

Mitochondrial metagenomics: How '-omics' is saving wild bees

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Mitochondrial genome (mitogenome) database demonstrated its great value on detecting wild bees in UK farms via mitochondrial metagenomics pipeline, a new approach developed by scientists from the China National Genbank (CNGB), BGI-Shenzhen.

The study published today in the journal *Methods in Ecology and Evolution* shows that, with mitogenome references, collecting [wild bees](#), extracting their mixed DNA, and directly reading the DNA of the resultant 'bee soup' could finally make large-scale bee monitoring programmes feasible. This new research demonstrates how the process could become quicker, cheaper and more accurate.

The approach used in the study would allow conservationists to detect where and when [bee species](#) are being lost, and importantly, whether conservation interventions are making effect.

Wild bees play a key role in pollinating wild plants and cultivated crops - maintaining both biodiversity and food production. They are however threatened by habitat loss, pesticides, climate change and disease. Safeguarding wild [bee populations](#) and their pollination services is therefore a top priority.

The UK's National Pollinator Strategy plans a large-scale bee monitoring programme. Traditional monitoring involves pinning individual bees and identifying them under a microscope. But the number of bees needed to track populations reliably over the whole country makes traditional

methods infeasible. Developing an efficient long-term monitoring programme to better understand the causes of their decline is one of the goals of DEFRA's National Pollinator Strategy. This will involve a massive collection of bees across the UK. Traditionally they would be pinned and identified under a microscope, but this is so labour-intensive and error-prone that the resulting data might not be available for years after the collections.

Prof. Douglas Yu, from University of East Anglia, UK and Kunming Institute of Zoology and Dr. Xin Zhou's group from the CNGB lead the research team to apply the mitochondrial metagenomics [pipeline](#) on bulk bee samples collected in the studied regions, which have been morphologically identified by scientists from University of Reading in the UK. Dr. Zhou's group firstly conducted biodiversity study using a PCR-free method in 2013 (Zhou et al. 2013), avoided PCR-bias and demonstrated the positive correlation between biomass and the sequence numbers. Mitogenomes are expanded DNA markers beyond the conventional DNA barcodes, providing >20X of informative references for species diagnosis, which would benefit not only researches on biodiversity and ecology but also phylogenetic and evolution studies. Last year, the CNGB initiated the MT10K (10,000 mitochondrion genome, <https://www.mt10k.org>) project, and developed a high-throughput and cost-efficient mitogenome construction pipeline (Tang et al. 2014). The successful application of mitochondrial metagenomics pipeline on the new beestudy is very encouraging, implicating promising applications on large-scale and long-term conservation projects.

In the pipeline, mitogenome references were built first under efficient time and cost, and then the raw DNA reads from the 'bee soup' were mapped against mitogenome references. The process did not require taxonomic experts and the result was proved to be more accurate. Also, by skipping the DNA-amplification step known as PCR, the method was able to estimate the biomass contributed by each species, which makes it

applicable to tracking population trajectories.

"We're trying to speed up ecological investigation on a monumental scale." said the lead researchers.

More information: Tang, M., Hardman, C. J., Ji, Y., Meng, G., Liu, S., Tan, M., Yang, S., Moss, E. D., Wang, J., Yang, C., Bruce, C., Nevard, T., Potts, S. G., Zhou, X. & Yu, D. W. (2015). High-throughput monitoring of wild bee diversity and abundance via mitogenomics. *Methods in Ecology and Evolution*.

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Provided by BGI Shenzhen

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