WHAT & WHO: Comparing the genetic variation of wild and selectively-bred B2 Sydney Rock Oysters. Research was undertaken by Macquarie University (Jessica Thompson, David Raftos & Adam Stow) in partnership with NSW DPI (Mike Dove & Wayne O'Connor)

BACKGROUND: The project was designed to compare wild oysters from the Georges River with B2 selective breeding line oysters. Oysters were ~3-year-old. There is evidence that selectively-bred B2 oysters perform differently to wild oysters under various conditions, with differences in traits such as growth rate and disease resistance. We wanted to know whether the differences between these oyster types could be seen in their genetics. This is important because if the different traits and performances have a genetic basis, then these traits can be passed down through generations. This is very important when developing and maintaining selective breeding programs.

WHAT WAS FOUND: We found a clear difference between the genetic composition of wild and B2 oysters. The genetic composition of the B2 oysters was much more variable than the wild oysters. This is important as higher levels of genetic variation can help to improve the overall survival of the population or group of oysters, particularly when there is a change in environmental conditions. We also identified 35 genetic markers that were unique to the B2 oysters, and could be associated with traits they were selected for (disease resistance and fast growth).

HOW WILL THIS HELP THE OYSTER INDUSTRY: The higher genetic variation in B2 oysters was completely unexpected and fantastic news for the industry. Animals in selective breeding programs almost always have lower genetic variation than the animals in the wild population that they were originally taken from, even after just one or two generations. The fact that the B2 oysters still have high genetic variation after so many generations of selective breeding means that the breeding program is being managed successfully. The genetic markers identified in the B2 oysters are currently being investigated further. If we can identify their function, hopefully this information can be used to assist the industry's selective breeding programs.
The findings of this study also present a major stepping stone towards further research comparing wild and selectively-bred Sydney rock oysters.

Over the next 2 years, Jessica's research will focus on specific comparisons between multiple selective breeding lines and crosses. This will hopefully allow us to identify specific genes associated with important traits for oyster production, such as disease resistance. Jessica will also compare a huge range of wild oysters collected across their entire distribution on the east coast. By examining the genetic variation of many wild oyster populations, this could help us to find 'hotspots' that contain oysters with genetic markers relating to important traits such as disease resistance. These oysters and their beneficial genes could then be incorporated into future breeding experiments.

FURTHER INFORMATION: Jessica Thompson on Jessica.Thompson2@students.mq.edu.au