



NGĀ ARA WHETŪ
CENTRE FOR CLIMATE,
BIODIVERSITY & SOCIETY



Center for Biodiversity & Biosecurity Sequencing Grants

Accepting applications until 5pm Friday 17 May 2024 or until all funding has been allocated

DNA-based approaches are becoming a mainstay in biodiversity assessment and biosecurity applications. We are looking to support a number of sequencing grants (until funding is exhausted) for CBB researchers and students in collaboration with Manaaki Whenua Landcare Research. MWLR have substantial expertise in the ecological application of next generation amplicon sequencing methods, specifically metabarcoding of vertebrate, invertebrate, plant, fungal and microbial community targets. Each sequencing grant includes 1x Illumina Miseq V3 300x2 bp run, sequencing library preparation (if required) and quality control and a consultation service on the project (if required). For further information on the MiSeq system, see: <https://www.illumina.com/systems/sequencing-platforms/miseq.html>

Example projects:

- 1: Diet study: Mora AJ, Prosse SWJ, Mora JA (2019) DNA metabarcoding allows non-invasive identification of arthropod prey provisioned to nestling Rufous hummingbirds (*Selasphorus rufus*). *PeerJ* 7: e6596 <https://peerj.com/articles/6596/>
- 2: Microbiome study: San Juan PA, Castro I, Dhami MK (2021) Captivity reduces diversity and shifts composition of the Brown Kiwi microbiome. *Animal Microbiome* 3: 48 <https://doi.org/10.1186/s42523-021-00109-0>
- 3: Soil eDNA community study: Drummond AJ, Newcomb RD, Buckley TR, et al. (2015) Evaluating a multigene environmental DNA approach for biodiversity assessment. *GigaScience* 4: s13742–015–0086–1 <https://doi.org/10.1186/s13742-015-0086-1>

Eligibility requirements & library format:

- 1, Projects must include CBB staff or affiliates. Student projects are encouraged, but applications should be submitted by their supervisor, who must be a CBB member. To join CBB, please fill this [form](#) and email it to j.beggs@auckland.ac.nz
- 2, Projects must contribute to the wider goals of [CBB](#)

3, Researchers may prepare their own sequencing libraries to their own specification or choose from a range of targets that MWLR supports. All libraries must be Illumina compliant (include P5/P7 adaptors) with a maximum library amplicon length of 600 bp.

For enquiries, contact dhamim@landcareresearch.co.nz or a.santure@auckland.ac.nz

To apply, please submit a short application to dhamim@landcareresearch.co.nz detailing your project, including the following:

Team: (must include one CBB staff or affiliate)

Project title:

Project description: (max 200 words)

Sample description: (please include sample/tissue type, amplicon target & total number of samples)

Sequencing library construction: (state if required)

Consultation: (state if required & nature, e.g., advice on DNA extraction, help with target selection/DNA amplification etc)

Timeline: (tentative timeline)