

# Genome-wide divergence history of Atlantic salmon *Salmo salar* across its native range

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## 1. Background - Atlantic salmon

Understanding the process of divergence requires knowledge of the underlying demographic history

Alternative histories can lead to similar patterns of genetic divergence and are difficult to exclude<sup>1</sup>

### The Atlantic salmon *Salmo salar* model

Wide northern distribution from Eastern Europe to East America<sup>2</sup>

Homing behaviour and straying generates complex genetic structure at different hierarchical scales<sup>2,3,4</sup>

Mitochondrial and SNP analyses suggest a more recent origin of American populations from a few European sources<sup>2</sup>

However, relatively little is known about the species divergence history

How many European refugia existed? How many populations contributed to the founding of American populations? Have European and American populations diverged with continuous gene-flow or were they isolated in the past?

## 2. Objectives

Reconstruct the global history of divergence of *Salmo salar* across its native range

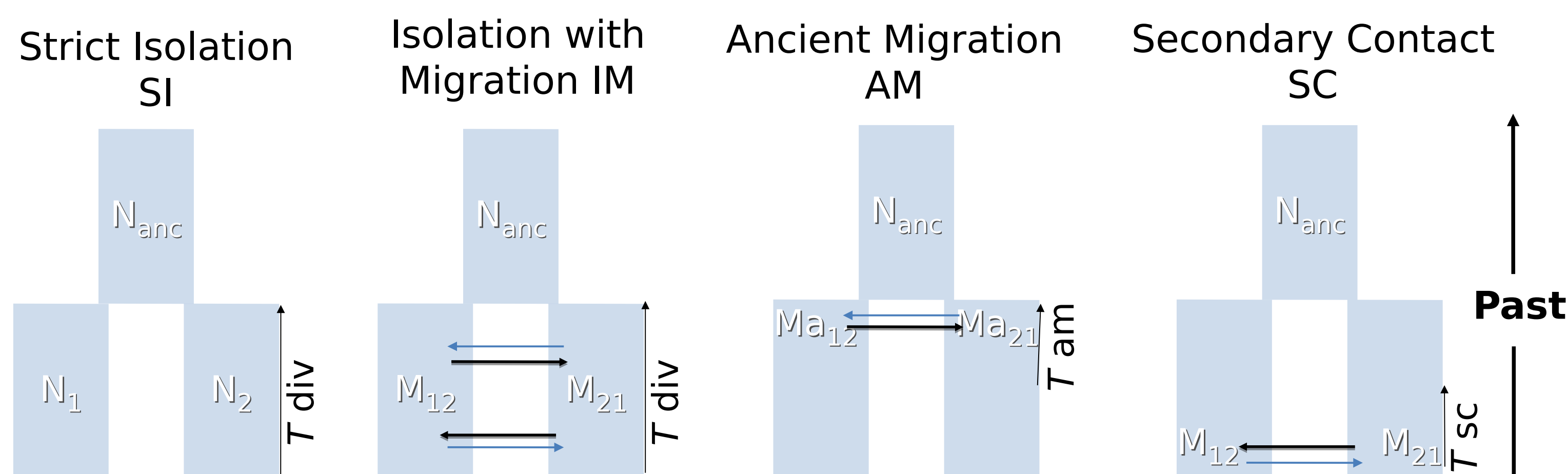
- Further characterize how European populations have diverged
- Determine whether American population divergence predates the last glacial cycle or is more recent
- Disentangle the effect of linked selection and restricted effective migration rates on demographic inference

## 3. Methods

Total of 77 sample sites and 4,656 SNPs from a SNP-array<sup>4</sup>

Inference of population structure and admixture and source of admixture using geogenetic maps<sup>5</sup>, tree-based approaches<sup>6</sup> and *F*<sub>3</sub>-statistics<sup>7</sup>

Explicit modelling of divergence history using an Approximate Bayesian Computation (ABC) previously developed<sup>8,9</sup>

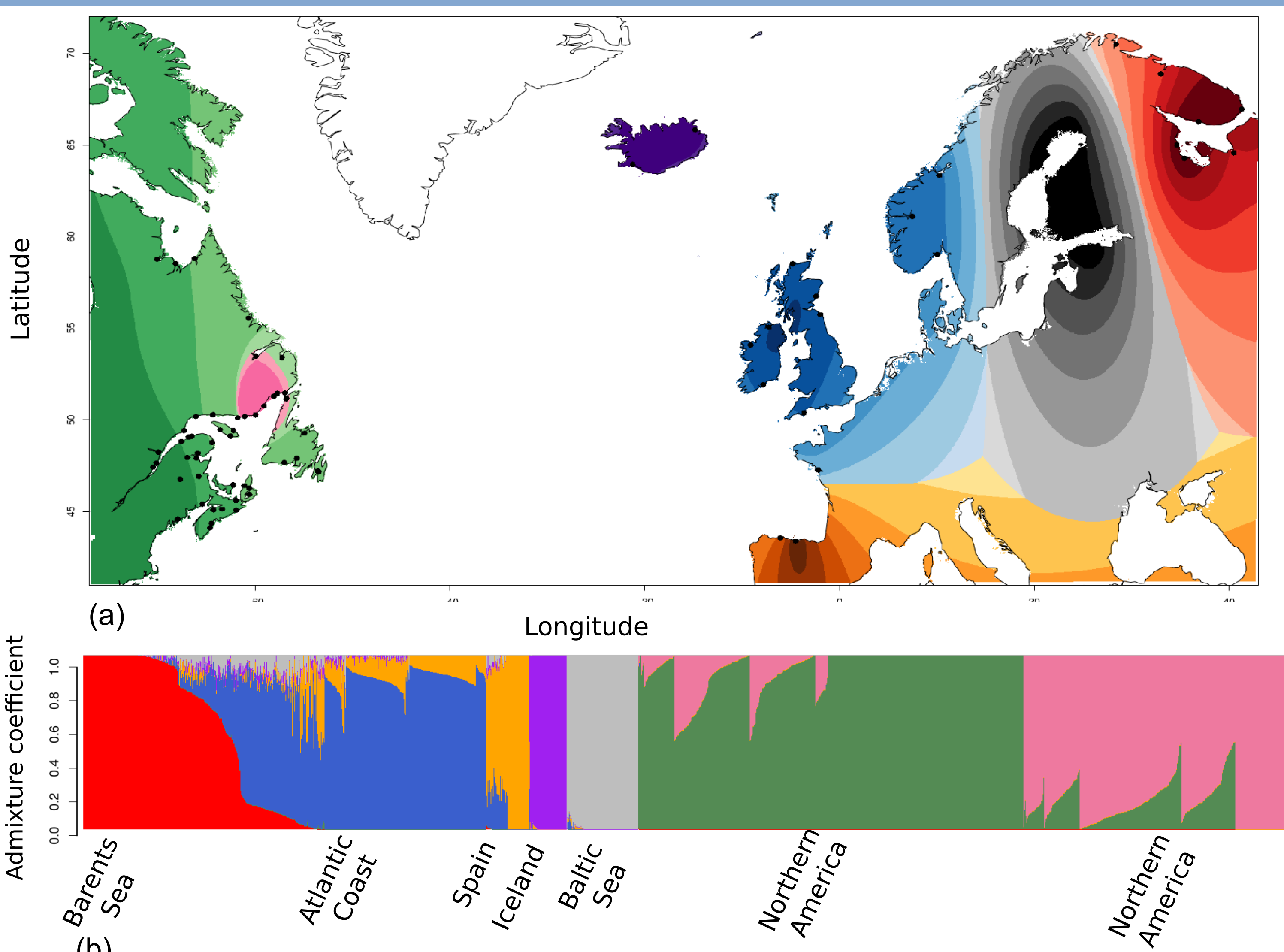


**Fig.1.** The four major scenarios compared

Incorporation of selective effects : Variation in  $N_e$  along the genome

Incorporation of variable introgression rate : Variation in  $m$  along the genome

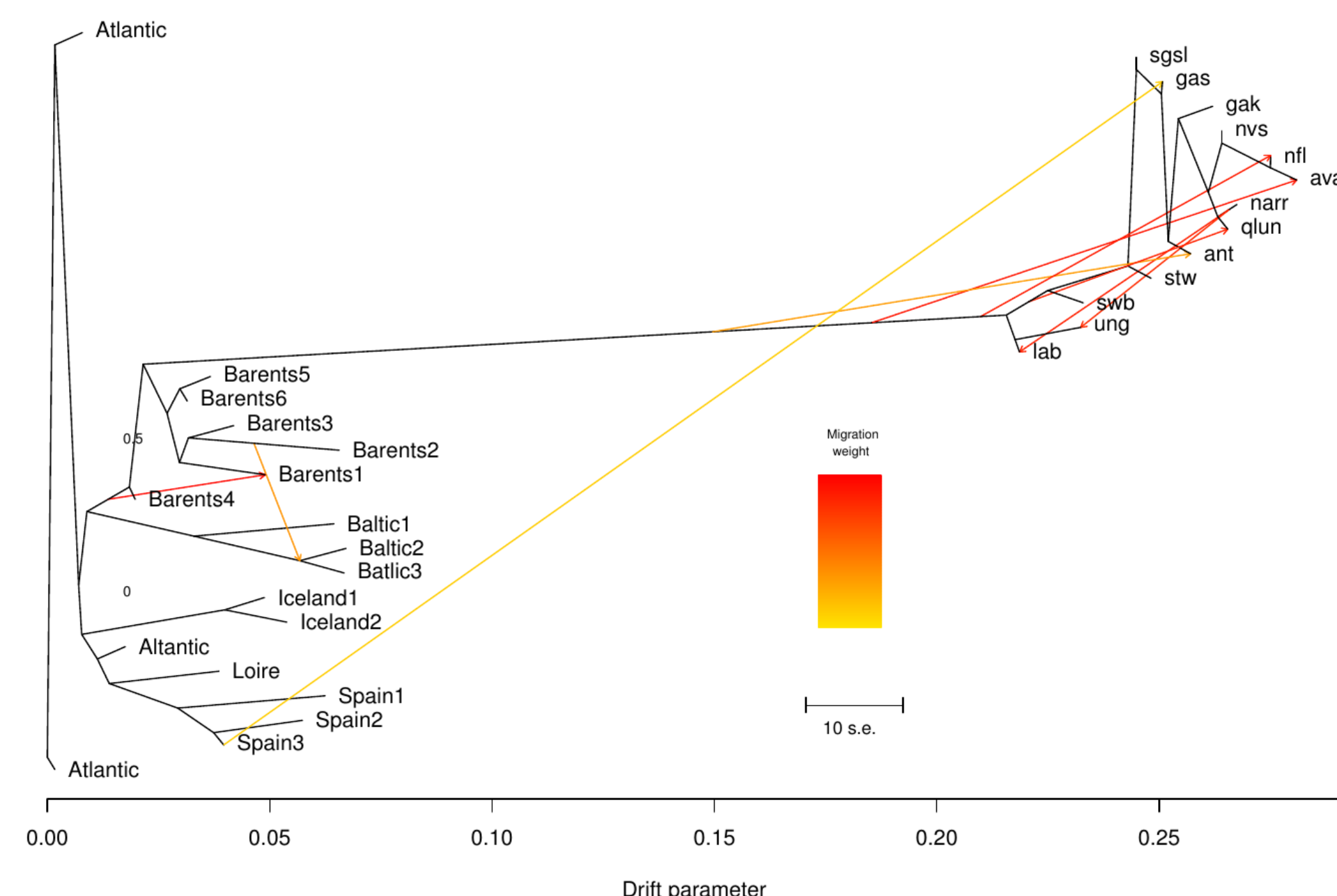
## 4. Ancestry coefficient and admixture



**Fig.2.** (a) Spatial interpolation of ancestry coefficients and (b) admixture barplot for the major genetic groups

European populations displayed stonger genetic structure corresponding to the major historical refugia while American populations appears more homogeneous

## 5. Evidence for intercontinental gene-flow



*F*<sub>3</sub>-test indicates significant admixture levels from Europe to American in ~60 % of the American populations

*F*<sub>3</sub>-tests suggest two American populations contributed significantly to admixture with all other American populations

Only one European population (Barents area) significantly admixed with contribution from both Europe and Americas

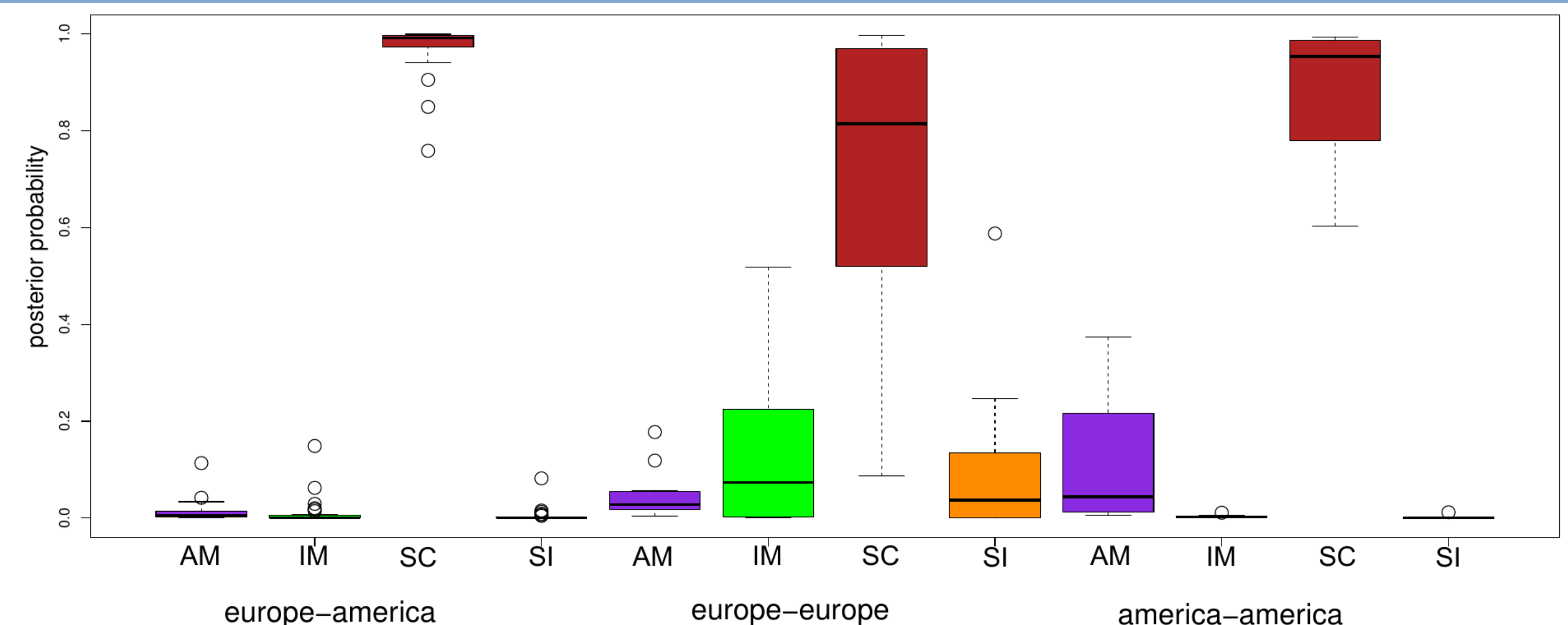
**Fig.3.** TreeMix analysis representing genetic relationship among populations (grouped by major cluster) and major migration among them depicted by arrows. Colour gradients indicate the weight of the migration events. nine migration events are shown here. Drift parameter used as relative temporal measure where the scale bar indicates 10 times the average standard error.

Over 99.9 % of variance explained with  $m = 9$ .

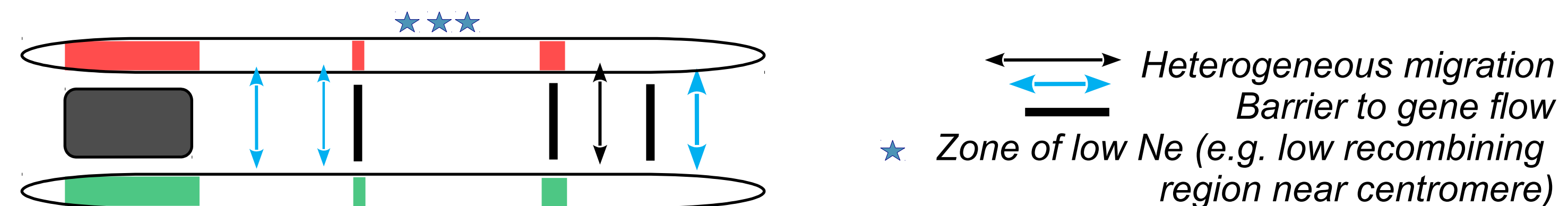
Evidence for admixture between European and most American populations

Strong admixture among American populations - Moderate admixture in Europe

## 6. A complex demographic history



**Fig.4.** Boxplot of model choice posterior probability. The x-axis shows the compared pairs. Europe-America ( $n=31$ ) comparisons, Europe-Europe : comparison between populations from different putative refugia<sup>4</sup> ( $n=14$ ), America-America : comparison between populations from genetically divergent areas<sup>10</sup>. Posterior probabilities (y-axis) are summed for the four alternative version of the AM, IM SC and SI models for ease of comparison. In three instances, homogeneous models provided a better fit than the three heterogeneous alternatives



In 94 % of the comparisons, models incorporating heterogeneous rate of migration and variable  $N_e$  outperformed models that do not take these into account e.g. averaged  $P(SC \text{ hetero}) > 0.83$

Europe-American comparisons : multiple **secondary contact** from at least two European sources

In Europe : populations from divergent refugia are now connected by secondary gene flow, although in two case, ongoing divergence and strict isolation were best supported

In America, preliminary comparisons suggest that populations have retained a signal of secondary contact

## 7. Conclusions & Perspectives

Demographic analyses suggest **secondary contact** between European and American populations, as well as between European populations from different putative historical refugia and between American populations from different regions

Salmon genomic landscape of divergence are shaped by **linked selective** effects and **differential introgression** rates

Demographic inferences may benefit from taking into account effects of linked selection and differential introgression when comparing divergence models

ABC modelling : Integrating periodic episodes of gene flow and allowing for variation in effective population size should provide a more accurate picture of the divergence history of Atlantic salmon

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