

## Genetic basis of Abnormal Mussel Mortality in France using a field and experimental infection investigations

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Abnormal mussel mortality (AMM) outbreaks started along the French Atlantic coasts in 2014 and varied among sites and years (30-100%). The etiology of AMM is still unknown. This study investigates the resistance to AMM in the two mussel species cultivated in France (*Mytilus edulis* and *M. galloprovincialis*) and mussels with genomic signatures from both species (NH). Six wild mussel populations were used to produce 100 families in January/February 2017. Mussels were deployed in two sites [La Floride (LF), and Maison Blanche (MB)] in October 2017, and their survival/growth were recorded until June 2018. AMM was only observed at MB during spring 2018, and reached 70%, 43%, and 63%, for *M.edulis*, *M.galloprovincialis*, and NH, respectively, at the endpoint. In contrast, low mortality was observed in LF, reaching 11%, 30%, and 22%, respectively. Heritability for survival was low to moderate in both sites, ranging from 0.06 to 0.34. Significant genotype-by-environment interaction for survival between sites was found with low genetic correlations (-0.05 to 0.43). In addition, experimental infection was performed in October 2018 using a pathogenic strain of *Vibrio splendidus* isolated during AMM in 2014. The mean mortality after 72 hours post-infection was 53%, 22%, and 31% for *M.edulis*, *M.galloprovincialis*, and NH, respectively. The lowest heritability was observed for NH (0.15) and highest for *M.galloprovincialis* (0.38), and more interestingly, the genetic correlation between AMM in MB and experimental infection was not significantly different from 0, suggesting that this *Vibrio* strain, is not the major cause of AMM outbreak in MB 2018.