	<p style="text-align: center;"><b>International Atlantic Salmon Research Board</b></p> <p style="text-align: center;"><i>Proposal for a New Single Nucleotide Polymorphism (SNP) Genetic Baseline to Assign Atlantic Salmon (<i>Salmo salar</i>) Sampled at Greenland</i></p>	<p style="text-align: center;"><b>ICR(22)08</b></p>
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***Proposal for a New Single Nucleotide Polymorphism (SNP) Genetic Baseline  
to Assign Atlantic Salmon (*Salmo salar*) Sampled at Greenland***

**Background**

At the 2021 Annual Meeting of the Board, [ICR\(21\)18](#) paragraph 8.1, the Board member for the UK referred to the potential development of a new north Atlantic single nucleotide polymorphism (SNP) baseline to assign Atlantic salmon sampled at Greenland to region of origin. She asked if this was something that could be referred to the Board's Scientific Advisory Group (SAG). The Chair noted that there may be an inter-sessional meeting of the Board in 2021-2022 and suggested that this could be discussed at that meeting. The Board member for the UK agreed to provide further information for the discussion.

However, there was no inter-sessional meeting of the Board in 2021-2022, as the inter-sessional work was completed by correspondence. The Board member for the UK provided information on this proposal in April 2022 for discussion at the 2022 Annual Meeting of the Board.

The proposal for a new single nucleotide polymorphism (SNP) genetic baseline to assign Atlantic salmon (*Salmo salar*) sampled at Greenland is in Annex 1.

**Decisions**

The Board may wish to consider the proposal in Annex 1 and agree whether to endorse the concept of composing a new North-East Atlantic salmon genetic baseline for the purpose of assigning salmon samples from Greenland to region of origin.

Secretariat  
Edinburgh  
6 May 2022

### ***A new Single Nucleotide Polymorphism (SNP) genetic baseline to assign Atlantic salmon (*Salmo salar*) sampled at Greenland***

#### **Introduction**

Genetic Stock Identification (GSI) can be a useful tool for fisheries managers as it can identify contributing stocks in Mixed-Stock Fishery (MSF) samples. This technique has been used on Atlantic salmon (*Salmo salar*) using various types of genetic markers such as minisatellites (e.g. Galvin *et al.*, 1995) and microsatellites (e.g. Ensing *et al.*, 2013). Single-Nucleotide Polymorphisms (SNPs) have also been used to investigate population structure in Atlantic salmon populations (e.g. Arnekleiv *et al.*, 2019) but examples of its use in GSI studies are – to date – notably absent from the scientific literature. The technique is however currently used in GSI studies, as will be discussed below, but references are limited to scientific reports and grey literature.

GSI studies depend on the existence of a comprehensive genetic baseline, including baseline samples from all stocks present in the assignment sample. They also require genetic markers able to discriminate between contributing stocks, as well as the existence of genetic differentiation between stocks, i.e. the existence of more-or-less discrete genetic populations. In other words, GSI does not work with panmictic stocks or when the chosen genetic marker is unable to determine the true levels of genetic differentiation between populations sufficiently.

#### **Greenland**

The ICES Working Group North Atlantic Salmon (WGNAS) has used a microsatellite genetic baseline originally developed for the SALSEA-Merge project (Gilbey *et al.*, 2018, Fig. 1) in order to assign Atlantic salmon samples collected during the International Sampling Programme at Greenland to region-of-origin, after having been separated according to continent-of-origin using a scale analysis (WGNAS, 2021). This SALSEA-Merge genetic baseline, which covers the North-East Atlantic (NEAC) area, is augmented with a North-West Atlantic (NAC) area component in order to conduct this analysis (WGNAS, 2018). From 2017 onward this was replaced by a SNP baseline which has much improved spatial coverage in the North-West Atlantic area (Fig. 2), but limited spatial coverage in the North-East Atlantic area, especially when compared to the previous SALSEA-Merge microsatellite baseline (compare figures 1 and 2).

#### **SNPs vs. microsatellites**

SNPs can have certain advantages over microsatellites, such as not requiring lengthy inter-calibrations between labs when combining genotypes generated in different labs or analysis platforms into a single baseline. The main advantage for North-East Atlantic salmon however is the potential for greater resolution compared to using the SALSEA-Merge microsatellite baseline. The main weakness of the SALSEA-Merge microsatellite baseline is the limited resolution within the Ireland/UK assignment group. Individuals cannot be assigned to river- or region of origin, but assign (weakly supported) to 4-5 very broad assignment groups, which is not very useful for management. This a result of the particular post-glacial colonisation history of Atlantic salmon in Britain and Ireland after the Last Glacial Maximum (LGM) causing shallow phylogeny, and the lack of power in the microsatellite baseline to resolve this. There are indications that certain SNP suits are better suited to find substructure within the

Ireland/UK assignment group compared to the SALSEA-Merge microsatellite baseline (pers. comm. J. Gilbey/P. Prodöhl). The problem is that not all populations analysed for the SALSEA-Merge baseline have been analysed for SNPs, let alone the same SNPs (so they can be included in a single baseline). After the SALSEA-Merge project some countries have continued to update and develop their Atlantic salmon genetic baselines, while others haven't. Some areas (Norway, Scotland) are well covered for SNPs, also with good overlap in SNPs. Other areas are less well covered, or not at all. This however can be addressed fairly easily by genotyping archival samples in these areas, some limited resampling, and work on rationalisation and fine-tuning of the North-East Atlantic SNP baseline.

A higher resolution North-East Atlantic SNP baseline would be major improvement over the currently North-West Atlantic-heavy SNP baseline with the limited number of added North-East Atlantic samples, as well as the historic SALSEA-Merge microsatellite baseline. The hope is a new fit-for-purpose North-East Atlantic SNP genetic baseline will allow genetic assignment of Atlantic salmon sampled at Greenland to be assigned to higher resolution genetic assignment groups beyond the current level of for example 'Irish Sea' or 'Northern Scotland/North & West Ireland'. This shallow level of geographical resolution is suboptimal for management, especially against a background of possible exploitation of Atlantic salmon at East-Greenland, an area where it is known NEAC origin fish dominate relative to NAC fish (WGNAS 2022, in press).

### **Proposal**

A meeting of North-East Atlantic salmon geneticists will take place in May 2022. At this meeting a proposal will be developed for a project to compose a new North-East Atlantic salmon genetic baseline for the purpose of assigning salmon samples from Greenland to region of origin. The project will combine existing SNP North-East Atlantic salmon genetic baselines, allow genotyping of archival samples and collection and genotyping of geographical gaps in the envisioned baseline. The work will be published in a peer-reviewed scientific journal.

We therefore seek the Board's endorsement of the concept of composing a new North-East Atlantic salmon genetic baseline for the purpose of assigning salmon samples from Greenland to region of origin.

### **References**

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Figure 1. SALSEA-Merge microsatellite baseline sampling spatial coverage in the North-East Atlantic area; 26 813 individuals from 467 locations in 284 rivers.

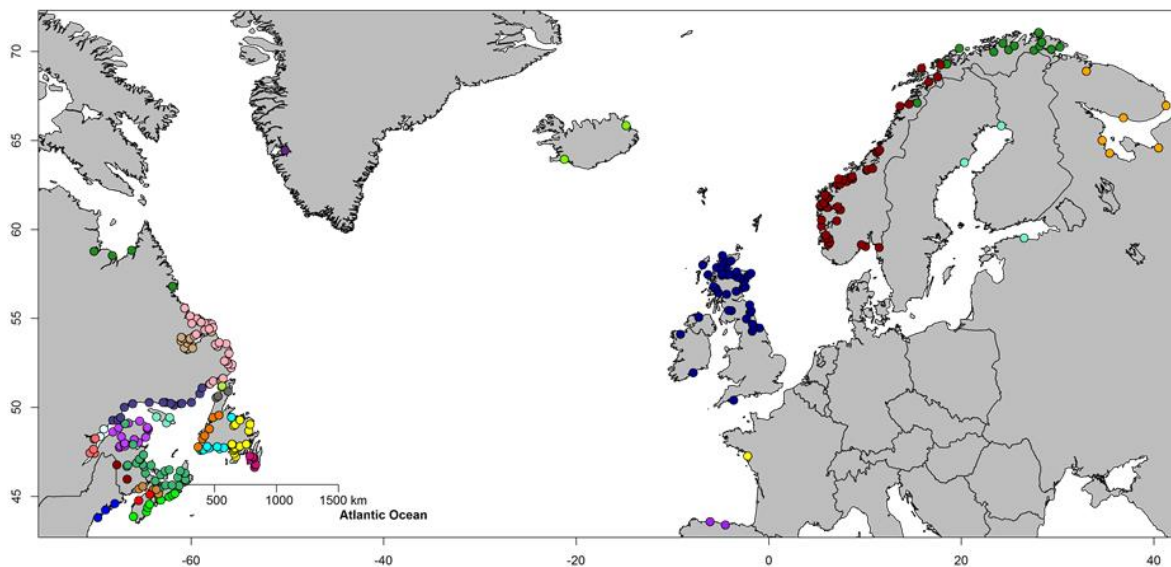


Figure 2. SNP genetic baseline sampling spatial coverage in the North Atlantic.