

	<p><b>International Atlantic Salmon Research Board</b></p> <p><i>Proposal for an Updated Comprehensive trans-European Genetic Reference Baseline to Assign Atlantic Salmon (<i>Salmo salar</i>) to Rivers and Region of Origin across the Eastern North Atlantic</i></p>	<p><b>ICR(24)07</b></p> <p>Agenda item: 6</p>
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***Proposal for an Updated Comprehensive trans-European Genetic Reference Baseline to Assign Atlantic Salmon (*Salmo salar*) to Rivers and Region of Origin across the Eastern North Atlantic***

**Purpose**

The purpose of this paper is to update the Board on the proposal submitted by the UK in 2023 for funding and provide details to enable the Board to consider the request for further funding.

**Decision**

- the Board may wish to agree whether to fund the updated ‘Proposal for an Updated Comprehensive trans-European Genetic Reference Baseline to Assign Atlantic Salmon (*Salmo salar*) to Rivers and Region of Origin across the Eastern North Atlantic’.

**Background**

At its 2023 Annual Meeting, the Board considered a proposal from the UK for an Updated Comprehensive trans-European Genetic Reference Baseline to Assign Atlantic Salmon (*Salmo salar*) to Rivers and Region of Origin across the Eastern North Atlantic’, [ICR\(23\)11](#). The proposal sought strategic funding of €41,000 from the Board.

In its consideration of the proposal, the Board noted that it was very supportive of the proposed work and agreed to make a decision on funding the scoping workshop by correspondence, once additional information had been provided.

The Secretariat sought the requested information and a modified proposal, [ICR\(23\)19](#), was received seeking funding of the lesser amount of €19,000 in 2023. The Board considered this proposal by correspondence and unanimously agreed to provide the €3,000 sought to support the hybrid meeting. The majority of the Board’s responses were also in support of providing the additional €16,000 to support 200 post-doc hours based at IMR in Norway, to collate information on the various sample and data availability across the eastern Atlantic and Baltic range and to perform both a power analysis of new baseline capabilities and to examine novel analytical methods of performing robust GSI. However, two members of the Board requested further consideration of this before making a decision. The Board agreed that once the ‘Draft Plan’ arising from the hybrid workshop (items one and two of [ICR\(23\)19](#)) had been provided, it would be considered by the Board and a decision could be taken on providing the additional funding.

The project consortium has now provided an update on the Proposal (Annex 1), the Report on the Baseline Workshop (Annex 2) and a presentation given to the WGNAS on the proposal (Annex 3) for the Board’s consideration. The update in Annex 1 seeks the additional €16,000 to fund the following deliverables:

- an enhanced resolution baseline for covering a significant proportion of the production in the Eastern Atlantic;
- enhanced resolution of archived marine samples to increase understanding of differential stock utilisation in the Atlantic;
- the enhanced ability to refine the ICES lifecycle model using finer resolution stock groups; and

- a report outlining data availability, power analysis results and outline for agreed future direction in baseline development.

On behalf of the project consortium, Phil McGinnity has been invited to attend the Board's 2024 Annual Meeting to make a short presentation to the Board.

The Board may also wish to take into consideration its recent 'Statement of the International Atlantic Salmon Research Board on Future Research Priorities', [ICR\(24\)01](#), which has been agreed since the original request for funding this project was submitted. In this statement, the Board

*'agreed the need to prioritise research into the future prospects for Atlantic salmon populations towards 2050, on both a basin-wide and regional scale, so as to support an adaptive management approach to their protection and conservation into the future.'*

The Statement also noted the Board's current top five research priorities and that it had agreed to pursue new research activities into addressing the top-ranked area at this time, namely 'Basin-wide patterns of marine growth and survival of Atlantic salmon'.

The Board currently has very limited resources available to fund new research projects. As shown in the '2023 Accounts for the International Atlantic Salmon Research Fund', [ICR\(24\)09](#), the Board has approximately £20,000 available in non-ring fenced funding.

Secretariat  
Edinburgh  
17 May 2024

### ***Proposal for an Updated Comprehensive trans-European Genetic Reference Baseline to Assign Atlantic Salmon (*Salmo salar*) to Rivers and Region of Origin across the Eastern North Atlantic***

#### **Update - May 2024**

Ensing, D., Gilbey, J., McGinnity, P., Verspoor, E., & Wennevik, V.

#### **Requirements**

There is a need for an enhanced genetic baseline which covers species distribution across the rivers in the entire eastern Atlantic, but at a much greater resolution than is currently available. New stock assessment initiatives and associated management such as for example the Life Cycle Model would benefit substantially from stock discrimination and assignment units across the range with a single European reference baseline at a much finer resolution than is currently available.

#### **Proposal**

To examine options for enhanced GSI resolution in the eastern Atlantic through collaborative discussions with all interested parties.

Thus, the plan for taking the work forward and associated funding requests are:

- 1) Funding to support a hybrid two-day meeting (workshop format) at Institute of Marine Research (IMR) in Norway of the five principal scientists who have been instrumental in previous baseline building collaborations and have been leading the preliminary discussions on future directions and new eastern Atlantic baseline requirements. This workshop will be used to produce an outline plan which will detail options for the development and application of a trans-European baseline to be discussed by a larger international consortium. **Estimated costs: ~€3,000**

#### **Update May 2024**

The virtual workshop was held in Newport, Ireland in April 2024. Discussions centred around the different questions of interest researchers have, the different available markers, the screening technologies and the availability and inclusion of existing marker sets. A summary of the discussions was presented at the ICES WGNAS. A report was produced and presented to IASRB which outlined the workshop discussions, the questions addressed, and which summarised the options going forward (NASCO\_Baseline\_Workshop\_Report\_April\_2024). These questions and options will act as initial discussion points for the larger virtual workshop which is in the process of being organised. Total costs for the workshop were less than the estimated €3,000 as advantage was taken to hold the meeting immediately before the ICES WGNAS annual meeting. The costs for the workshop were thus just T&S for two participants of €2104.44 (to be claimed).

- 2) The draft plan developed during the workshop will be presented in advance to representatives with genetic expertise from all countries with salmon rivers in the eastern Atlantic and Baltic Sea. Preliminary discussions have already been had with these representatives, and a high level of interest has been expressed in the development of a new baseline. Countries which have expressed an interest are Denmark, England, Finland, France, Germany, Iceland, Ireland, Northern Ireland, Norway, Portugal, Scotland, Spain, Sweden, and Wales. A virtual workshop will then be held where all collaborators can

discuss the draft plan and outline what data/coverage/markers they have, the issues they would like to be able to address, and the preferred methods of taking things forward. Discussions will also be had regarding technical issues around the development of a new baseline (marker choice, platforms for screening etc). Following the meeting the principal project partners will draw together and circulate an updated draft project proposal which will aim to address all issues raised at the virtual workshop and outline the approach to be taken going forward. **Costs: Nil** (virtual meeting and time given by principal scientists pro bono).

#### **Update May 2024**

Interest has been received from representatives from 14 countries covering the entire eastern Atlantic salmon range. Further participants are in the process of being identified and contacted with the aim of inviting interested parties from both sides of the Atlantic such that insights from across the range can be put forward, and potentially a joint approach agreed if possible/required. The report from the initial workshop will be shared with participants before the meeting and act as a start for discussions. It is envisaged the virtual meeting will be held ~October 2024. **Costs: Nil.**

- 3) Following the virtual meeting and the development of the plan to take the project forward, a small amount of funding will be required to support 200 post-doc hours based at IMR in Norway to collate information on the various sample and data availability across the eastern Atlantic and Baltic range. Time to be also used to perform both a power analysis of new baseline capabilities and to examine novel analytical methods of performing robust GSI. **Estimated costs: €16,000**

#### **Update May 2024**

Initial scoping analysis of Norwegian, Irish and Scottish data has already been performed, by the authors of this proposal, and/or is underway. Further work would be targeted on identification of datasets, power analysis, and determining the options for integration of data from across the range. Currently, the eastern Atlantic baseline utilises 18 assignment units, it is envisaged that the power analysis of the microsatellite extended baseline across Norway, Scotland and Ireland will significantly increase this resolution, with an expected as seen in the Barents Sea where resolution was increased from 4 to 26 assignment units (Ozerov et al., 2017; Gilbey et al., 2018). Once developed, available archived marine samples will be reassigned to the new assignment units.

Deliverable: Enhanced resolution baseline for covering a significant proportion of the production in the Eastern Atlantic. Enhanced resolution of archived marine samples giving great understanding of differential stock utilisation in the Atlantic. Enhanced ability to refine ICES lifecycle model using finer resolution stock groups. Report outlining data availability, power analysis results and outline for agreed future direction in baseline development. To be presented at ICES WGNAS and IASRB in 2025. Estimated costs: €16,000

- 4) The principal scientists will bring together the information from the collaborators captured from the virtual workshop, together with the power and analytical information gained from the preliminary analysis, to begin the development of a full project proposal. **Costs: Nil** (virtual meetings and time given by principal scientists pro bono).

## **Update May 2024**

Project shape and partners will be determined following completion of tasks 1,2, and 3. Project leads and funding streams to be identified following discussion with interested collaborators.

**We therefore this year seek total funding of €18,104.44.**

## **Roadmap**

### Short-term (over next 6 months)

- QC existing 31-microsatellite reference data.  
Update May 2024: Complete
- Perform power analysis to examine levels of resolution  
Update May 2024: Complete for Scotland and Ireland, ongoing for Norway
- Identify datasets/samples  
Update May 2024: Complete for Scotland, Ireland, and Norway
- Investigate new developments in screening platform and genetic marker options  
Update May 2024: Completed at hybrid workshop, report produced outlining discussions and options
- Hold meeting with interested parties to examine options for eastern Atlantic genetic baseline coverage  
Update May 2024: Initial contact made with interested parties from 14 countries from the Eastern Atlantic. Wider consortium being developed
- Identify topics of international, pan-Atlantic, interest and research questions that can be addressed with the updated genetic baseline, with input from NASCO Parties, ICES Expert Groups, and project partners  
Update May 2024: Topics and partners to be identified at virtual meeting.

### Medium-term (over next 6 months-2 years)

Update May 2024: Medium-term goals to be addressed following short term discussions as set out above.

- Set-up consortium/project to update reference baseline across the species range in the eastern Atlantic
- Screen samples from across eastern Atlantic with optimum marker set
- Perform and publish marker set and power analysis
- Publication of Report to ICES WGNAS and IASRB
- Establish a large-scale international collaborative project and in conjunction with partners from the western Atlantic to update and apply the enhanced baseline across the species range to address questions of international importance relating to the biology of Atlantic salmon at sea
- Acquire appropriate- scale funding for this project (estimated at €1.0-3.0 million)

### Longer-term (2+ years)

Update May 2024: Longer-term goals to be addressed when possible.

- Screen marine samples from areas of interest, and/or to address specific questions of importance and use enhanced resolution to examine stock specific distributions
- Establish an open Database of genetic baseline data
- Communicate project findings to stakeholders such as ICES Expert Groups and NASCO

### **References**

Gilbey, J., Coughlan, J., Wennevik, V., Prodohl, P., Stevens, J. R., Garcia-Vazquez, E., Ensing, D., *et al.* 2018. A microsatellite baseline for genetic stock identification of European Atlantic salmon (*Salmo salar* L.). ICES Journal of Marine Science 75, 662-674.

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### ***Options for an Updated Comprehensive trans-European Genetic Reference Baseline to Assign Atlantic Salmon (*Salmo salar*) to Rivers and Region of Origin across the Eastern North Atlantic***

Ensing, D., Gilbey, J., McGinnity, P., Verspoor, E., Wennevik, V. & Cross, T.

#### **Executive summary**

This paper summarises the management drivers and development options for enhancing the resolution of the existing methodology for Genetic Stock Identification of Atlantic salmon in the eastern North Atlantic. Its objective is to provide the important background information needed for an informed discussion with all interested parties on defining the optimum ways forward to advance the methodology and support advancement of understanding of the distributional biology of eastern Atlantic salmon stocks which will in turn inform management and conservation strategies.

The various drivers for an enhanced resolution reference baseline are described and the existing available resources are summarised. The various options for further development are then examined and reviewed in light of their strengths and weaknesses. A number of emergent points are listed to provide a starting point for discussions by researchers with interest in GSI for salmon from the eastern Atlantic. These will in turn provide the basis for a draft agenda for a virtual meeting to be held with those with an interest in the topic from across the species range. The outline and discussion points raised here are intended to allow structured discussion and agreement on the optimal strategy for development of an enhanced reference baseline. The objective is that this will become the starting point for the development of a research collaboration to advance the NE Atlantic GSI tool.

Interest in the aim of enhancing GSI resolution and for attending the virtual meeting have already been expressed by researchers from 14 countries, and further contacts being made and further invitations extended to ensure the broadest engagement in the process.

#### **Background**

Genetic Stock Identification (GSI) based on molecular genetic markers has over time become an increasingly essential tool in salmon fisheries management to identify mixed-stock fisheries (MSF), contributing component stocks, and the relative contributions of those components. In the marine environment, in particular, they are also critical for advancing understanding of the distributional and demographic biology of those components, and the overall eco-evolutionary dynamics of the species during its marine phase.

GSI methodology and its informativeness is contingent on the development work related to three interlinked requirements: resolving stock structuring; identifying informative, practical molecular genetic markers for resolving that structuring; and creating geographically comprehensive genetic baselines. Stock structuring in Atlantic Salmon, a reflection of historical, evolved reproductive and genealogical division of a species into distinct biological units, is hierarchical from the transatlantic to the tributary scale. GSI development involves the simultaneous resolution of this structuring, the identification of optimal molecular genetic marker panels that allow assignment of individuals to different phylogeographic stock groups, and the creation of geographic baselines for these markers that provide accurate assignment of individual river stocks to their higher order phylogeographic stock groups.

A number of different genetic reference baselines are currently in use across the Atlantic

Salmon's range and these facilitate assignment of individuals in different areas, at different levels of phylogeographic stock resolution, and different levels of assignment certainty (see below). However, it is being increasingly recognised that the levels of resolution and/or geographic coverage of these baselines, in many contexts, is insufficient to address important management issues and conservation concerns. Thus there is a widespread interest in investigating the potential of integration and extension of genetic reference baseline coverage for salmon across the range increasing resolution and assignment accuracy, particularly in the eastern Atlantic. To address the increasingly focused questions being raised, will require increasing understanding of finer scale stock structuring, the inclusion of samples from more rivers for stock units of interest and identifying marker sets with higher resolving power. Ideally, this will require inclusion of samples from all river stocks likely to be present in the assignment sample and consist of genetic marker panels of sufficient discriminatory power to be able to differentiate among contributing stocks to a useful level of resolution.

### **The case for enhanced resolution**

A number of management and conservation contexts are emerging within which an enhanced GSI resolution would be beneficial. These cover geographical scales from the intercontinental to the local. In each case the ability to refine the stock composition of fish would provide increased understanding of the questions being raised in these contexts. In turn this would strengthen evidence-based fishery management, and help develop conservation strategies that could better focus on river stocks of conservation concern. Some, but not all, of the particular issues of prominent concern that would benefit from enhanced GSI tools are detailed below. However, the reality is that most any question on stock specific marine distributions of salmon could be better answered if the geographic origin of marine captures of salmon could be assigned with finer-scale resolution and higher certainty.

### **Fisheries**

Most, if not all, marine fisheries for salmon are mixed stock, as well as some freshwater fisheries in large river systems. As such, it is of particular management importance that the stock composition of all fisheries, directed or by-catch, can be accurately quantified, ideally to the river stock level. This would allow management strategies to be developed that would better protect stocks at risk, including the setting of sustainable limits for exploitation that provide for keeping all stocks above Maximum Sustainable Yields.

#### *ICES lifecycle model stock delineation enhancement*

The ICES benchmark, for the assessment and forecast models currently used by ICES for Atlantic salmon stock assessment in the North Atlantic, is based on a hierarchical Bayesian life cycle model (ICES, 2023). This simultaneously estimates the abundance of post-smolts at sea, post-smolt survival rates, and proportions maturing as 1SW, for all SU in Northern Europe, Southern Europe and North America (Olmos *et al.*, 2019). This insight provides a way of understanding the mechanisms driving the response of Atlantic salmon populations to variations in biological and environmental factors among different river stocks that have overlapping marine migration routes and may be exploited by the same marine fisheries. The insight gained from this model would benefit substantially from a finer scale insight into the migration patterns of river stocks across the range, something that can best be realised by creation of a single, higher resolution European reference baseline.

#### *West Greenland*

GSI is currently used to monitor the composition of salmon stocks in the West Greenland fishery at the intercontinental level of stock resolution (Sheehan *et al.*, 2010). For western Atlantic stocks, GSI can provide further assignment to 20 regional phylogeographic assignment



units (Jeffery *et al.*, 2018). In contrast, currently further assignment of eastern Atlantic origin river stocks, encompassing a much larger area, is less refined, encompassing only 8 regional phylogeographic stock units (Jeffery *et al.*, 2018). However, with a more refined GSI methodology, higher spatial resolution regional assignment would be possible and enable development of a much more detailed understanding of the stock composition of the fishery from both sides of the Atlantic, and of the conservation priorities of eastern Atlantic river stocks in a similar way as now is the case with western stocks.

### *East Greenland*

The Labrador and Irminger seas and their associated coastal waters have long been known to be important feeding areas for Atlantic salmon. In contrast, very little historical information exists regarding Atlantic Salmon off the coast of East Greenland. Yet new tracking studies are now providing some initial insights with regard to this area (e.g. SMOLTRACK; ICES, 2022) and suggest that it may be more important than thought, at least for some regional stock groups. However, how important and which stocks are not known and a better understanding of the contemporary dynamics of Atlantic salmon is needed and especially important if the exploitation in the fishery in this area is to increase (ICES, 2022). GSI assignment of captures from this area in support of biological studies in this area would help to understand which stocks and how important it is.

### **Ecological**

River stocks and even tributary specific populations are evolutionarily diverse and locally adapted to their freshwater environments and to varying degrees appear to have unique marine ecologies, if only in their spatial and temporal patterns of marine migration (Gilbey *et al.*, 2021). Characterising differences in their freshwater ecology is facilitated by their homing to natal rivers where river stock and tributary population level studies can be carried out. However, studies of the marine ecology of individual populations, river stocks, or regional stock groups are problematic, even using physical tags to track individuals from a given group. Yet results of tagging studies, combined with biological and geographical considerations, indicate that, at least on a regional stock group level, large and potentially important differences can exist in the marine environments they utilise (Drenner *et al.*, 2012). However, overall, the extent to which stocks at different levels of population aggregation differ in their eco-evolutionary dynamics remains poorly understood. This needs to be addressed as these dynamics are underlying processes which are major determinants of demographic outcomes which may vary dramatically among populations, river stocks and regional stock groups. Establishing the full extent of differences in the marine ecology of these groups can only be realised if the origin of fish captured at sea can be determined. Ideally, this would be at the river stock if not tributary population level though this would require a large amount of genomic work to identify molecular markers that would allow this to be achieved.

### **Management of anthropogenic stressors**

Better understanding of the origin of stocks can greatly enhance knowledge based management strategies for salmon. Anthropogenic impacts have the potential to disproportionately impact different stocks, some of which may already be at critical levels. As such the ability to identify these stocks at higher resolutions will aid in the management of interactions between fish in the marine environment and processes such as aquaculture interactions, offshore power, bycatch, and MPAs locations (Forseth, 2023).

### **Present situation**

There are several genetic reference baselines in use presently across the Atlantic salmon species range facilitating stock assignment at different levels of resolution (Table 1). At a continental

level of resolution, fish have been assigned with high accuracy to either North American or European rivers using microsatellites (e.g. Sheehan *et al.*, 2010), and Single Nucleotide Polymorphisms (SNPs) (e.g. Jeffery *et al.*, 2018). In the western Atlantic area a SNP baseline is also used to assign fish from the western Atlantic at a relatively high-resolution to 26 regional groups (Bradbury *et al.*, 2018). The baseline of Bradbury *et al.* (2021) builds on that of Jeffery *et al.* (2018) and allows assignments simultaneously to both sides of the Atlantic. However, whilst the resolution of this baseline is relatively good on the western Atlantic where it was developed (23 units in total including Greenland) it is relatively poor on the eastern side (7 units including Iceland and the Baltic).

In the eastern Atlantic area assignment using a microsatellite genetic baseline originally developed for the SALSEA-Merge project provides the most comprehensive geographic coverage with accurate individual assignment of fish to 18 European regional stock groups (Gilbey *et al.*, 2018), with relatively coarse spatial assignment units in a number of areas of its coverage (e.g. the salmon populations of Britain and Ireland are assigned as a single group, similarly it is difficult to separate populations and regional groups in large parts of Norway). Further the spatial coverage in certain parts of the range, especially the south, is relatively sparse.

Within Europe there are also several other reference genetic baselines which provide enhanced resolution across limited countries or within individual countries but these are not based on standardised marker panel sets and as a result have limited applicability across the range. For example the ASAP baseline covers much of the southern salmon range (Griffiths *et al.*, 2010) with a resolution of 8 assignment units. In Scotland a 288 SNP marker baseline allows Scottish fish to be assigned to 18 assignment units (Gilbey *et al.*, 2016). In Ireland a 15 microsatellite panel baseline has been used to assign to individual rivers (Anon, 2008). In the northern European part of the range a 31-microsatellite baseline is available that enables assignment to 26 reporting groups (Ozerov *et al.*, 2017) within northern Norway and Russia. The coverage of this baseline has now been extended to include also southern Norway and is expected to increase the number of reporting groups in Norway significantly (analysis ongoing at present). The same marker set has also been applied to extend the number of markers for a select set of Scottish and Irish rivers that were included in the SALSEA-Merge baseline with work ongoing to examine resolution in this dataset.

**Table 1.** Available genetic regional reference baselines for salmon in the eastern Atlantic.

Geographic Coverage	Samples	Markers	Assignment Resolution	Reference
Trans-Atlantic	80 fish, 2 rivers	11 microsatellites	2 units, EU/NA	King <i>et al.</i> (2005)
Trans-Atlantic	12 rivers	1 microsatellite, 1 mtDNA haplotype	2 units, EU/NA	Gilbey <i>et al.</i> (2005)
Trans-Atlantic	4,942 fish, 46 rivers	11 microsatellites	3 units, EU/US/CAN	Sheehan <i>et al.</i> (2010)
Trans-Atlantic	1,930 fish, regions	466 microsatellites	2 units, EU/NA	Gilbey <i>et al.</i> (2017)
Trans-Atlantic	3,406 fish, populations	28596 SNPs	28 units	Jeffery <i>et al.</i> (2018)

Trans-Atlantic	319 populations	96 SNPs	30 units	Bradbury <i>et al.</i> (2021)
Eastern Atlantic	26,822 fish, 28214 rivers, 467 sites	28214 microsatellites	18 units	Gilbey <i>et al.</i> (2018)
Barents sea	185 populations	33 microsatellites	26 units	Ozerov <i>et al.</i> (2017)
Scotland and England	NE3,787 fish, 147 sites, 27 rivers	288 SNPs	18 units	Gilbey <i>et al.</i> (2016)
Northern Ireland	673 fish, 27 sites	7 microsatellites	6 units	Ensing <i>et al.</i> (2011)
Ireland	7,924 fish, 322 sites, 143 rivers	15 microsatellites	20 units	Anon (2008)
Southern Europe	3,730 fish, 57 rivers	12 microsatellites	8 units	Griffiths <i>et al.</i> (2010)
France	199 fish, 6 regions	17 microsatellites	6 units	Perrier <i>et al.</i> (2009)
Baltic Sea	2,337 fish, 32 stocks	8 microsatellites	3 units	Koljonen (2006)
Baltic Sea	3,394 fish, locations	3633 microsatellites	28 units	Vähä <i>et al.</i> (2016)
Baltic Sea	39 stocks	14 microsatellites	14 units	Koljonen <i>et al.</i> (2021)
Western Atlantic	9142 fish, 50 sites	3000 SNPs	14 units	Moore <i>et al.</i> (2014)
Western Atlantic	12,409 fish, rivers	19415 microsatellites	12 units	Bradbury <i>et al.</i> (2016)
Western Atlantic	1,485 fish, populations	35101 microsatellites	26 units	Bradbury <i>et al.</i> (2018)

### Requirements going forward

Understanding the marine ecology of eastern Atlantic salmon would benefit greatly from an enhanced resolution genetic baseline. However, the requirements of such a baseline will depend to a large extent on the questions being asked and the particular situation. For example, existing inter-continental resolution may be enough for some questions, whereas intra-river level assignments may be required for others. As such it would be of particular use if the various groups working with GSI of eastern Atlantic origin salmon could come together, discuss, and come to some sort of agreement on just what is needed.

Questions for discussion would include:

- Would a single trans-range (west and east Atlantic) baseline with the same set of markers be optimal?
- Is a single reference baseline required, or a hierarchy of baselines and associated hierarchical assignment analysis?
- However, it may be sub-optimal screen fish at multiple marker sets - so how to reconcile the issue of questions/markers/coverage?

- What sort of marker type/s and technologies should the focus be on in any new development?
- How and whether it would be possible or desirable to include existing reference baselines/marker types in areas with dense coverage and good resolution?
- Should the screening be able to be done in individual laboratories, or could/should a commercial option and/or a central laboratory be utilised?
- How would any new marker panels be developed? Existing loci v new marker development from high density chips/whole genome scans across range?
- How and if to include adaptive loci?
- How to ensure as best as possible that new loci identified in the future can be incorporated into the panel if desired?
- Should there be a central open access database for the baseline and if so how to manage?
- Is there an opportunity and would it be useful to include other metrics into the assignment structure (e.g. otolith/lens/scale microchemistry/stable isotope)?
- Need to think about immediate development v long term considerations. For example it might be relatively easy to build on what is available now, but should more effort be put into a larger project utilising whole genome scans across the range at high density to develop the optimal panel/s which might future proof the baseline/s?
- Is there any requirement for GSI analytical method development into usable R packages, especially if a hierarchical approach is to be considered (e.g. Hsu and Habicht, 2024).

### Technical considerations

Table of options for discussion

Technology	Markers	Pros	Cons
Fragment analysis	Microsatellites	Considerable existing data Cheap for small marker numbers	Old technology, not many labs can screen anymore Hard to expand marker numbers Cannot include other marker types at screening (SNPs)
Digital PCR	SNPS / Adaptive	Easy to calibrate between labs Many labs have the technology Fast development platform	Marker number limited due to costs Marker numbers need to be based around IFC capabilities
Micro-array	SNPS / Adaptive	Large numbers of markers can be screened Cost effective Central screening option	Small number of labs have capacity for inhouse screening Hard to add new markers once developed

			Limited marker types
Genotyping by sequencing	Microsatellites / SNPS / Adaptive	<p>Large numbers of markers can be screened</p> <p>Can screen many marker types</p> <p>Can add new markers relatively easily</p> <p>Easy to calibrate between labs</p> <p>Many labs have the technology</p>	<p>Length of reads may limit some long allele markers</p> <p>May be costly compared to other high density screening options</p>
Whole genome scans	Microsatellites / SNPS / Adaptive	<p>Complete genome coverage</p> <p>New marker discovery</p> <p>Data can be mined for specific questions/panels</p>	Costly for high numbers of samples

### Conclusions

As with many decisions, there is always a trade-off between what is optimal and what is practical while taking into consideration the questions being asked and the available technology and resources. However, the practical and optimal outcomes are not mutually exclusive. Enhancements can be made in the short and medium term while at the same time focus being given to the development of an optimal resolution, and if the end goal is known, the immediate enhancements can be directed to help achieve this goal where possible.

It will probably never be the case that a brand new baseline could be developed which will cover all rivers in the maximum detail and be able to answer all research questions from the off. However, if researchers looking at particular rivers/questions can also add their new sites and/or marker panels, as they are developed, to an existing range-wide reference baseline, then, a continuously improving resource will be available to all.

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***Developing a new genetic baseline for NEAC – Presentation by Vidar Wennevik at WGNAS 2024***

There is a need for an enhanced genetic baseline which covers species distribution across the rivers in the entire eastern Atlantic, but at a much greater resolution than what is currently available. New stock assessment initiatives and associated management such as for example the LCM would benefit substantially from stock discrimination and assignment units across the range with a single European reference baseline at a much finer resolution than what is currently available. Also, determining the origin of salmon caught at sea will aid in identifying important migration corridors and feeding areas, provide a more detailed estimate of which European populations are exploited in the fisheries at Greenland, and in general increase the understanding of the marine ecology of Atlantic salmon.

There are several genetic reference baselines in use presently across the Atlantic salmon species range facilitating stock assignment at different levels of resolution. At a continental level of resolution, fish have been assigned with high accuracy to either North American or European rivers using microsatellites (e.g. Sheehan *et al.* 2010), and Single Nucleotide Polymorphisms (SNPs) (e.g. Jeffery *et al.* 2018). In the NAC area a SNP baseline is also used to assign fish from the Northwest Atlantic at a relatively high-resolution to 22 regional groups (Bradbury *et al.* 2021). In the NEAC area assignment a microsatellite genetic baseline originally developed for the SALSEA-Merge project (Gilbey *et al.* 2017) provides accurate individual assignment of fish to 18 European regional stock groups.

However, the SALSEA reference baseline of Gilbey *et al.* (2017) has relatively coarse spatial assignment units in some areas of its coverage e.g., the salmon populations of UK and Ireland are assigned to a single group, similarly it is difficult to separate populations and regional groups in large parts of Norway. Within Europe there are also several other reference genetic baselines which provide enhanced resolution at a within country level but are not based on standardised marker panel sets and as a result have limited applicability across the range. For example, in Scotland a 288 SNP marker baseline allows Scottish fish to be assigned to 18 assignment units (Gilbey *et al.* 2016). In Ireland a 17-microsatellite panel baseline has been used to assign to individual rivers (P McGinnity *pers. comm.*). In the northern European part of the range a 31-microsatellite baseline is available that enables assignment to 26 reporting groups (Ozerov *et al.* 2017) within northern Norway and Russia. The coverage of this baseline has now been extended to include also southern Norway and is expected to increase the number of reporting groups in Norway significantly (analysis ongoing at present). The same marker set has also been applied to extend the number of markers for a select set of Scottish and Irish rivers that were included in the SALSEA-Merge baseline.

A project to plan the way forward towards a functional pan-European baseline has been initiated. The project plan outlines two workshops; a planning workshop to develop a draft plan for issues to be discussed and a virtual workshop planned for late 2024. A summary of the issues discussed at the planning meeting was presented to the Working Group. The preliminary plan will be presented in advance to representatives with genetic expertise from all countries with salmon rivers in the eastern Atlantic and Baltic Sea. Preliminary discussions have already been had with these representatives, and a high level of interest has been expressed in the development of a new baseline, from Denmark, England, Finland, France, Germany, Iceland, Ireland, Northern Ireland, Norway, Portugal, Scotland, Spain, Sweden, and Wales. A virtual workshop will then be held where all collaborators can discuss the draft plan and outline what



data/coverage/markers they have, the issues they would like to be able to address, and the preferred methods of taking things forward. Discussions will also be had regarding technical issues around the development of a new baseline (marker choice, platforms for screening etc). Following the meeting the principal project partners will draw together and circulate an updated draft project proposal which will aim to address all issues raised at the virtual workshop and outline the approach to be taken going forward.

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