
The population genetics of hybrid zones between introduced and native mussels at the sea-port interface

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Abstract

Anthropic activities are creating new contacts between genetically differentiated lineages that start to exchange genes again before our eyes. These contacts provide the opportunity to investigate the importance of demography, environmental conditions, reproductive isolation and contingency on the outcome of hybridization between introduced and native lineages. In the opposite direction, a better understanding of the importance of those parameters is essential to hope to control invasions with hybridization, both spatially and genetically. We studied the population genetics of non-indigenous mussels in French ports. The blue mussel species complex (*Mytilus sp.*) is composed of three species distributed in the Northern hemisphere (*M. edulis*, *M. galloprovincialis* and *M. trossulus*), that naturally hybridize each time they meet. *M. galloprovincialis* is also found worldwide due to its invasive potential (e.g. in South Africa, the US West coast or Asia). Using a set of ancestry informative markers we recently uncovered that the mediterranean lineage of *M. galloprovincialis* has been introduced in multiple French ports (Le Havre, Cherbourg, Saint Malo, Brest) and has been extensively introgressed by *M. edulis*. Sharp genetic shifts are observed at a very fine spatial scale at the sea-port interface where the native population is *M. edulis*. In the roadstead of Brest

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however, where the native population is the Atlantic lineage of *M. galloprovincialis*, we found that the invading lineage started to spread and to introgress the native background. We used adjustment to the migration-selection tension zone model to better understand the relative importance of connectivity, reproductive isolation and adaptation to the port environment in maintaining the spatial structure.