

Unleashing the genetic potential of black tiger shrimp

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New research hub in Australia to develop advanced breeding program

The black tiger shrimp (*Penaeus monodon*) is globally the second most farmed penaeid species, accounting for about 15 percent of total shrimp production in 2014, totaling 634,521 metric tons (FAO 2016).

Despite early growth in production in the mid-1980s, continued expansion of the farmed black tiger industry has not fulfilled initial expectations, primarily due to difficulties in broodstock supply and domestication of the species, devastating viral diseases, increased market competition from other penaeids, and trade restrictions.

As a result, there has been a widespread trend towards farming of the fully domesticated and genetically improved white-tailed shrimp (*Penaeus vannamei*), particularly in Asia, where this species was commercially introduced in 1996.

In Australia, the black tiger shrimp is still the primary crustacean farmed, representing about 95 percent of total shrimp production in 2014 (5,000 metric tons; APFA 2016). Historically, the Australian industry has been heavily reliant on the collection of wild broodstock to propagate the seedstock needed to stock farms, although recent advances in husbandry and domestication by some companies are decreasing this reliance.

Semi-commercial domestication – coupled with selection for enhanced growth, survival and pathogen resistance – has highlighted the benefits and increases in productivity that can come from the genetic improvement of the species (i.e., up to 39 percent higher over wild stocks; Norman-Lopez et al. 2015. Aquaculture Research. doi: 10.1111/are.12782). As such, there is great interest in Australia in selective breeding of black tiger shrimp. To date, however, the Australian industry has not widely capitalized from selective breeding of the species.



ARC Hub for Advanced Prawn Breeding

In recognition of the importance of Australian aquaculture as an industry to provide healthy and sustainable seafood to the global community, the Australian Research Council (ARC) funded a five-year Industrial Transformation Research Hub comprising leading animal geneticists, genomists, virologists and aquaculturists from James Cook University, the Commonwealth Scientific and Industrial Research Organization (CSIRO) and the University of Sydney, genome sequencing expertise from the Australian Genomics Research Facility (AGRF) and Ghent University, and one of the country's largest producers of farmed shrimp, Seafarms Group. (Seafarms Group is the proponent for Project Sea Dragon, which aims to develop one of the largest shrimp farms in the world comprising 10,000 ha of ponds in northern Australia.)



Examples of black tiger shrimp being phenotyped for cooked coloration.

The resultant ARC Hub for Advanced Prawn Breeding has the ambiguous mission of bringing the genetic knowledge of the black tiger shrimp to a comparable level as that in livestock and to generate the tools and processes needed to conduct a highly-advanced breeding program for the species that has industrial scalability. In particular, the Hub endeavors in one effort to bring the state of genetic and phenotypic knowledge to the point where highly accurate statistical methods based on genome-wide markers can be used to predict the genetic merit of a breeding animal.

This approach is termed genomic selection and has recently established itself as the gold standard in livestock and crop improvement programs. Incorporating genomic selection into breeding programs has been shown to increase genetic gain for some traits by as much as 81 percent and have an average increase in breeding value accuracy of 33 percent over purely traditional phenotypic- based methods (Nielson et al. 2009. *Aquaculture* 289:259-264 & Nielson et al. 2011. *Journal of Animal Science* 89:630-638).

Furthermore, genomic selection has the highest potential for the selection of traits that cannot be directly measured on the selection candidates themselves (like disease tolerance, carcass quality and feed conversion ratio, or FCR), as it captures both the within and between family components of genetic variance. Integration of genomic selection methods into shrimp breeding programs, particularly those incorporating disease and physiological tolerance traits,

promises to rapidly increase genetic gains over that of traditional phenotype selection.



Sampling black tiger shrimp for DNA analysis (Researchers Quyen Quyen Banh and Tansyn Noble).

What the ARC Hub will deliver to the Australian industry

Activities for the ARC Hub for Advanced Prawn Breeding fall under five workpackages, each of which either deliver foundation knowledge, or cutting-edge genetic tools to achieve the overarching objective of implementing genomic selection. These scientific themes include:

Family production – For any breeding program to be successful it has to have a reliable supply of broodstock. Working with Seafarms staff, innovative husbandry approaches will be used to produce large numbers of domesticated broodstock. It is a major goal of the ARC Hub to leave in place numerous domesticated shrimp lines that also have extensive genomic and phenotypic data records and that can become foundation stocks for Seafarms' future selection program.

Draft shrimp genome – Knowledge on genome structure of the black tiger shrimp can provide information essential to the downstream development of genetic maps and advanced genomic breeding programs, along with providing the capacity to better understand the function of genes linked to commercially important traits. The ARC Hub is utilizing a combination of the latest next-generation sequencing technologies and assembly pipelines to produce a draft genome, and tissue-specific transcriptome. It will also apply comparative mapping methodologies of the black tiger genome with that of other crustaceans to further refine the draft genome. The goal is to produce the most

comprehensive shrimp genome assembly to date.

Production of genomic resources – Understanding genome structure and trait genetic architecture is an important prerequisite of any advanced selective breeding program. The ARC Hub will generate comprehensive genome-wide resources for the black tiger shrimp using genotype-by sequencing methodologies. This approach will identify 50,000-plus single nucleotide polymorphism (SNP) markers, which, through the use of pedigree data, will be anchored to genetic linkage maps. These markers will form the basis of predicting the genetic breeding value of an individual when correlated with phenotypic information.

Collection of phenotypic data and the development of industrial multi-trait phenotype acquisition technologies

– Shrimp breeding programs require the collection of phenotypic records from tens of thousands of individuals per generation. Even for a single trait this represents an enormous labor investment in order to collect adequate amounts of data to make reliable selection decisions. As a result, shrimp improvement programs have generally been restricted to selection for growth, survival and disease resistance.

One of the major goals of the ARC Hub is to collect phenotypic data on an industrial scale for many traits simultaneously using automated approaches. As such, Hub researchers have developed software to estimate shrimp weight and body parameters from digital images and are also trialing near-field infra-red spectroscopy (NIRS) to quickly phenotype shrimp for important biochemical traits like protein content, and omega-3 fatty acids.

Genetic parameter estimation and genomic selection

– Ultimately the ARC Hub aims to undertake genomic selection in the black tiger shrimp for the first time. To do this, all pedigree, genomic and phenotypic information collected throughout the work packages will be integrated using a purpose built database, linking the genome with the phenome, and predictive algorithms that estimate an individual's genomic breeding value. The ARC Hub will validate predictive algorithms in the real-world, delivering the worlds most advanced multi-trait genomic selection breeding program for shrimp.

Perspectives

The ARC Hub for Advanced Prawn Breeding has been underway for one and a half years, during which time our researchers have sampled and phenotyped more than 22,000 shrimp from 130 families harvested from Seafarms commercial ponds. DNA has been taken for parentage and genomic analyses, while at the same time shrimp have been sampled for viral loads to gill-associated virus (GAV) and stress tolerance markers. In total, it is anticipated that around 35,000 shrimp will be phenotyped and genotyped to establish the predictive algorithms needed for genomic selection. Read more and follow our progress at <https://research.jcu.edu.au/itrh-apb>.



[selection](#), [genomic selection](#), [husbandry](#), [Jerry](#), [near-field infra-red spectroscopy](#), [NIRS](#), [nucleotide polymorphism \(SNP\) markers](#), [Penaeus monodon](#), [phenotype](#), [Sellars](#), [shrimp genome](#)

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