



## Effective monitoring of terrestrial ecosystems with honeybees and DNA metabarcoding

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### Speaker Bio

Francisco is a research scientist at the Centre of Australian National Biodiversity Research (CSIRO) working on pollination biology, plant conservation ecology and evolutionary biology. He has been working on the application of genomic tools for pollination research, biosecurity and biodiversity monitoring.

### Presentation

Monitoring biodiversity is a growing and pressing challenge as climate change threatens species with extinction and leads to widespread shifts in plant distribution and phenology. Traditional vegetation surveys are costly and time-consuming, therefore the characterisation of complex and heterogeneous communities remains an ongoing challenge. Molecular environmental DNA (eDNA) methods are rapidly being developed to provide fast and reproducible results for ecosystem monitoring and they can also provide valuable information for beekeepers about honeybee foraging behaviour, and presence of pests and weeds. We investigated the potential of using DNA metabarcoding of pollen foraged by European honeybees (*Apis mellifera*) to survey plant communities. Using managed beehives located within an urban bushland reserve, we collected samples of three different pollen sources: individual bees, raw honey and pollen traps. The plant community identified from the pollen with two DNA barcode markers (ITS2 and trnL) was compared to a vegetation survey carried out by plant specialists. DNA metabarcoding detected 200 taxa (66.5% identified to species) across all pollen sample types, compared to 44 taxa recorded by the conventional survey (93% identified to species). Within the metabarcoding results, we identified 66% of the genera and 27% of the species found during the survey, with all of the top ten flowering genera represented. While honey was the most taxa-rich pollen source, followed by pollen traps and honeybees, pooling six individual bees could detect similar taxa numbers to honey, while two bees were sufficient to detect as many taxa as the survey. We demonstrate that DNA metabarcoding of pollen foraged by honeybees is a suitable alternative and complementary tool for biodiversity monitoring as well as honeybee foraging behaviour.

