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# Using molecular tools to shed light on trophic interactions in agricultural systems

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## Abstract

Modern monocultural agro-ecosystems can be perceived as a simplification of natural ecosystems, where a single plant species is usually grown over vast areas. Because of this apparent simplicity, species interactions have often been treated as linear in agricultural landscapes. For example, in these systems, it has historically been assumed that the concept of a food chain can describe the relationships between an insect pest and a single biocontrol agent. In reality, multiple ecological interactions are involved, comprising potentially complex food webs. The disentangling of these interaction networks and quantification of the relative strengths of the multi-trophic interactions are very difficult using orthodox methods such as dissection and subsequent visual gut-content identification. An emerging field of study using molecular tools to analyse these interactions in agricultural systems can now begin to address these impediments and help to better understand multi-trophic dynamics. In this presentation, we will present cases studies focusing on host parasitoid, plant-pollinator and plant-phytophagous insect networks for which we used molecular tools to reveal trophic interactions. For each of these studies we used a DNA metabarcoding approach to describe the breath of biotic interactions among our species of interest. Our results show that high-throughput DNA sequencing can reveal a world of otherwise unseen trophic relationships within agricultural ecosystems. Based on our results and our review of the literature, we propose recommendations and future directions for the use of molecular methods (including high-throughput DNA sequencing) for a better understanding of trophic interactions in agricultural landscapes and potential applications for improved biological control.

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