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METAGENOMIC SHOTGUN SEQUENCING OF DIVERSE ARTHROPOD ASSEMBLAGES

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ABSTRACT

Metagenomic shotgun sequencing of mixed species assemblages can provide important information beyond what is obtained by amplicon-based metabarcoding. Using examples from mass-trapped arthropods, we show the relative ease of extracting entire mitochondrial genomes from complex specimen mixtures and demonstrate the power of 'mitochondrial metagenomics', whereby sequence reads from low coverage shotgun sequencing of unsorted samples are mapped against full-length mitochondrial genomes or COI barcode reference sets to make high confidence species identifications. Our case studies include communities of soil arthropods, insect pollinators and herbivores, and we show that the method can establish species /absence and estimate their abundance (biomass) in mixtures. The use of a PCR-free approach overcomes many of the biases inherent in metabarcoding, which can hamper recovery of the full set of species in the sample and preclude inferences about abundance; it also reduces the risk of contamination. By allowing rapid assembly of mitogenome reference libraries from mixtures of specimens and the use of read counts for accurate estimates of key parameters metagenomics represents a powerful new tool for environmental monitoring in a wide variety of contexts..of biodiversity directly from environmental samples, mitochondrial

References:

Gómez, Rodríguez, C., Crampton, Platt, A., Timmermans, M.J.T.N., Baselga, A. Vogler, A.P., 2015. Validating the power of mitochondrial metagenomics for community ecology and phylogenetics of complex assemblages, *Methods in Ecology and Evolution*

Andújar, C., Arribas, P., Ruzicka, F., Crampton Platt, A., Timmermans, M.J.T.N.; Vogler, A.P., 2015. Phylogenetic community ecology of soil biodiversity using mitochondrial metagenomics. *Molecular Ecology*

Paula, D.P., Linard, B., Andow, D.A., Sujii, E.R., Pires, C.S.S. Vogler, A.P., 2015. Detection and decay rates of prey and prey symbionts in the gut of a predator through metagenomics, *Molecular Ecology Resources*

Tang, M; Hardman, C; Ji, Y; Meng, G; Liu, S; Tang, M; Yang, S; Moss, E; Wang, J; Yang, C; Bruce, C; Nevard, T; Potts, S; Zhou, X Yu, D., 2015. High-throughput monitoring of wild bee diversity and abundance via mitogenomics. In Review



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