

Exploring local reproductive differentiation of Pacific oyster population recently settled in northern Europe by transcriptomic approach

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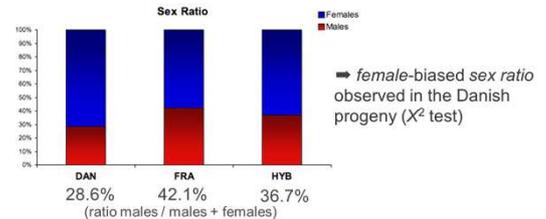
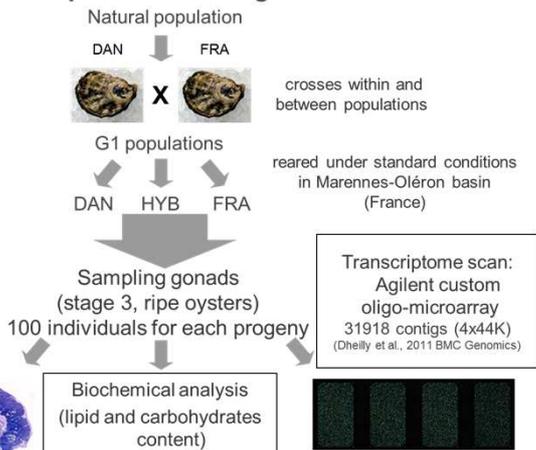
Abstract Originating from north-eastern Asia, the Pacific oyster *Crassostrea gigas* has been introduced, mainly for aquaculture purpose, into a large number of countries. Although highly variable, its invasive nature has been reported in an increasing number of coastal areas, notably Northern Europe. We set up a common garden experiment based on the comparison of progenies of Pacific oysters sampled in France, where populations settled since the introduction of the species in the 70's, and Denmark, where established populations were observed since the beginning of 90s. Pure and hybrid progenies, resulting from crosses within and between adults sampled in both populations, were studied for their sex-ratio, condition index, transcriptomics, and biochemical parameters.

A female-biased sex-ratio and a higher condition index, which reflects a greater reproductive effort, were observed in the Danish progeny, both being hypothesized as a possible reproductive strategy to increase the potential success of natural recruitment in this recently settled population. Overall the 31,918 mRNAs assayed, the mean phenotypic differentiation (P_{ST}) was 0.29. The degree of differentiation in quantitative traits (Q_{ST}) were estimated on intermediate mRNA levels in hybrid progeny (suggesting additive genetic bases), outliers Q_{ST} estimates between the two progenies were 55 and 52 in male and females respectively, giving a mean value of 0.5. Among the over-expressed genes observed in the Danish progeny, candidate genes for sperm quality and insulin metabolism were found. Carbohydrate and lipid measurements showed higher levels for hybrid progeny suggesting hybrid vigor for these biochemical characters.



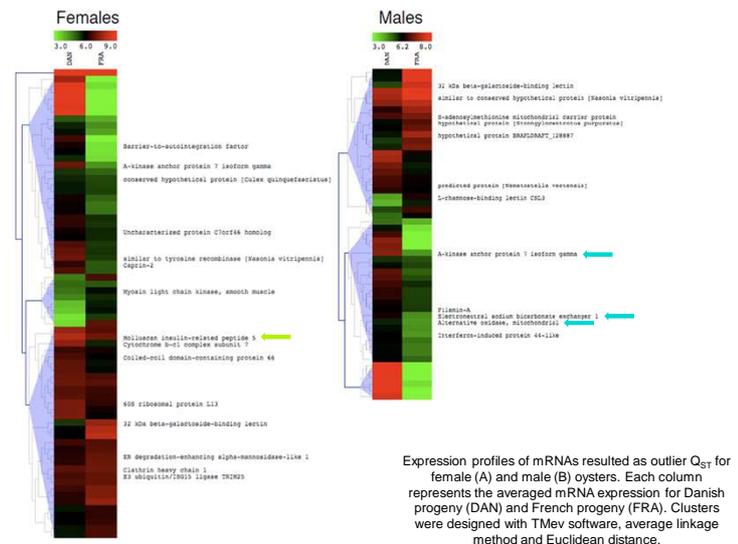
Populations present from Portugal to Norway and in the Mediterranean sea with an established genetic structure between Northern and Southern populations

Experimental design



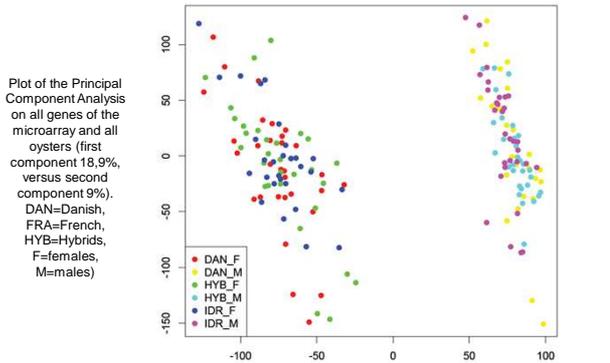
Reproductive strategy for an unlimited male gametes species to increase the potential success of natural recruitment?

Only 3% features of the microarray showed mRNA level strictly intermediate in hybrids and thus their variation presumed to be under additive genetic determinism. Average Q_{ST} values were 0.50 for males and 0.51 for females while phenotypic differentiation mean values on all genes, P_{ST} , were of 0.29; clearly higher to the genetic differentiation F_{ST} (0.046 for SNPs and 0.037 for microsatellites; Rohlfritsch et al. 2013). Over-expression in the Danish progeny of candidate genes for sperm quality (oxidative protection of spermatozoa) and insulin metabolism.



Expression profiles of mRNAs resulted as outlier Q_{ST} for female (A) and male (B) oysters. Each column represents the averaged mRNA expression for Danish progeny (DAN) and French progeny (FRA). Clusters were designed with TMEV software, average linkage method and Euclidean distance.

A strong gender effect requiring calculate separate sex Q_{ST}



Conclusions

-Reproductive strategies to increase the potential success of natural recruitment and favor colonization of new habitats:

A higher quantity of female gametes shown by the female biased sex-ratio

A greater gamete quality would also enhance the chance of success to the fertilization revealed by the over-expression of candidate genes for sperm quality and insulin metabolism.

-Diversifying selection is probably acting on outlier gene expression: Divergence in neutral markers F_{ST} compared to divergence in phenotypic traits is typically used to estimate whatever populations are submitted to genetic drift or selection. The Q_{ST} levels exceed that observed in F_{ST} on the same populations by Rohlfritsch et al. (Evol Appl 2013) suggesting an important role of natural selection on traits associated with differentially expressed mRNAs.

