

Divergent history, linked selection and deleterious mutations in Coho salmon across its native range

Quentin Rougemont¹, Jean-Sébastien Moore¹, Ben Koop², Louis Bernatchez¹

¹IBIS, Université LAVAL, Quebec City, Canada, ²Department of Biology, University of Victoria, BC, Canada
quentinrougemont@orange.fr



1. Demographic history & linked selection

Understanding population divergence and adaptation requires knowledge of the underlying demographic history

Alternative histories can lead to similar patterns of genetic divergence and are difficult to exclude¹
Demographic inference can be obscured by linked selection and should be accounted for

The Coho salmon *Onchorynchus kitsuch* model :

Wide distribution in **Western North America**²

Relatively **little is known about the species divergence history**³:

- * How population sizes have changed through time?
- * How many populations contributed to the founding of populations ?
- * Have populations diverged with gene-flow or were they isolated in the past?
- * Did population size reductions result in an increased genetic load?

2. Objectives

Reconstruct the global history of divergence of Coho salmon across its native range

- Determine whether contemporary populations originated from a single or multiple refugia
- Determine the extant of population size change through time
- Disentangle the effect of linked selection on demographic inference
- Determine if demographic history favored an accumulation of deleterious mutations

3. Methods

Total of 59 sampling sites, ~2000 individuals, and ~80K SNPs from RADseq

50 individuals with WGS data (>15 millions SNPs)

Inference of population structure and admixture and source of admixture using PCA, tree-based approaches, *F*₃-statistics, *f*₃-statistics⁴

Modeling divergence history with Approximate Bayesian Computation (ABC)⁵, Random-Forest⁶, and smc++⁷

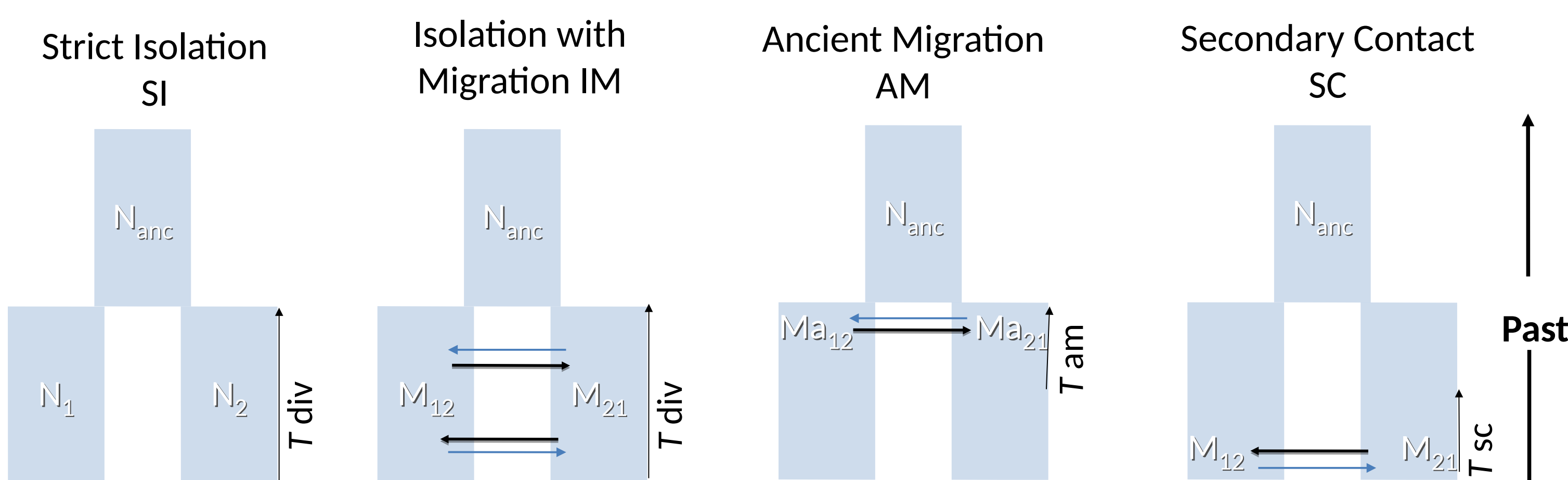
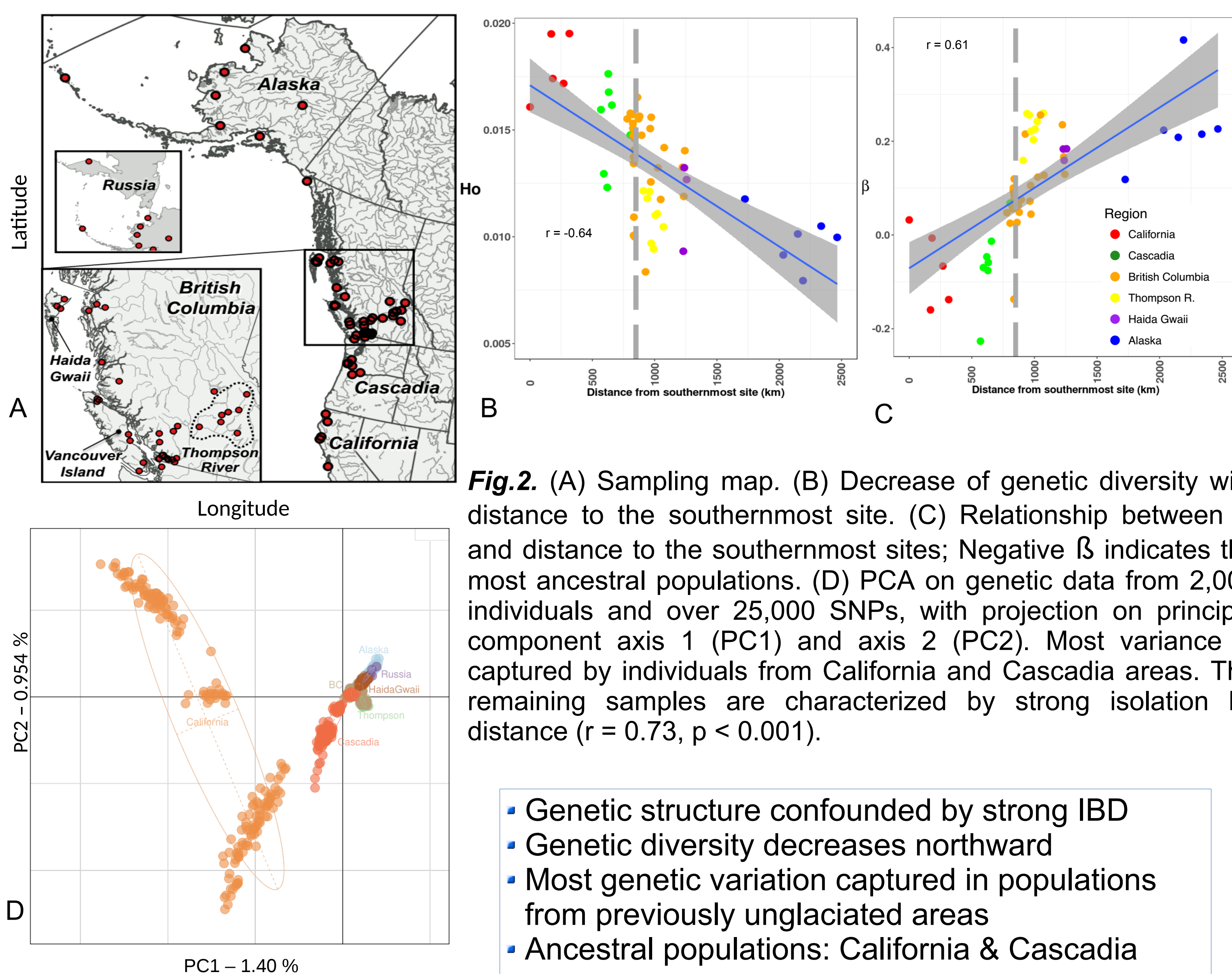


Fig.1. The four major scenarios compared

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

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

4. Structure, diversity and ancestral populations



5. Demographic history : migration and size change

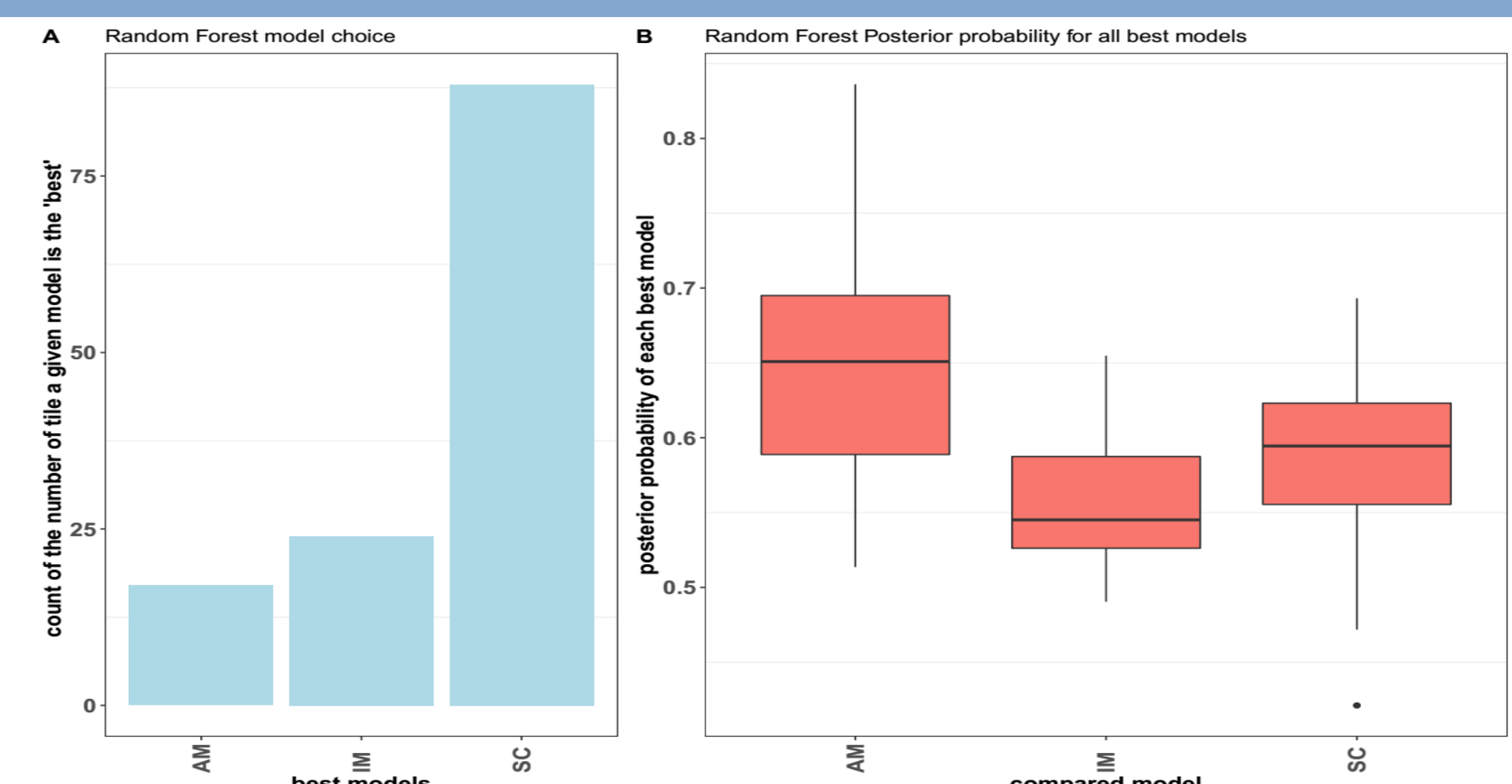


Fig.3. Model choice among alternative divergence scenarios with (A) number of times a given model was designated as the best, and (B) posterior probability of the designated best model in (A). Although the SC model was more often selected, its posterior probability was low and it cannot be robustly distinguished from the IM model (i.e. classification error of ~50%). The SI model did not received any support.

- Rejection of models without gene flow
- Higher support for models with linked selection (not shown)
- Models with gene flow cannot be distinguished indicating that populations are lying in the grey zone of divergence⁸

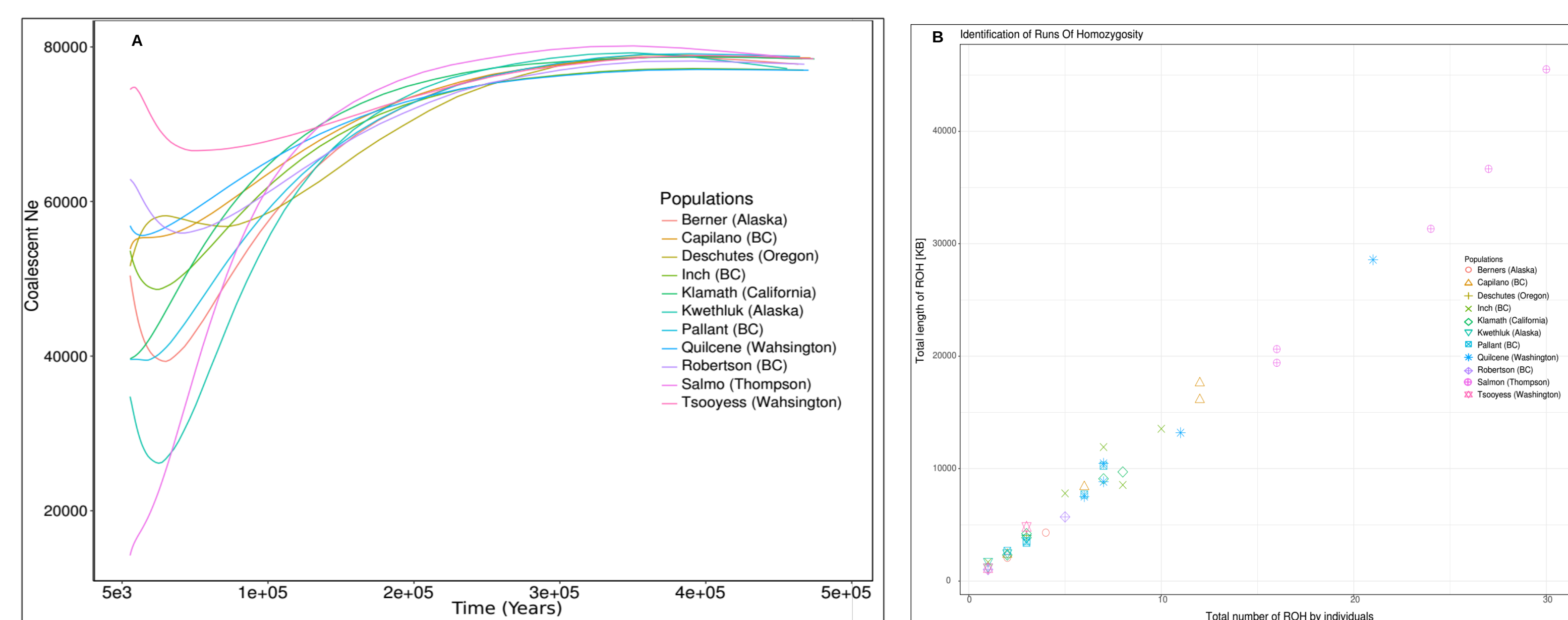


Fig.4. (A) Changes in population size through time inferred from SMC++ with whole genome data and (B) identification of Runs Of Homozygosity (ROH) in the same dataset in each individuals.

- Little population size change until recently
- One population (Thompson) has undergone a continuous decline, confirming results from RADseq (not shown)
- The Thompson population also displays the highest amount and longer ROH, supporting its strong decline

6. History and load of deleterious alleles

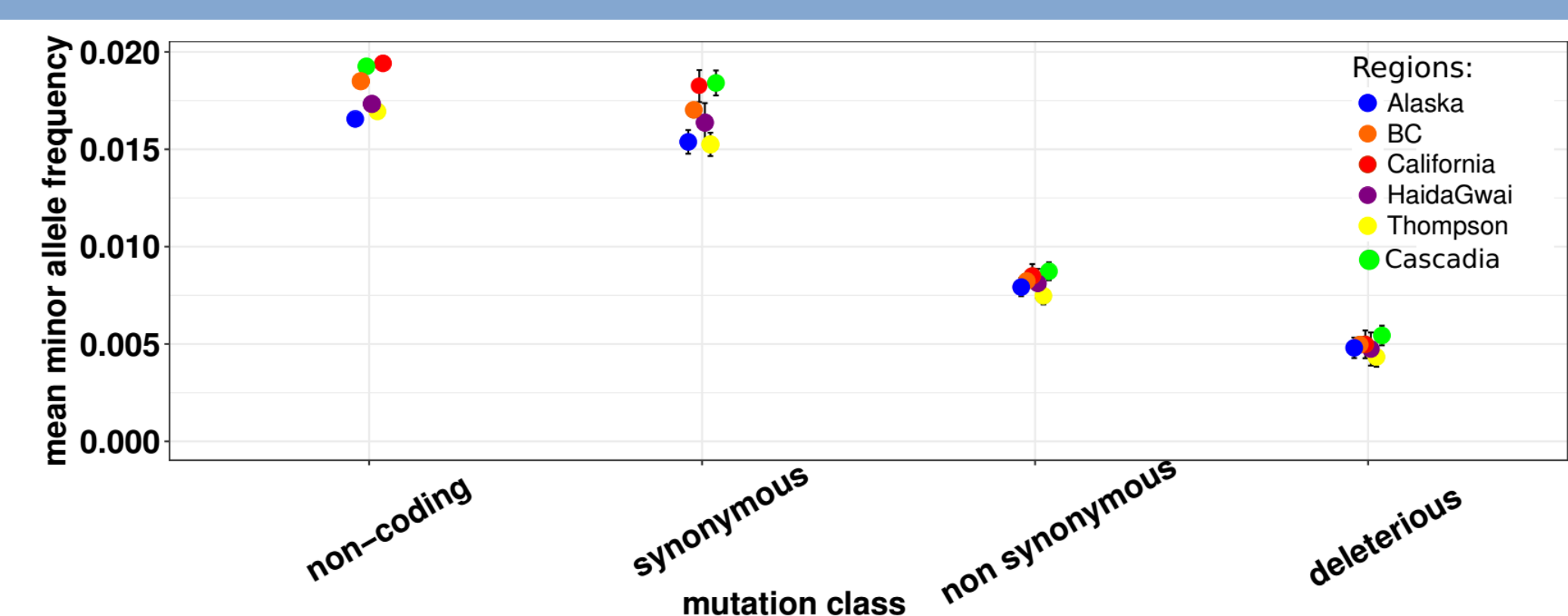


Fig.5. Distribution of mean minor allele frequency for different classes of mutation in RADseq data. Due to strong bottlenecks (Thompson) and possible founder event following expansion from a single refugium, we tested for an increased load of deleterious mutation in Northern population.

- As expected, deleterious alleles are maintained at low frequency.
- No differences among population detectable with RADseq data
- To be confirmed with WGS data.

7. Conclusions & Perspectives

Demographic analyses support **ongoing gene flow** between diverging pairs of populations but failed to rigorously distinguished between IM and SC.

Demographic analyses and independent estimates (not shown) indicate that Salmon genomic landscape is shaped by **linked selective** effects.

Available evidence suggests **expansion from a single unglaciated area** with **northward recolonization** inducing various bottleneck and genetic diversity reduction.

No clear difference in frequencies of deleterious alleles in bottlenecked populations (Thompson) or in population with reduced diversity (Alaska).

Absence of differences in load to be confirmed by WGS data. Difference in the distribution of deleterious alleles in and outside ROH and in region of various recombination rate should help untangle how purifying selection is acting throughout the genome in different populations.

References:

1. Bierné N, Gagnaire P.A., David P. (2013) *Curr. Zool.* 59: 72-86
2. Quinn, (1993) *Fisheries Research* 18:29-44
3. Smith et al (2001) *Mol Ecol.* 10 : 2775-2785
4. Weir & Goudet (2017) *Genetics*, 206 : 1-19.
5. Beaumont et al. (2002) *Genetics*, 162: 2025–2035
6. Pudlo et al. (2015) *arXiv*:1406.6288v3
7. Terhorst et al. (2016) *Nat Genet* 49: 303–309
8. Roux et al. (2016) *PLoS Biol* e2000234

Acknowledgments:

We thank B. Bougas, B. Boyle, C. Hernandez, A. Peyrault and E. Normandeau for laboratory and bioinformatics support. Computations were carried out on the supercomputer Colosse (Calcul Québec) and on Cedar and Graham (Compute Canada). This research was carried out in conjunction with EPIC4 (Enhanced Production in Coho: Culture, Community, Catch), a project supported by the government of Canada through Genome Canada, Genome British Columbia, and Genome Quebec.