Novel molecular ecology tools to predict harmful algal blooms in oyster-producing estuaries

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Harmful algal blooms (HABs) leading to the accumulation of marine biotoxins in seafood are one of the primary risk factors for aquaculture worldwide, including in Australia. Information on the abundance of harmful algae is obtained by transporting water samples to laboratories where light microscopy is used to identify HAB species, taking ~ 2-7 days. For the shellfish aquaculture industry to be able to monitor for HABs in real time, prior to the accumulation of biotoxins in seafood, on farm methods are required that can be conducted simply and quickly. As part of a large-scale project, we have developed and implemented on-farm methods of weekly HAB sample collection using eDNA for molecular genetic analyses in 11 estuaries. This method coupled with on farm qPCR pipelines that we have developed can aid in rapid and precise species identification and the identification of genes responsible for marine biotoxin biosynthesis. The information obtained in this project will allow for fine scale modelling of factors influencing marine water quality using much larger and more precise datasets than have been previously available, including the prediction and mitigation of the impacts of marine HABs.