

Genetics of Scottish populations of the native oyster,



The European, native or flat oyster, *Ostrea edulis*, has been the subject of human-mediated translocation and aquaculture in Europe for centuries and may have diluted or masked natural population genetic structure. Samples of *O. edulis* from 10 sites in Scotland and The Netherlands, Brittany and Norway were collected and genotyped at up to six microsatellite loci. Numbers of alleles and heterozygosity per locus were high in all populations and were consistent with previous microsatellite studies. There is no evidence that extensive traditional oyster aquaculture has led to loss of allelic diversity. Deficiencies of heterozygotes against Hardy-Weinberg predictions were common and were probably mainly due to the presence of null alleles. Overall, population differentiation ($F_{st} = 0.05$) was estimated to be higher than previous studies and could be resolved into four main genetic groups (1) Norway, (2) The Netherlands and Brittany, (3) Scotland apart from (4) Skye. The genetic distinctness of Norway oysters agrees with previous findings.

The distinctiveness of the Skye population could be partly due to an artefact of small sample sizes and partly due to the founder effect of importation of Brittany oysters in the 1950s. Further studies are required to ascertain whether the Skye population may be deserving of special conservation status. The results suggest that human aquaculture activities over recent centuries have probably diluted any original local genetic differentiation within Scotland, but that potentially important genetic differentiation still exists at the wider scale across Europe

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