

Development of microsatellite markers from 454 transcriptome derived sequences for the scallop *Pecten maximus*

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ABSTRACT

Twelve microsatellite markers were developed for the scallop *Pecten maximus*. The markers were tested in three geographically diverse populations and all markers were polymorphic in all three populations. The mean number of alleles per locus ranged from 2 to 10.67 and the observed and expected heterozygosity ranged from 0.05 to 0.67 and 0.05 to 0.81 respectively. Some loci showed evidence of null alleles and an excess of homozygotes in some populations but 9 loci conformed to Hardy–Weinberg expectations. These new loci can be combined with previously published microsatellites to create a powerful suite of markers for genetic analyses.

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