World-first mapping of the Aussie tiger prawn genome
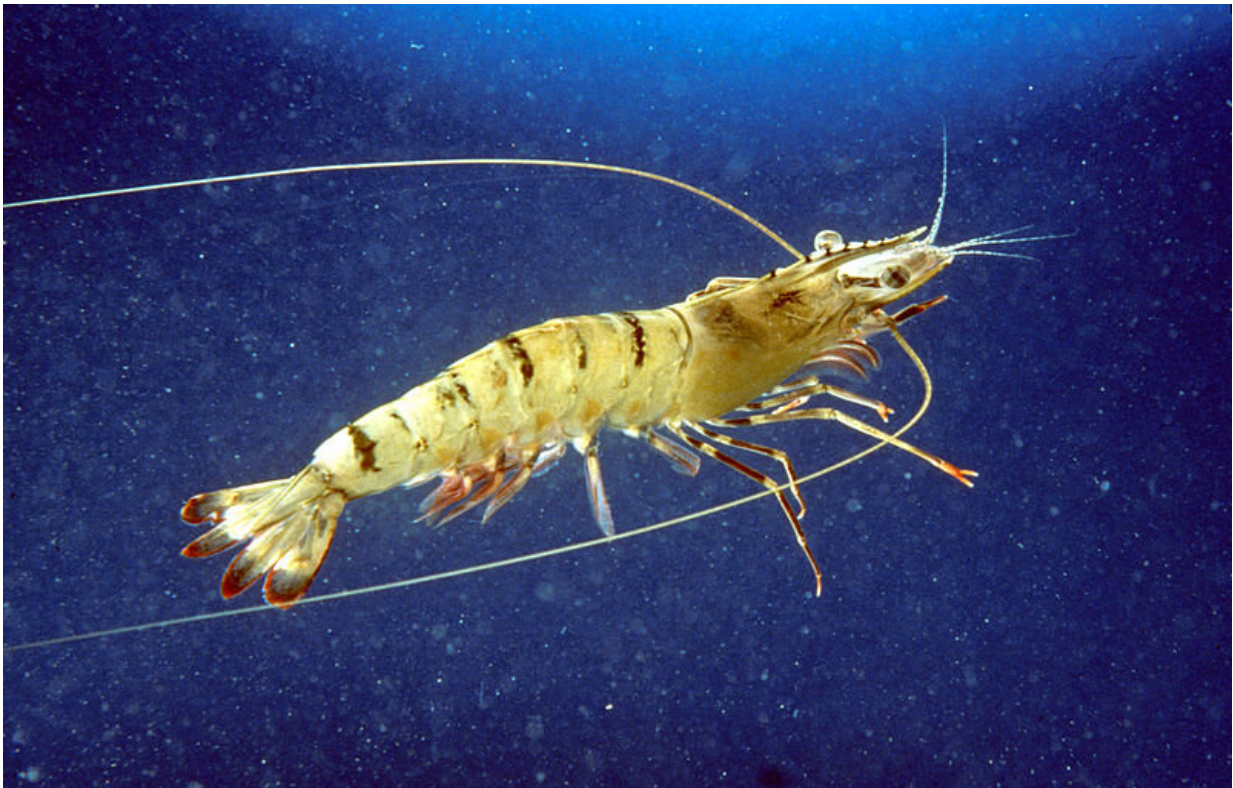
March 14 2022

The giant tiger prawn (Penaeus monodon) is the dominant prawn species farmed in Asia and Australia. Scientists at CSIRO Marine Research are working to improve the average productive output of the giant tiger prawn, improve the capacity of prawn farms to stock ponds with progeny from domesticated broodstock, and develop and introduce selective breeding for commercially useful traits. Credit: CSIRO Marine Research/Wikimedia Commons, CC BY 3.0

James Cook University researchers have been part of the first-ever successful effort to map the genome of an iconic Australian seafood species—that of the Australian black tiger prawn—which may lead to bigger and more disease resistant farmed stock in the future.

JCU Professor of Aquaculture Dean Jerry said the research came out of the ARC Industrial Transformation Research Hub for Advanced Breeding, a collaboration between JCU, the Australian Genome Research Facility (AGRF), the University of Sydney, CSIRO and Seafarms Group. The partnership aimed to improve productivity and efficiency of farming prawns through the use of genetic selection.

"The idea was to improve the capability of Australian prawn farmers to apply selective breeding practices to produce larger and healthier farmed prawns. As part of this project, we set out to sequence the genome of the black tiger prawn. The information in the genome is important for us to know, as it essentially contains the blueprint that determines the makeup and behavior of the prawn," said Professor Jerry.

He said one benefit of having this genome is that it can significantly help with the selective breeding efforts of prawns, similarly to what has happened with livestock and crop species over the last few thousand years.

"The prawn is a tiny animal, but its genome is almost as large as a human, and is much more complicated in its structure," said Professor Jerry.

AGRF Bioinformatics Manager Dr. Kenneth Chan said the genetic mapping process to reconstruct the genome of the black tiger prawn was diabolically tricky.

"Imagine the task of putting together a 1.9 billion piece double-sided

puzzle with no borders, long repeated overlapping sections, millions of missing pieces, multiple pieces that can fit in the same place, no picture on the box to follow, and possibly lots of pieces from another unrelated puzzle," said Dr. Chan.

The scientists also found something very unusual in the way the tiger prawn fought viral infections.

Dr. Nick Wade, Senior Research Scientist with CSIRO explained that the Viral elements in the genome that help fight viral infections (known as the Endogenous Viral Element or EVE) is truly unique in the Australian tiger prawn.

"No EVE found in any other animal looks like this," said Dr. Wade.

"Discovery of this EVE allows for further research into understanding how prawns deal with infections by viruses and perhaps into new therapies that can be applied to make prawns more resistant to viral diseases," he said.

Professor Jerry said the benefits of mapping the genome will come in a whole range of complementary areas.

"It radically changes the landscape for prawn research, enabling a whole suite of other functional biological studies, including on how to target particular genes for improved selection outcomes, through to precision genome engineering," said Professor Jerry.

More information: Roger Huerlimann et al, Genome assembly of the Australian black tiger shrimp (Penaeus monodon) reveals a novel fragmented IHHNV EVE sequence, *G3 Genes|Genomes|Genetics* (2022). DOI: 10.1093/g3journal/jkac034

Provided by James Cook University