Poster # 9

Using omics tools in aquaculture organisms

Complexities of working with non-model organisms

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Aquaculture is the farming of aquatic animals and plants for commercial food production and has become the fastest growing food production sector in the last 30 years. Enhanced growth, immunity, and resilience are highly sought-after phenotypic traits in aquaculture. Omics approaches are powerful tools to unravel the effects that environmental stimuli exert upon aquaculture organisms and the relevance of this in growth immunity and resilience. omics technologies in aquaculture can enable manufacturing of advanced diets that provide specific nutrients intended to attain enhanced growth, immunity, resilience leading to increase production yield while ensuring environmental sustainability and promoting animal welfare and social license

Prawn nutrition - proteomics & metabolomics

Prawn hepatopancreas and haemolymph were analysed by proteomics and metabolomics following one week feeding. Prawns were fed a fishmeal control diet and a diet supplemented with krillmeal. A third group of prawns was maintain in fasting conditions for seven days.

From prawn to fruit fly – Information loss. Gene ontology analysis



Climate change - Salmon heat stress in Tasmania

Fish cannot regulate body temperature¹. The salmon industry in Australia has been affected by summer heatwaves where affected fish experienced reduced feed intake, impaired metabolism, and flesh decolouration².

Targeted proteomics – heat stress markers in salmon liver

Atlantic salmon were subjected to temperature increase and liver was monitored for heat stress markers using targeted proteomics.

Α

Figure 1: A, Schematic representation of information loss in proteomics workflow. Entrez gene ID search carried out in https://david.ncifcrf.gov/. KM, krillmeal. FS, fasting. B, Gene ontology analysis. Functional protein groups identified as significant in hepatopancreas of fasted prawns compared to prawn fed fishmeal. C, Gene ontology analysis. Functional protein groups identified as significant in hepatopancreas of shrimp fed krillmeal compared to prawn fed fishmeal. Gene ontology chord diagrams generated on MonaGo https://monago.erc.monash.edu/





Figure 2: Metabolomics analysis of haemolymph and joint-pathway analysis in hepatopancreas and haemolymph of shrimp Penaeus monodon under different feeding regimes. A, metabolite classes with differential expression in haemolymph. Proteins and metabolites with significant high abundance were used to identify metabolic pathway perturbations. B, pathways identified in shrimp fed KM compared to FM diet. C, pathways identified in FS shrimp compared to FM diet. All pathways shown here were significantly upregulated (<0.05). Scale and circle colour intensity indicate the level of significance of -log(p-value). Circle size indicates level of pathway impact.

Figure 3: Monitoring heat stress markers in liver of salmon subjected to heat stress. A, experimental temperature ramp. B, transitions for ferritin peptide. C, experimental mass spectral evidence for ferritin peptide. D, principal component analysis of total protein variance observed in individual samples compared to pool samples from liver of salmon reared at 15°C and 20 °C to determine the effects of heat stress. E, significant abundance of serpinH1 in liver of salmon reared at 20°C compared to a control group (15°C). F, validated markers for heat stress.

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