

Invasion genetics of the Pacific oyster *Crassostrea gigas* in the British Isles following its introduction for aquaculture production

D. Lallias¹, P. Boudry², F.M. Batista³, A.R. Beaumont¹, J.W. King¹, J.R. Turner¹, S. Lapègue⁴

¹ School of Ocean Sciences, Bangor University, Bangor, UK

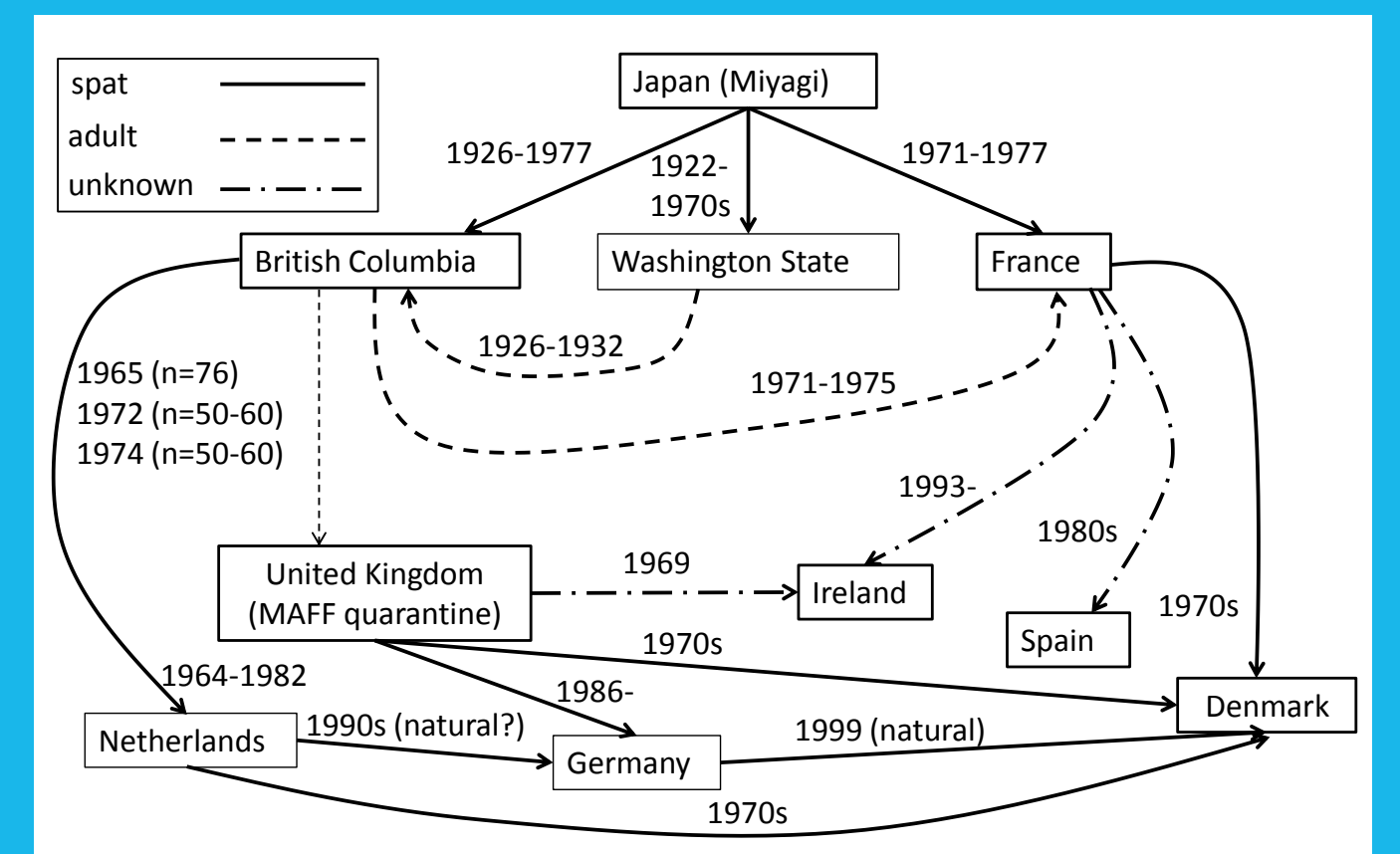
² Ifremer, UMR 6539 Laboratoire des Sciences de l'Environnement Marin, Plouzané, France

³ Instituto Português do Mar e da Atmosfera, Estação Experimental de Moluscicultura de Tavira, Portugal

⁴ Ifremer, Laboratoire Génétique et Pathologie des Mollusques Marins, La Tremblade, France

BACKGROUND

- Pacific oyster *Crassostrea gigas*: native to Japan, introduced in Europe following the collapse of Portuguese oyster *Crassostrea angulata* production in the early 70's. Today one of the most important cultured shellfish in Europe
- First settlement along the French Atlantic coasts but expansion in Northern Europe up to Norway, often as feral populations from aquaculture sites
- In the UK and Ireland: patchy distribution, forming locally dense populations; environmental concerns that its range may further expand
- Good records of introduction and expansion in Europe



AIM OF THE STUDY

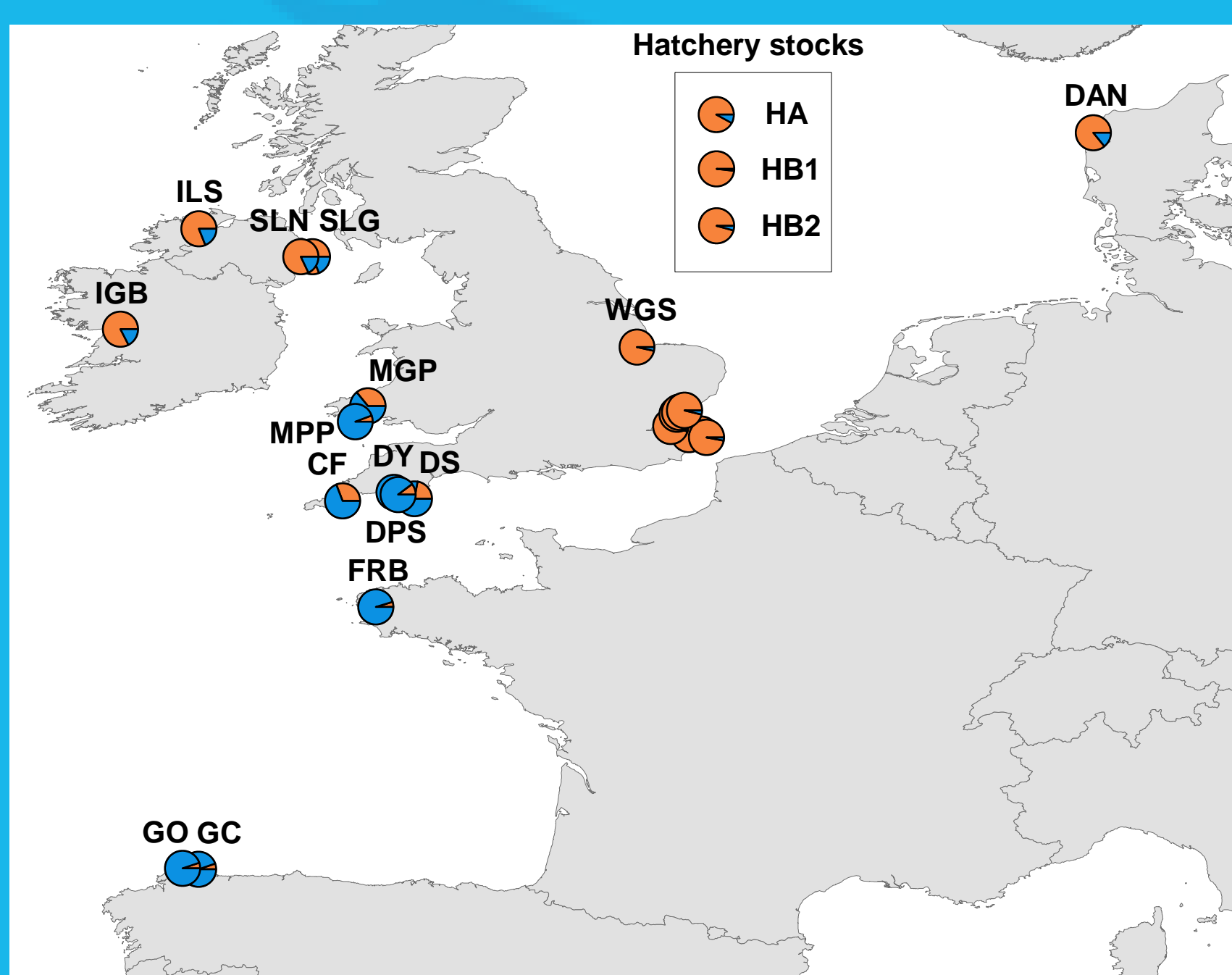
- Assess the genetic diversity and population differentiation of feral populations of *C. gigas*
- Attempt tracing the origin of non-native populations, notably by including samples from 3 British hatcheries and Japan



MOLECULAR MARKERS

- 11 microsatellites (nuclear markers) - 25 populations (n=37-200)
- Major Noncoding Region (mitochondrial marker) - 13 populations (n=18-25)

RESULTS: MICROSATELLITES



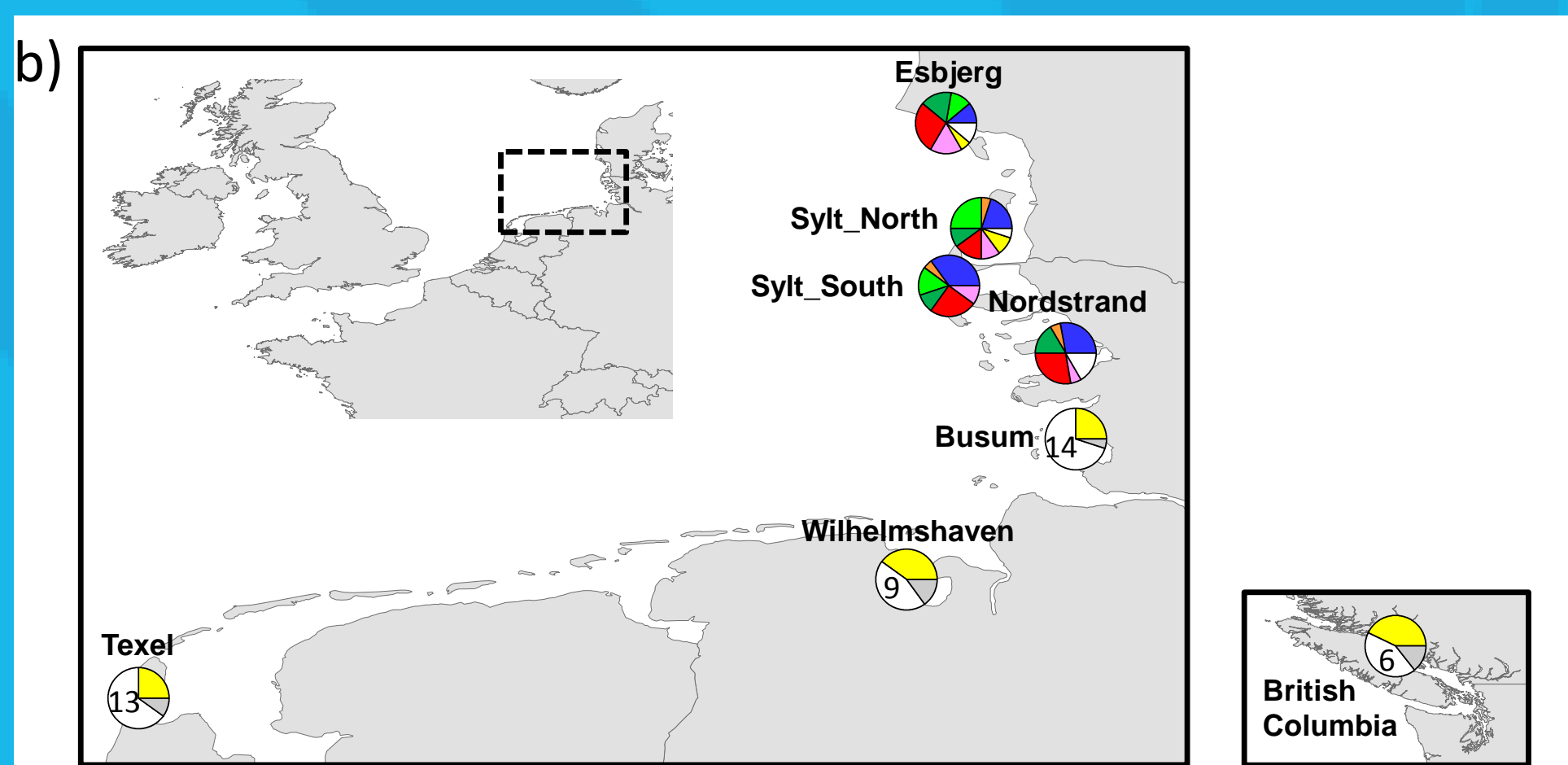
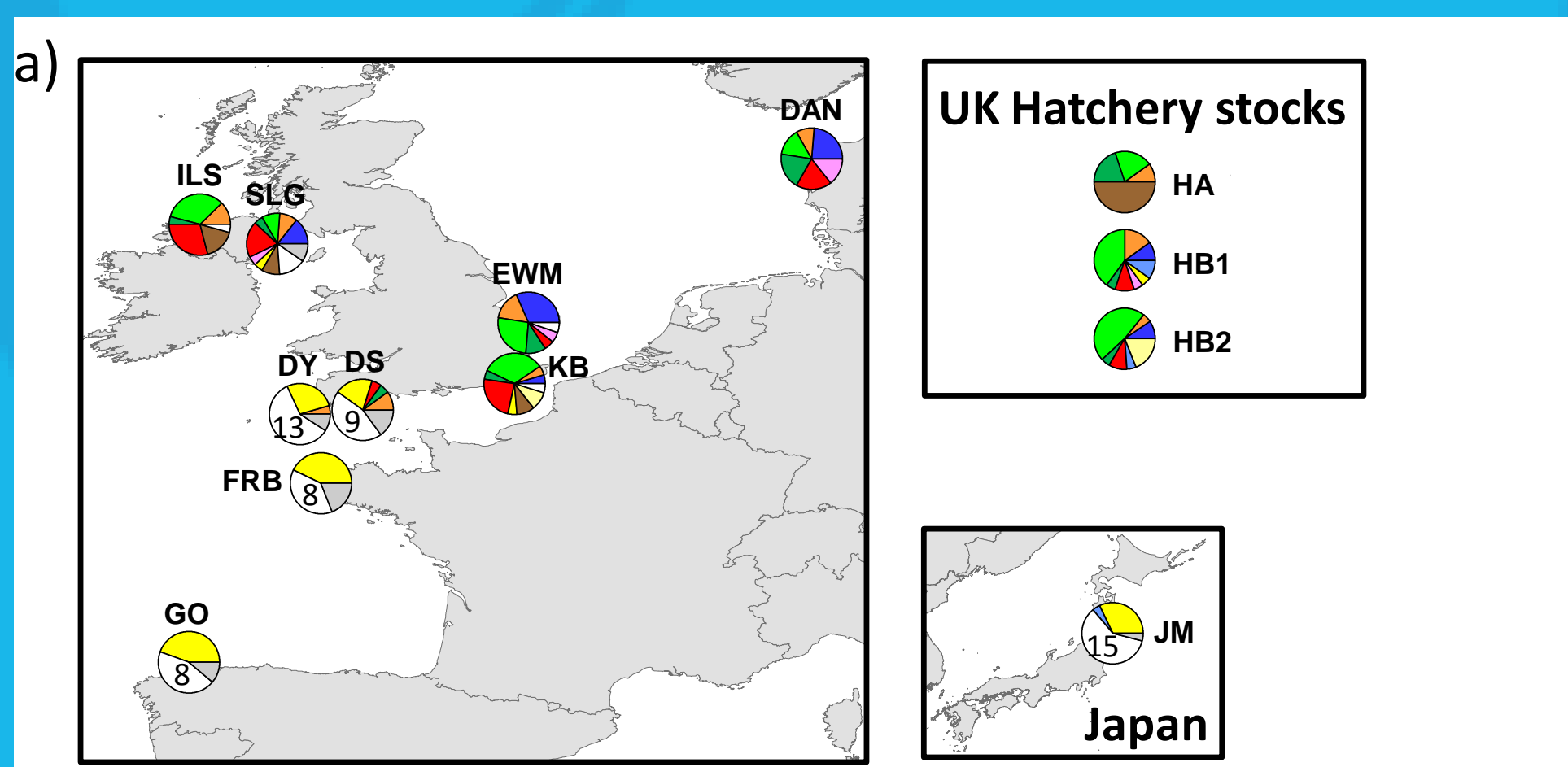
Map of sampling sites, with coloured pie charts showing the contribution of the two main genetic clusters identified by STRUCTURE analysis.

Cluster	A	He	Private
South West	45.68	0.928	16.091
EE/I/D/H	26.58	0.883	1.364
Hatchery A	11.47	0.844	0.090

A: allelic richness
He: expected heterozygosity
Private: no. of private alleles

- 2 main genetic clusters:
 - ✓ South West
 - ✓ East England / Ireland / Denmark / Hatcheries (EE/I/D/H)
- Hatchery A forming a 3rd cluster in most analyses
- $F_{st} = 0.022$ [0.017-0.028]
- Significantly higher A, He and Private in South West cluster

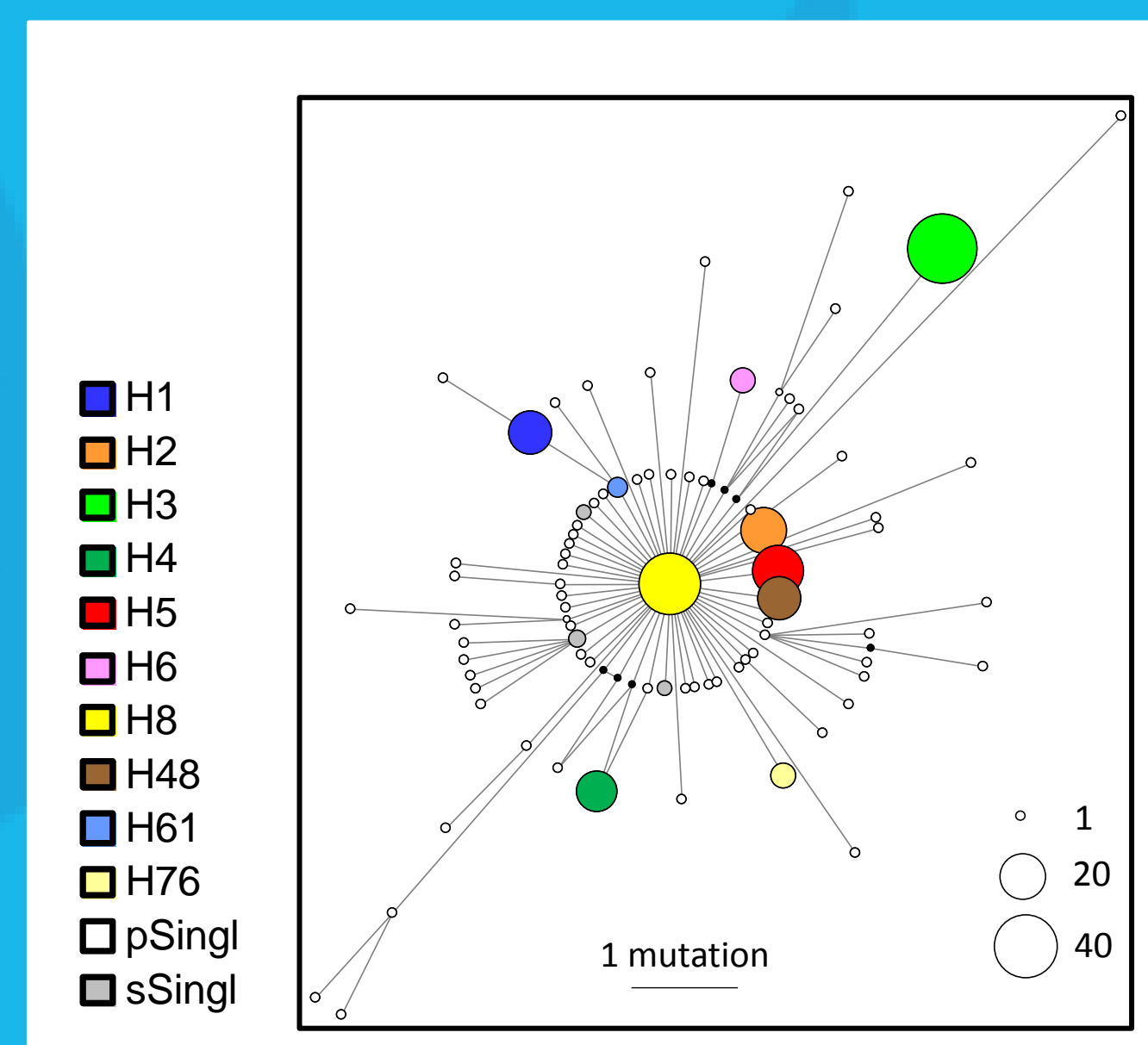
RESULTS: MITOCHONDRIAL DNA



Maps of MNR haplotype frequencies. a) This study; b) Samples analyzed by Moehler et al 2011 (J Sea Res 66: 256-262).

Cluster	H _t	H _d
SW/JM	69	0.879
EE/I/D/HB	18	0.851
HA	4	0.695

H_t: no. of haplotypes
H_d: haplotype diversity



Median-joining network for the 81 MNR haplotypes of *C. gigas*. pSingl: private singletons; sSingl: shared singletons

- Alignment: 674 bp - 109 variable positions (16.2%)
- 81 haplotypes
- 3 main genetic clusters
 - ✓ South West / Japan (SW/JM)
 - ✓ East England / Ireland / Denmark / Hatchery B (EE/I/D/HB)
 - ✓ Hatchery A (HA)
- Star-like pattern (central haplotype: H8)
- Significantly higher H_t and H_d in South West / Japan cluster

CONCLUSIONS

- Good agreement between nuclear and mitochondrial markers
- Two or three main genetic clusters
- Genetic diversity patterns generally follow history of introduction and aquaculture practices
- Our population genetics study illustrates the potential of such approaches to unravel the recent history of a marine bivalve now invasive in Northern Europe