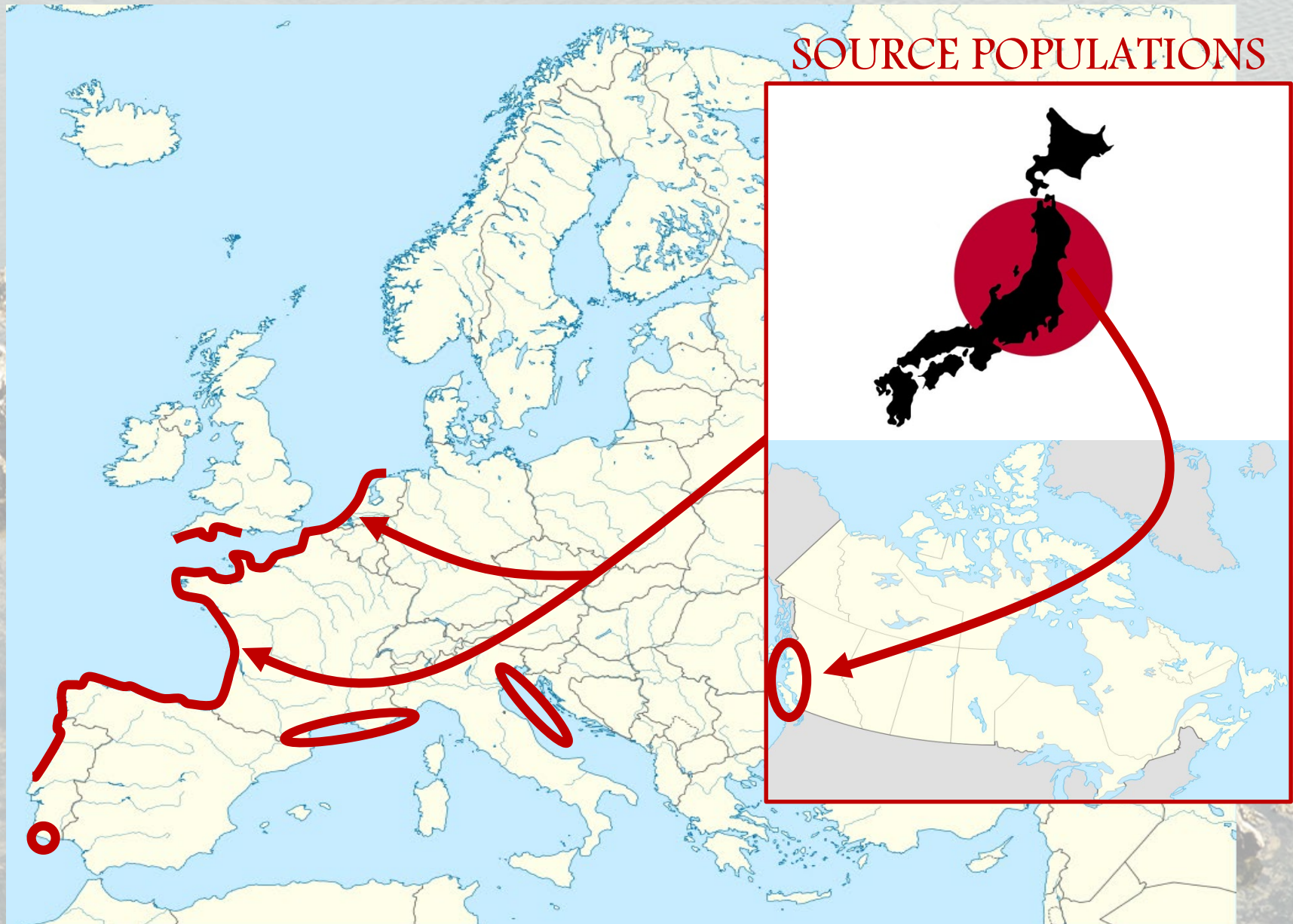


Investigation of the genetic structure of the pacific oyster (*Crassostrea gigas*) in Europe using a high density SNP array

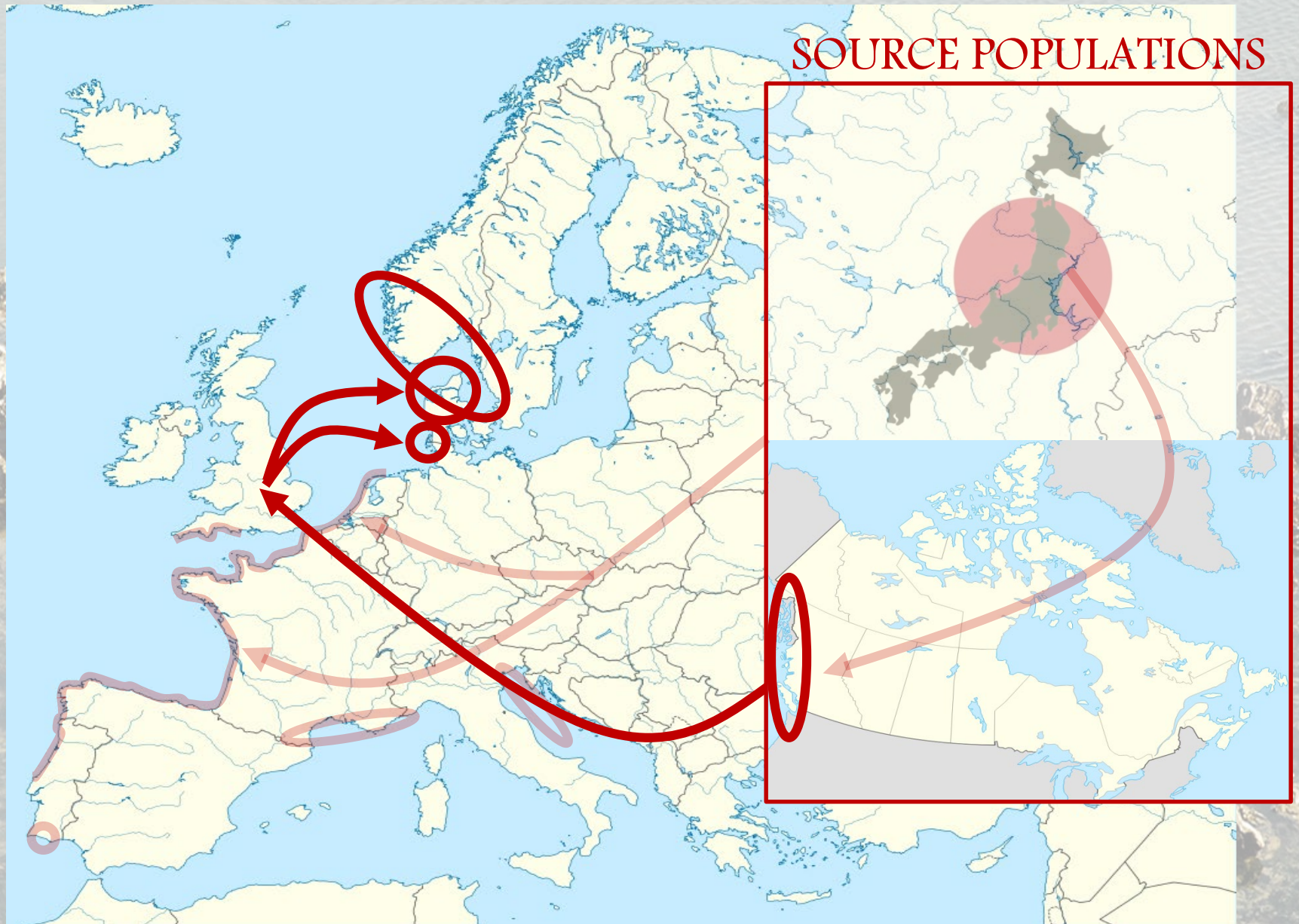
David L. J. Vendrami



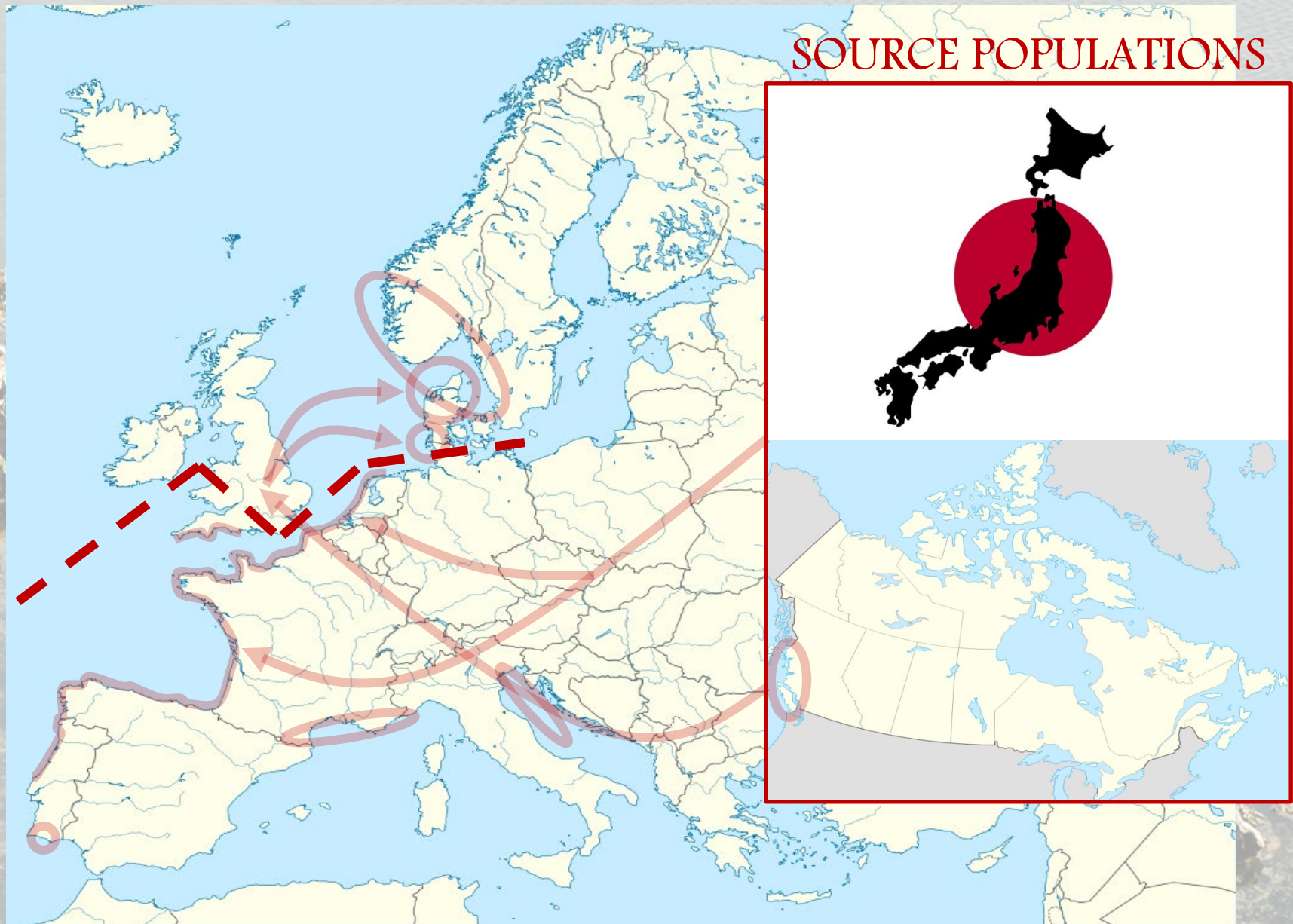
History of oysters in Europe



History of oysters in Europe



History of oysters in Europe



Galil 2000, Moehler *et al.* 2011, Meistertzheim *et al.* 2012, Rohfrisch *et al.* 2013, Lallias *et al.* 2015, Anglès d'Auriac *et al.* 2017

Aim of the study

Investigate the genetic structure of *Crassostrea gigas* populations in Europe

Samples genotyped at over 30,000 SNPs !!!

Samples collected within an unprecedentedly wide latitudinal range !!!

Our sample collection



Our sample collection



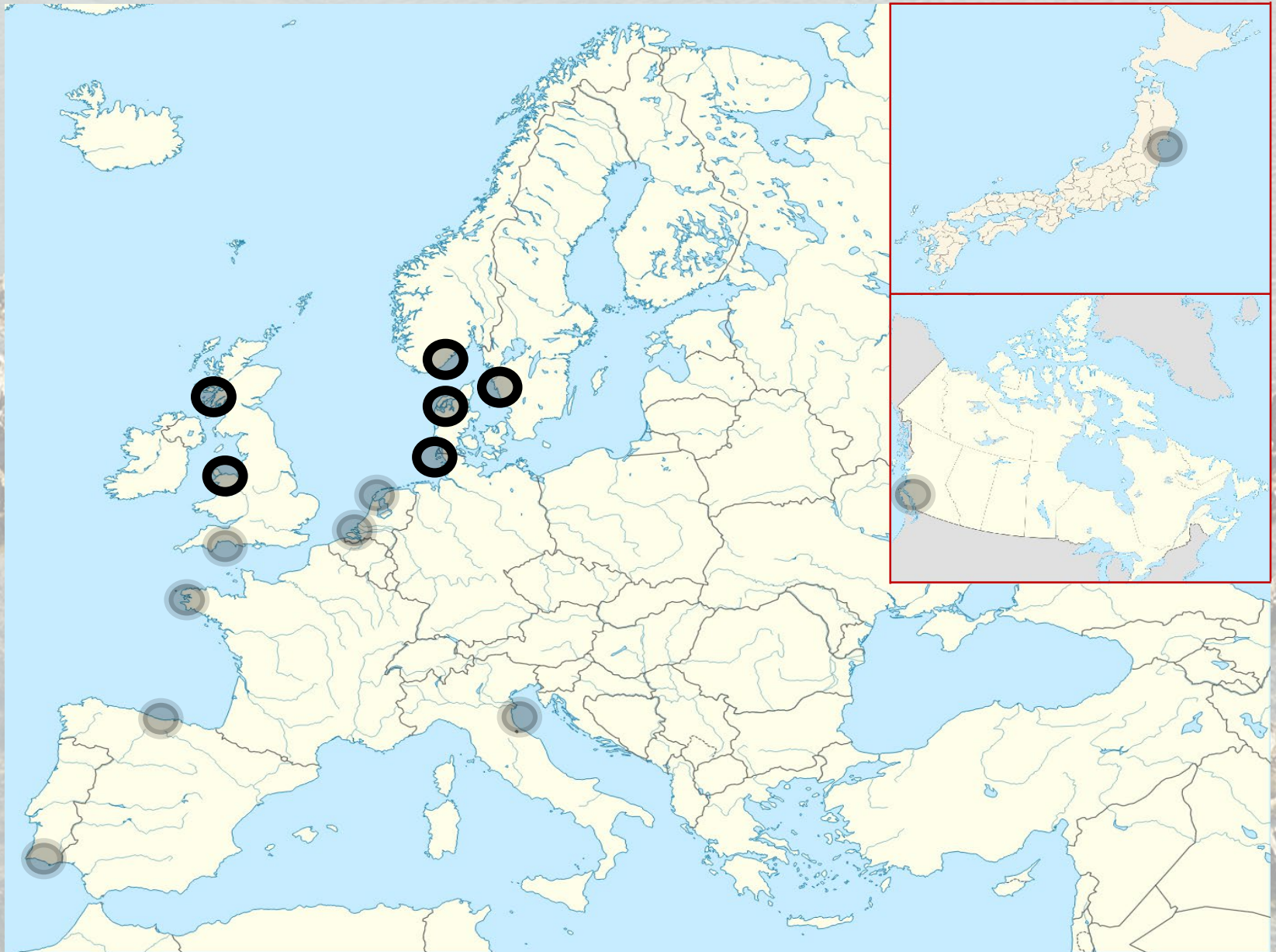
Our sample collection



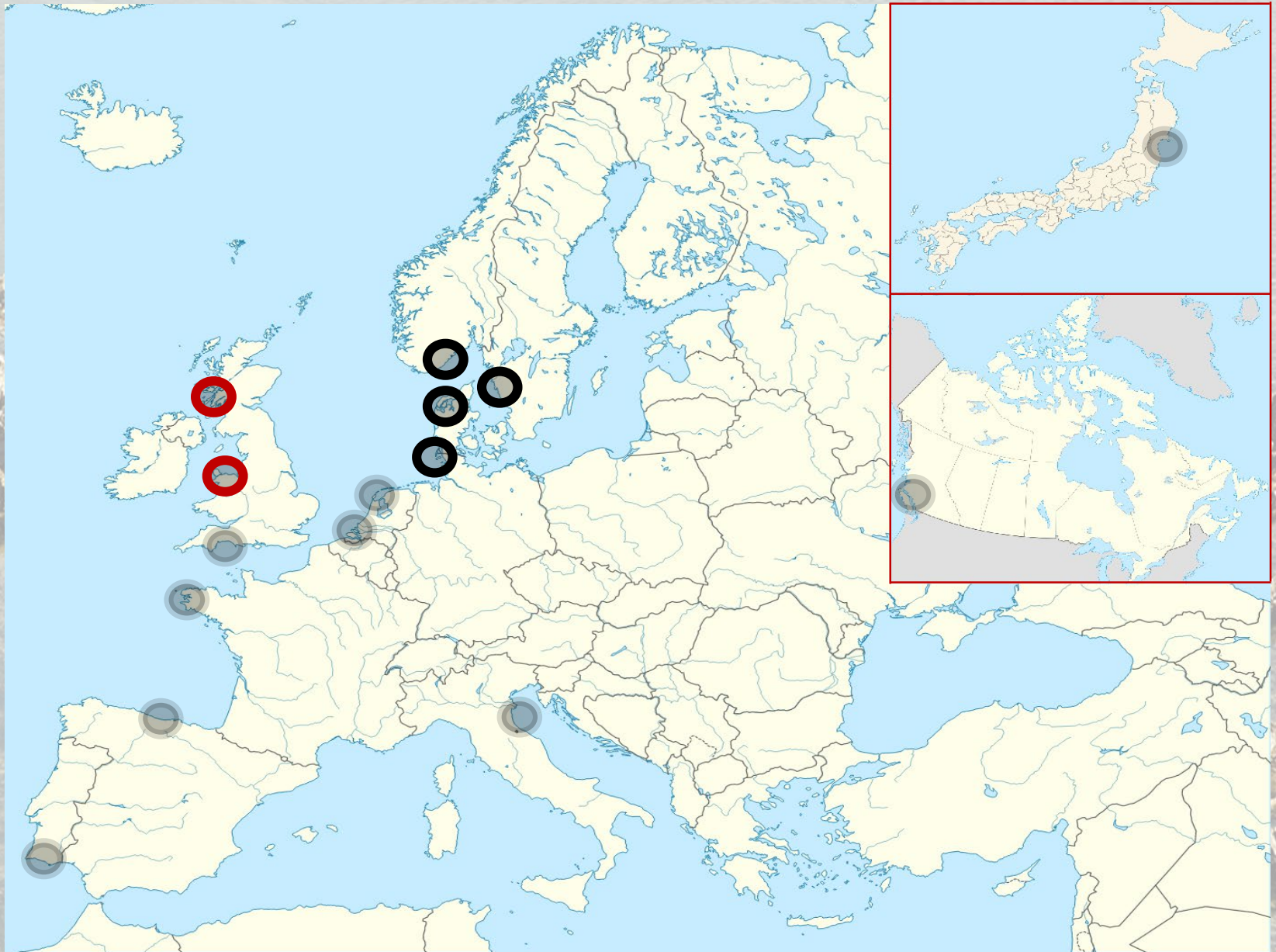
Our sample collection



Our sample collection



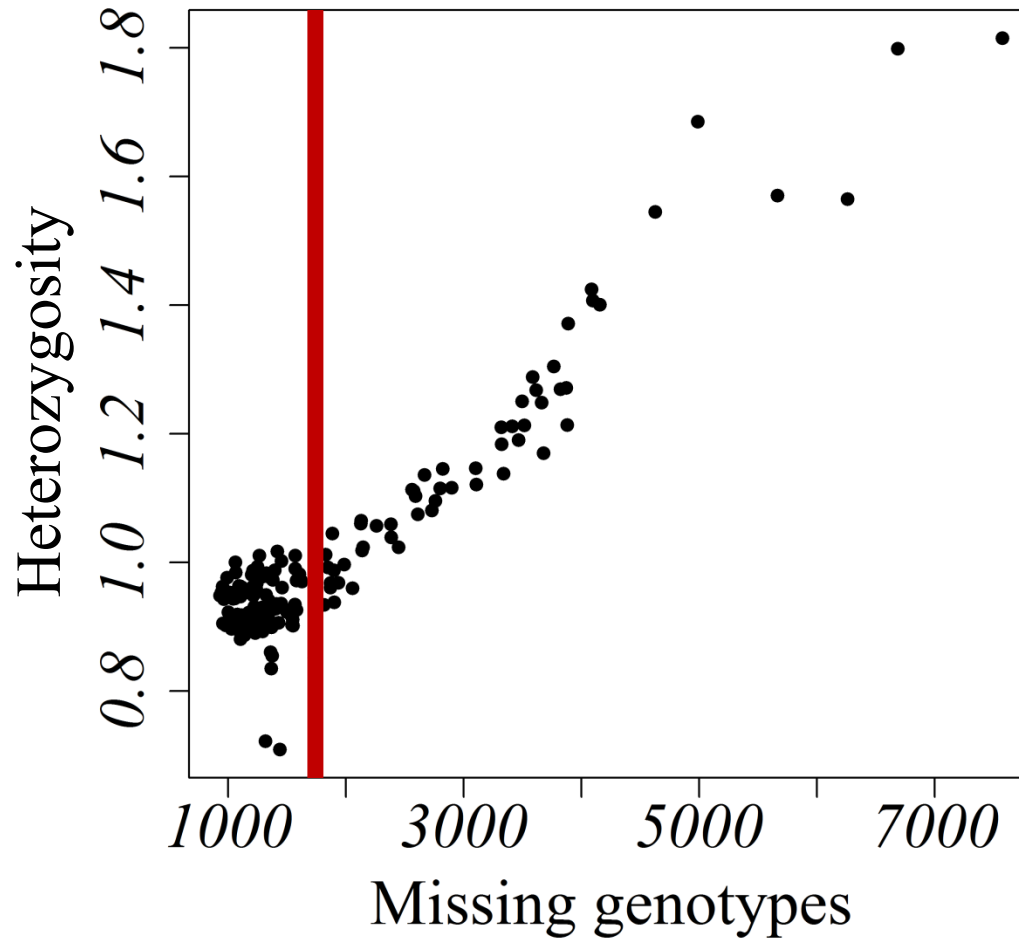
Our sample collection



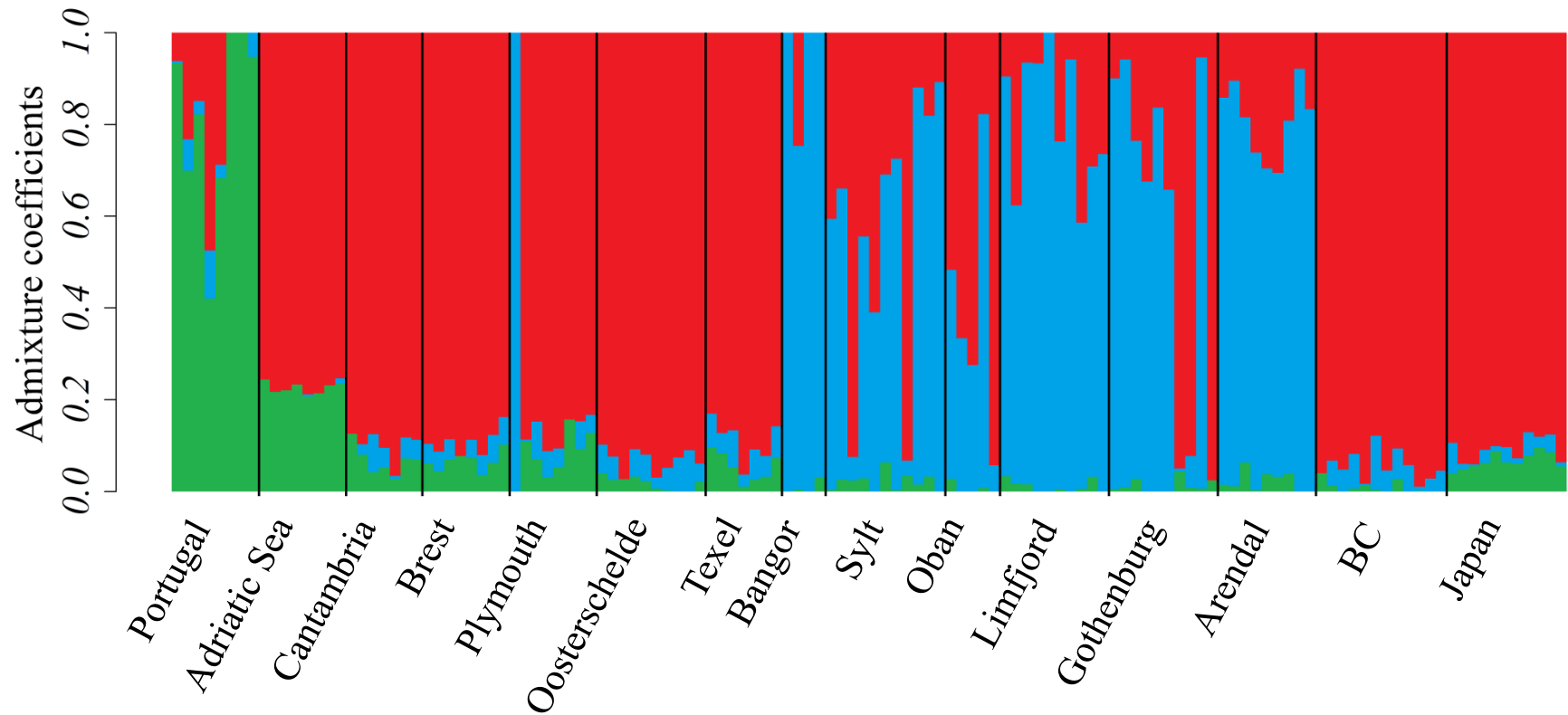
Our sample collection



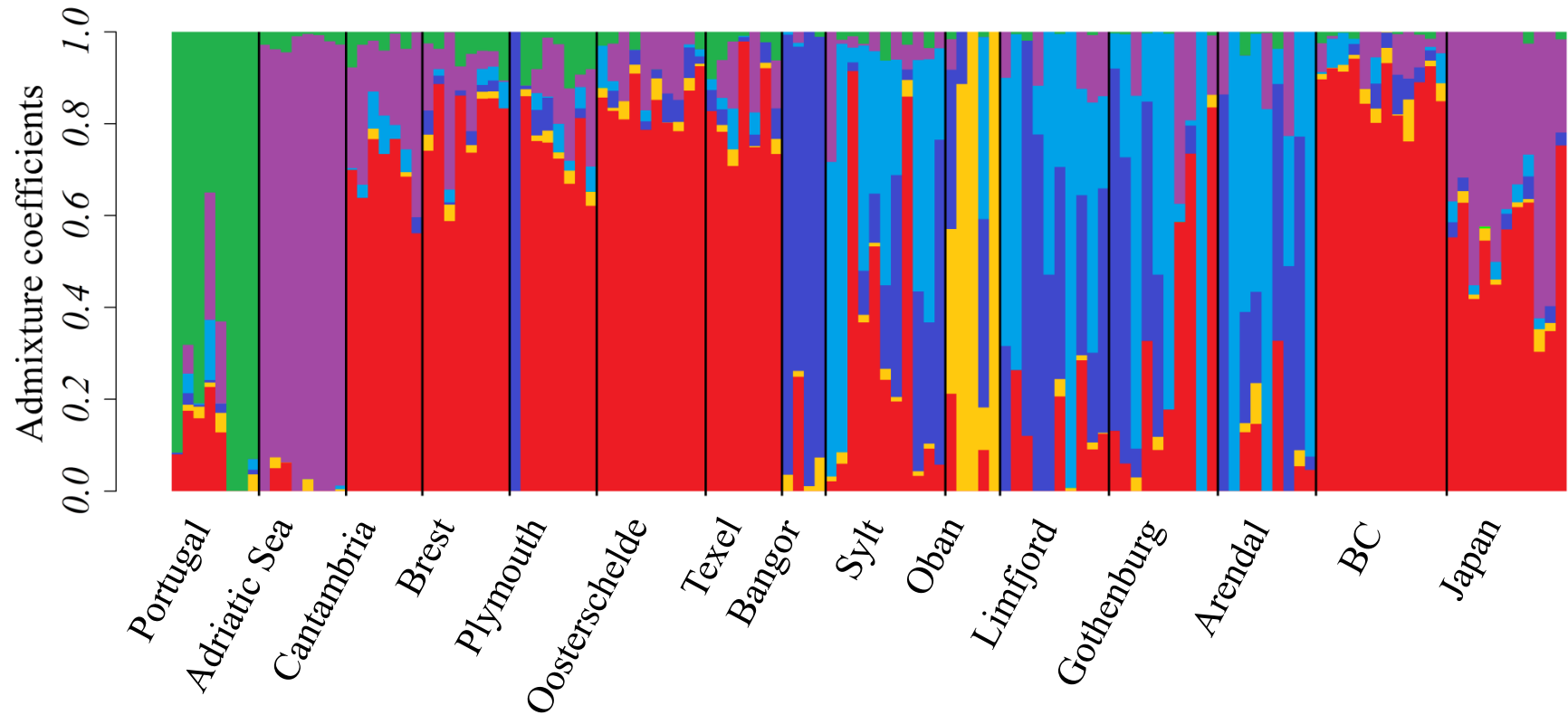
Problematic artifact



Genetic structure results: sNMF

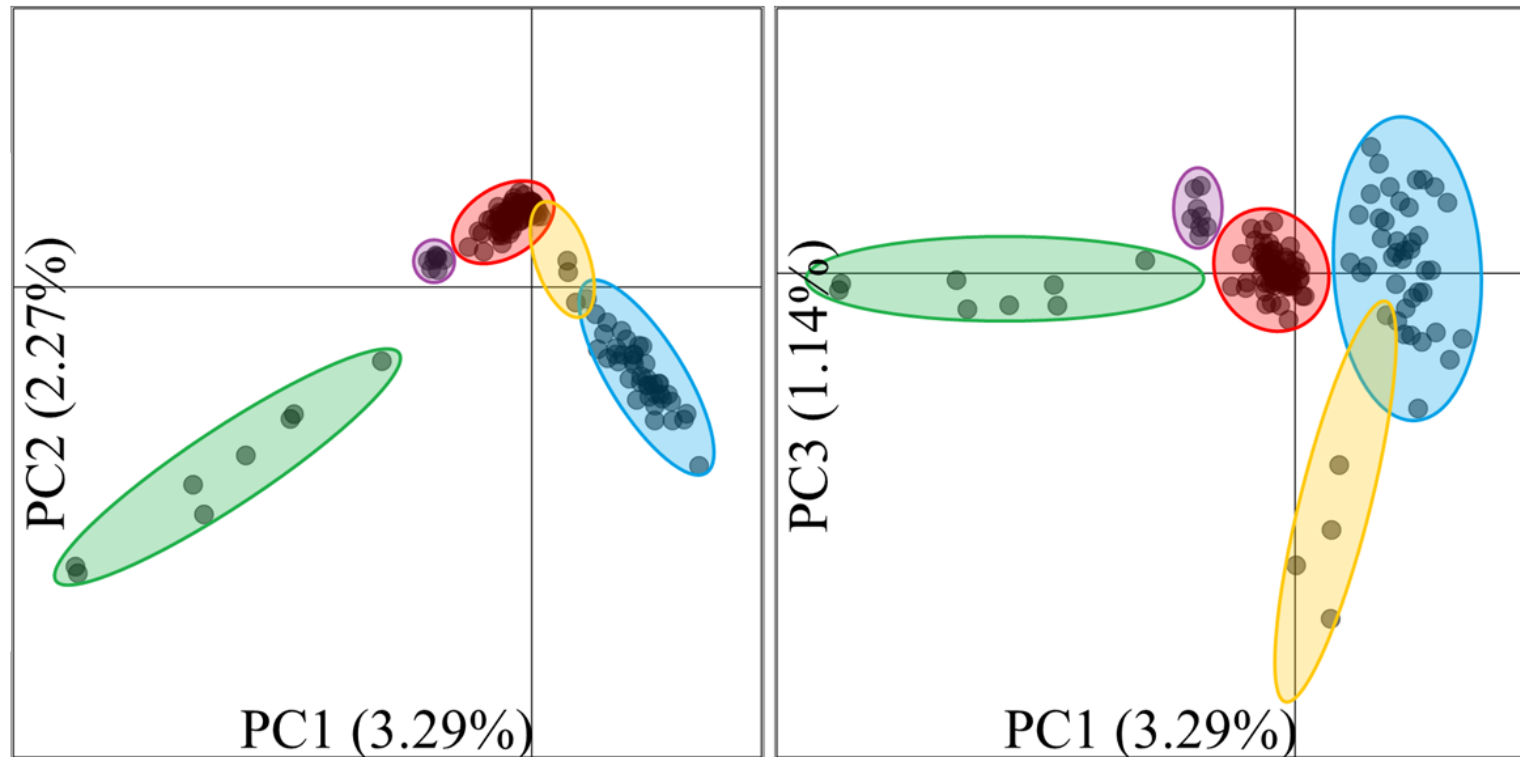


Genetic structure results: sNMF



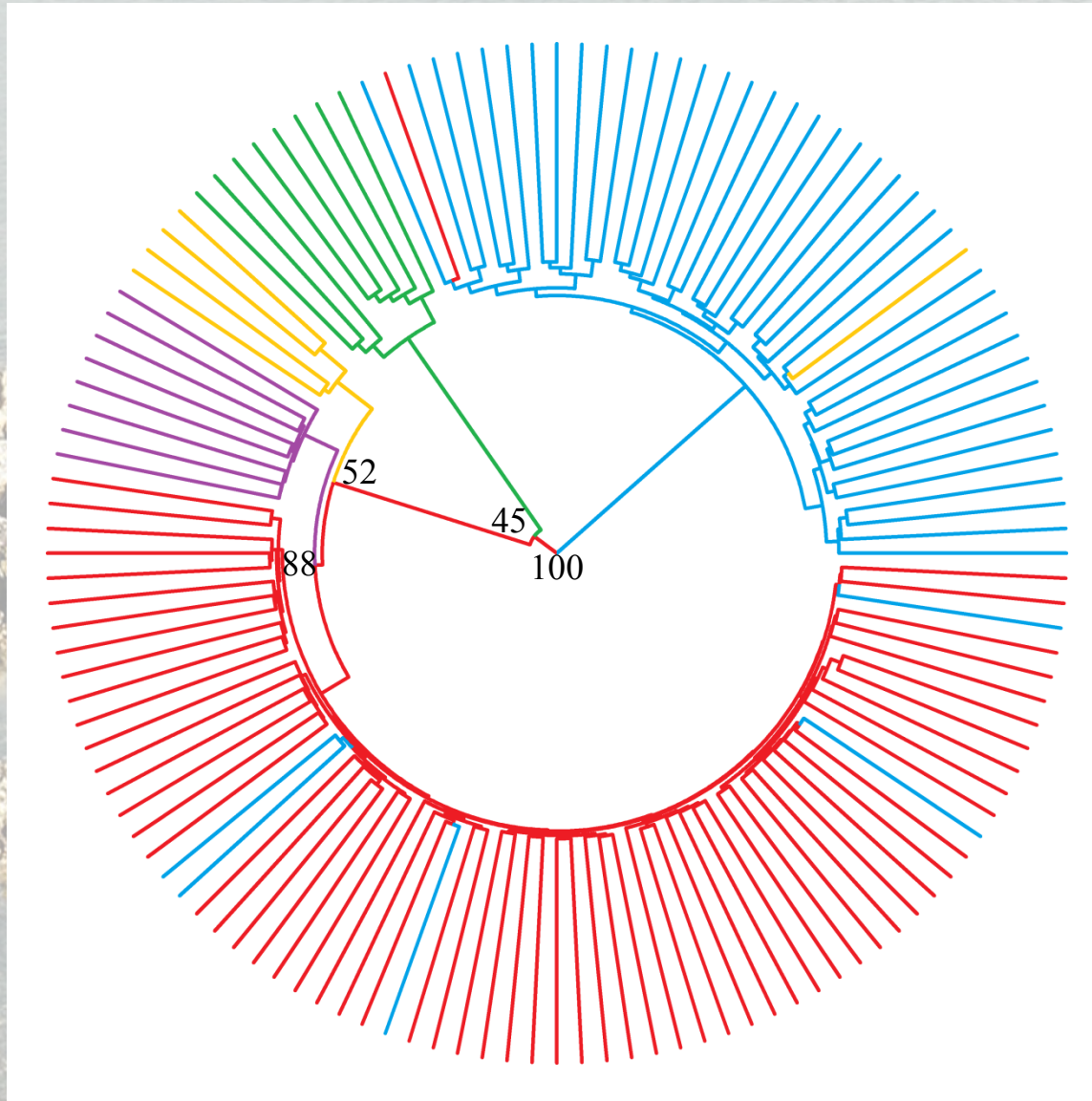
Genetic structure results: PCA

Portugal
Adriatic Sea
S-Europe &
Source pops
N-Europe
Oban



Genetic structure results: phylogenetic tree

Portugal
Adriatic Sea
S-Europe &
Source pops
N-Europe
Oban



Summary 1: genetic structure

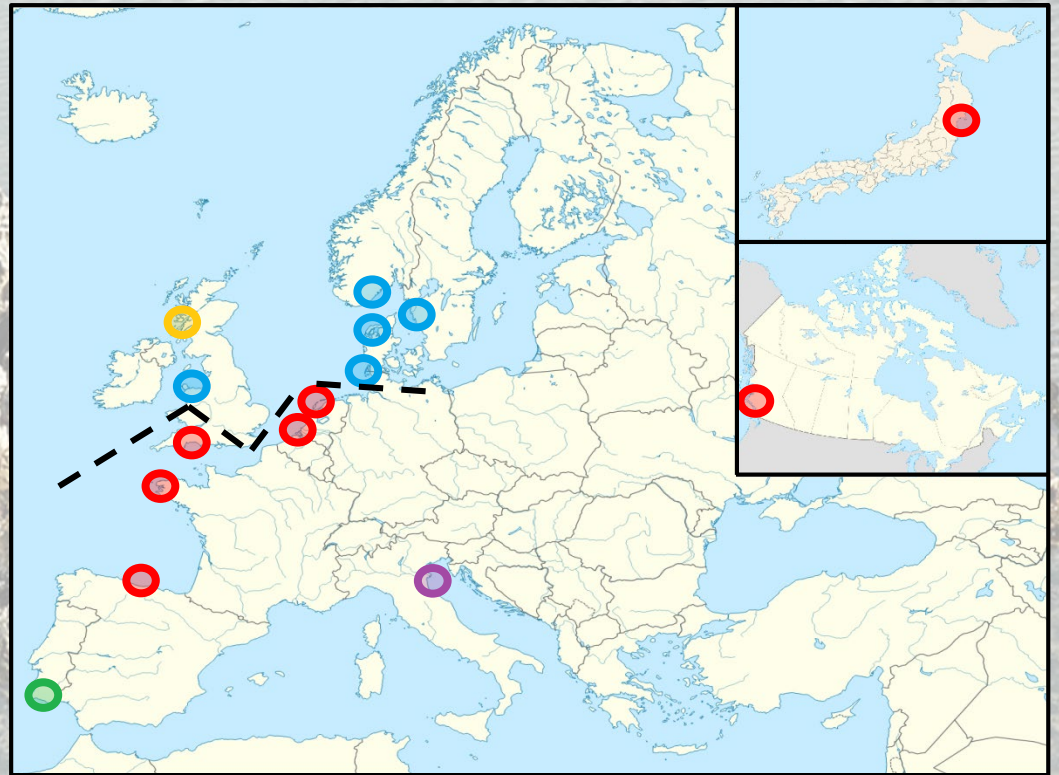
Confirmed the presence of a northern and a southern genetic group.

Samples from the southern cluster do not differ from the ones collected from the source populations

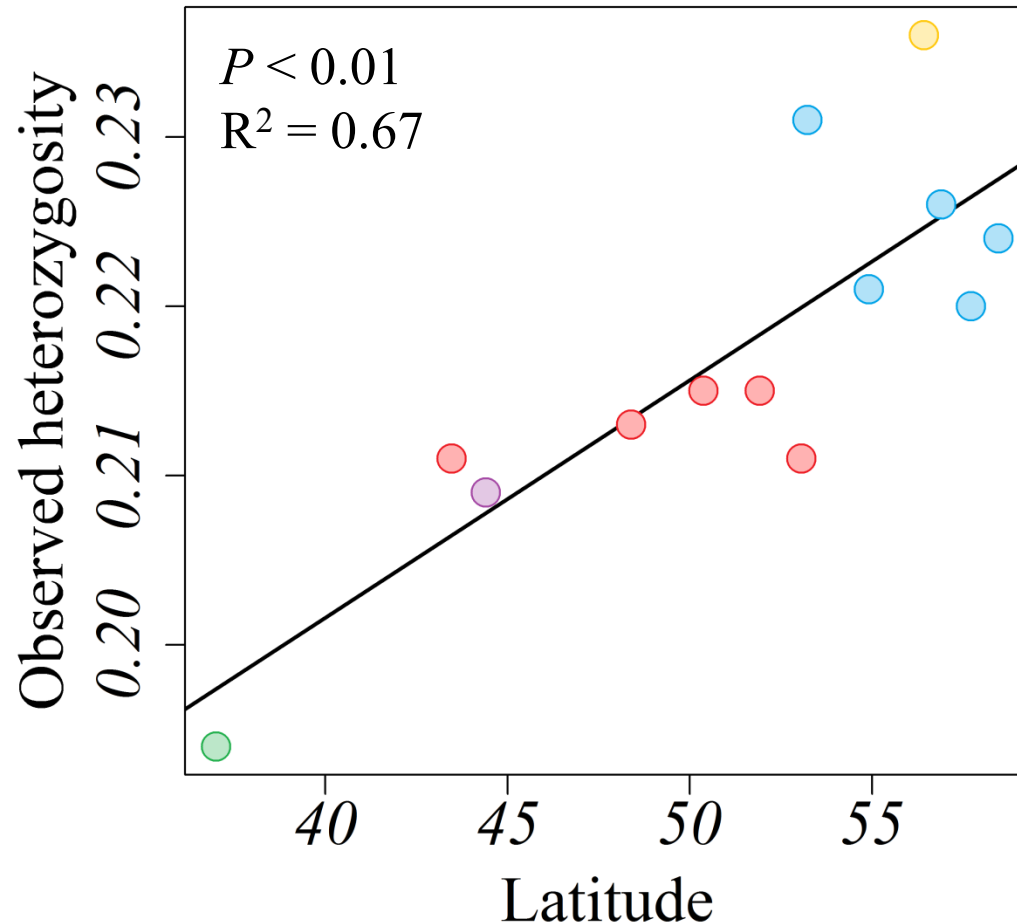
Detected the presence of two additional genetic groups in the southern cluster.

The population from Oban seems to be different from the others.

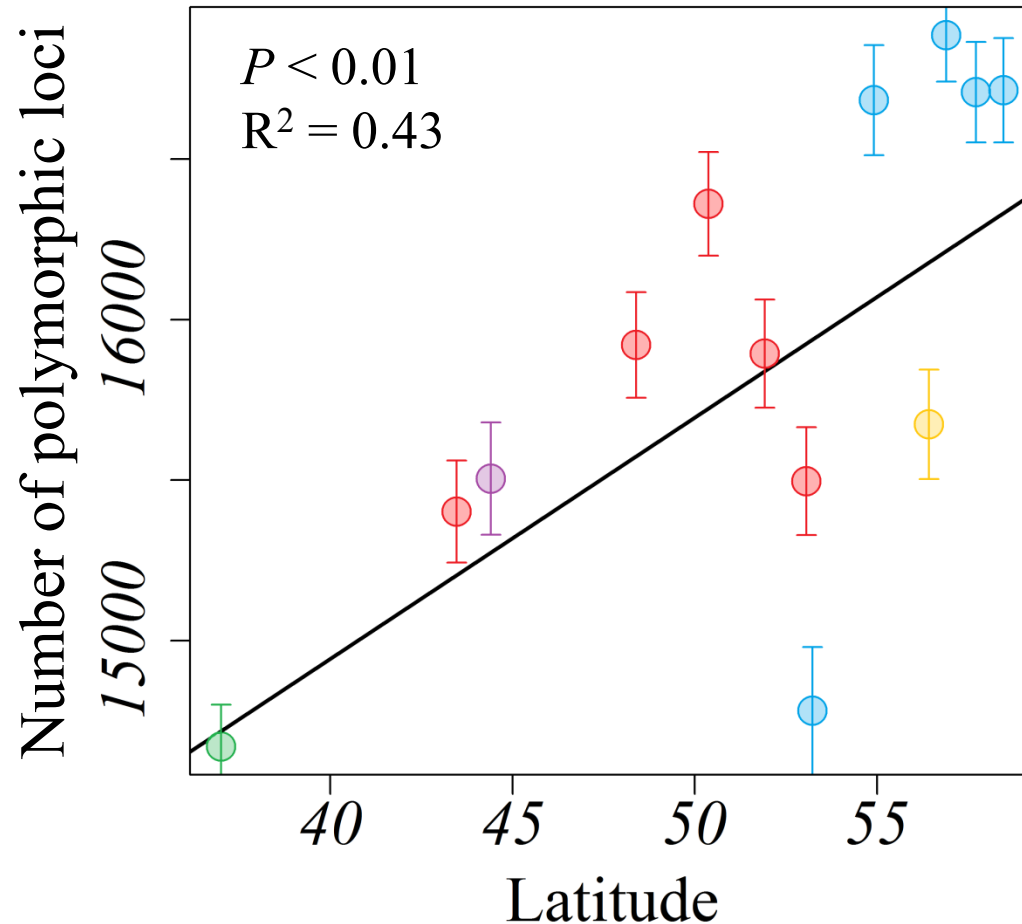
Potential evidence of larval drifting



Genetic diversity results: heterozygosity

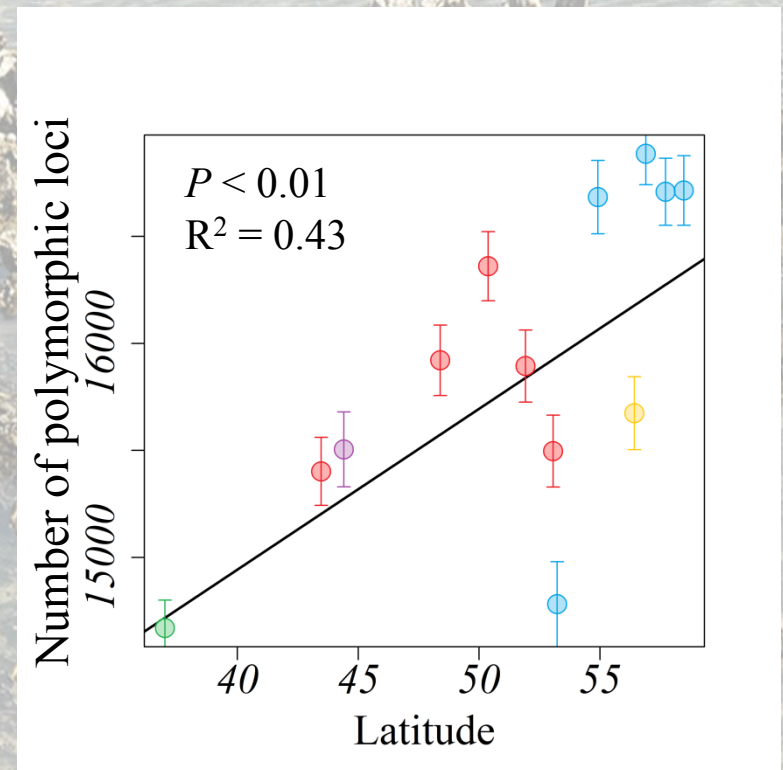
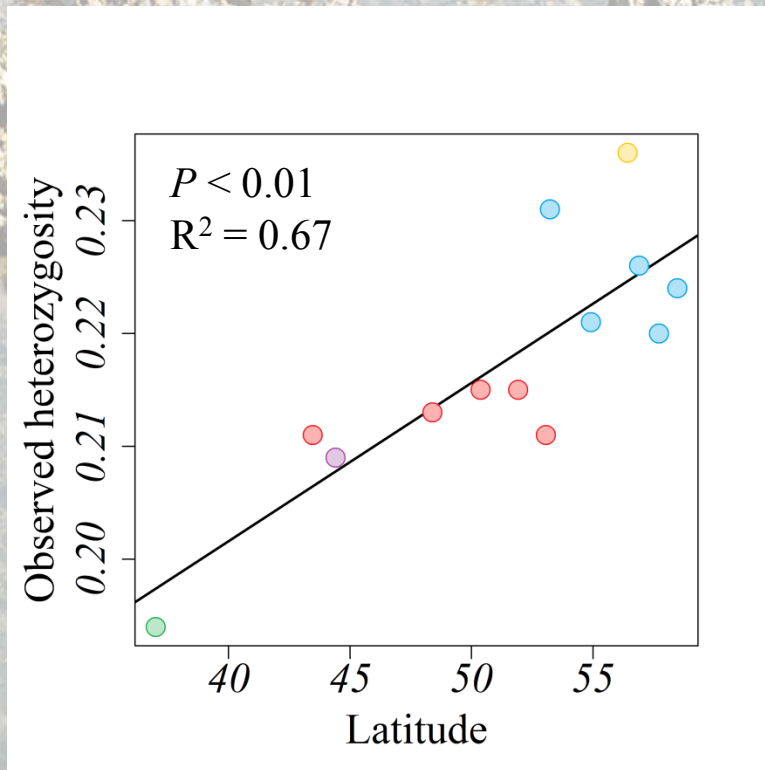


Genetic diversity results: polymorphic loci



Summary 2: genetic diversity

Populations from the northern cluster show higher levels of genetic diversity!!



Loci potentially under selection

> 30,000 SNPs



pcadapt

148 SNPs potentially under selection



univariate logistic
regressions

21 correlated with Sea Surface Temperature



BLAST

14 located within genes

Acknowledgement

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Ross D. Houston
Philip Ellis
Martin Stoffel
Pierre Boudry
Oliver Kruger



Thank you!!!

21 SNPs correlated with SST

SNP	Within_gene	intron/exon	product/closest_product	Distance (bp)
AX.169158107_T	no	NA	cadherin-87A	49
AX.169161967_G	no	NA	retinoic acid receptor gamma	665
AX.169186764_C	no	NA	probable G-protein coupled receptor B0563.6	310
AX.169186786_A	no	NA	uncharacterized LOC105321674	7859
AX.169188930_C	no	NA	uncharacterized LOC105326436	3871
AX.169176222_G	no hits	no hits	no hits	no hits
AX.169179891_G	no hits	no hits	no hits	no hits
AX.169158397_A	yes	intron	uncharacterized LOC105338594	0
AX.169158521_T	yes	intron	calcium homeostasis endoplasmic reticulum protein	0
AX.169162580_T	yes	intron	kin of IRRE-like protein	0
AX.169165078_T	yes	intron	uncharacterized LOC105341373	0
AX.169165757_C	yes	intron	large neutral amino acids transporter small subunit 1-like	0
AX.169167818_T	yes	exon	HAUS augmin-like complex subunit 3	0
AX.169170272_T	yes	intron	transmembrane channel-like protein 7	0
AX.169174221_G	yes	exon	RNA exonuclease 1 homolog	0
AX.169185811_G	yes	intron	cysteine protease ATG4C-like	0
AX.169201293_T	yes	intron	dual adapter for phosphotyrosine and 3-phosphotyrosine and 3-phosphoinositide	0
AX.169206115_T	yes	intron	innexin unc-9	0
AX.169206970_A	yes	intron	ABC transporter F family member 4	0
AX.169207719_T	yes	intron	E3 ubiquitin-protein ligase CBL	0
AX.169208951_G	yes	intron	hemicentin-2	0

Limfjord – Denmark

