

Using Next Generation Sequencing to identify botanical origin of pollen collected from foraging honeybees

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Next Generation Sequencing (NGS) of DNA is a promising new method for the identification of plant species visited by bee foragers. This study demonstrates how honey bee pollination activity can be analysed using a non-invasive DNA-based method. This study also aimed at assessing the consistency of NGS to accurately detect the presence and estimate the abundance of plant species in honeybee pollen.

We collected pollen pellets using pollen traps installed on two honeybee hives in Canterbury, NZ during the summer 2013-2014.

Samples were homogenized and DNA extracted in triplicates from each samples. Universal ITS primers were used to amplify plant DNA from the samples and NGS was performed using the 454-pyrosequencing technology. We detected a total of 28 plant species from the collected samples. Six species represented 92% of the DNA sequences retrieved. Among these, our results showed that common crop (Brassicaceae, radish, clover) were foraged for equally in the morning and in the afternoon while dandelion for example was preferentially foraged in the morning. The most common native plant was lancewood, which was detected in 18% of the samples.

Plant species presence and DNA abundance were compared in triplicates of the same samples to assess the consistency of the NGS approach. We found that species presence and DNA abundance can vary significantly from one triplicate to another, which justifies analyzing multiple replicates for each sample.

However, the more abundant the species was, the more likely it was to be detected in all triplicate.

The NGS approach used here proved a cost- and time- effective method for surveying the species on which honeybees frequently forage for pollen. This method allows fine time scale analysis (such as morning versus afternoon). However, for maximum accuracy and detection of plant species rarely exploited by bees, replicated analyses are recommended.