

# ABSTRACTS

## SESSION 10: GENOMICS AND METABIOMES

## CAN CHANGES IN POND YIELD IN THE BLACK TIGER SHRIMP *PENAEUS MONODON* BE DETECTED BY STUDYING THE BACTERIAL MICROBIOTA?

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### Abstract

The relationship between bacterial microbiota and host health has been recognized across different taxa in both vertebrate and invertebrate lineages. In aquatic environments such as shrimp farms host-pathogen interactions are common, and infectious diseases pose a major risk to the expansion of the shrimp aquaculture industry. While the main disease management strategy aims for disease freedom through biosecurity procedures, the emergence of previously unknown diseases is common. Therefore, additional measures to control pathogens and improve shrimp health and system performance should be considered, including managing the microbiota in the pond and the animals. However, bacterial culture methods focusing on single-pathogen detection (e.g. *Vibrio* spp) have been the main method traditionally, limiting information about bacterial species diversity and composition in the shrimp hosts and ponds. Nowadays, high throughput sequencing (HTS) is used to characterize the entire bacterial community, increasing the understanding of environment-bacteria-host interactions under normal production and disease outbreak conditions. Investigating this interaction is essential to facilitate future management of the pond and intestinal microbiota to decrease the risk of disease and increase productivity. We investigated the bacterial microbiota using 16s rRNA metabarcoding in the pond environment (n=4), gut and gastric mill (GM) of cultured *P. monodon* (n=12/pond), where significant differences were seen in harvest yield. nMDS ordination and ANOSIM analyses detected significant changes in bacterial assemblages in the water, gut and GM of shrimp from ponds with low and high productivity. Low productivity ponds exhibited decreased bacterial diversity and richness. A LEfSe analysis indicated that the gut and GM in shrimp of low productive ponds were enriched in *Vibrio* and *Fusibacter* (LDA  $\geq 4$ ); cyanobacteria were enriched in the water (LDA = 4.38), and the Desulfobacteraceae family was more abundant in sediments (5% on average). These shifts in bacterial composition can serve as indicators of stress and low yielding ponds during summer months in North Queensland shrimp aquaculture. This pilot study represents the first advances in characterizing the bacterial community in the pond and gut of Australian farmed *P. monodon*.

*Keywords: Penaeus monodon, bacterial community, productivity, gut, environment*

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## METAGENOMIC ASSESSMENT OF THE BODY SURFACE MICROBIAL COMMUNITIES OF THE SEA URCHIN, *TRIPNEUSTES GRATILLA*.

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### Abstract

The sea urchin, *Tripneustes gratilla*, has gained popularity as a potential aquaculture species in South Africa. However, sea urchins are susceptible to 'bald sea urchin disease', which has resulted in great economic losses within already established aquaculture environments in Japan. This disease is characterised by lesions that form on sea urchin body surfaces in both natural and cultured sea urchin populations. Therefore, this study aimed to characterise the body surface microbial communities from healthy and diseased *T. gratilla* individuals, using a 16S rDNA metagenomics approach to provide insight into this balding disease. Microbial samples were collected from non-lesioned healthy animals from natural locations along the eastern coast of South Africa, as well as from different cultured cohorts: non-lesioned healthy animals, lesioned diseased animals and non-lesioned stressed animals. A total of 1 067 515 individual bacterial operational taxonomic units (OTUs) were identified, belonging to 257 family-, 411 genus- and 612 species level OTU groups. Alpha diversity analyses, based on Chao1, Shannon and Simpson indices, showed that there were no statistically significant differences (ANOVA;  $P > 0.05$ ) between the respective cohorts, as all cohorts displayed a high degree of bacterial diversity. Similarly, beta diversity analyses showed a large degree of overlapping OTUs across the four cohorts, suggesting that similar OTU sets are found across the respective health statuses. Within each cohort, various OTUs commonly associated with marine environments were found, including several species predominantly belonging to the families Vibrionaceae, Saprospiraceae, Flavobacteriaceae and Sphingomonadaceae. Differential abundance analysis (DESeq2) showed that 25 family-, 28 genus- and 36 species level OTUs were differentially abundant across cohorts, but the majority of these were not specifically associated with the diseased cohort. Furthermore, putative metabolic functions assigned to the microbial communities showed that heterotrophic bacteria appear to be responsible for tissue lysis of degrading animal matter, and therefore potentially play an integral role in disease progression. The results from this study, obtained through univariate and multivariate-based approaches, suggests that this disease is more likely caused by complex interactions between opportunistic bacteria, rather than by a specific pathogenic agent.

*Keywords:* 16S rDNA, bald sea urchin disease, collector sea urchin, next-generation sequencing, opportunistic bacteria

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## GENETICS, GENOMICS AND MICROBIOMICS, UNDERLYING COLD TOLERANCE IN THE BLUE TILAPIA (*OREOCHROMIS AUREUS*)

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### Abstract

Cold is an environmental challenge that greatly affects physiological processes. When exposed to cold temperatures, poikilothermic animals, such as fish, undergo remarkable physiological adjustments to maintain homeostasis. Such adjustments may occur through genetic and/or non-genetic mechanisms and may vary across populations and individuals, depending of factors such as life history, nutritional status or genetic background. Understanding the mechanisms that underlie the variation of phenotypic responses can open new directions to improve brood-stocks, and provide insights into the nature of environmental tolerance and adaptation. Here, we aim to explore potential mechanisms of thermal tolerance in tilapias, one of the most important aquaculture fish group. For this purpose, we used unique experimental setups, based on tilapia families with low or high tolerance to low water temperatures, originating from a selective breeding scheme for cold tolerance in the blue tilapia (*Oreochromis aureus*). We performed cold challenge trials and families were selected based on the performance in low temperatures. The inheritance of cold tolerance was evaluated in order to understand its genetic components, while the transcriptomic response and the microbiome composition were also examined using next generation sequencing (RNAseq and amplicon sequencing), in order to understand the fish physiological response and potential effects on host-microbe interaction. Our results showed strong maternal effect in the inheritance of cold tolerance, likely due to epigenetic effect rather than mitochondrial inheritance. Transcriptome analysis revealed biological pathways which are the core response to low temperatures, common to all analysed fish and tissues, as well as pathways which are the differential response between cold-tolerant and cold-sensitive fish. Over all, at the gene expression level, cold-tolerant fish showed milder response to declined temperatures compared to the sensitive fish. Similar pattern observed in the response of these fish microbiome composition, indicating that the microbiome is potentially shaped by its host thermal acclimatization.

*Keywords: Environmental stress, Heritability, Maternal effect, Transcriptome, Microbiome*

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