

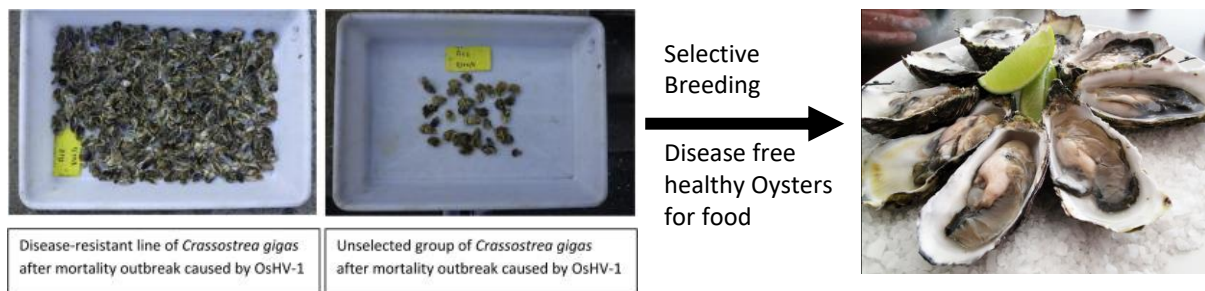
Topic/Title

Fin kartlegging for å kartlegge gener for resistens mot OsHV-1-virus i stillehavsosters.

Topic/Title

Fine mapping to unravel genes for resistance to OsHV-1 virus in pacific oyster.

Picture



Summary

Background: The Pacific oyster (*Crassostrea gigas*) is a highly important shellfish species, accounting for roughly 98 percent of global oyster aquaculture. Infectious diseases pose a significant threat to sustainable production, with high economic losses due to mortalities. The Ostreid herpesvirus type 1 (*OsHV-1*) is highly contagious, with a relatively short lifecycle and can cause up to 100 percent mortalities. We detected a strong signal of QTL for survival against *OsHV-1* explaining large proportion of genetic variance ¹.

The topic of this thesis: Fine mapping to unravel genes underlying resistance to *OsHV-1* virus in pacific oyster.

Type of work: The QTL mapping was previously performed using axiom array with sparsely distributed SNP markers (n~14000). We also have the sequence data from the parents and sibs available. The objective of this thesis would be to determine position of array SNPs in newly assembled genome assembly (https://www.ncbi.nlm.nih.gov/assembly/GCF_902806645.1/) perform imputation to increase resolution, and execute fine-mapping of the genomic QTL regions.

Relevant literature:

1. M. L. Aslam, Dagnachew, B. S., Heurtebise, S., Maurouard, E., Dégremont, L. and Lamy, J-B. 2021. GWAS and accuracy of predictions for resistance against *OsHV-1* in pacific oyster *Crassostrea gigas*. Proceedings of EA-2021, Madeira, Portugal, pp. 79-80. <https://eposters.blob.core.windows.net/eas-eposters/AE2021AbstractBook.pdf>
2. S. van den Berg., Vandenplas, J., Eeuwijk, F. A-van., Bouwman, A. C., Lopes, M. S., and Veerkamp, R. F. 2019. Imputation to whole-genome sequence using multiple pig populations and its use in genome-wide association studies. Genet. Sel. Evol. doi: 10.1186/s12711-019-0445-y.

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