

CRC TiME Project Concept Brief Environmental Genomics for Life-of-mine Biomonitoring and Biodiversity Assessments

Proposal proponents

Curtin University, Department of Climate Change, Energy, the Environment and Water (DCCEEW), Illumina

What is the problem?

There is a growing array of genomic-based methods that are promising to transform biological monitoring and assessments. DNA recovered from water, soil, sediment, or air samples can provide information on the living parts of ecosystems. Invertebrate-derived DNA extracted from carrion flies, mosquitoes and leeches has been used to conduct biodiversity surveys. DNA-based taxonomic identification of invertebrates and vegetation from whole/parts of organisms is also becoming common. The mining industry is increasingly using genomic-based approaches to evaluate and manage species and biodiversity risks, and to meet environmental regulations (e.g., threatened, and invasive species), track progress towards biodiversity targets, and determine effectiveness of mitigation measures.

The use of genomics can overcome limitations with traditional morphological methods for species detection and studying biodiversity changes, such as the need for taxonomic expertise; intensive data capturing efforts (time consuming and labour intensive); the challenge of detecting rare, elusive or low abundance species; and high costs. Genomic-based surveys can involve targeted monitoring of key single species, or monitoring using DNA combined with high throughput sequencing for whole-community assessments (also known as metabarcoding).

Despite the rapid advancements in genomic-based approaches, environmental regulators and managers are often reluctant to apply this technology as standalone evidence for assessments and decision-making. The reluctance stems from:

- uncertainties in species detection and abundance estimates, e.g., false positives, false negatives and other potential sources of error (signal detection, contamination, life history of species, environmental conditions)
- a lack of understanding around how genetic material behaves in the environment, e.g., persistence and distribution
- absence of standardised protocols for DNA field collection, laboratory analysis, bioinformatics analysis and communication to regulators and managers
- validation of genomic results with traditional morphological methods at sites, with time.

How could it be solved?

<u>Stage 1</u>

- Undertake a series of CRC TiME Partner workshops/conversations to:
 - a. assess the usefulness of genomic-based tools for understanding ecological communities at a landscape; the presence of rare, invasive and low abundant species; and demonstrating the effectiveness of mitigation measures at mine sites
 - b. identify CRC TiME Partner mines where genomic (and traditional morphological) data is currently being collected or has been collected for biomonitoring and biodiversity assessments, and where results are being collated (repository) and reported







- c. identity standard practices and procedures used to ensure the robustness, sensitivity and reproducibility of genomic results
- d. determine the key enablers of and barriers to the uptake of genomic data for biomonitoring and biodiversity assessments at mine sites.
- Undertake a review of national and international standard protocols and procedures for DNA collection, analysis and reporting, (e.g., Australia/New Zealand eDNA best practice guidelines (<u>https://research.csiro.au/environomics/australia-new-zealand-edna-best-practice-guidelines/</u>) for guidance to the mining industry.

Stage 2 (If Partner agreement on a need. and sufficient evidence exists)

- Develop case studies that demonstrate the application of genome-based biomonitoring and biodiversity assessments within the mining industry, preferably within regulatory decision-making.
- Develop guidance(s) to the mining industry on DNA collection, analysis and reporting, for the uptake of results to evaluate and manage species and biodiversity risks, and to meet environmental regulations and track progress towards biodiversity targets.
- Establish a pathway/link(s) for mining environmental genomics data to repositories in Australia (e.g., Atlas of Living Australia
 (https://www.ala.org.au/environmentaldna/;
 https://www.csiro.au/en/research/natural-environment/biodiversity/ala) to make data/results accessible and showcase species and biodiversity information.

What are the benefits/proposed outcomes?

The following are the proposed outcomes of Stage 1 (and Stage 2 if to occur):

- workshop(s) with CRC TiME Partners on the usefulness of genomic-based data, best practices and procedures, and key enablers of and barriers to the uptake for biomonitoring and biodiversity assessments at mine sites
- a review of standard protocols and procedures for DNA collection, analysis and reporting for biomonitoring and biodiversity assessments, with a focus on the specific needs within the mining industry
- case studies that demonstrate the application of genome-based biomonitoring and biodiversity assessments within the mining industry
- guidance document(s) on DNA collection, analysis and reporting to the mining industry
- established pathway/link(s) for mining genomics data to repositories in Australia.

Why should my organisation be involved?

The project has the support of DCCEEW, Illumina and CSIRO.

We are seeking additional mining industry partners/organisations to be involved, to ensure focused R&D delivers mining industry outcomes that use genomic-based methods for regulatory decision-making and management actions.

Contact

For further details or to indicate your interest, please contact Dr Jason Kirby (Jason.Kirby@crctime.com.au).



