W8 DNA Barcoding: Improving stream management using ecological modelling and DNA barcoding.

Objective(s)

To: i) develop robust DNA barcoding methods and DNA reference barcode library to enable routine *species-level* macroinvertebrate identification; ii) build knowledge of *species-level* macroinvertebrate distributions, environmental habitat determinants, and responses to human activities; and iii) better quantify and track macroinvertebrate species losses or gains in response to pressures as well as to mitigation actions.

Why this research is important

Freshwater macroinvertebrates contribute to many ecological processes and functions and are essential to maintaining waterway health and ecosystem services such as water filtration and nutrient cycling. Their diverse ecological roles across multiple trophic levels and varying sensitivity to disturbances make macroinvertebrate assemblages sensitive, informative ecological indicators for biological monitoring of freshwaters. This monitoring function is critical for adaptive management, planning and accountability.

This research will generate new *species-level* macroinvertebrate data and a robust DNA reference barcode library for the Port Phillip and Westernport region. These biological datasets will support greater understanding of key values across the region, and bioassessment of stream health and multipurpose reporting.

In doing so, this project will improve the ability of Melbourne's waterway managers to monitor and improve stream health and biodiversity by developing a suite of interconnected molecular (DNA), spatial and quantitative tools to provide data-driven, comprehensive, landscape-scale decision support

Contribution to Melbourne Water research priorities

- MWRPP-8 (W1, W2, W5): Models and decision support tools to model the status of waterway and wetland environmental values, explore threats and likely future conditions and prioritise management interventions most likely to protect or improve waterway and wetland values.

Approach

This project will be conducted over four years, beginning with site selection in the first months, then sampling from 400 sites (300 in year 1 and 100 in year 2) and DNA metabarcoding in years 2-3. A trial testing DNA metabarcoding of bulk material will be conducted in years 1-2 to inform the sub-sampling approach

(laboratory sorting or direct DNA processing of bulk material). DNA metabarcoding will be followed by individual DNA barcoding of new species.

The first modelling will be undertaken at the end of the second year when high-quality species data will be available for 300 sites. Species data for the final 100 sites will be available in year 3, permitting validation and refinement of the models, biodiversity ranking and action prioritisation in years 3 and 4, with an increasing focus on publishing of the project outcomes, knowledge exchange and promoting the project outputs

Key outputs

- Standardised sampling method for DNA metabarcoding, a high-quality species dataset for ~400 sites and 600 new macroinvertebrate DNA barcodes to public repositories
- Species-level macroinvertebrate biodiversity priority rank map for Melbourne's waterways
- Development of a suite of interconnected molecular (DNA), spatial and quantitative tools to provide data-driven, comprehensive, landscape-scale decision support.

Expected benefits

- Significant advances in understanding of poorly-known freshwater macroinvertebrate species biodiversity and how it is impacted by natural environmental and human impact gradients.
- Improved the ability of Melbourne's waterway managers to monitor and improve stream health and biodiversity.
- Characterisation of biodiversity patterns including identification of high biodiversity areas, strongholds for particular species
- Better understanding of candidate management actions and determinants of where they can be applied.
- Better understanding of detailed cost estimation process for candidate actions and spatial variation of costs for a given action.

Project teams

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