LC-MS-Based Metabolomics and Lipidomics Investigation of Abalone Mortality in Cook Strait, New Zealand

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Fig 1. Experimental workflow

▲ M_A ▲ M_H

RESULTS

physiology.

METABOLOMICS

The targeted LC-MS metabolomics analysis of central carbon metabolites yielded 182 annotated compounds in abalone gill and muscle tissues. These metabolites belong to diverse chemical classes, including amino acids, citric acid cycle intermediates, other carboxylic acids, nucleobases, nucleosides, phosphosugars and fatty acids.

The PLS-DA score plot showed good separation between healthy and unhealthy abalone in both gill and muscle tissues, suggesting a good classification model (Fig 2A, B). The volcano plot identified 32 metabolites in gill tissues and 31 metabolites in muscle tissues that were significantly different between healthy and unhealthy abalone (Fig 2C, D).



LIPIDOMICS

The lipid analysis of abalone gill and muscle samples yielded 1450 features from the negative mode and 357 features in the positive mode in each tissue. Among these, there were 412 and 407 annotated lipids in gill tissues and muscle tissues, respectively. They belong to 24 lipid classes which glycerophospholipids (GPLs) were the most abundant lipids in the abalone tissues.

The separations between lipid profiles of healthy and unhealthy abalone were clear in the negative mode but not good in the positive mode in both gill and muscle tissues (Fig. 3). The univariate analysis via t-test did not show any difference between healthy and unhealthy abalone.



Fig 2. PLS-DA score plot of gills (A) and muscle tissues (B); and volcano plot of metabolites in gills (C) and muscle tissues (D) that significantly different between healthy and unhealthy abalone experienced a heatwave event

CONCLUSIONS

The present study represents the first application of metabolomic and lipidomic approaches to investigate a heatwave mortality event affected abalone wild populations. Although the abalone lipid profiles were not significantly influenced by the heatwave event, metabolomics data were able to discriminate healthy abalone from unhealthy abalone via many key central carbon metabolites. These different metabolic signatures indicate several disturbances in the physiological state (e.g., mitochondrial failure, cell and tissue damage, impairment in aerobic respiration and a metabolic switch from aerobic to anaerobic metabolism) of abalone.

It is envisaged from this study that future metabolomics and omics investigation studies for these events with more frequent samplings would lead to novel discoveries about mechanism underpinning the heat adaptation and resilience of abalone as well as marine molluscs. This fundamental information would be critical for development of fishery management strategy or selective breeding of better heat-tolerant lines in aquaculture.

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