese samples from different cohorts (FI-2023, FI-2024, FI-2025) largely overlapped in PCA space, suggesting limited temporal genetic differentiation among cohorts and a shared breeding pool.

The genomic relationship matrix (GRM) shows closest genetic similarity between Faroese Atlantic salmon and Icelandic Atlantic salmon, reflecting the shared origin of these samples (Figure 3).

Pairwise FST estimates supported the GRM results and revealed clear patterns of genetic differentiation among populations (Figure 2). The highest levels of differentiation were observed between Norwegian farmed salmon and Icelandic populations (FST ≈ 0.144–0.174), with moderate genetic structure observed between Norwegian farmed salmon and Faroese salmon (FST ≈ 0.073–0.083) confirming that the Norwegian farmed individuals are genetically distinct from both Faroese and Icelandic populations.

Faroese and Icelandic populations showed moderate differentiation, with FST values generally ranging from approximately 0.044 to 0.072. Moderate differentiation was also observed between the Faroese and Norwegian Farmed salmon, (0.073-0.083), likely a reflection of the original stocking of breeding programs from Norwegian stock in the mid- late 20th century. The lowest differentiation was observed among Faroese cohorts, with pairwise FST values between FI-2023, FI-2024, and FI-2025 ranging from 0.004 to 0.009, indicating that these cohorts represent a single, genetically cohesive population, with temporal stability.

Among Icelandic populations, relatively low differentiation was observed between temporal samples of Elliðaár (e.g. IS-2017 vs IS-2020, FST ≈ 0.012), while slightly higher values were observed between Eystri-Rangá (IS-2019) and the Elliðaár samples (FST ≈ 0.046–0.056). These results suggest modest structuring within Iceland but overall genetic similarity between source populations.

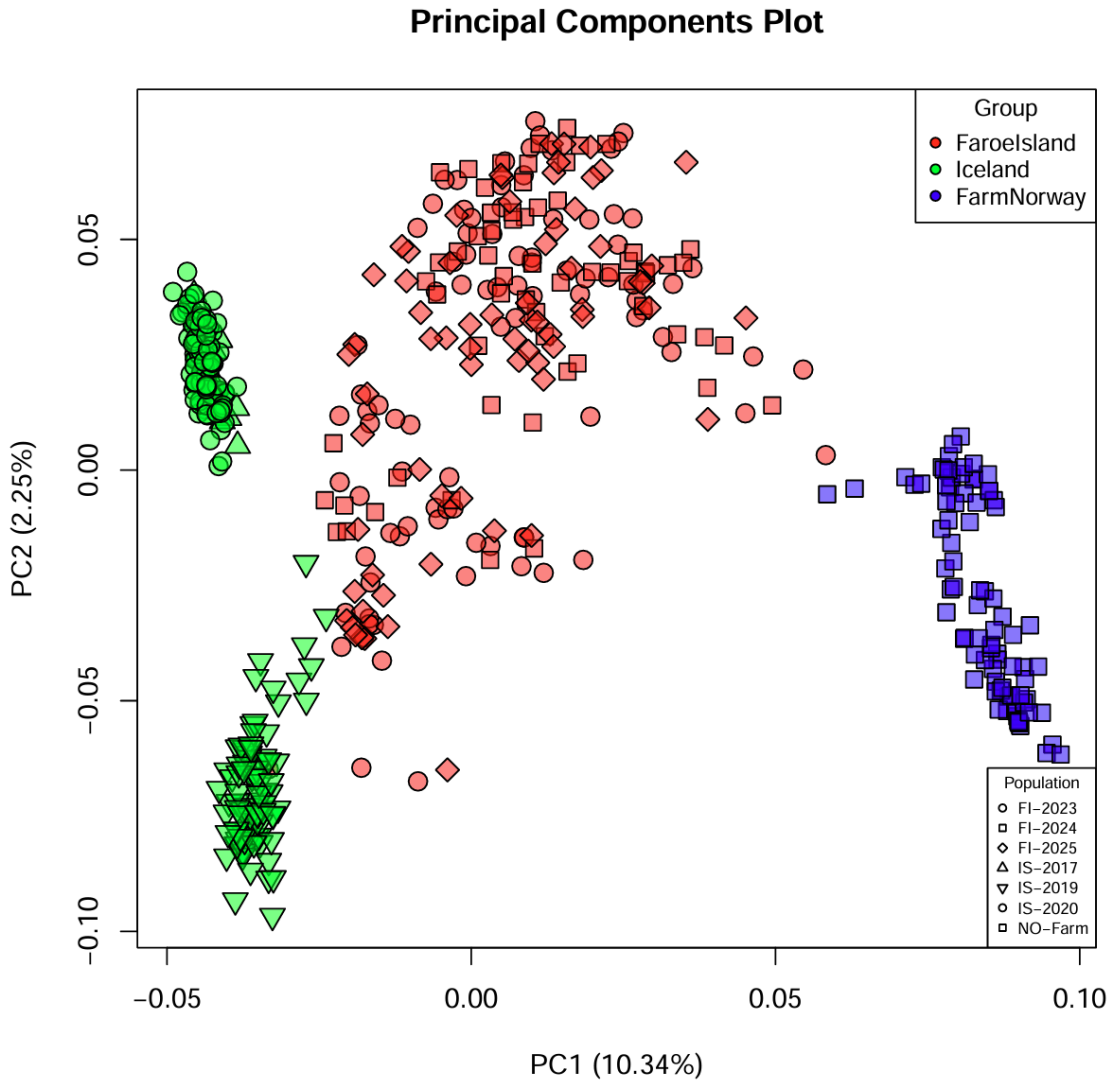

Figure 1 Principal components PC1 (x-axes) and PC 2 (y-axes) calculated from the genomic relationship matrix of all individuals. Samples are colour-coded by sampling site, and shape is defined by cohort as given in legend.

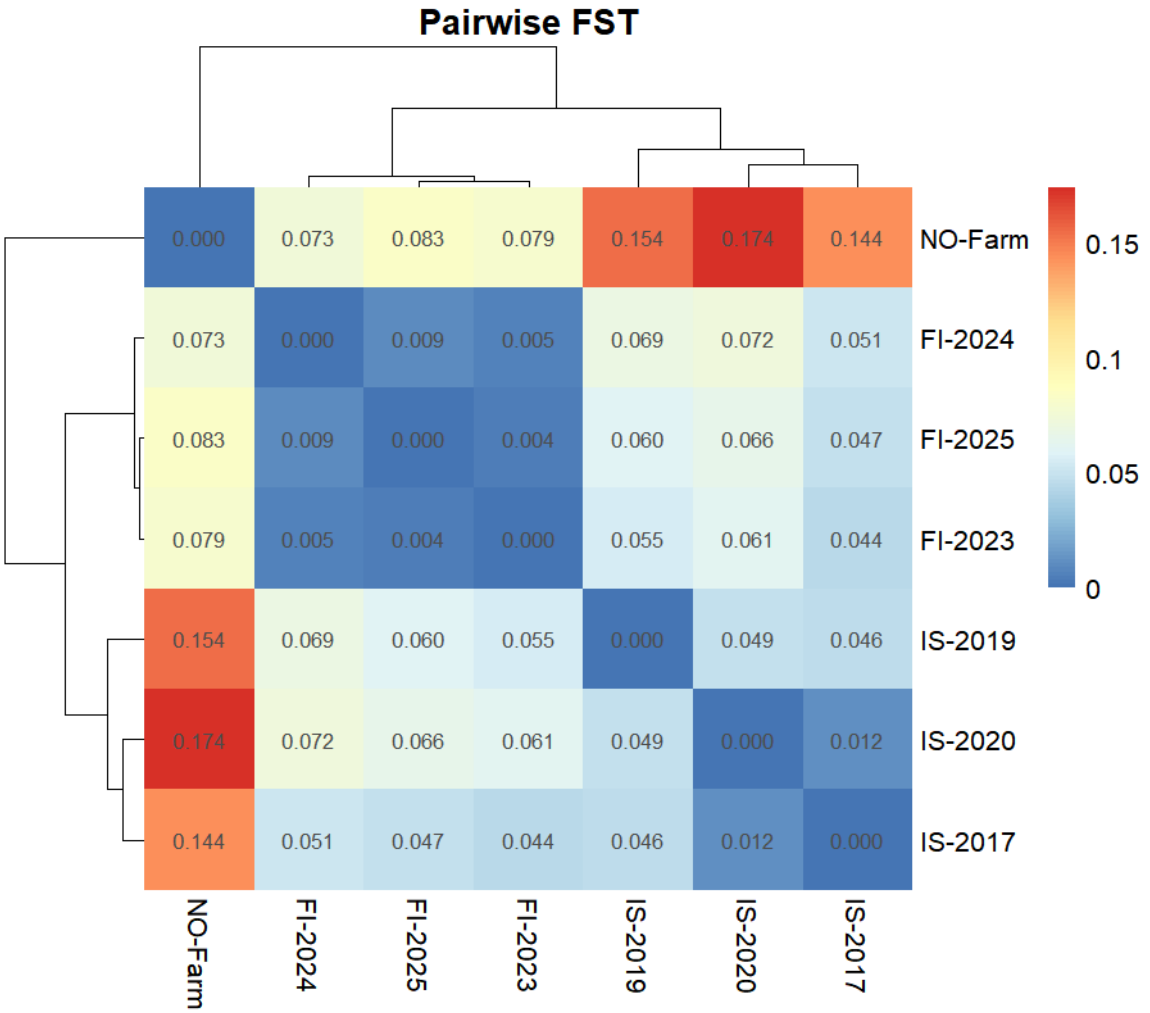

Figure 2: Heatmap matrix of pairwise population FST values. Low population differentiation is denoted by small FST values and "colder" colours, larger population differentiation is denoted by "warmer" colours and larger FST values.

Genomic Relatedness and Inbreeding

Patterns of genomic relatedness further supported these findings (Figure 3). Mean genomic relationship matrix (GRM) values within populations were highest for Norwegian farmed salmon (mean GRM ≈ 0.410), reflecting the high degree of relatedness expected in selectively bred aquaculture stocks. In comparison, Faroese populations showed substantially lower within-population relatedness (mean GRM ≈ 0.020–0.036), consistent with a more diverse breeding pool. Between-population GRM values were close to zero or negative for comparisons involving Norwegian farmed salmon and the other populations, indicating little shared recent ancestry. In contrast, Faroese and Icelandic populations exhibited small but positive between-population GRM values, consistent with shared ancestry due to historical translocation from Icelandic source populations.

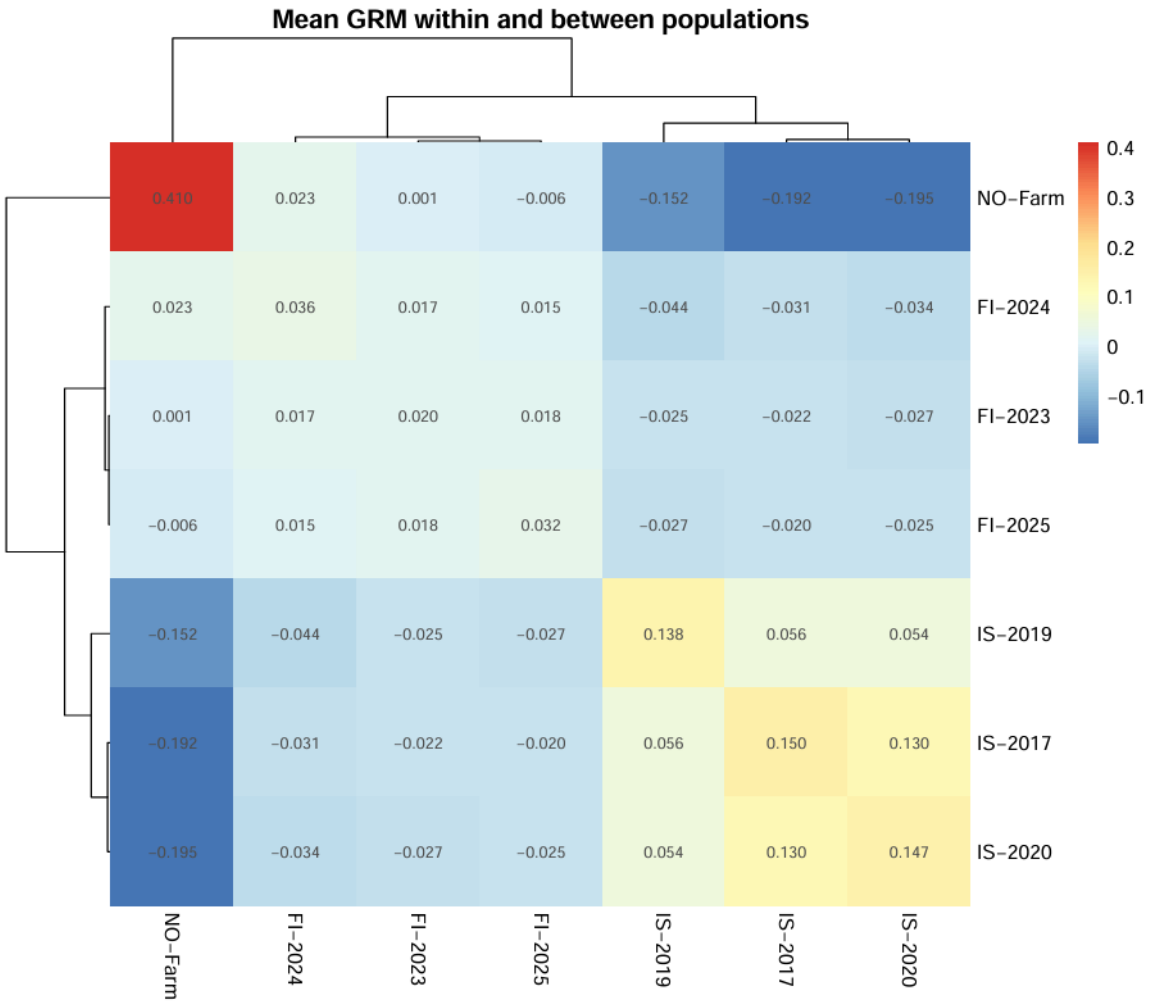

Figure 3: Heatmap matrix of mean pairwise genomic relationship (GRM) among populations. More remote genomic relatedness is denoted by small values and "colder" colours, closer population relatedness is denoted by "warmer" colours and larger values.

Identity-by-descent (IBD) network analysis

Network analysis of identity-by-descent (IBD) relationships revealed clear clustering patterns corresponding to population origin (Figure 4). Faroese and Icelandic individuals formed interconnected networks with numerous relationships of varying degrees, including full-sibling, parent–offspring, and second-degree relationships. These patterns reflect both shared ancestry and ongoing relatedness within these populations.

In contrast, Norwegian farmed salmon formed distinct clusters that were largely separated from the Faroese and Icelandic networks, with minimal connectivity between groups. This further supports the conclusion that farmed escapees represent a genetically distinct group with limited integration into the Faroese population.

Within the Faroese samples, the IBD network showed multiple clusters of closely related individuals, indicating the presence of family structure within cohorts. This is consistent with the use of supportive breeding programs and suggests that a relatively limited number of breeders may contribute disproportionately to subsequent generations.

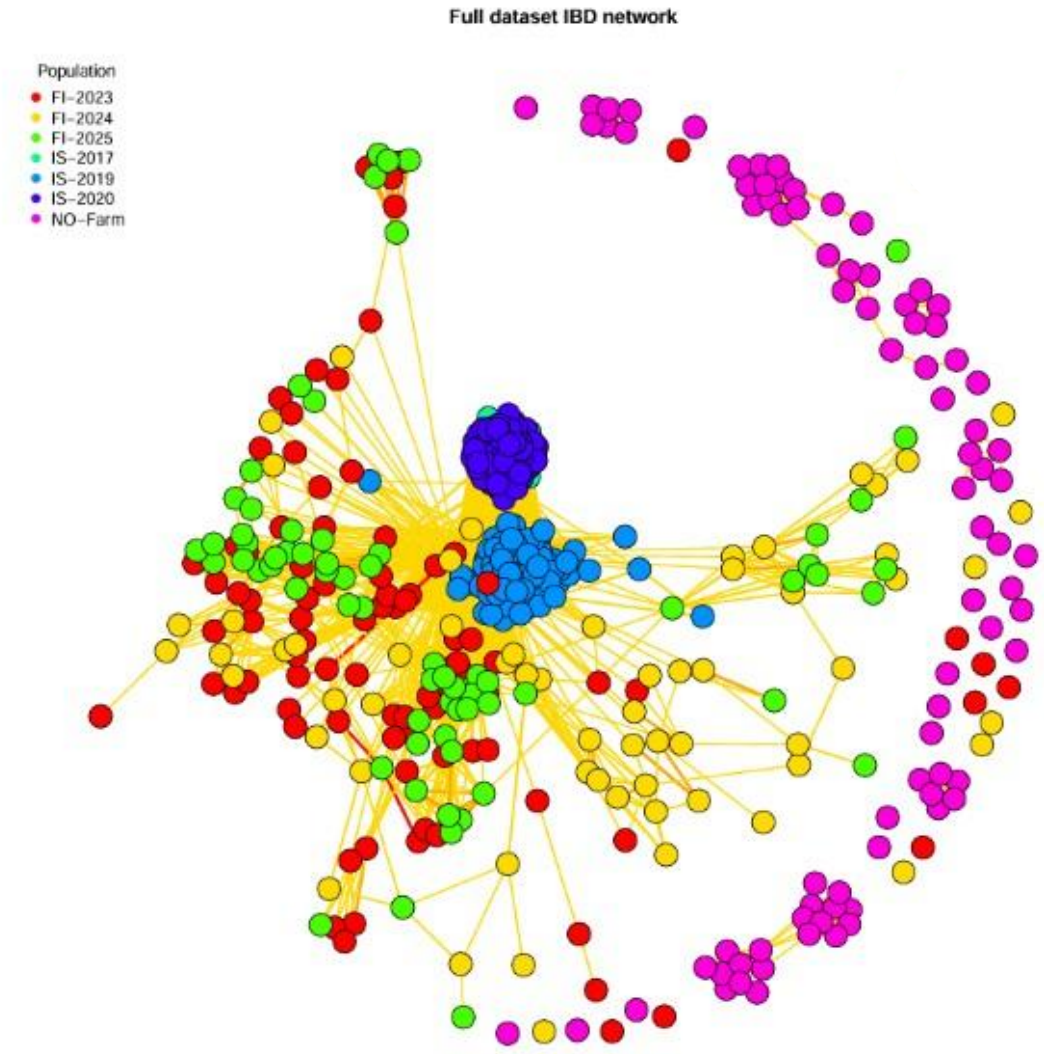

Figure 4: Identity-by-descent (IBD) Network. Dense clusters indicate close familiar relationships, common recent ancestry is denoted by connected lines. Populations and cohorts are coloured as per figure legend.

Summary of Part 1

Overall, these results demonstrate that Faroese Atlantic salmon retain a close genetic affinity to their Icelandic source populations, and moderate levels of genetic structuring from Norwegian farmed salmon. The low differentiation among Faroese cohorts indicates temporal stability in the population, whereas the presence of relatedness within cohorts suggests that breeding practices may influence genetic structure at a finer scale.

It is important to note that the farmed comparison in this study is from relatively recent Norwegian aquaculture samples. No comparison has been made to Faroese or Icelandic aquaculture samples, and thus a general conclusion on genetic influence of these aquaculture samples to Faroese populations cannot be made. Nevertheless, Faroese and Icelandic aquaculture stock is based on breeding material originating from Norway in the 20th century, and this can be observed in only moderate levels of genetic structuring between the Norwegian material in this study and the Faroese samples.

Part 2: Faroese Atlantic salmon - genomic relatedness and genetic diversity

Within-cohort relatedness in Faroese salmon

Analysis of identity-by-descent (IBD) relationships within the Faroese dataset revealed extensive relatedness among individuals across all cohorts. The full dataset network showed a highly connected structure, with multiple clusters linked by first-, second-, and third-degree relationships, as well as occasional parent–offspring and full-sibling pairs (Figure 5). This indicates that many individuals within the Faroese population form a network of interconnected families.

When examined by cohort, distinct patterns of relatedness were evident (Figure 6). The 2023 broodstock cohort displayed numerous close relationships, including full-sibling and parent–offspring connections, forming several tightly connected clusters. Similarly, the 2024 and 2025 broodstock cohorts exhibited multiple family groups, with clear clusters of closely related individuals and evidence of repeated use of related breeders. The 2023 smolt cohort also showed evidence of family structure, with clusters of related individuals consistent with offspring originating from a limited number of parental crosses.

Across all cohorts, the presence of numerous second- and third-degree relationships further indicates that relatedness extends beyond immediate families, reflecting shared ancestry across generations. Together, these results demonstrate that the Faroese salmon population exhibits substantial pedigree structure, likely reflecting the effects of supportive breeding and a limited effective number of breeders contributing to each cohort.

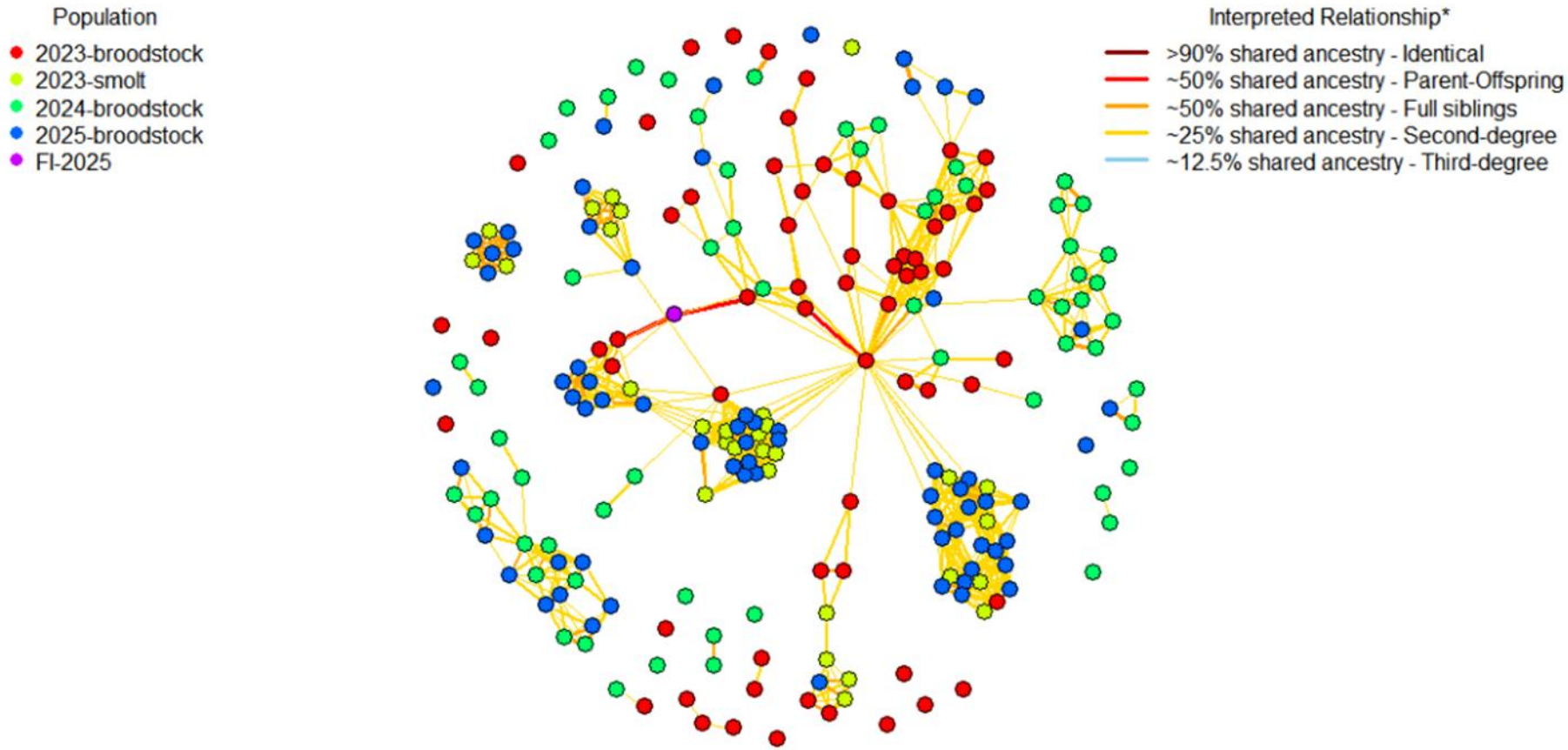

Figure 5: Identity by descent (IBD) network of Faroe Island Atlantic salmon, including a mis-labelled salmon (FI-2025). Dense clusters indicate close familiar relationships, common recent ancestry is denoted by connected lines and the estimated relationship based on patterns of allele sharing across the genome are denoted as per the legend. Populations and cohorts are coloured as per figure legend.

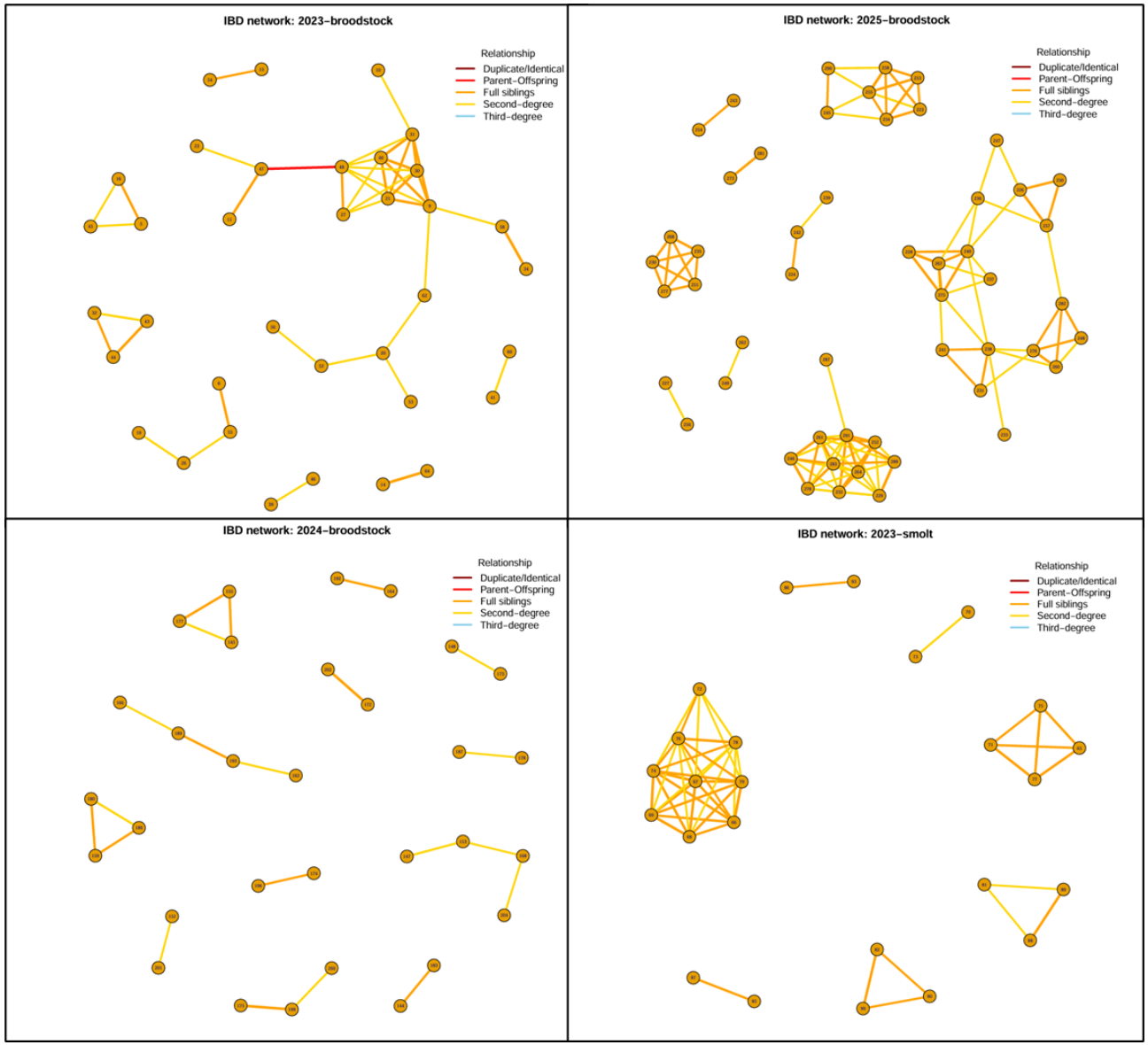

Figure 6: Identity by descent (IBD) networks per cohort of Faroe Island Atlantic salmon.

Genetic diversity and inbreeding

Genome-wide analysis of runs of homozygosity (ROH) revealed considerable variation in the extent and distribution of homozygous segments among individuals. Both the number and length of ROH varied widely across samples, indicating variation in individual inbreeding histories (Figure 7).

Long ROH segments were observed in a subset of individuals, consistent with recent inbreeding events (e.g. mating between close relatives), whereas shorter and more numerous ROH were present in other individuals, reflecting more distant shared ancestry. Differences in ROH patterns were also apparent among cohorts, with some broodstock individuals exhibiting particularly high ROH burden compared to others.

Chromosome-level analysis of FROH showed broadly consistent patterns across the genome, with no single chromosome disproportionately contributing to overall inbreeding. This suggests that inbreeding is genome-wide rather than driven by localized selection or structural variation (Data not shown).

Estimates of genomic inbreeding (FROH) further highlighted variation among individuals and cohorts (Figure 8). FROH values ranged from low levels (~0.03) to relatively high levels (>0.30), indicating a broad spectrum of inbreeding within cohorts. Most individuals fell within an intermediate range (~0.08–0.18), suggesting moderate levels of inbreeding across the population as a whole. Overall, the distribution of FROH indicates that while the population retains genetic diversity, there is clear evidence of inbreeding in a subset of individuals.

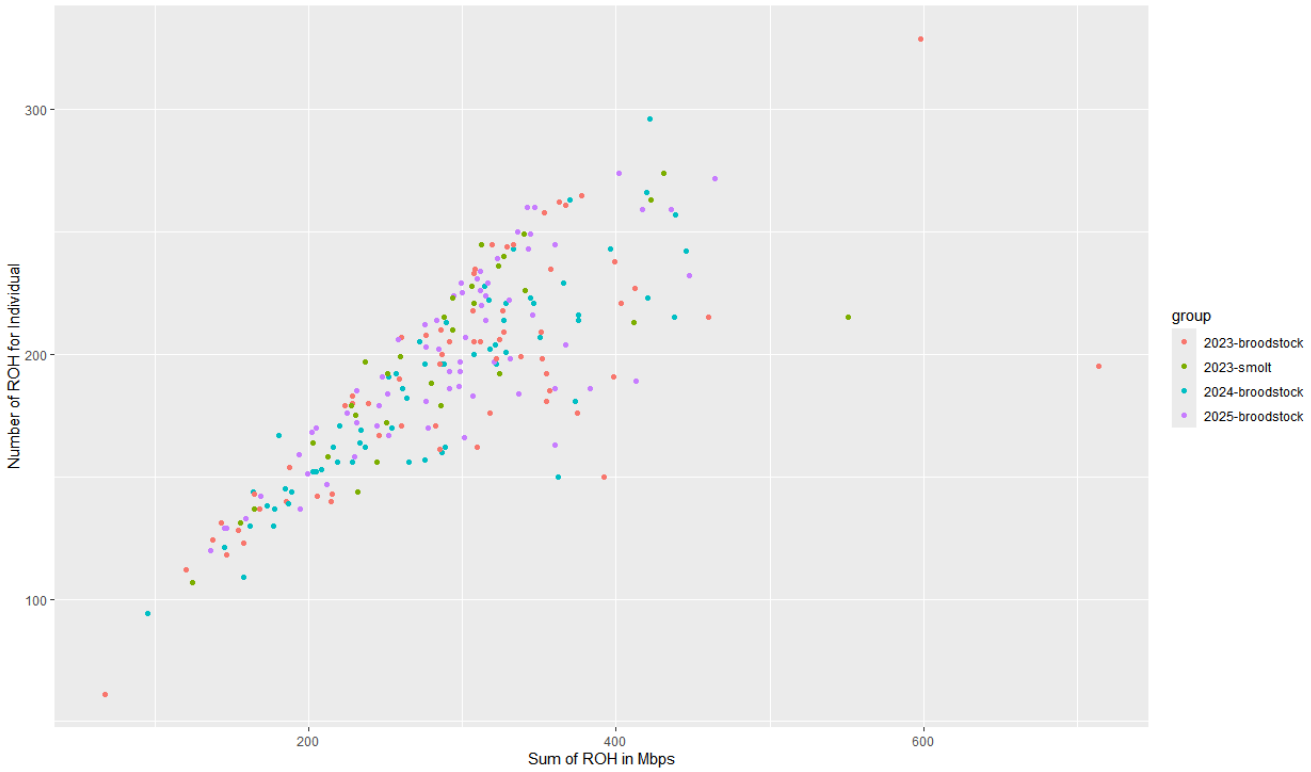

Figure 7: Scatterplot of number of detected runs of homozygosity (ROH) – Y-axis) and the size of the detected ROH. Large ROH can identify patterns in the distribution of runs in different cohorts (e.g. few long runs vs many short runs). Runs of homozyosity accumulate with inbreeding, thus both longer segments of homozygous regions or more ROH are indicative of inbreeding history.

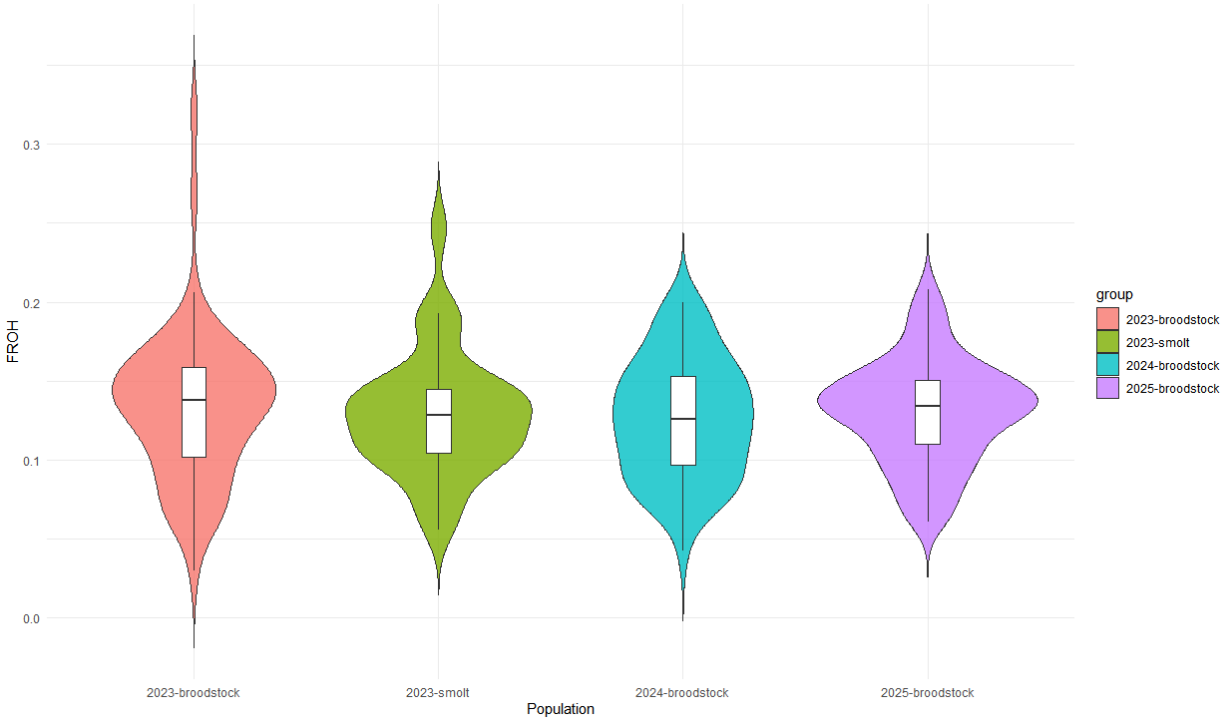

Figure 8 Distribution of inbreeding estimates of inbreeding from ROH per cohort. The box plot represents the quartiles (lowe and upper 75% of the data) with the line in the middle denoting the median FROH for each group.

Summary of Part 2.

Taken together, the genetic relatedness and inbreeding analyses indicate that the Faroese salmon population is characterised by a mixture of moderate genetic diversity and substantial relatedness among individuals. The presence of multiple family clusters within cohorts, combined with elevated inbreeding in some individuals, suggests that a relatively small number of breeders may contribute disproportionately to successive generations.

Despite this, the wide range of inbreeding values indicates that only some individuals are highly inbred; there are also many individuals with moderate and low levels of inbreeding, indicating sufficient genetic variation in the population as a whole. This presents an opportunity for genetic management to maintain or improve diversity through informed broodstock selection.

The integration of genetic relatedness (IBD) and inbreeding (FROH) information provides a practical framework for breeding management. Specifically, avoiding matings between closely related individuals (e.g. full siblings or parent–offspring pairs) and prioritising individuals with lower genomic inbreeding coefficients would help to reduce the accumulation of inbreeding over time. In addition, balancing parental contributions across cohorts could further enhance effective population size and maintain long-term genetic diversity.

Part 3: Faroese trout - Population structure and relatedness

Population structure of trout

Note: The sample sizes are low in several of these populations, and as such, inferences of inbreeding, population structuring and genetic diversity may not be representative of the entire population.

Population structure analyses of trout revealed clear genetic differentiation among sampling locations, despite the reduced SNP density (~1,000 SNPs). Principal component analysis (PCA) showed distinct clustering of individuals according to their population of origin, indicating that the marker set was sufficient to resolve broad-scale population structure (Figure 9).

Several populations formed well-defined and separated clusters in PCA space, these represent lakes with the seatrout populations clustering together. Individuals from Leitisvatn were clearly differentiated along the primary axis of variation (PC1), forming a distinct cluster separated from all other populations. Other populations, such as those from Niðara vatn Eiði and Saksun, also showed clear grouping patterns, although some degree of overlap was observed among geographically or genetically closer populations.

Pairwise FST estimates revealed moderate to high levels of genetic differentiation among trout populations (Figure 10). The highest differentiation was observed between Leitisvatn and other populations (FST ≈ 0.16–0.28), indicating strong genetic divergence and suggesting limited gene flow between this population and others.

Other population comparisons showed moderate differentiation, with FST values typically ranging from approximately 0.03 to 0.10. Lower FST values were observed among several populations (e.g. Sandá, Dalsá, and Leynar), suggesting greater connectivity or more recent shared ancestry among these locations. In contrast, higher values involving populations such as Áin norðuri við Á and Niðara vatn Eiði indicate stronger genetic structuring as would be expected in lake populations. Hviltkinnvatn (1 sample) does not cluster with other samples, and although a population inference from 1 sample is not possible, this genetic separation is likely a result of the geographic separation of the lake it inhabits.

Overall, the FST results demonstrate that trout populations in the Faroe Islands are genetically structured, with some populations showing pronounced isolation.

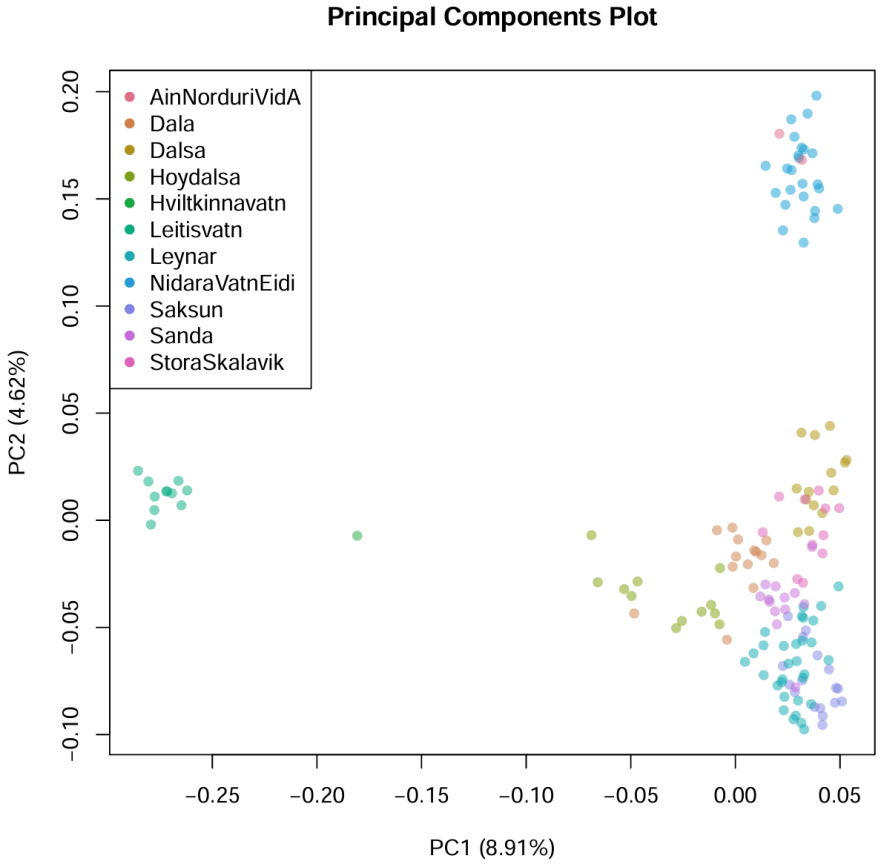

Figure 9 Principal components PC1 (x-axes) and PC 2 (y-axes) calculated from the genomic relationship matrix of all individuals. Samples are colour-coded by sampling site, and shape is defined by cohort as given in legend.

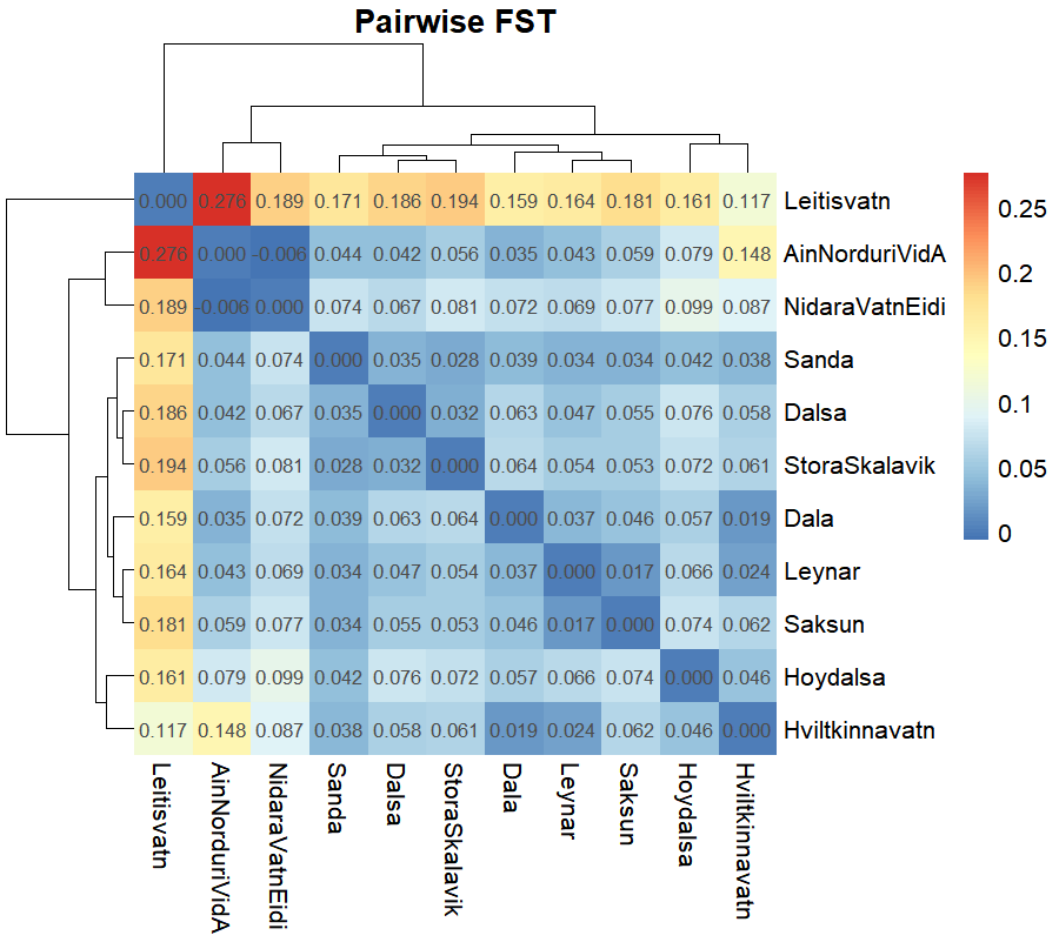

Figure 10: Heatmap matrix of pairwise population FST values. Low population differentiation is denoted by small FST values and "colder" colours, larger population differentiation is denoted by "warmer" colours and larger FST values.

Genetic diversity (heterozygosity and inbreeding)

Estimates of observed heterozygosity (Ho) indicated moderate levels of genetic diversity across populations, with values ranging from approximately 0.25 to 0.30. Most populations exhibited similar levels of heterozygosity, suggesting broadly comparable levels of genetic variation. However, some variation was observed among populations. The single sample from Hviltkinnavatn showed the lowest heterozygosity (Ho ≈ 0.247), indicating reduced genetic diversity relative to mean levels in other populations, whereas populations such as Dalá, Hoydalsá, and Sandá exhibited higher values (Ho ≈ 0.297–0.300), suggesting relatively higher diversity.

Inbreeding coefficients (F) were generally low or negative across most populations, indicating little evidence of inbreeding and, in some cases, a slight excess of heterozygosity relative to a neutral population expectation. Negative F values were observed in several populations (e.g. Dalá, Hoydalsá, and Sandá), consistent with outbreeding or mixing of genetically distinct lineages (Table 2). Hviltkinnavatn

contained just a single sample which had a positive inbreeding coefficient (F ≈ 0.11), suggesting a degree of inbreeding in this sample, no inference on the remaining population can be made without more samples. Likewise, Áin Norður við Á contained just two samples and as such limited inference on the population as a whole can be made, yet these two samples had low inbreeding coefficient and moderate level of genetic diversity as measured by the observed heterozygosity.

Table 2: estimates of inbreeding coefficient (F) and observed heterozygosity among populations. Number of individuals sampled per population is provided (N) and must be taken into account when interpreting genetic diversity as a whole.

Population ID	N	Mean F	Mean Ho
Áin Norður við Á	2	0.009921	0.276057
Dalá	14	-0.07567	0.299697
Dalsá	14	-0.00505	0.280117
Hoydalsá	12	-0.06891	0.29774
Hviltkinnavatn	1	0.1132	0.24707
Leitisvatn	11	-0.02413	0.285169
Leynar	31	-0.06845	0.29781
Niðara vatn Eiði	24	-0.02295	0.284789
Saksun	17	-0.02004	0.284207
Sandá	13	-0.06891	0.298046
Stórá - Skálavík	11	-0.02459	0.285555

Genomic relatedness within populations

Analysis of genomic relatedness within populations revealed substantial variation in mean relatedness levels (Figure 11). Most populations exhibited low to moderate mean genomic relationship matrix (GRM) values (e.g. Leynar ≈ 0.066, Sanda ≈ 0.064), consistent with relatively low levels of relatedness among individuals.

However, some populations showed elevated relatedness. For example, Hoydalsá (mean GRM ≈ 0.198) and Niðara vatn Eiði (mean GRM ≈ 0.175) exhibited higher within-population relatedness, suggesting smaller effective population sizes or stronger family structure. Notably, Leitisvatn displayed extremely high mean relatedness (mean GRM ≈ 0.96), indicating that sampled individuals are highly related and potentially represent a very small or isolated population.
The individual-level GRM heatmap further supports these findings, showing clear blocks of high relatedness within populations and lower relatedness between populations, consistent with the presence of structured and partially isolated populations. Note again that sample sizes in some populations are small and therefore give a biased picture of the population as a whole.

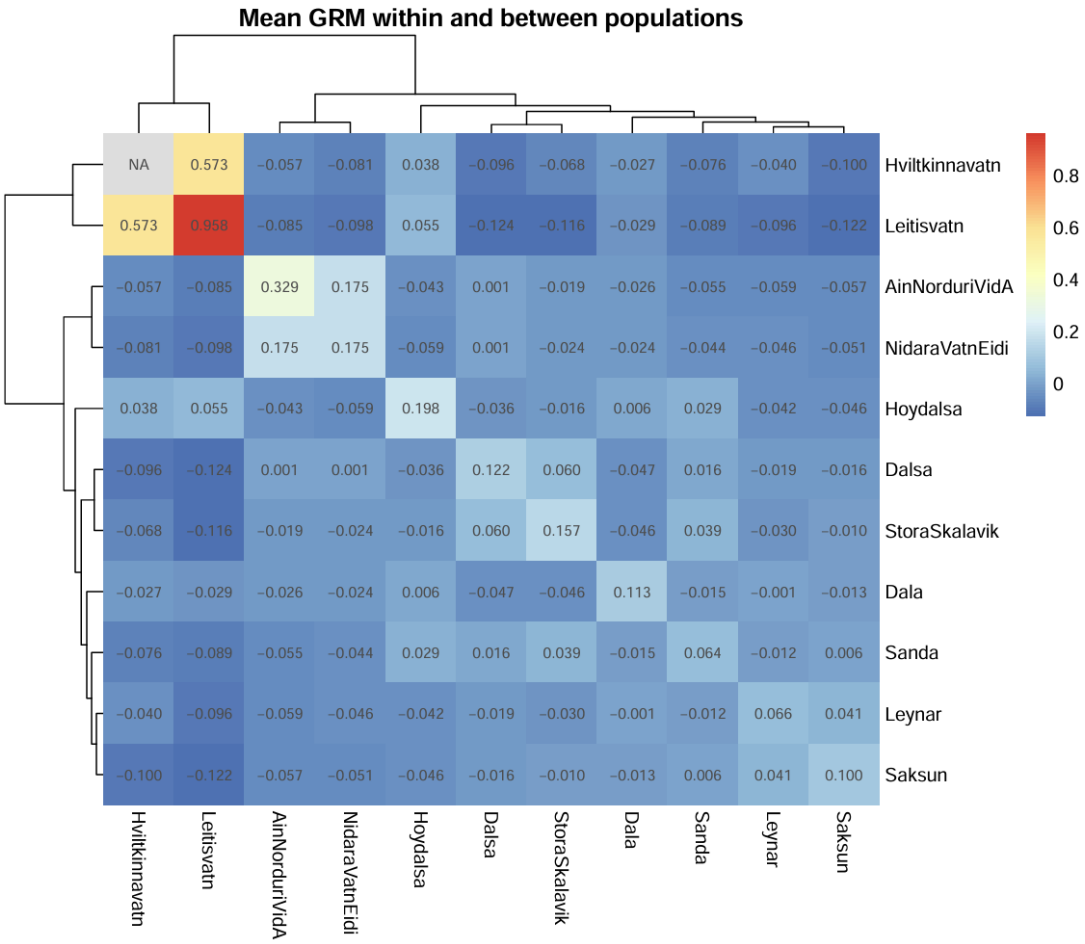

Figure 11: Heatmap matrix of mean pairwise genomic relationship (GRM) among populations. More remote genomic relatedness is denoted by small values and "colder" colours, closer population relatedness is denoted by "warmer" colours and larger values.

Summary of Part 3

Despite the reduced SNP density, and low sample sizes, the analyses consistently demonstrate that brown trout populations in the Faroe Islands are genetically structured, with varying degrees of differentiation and connectivity among locations. While most populations maintain moderate genetic diversity and low inbreeding, certain populations, particularly Leitisvatn, show signs of reduced diversity or elevated relatedness, suggesting potential isolation and reduced effective population size.

Detailed analysis methods

DNA from Faroe Island samples (both salmon and trout) was extracted and genotyped on the SsaTrack microarray. Genotype data for Faroe Island salmon and trout genotyping analysis was performed separately in Axiom Analysis Suite v5.4.0.23 using default SNP clustering and settings for Atlantic salmon and customised SNP clustering for Salmo trutta made using the Axiom Batch SSP tool.

Dataset 1. Faroe Island – Icelandic – Norwegian Atlantic salmon dataset.

Icelandic salmon raw genotype data (also genotyped on the SsaTrack array) was combined with the Faroe Island salmon data and data from confirmed escaped aquaculture salmon assigned by Sporbarhet AS from several escapee investigations. The Sporbarhet genotype data were genotyped on the Sporbar1 array, however this array contains many DNA markers in common with the SSaTrack array. Genotype data from Faroe Island, Icelandic and Farmed Norwegian salmon samples were thus combined and filtered using the software Plink 2.0[i, ii], to exclude individuals that were missing more than 5% of SNP data, SNP markers that had missing calls for more than 5% of the individuals, and SNPs that had a minor allele frequency of less than 5%.

After QC steps, 19021 SNP markers were analysed for 512 individual samples in dataset 1.

Dataset 2. Faroe Island Atlantic salmon dataset.

Genotype data from the Faroe Island salmon samples were filtered using the software Plink 2.0[i, ii], to exclude individuals that were missing more than 5% of SNP data, SNP markers that had missing calls for more than 5% of the individuals, and SNPs that had a minor allele frequency of less than 5%.

After QC steps, 51538 SNP markers were analysed for 224 individual samples in dataset 2.

Dataset 3. Faroe Island trout dataset.

Genotype data from the Faroe Island trout samples were filtered using the software Plink 2.0[i, ii], to exclude individuals that were missing more than 5% of SNP data, SNP markers that had missing calls for more than 5% of the individuals, and SNPs that had a minor allele frequency of less than 5%.

After QC steps, 1033 SNP markers were analysed for 150 individual samples in dataset 3.

Analyses.

Analyses were performed in Plink v2.0[1], GCTA[2], and detectRUNS[3] and plotted in R using in-house pipelines.

References

[1] Plink 2.0 Shaun Purcell, Christopher Chang www.cog-genomics.org/plink/2.0/

[2] Yang J, Lee SH, Goddard ME, Visscher PM. GCTA: a tool for genome-wide complex trait analysis. *Am J Hum Genet*. 2011;88(1):76-82. doi: 10.1016/j.ajhg.2010.11.011

[3] Biscarini, F., Cozzi, P., Gaspa, G & Marras, G. 2019 detectRUNS DOI: 10.32614/CRAN.package.detectRUNS