



Editorial: Molecular and isotopic approaches to food webs in agroecosystems



Stéphane Boyer ^{a,b,*}, William E. Snyder ^c, Stephen D. Wratten ^b

Applied Molecular Solutions Research Group, Environmental and Animal Sciences, Unitec Institute of Technology, Private Bag 92025, Victoria Street West, Auckland 1142, New Zealand
Bio-Protection Research Centre, PO Box 85084, Lincoln University, Lincoln 7647, New Zealand
Department of Entomology, Washington State University, Pullman, WA 99164-6382, USA

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ABSTRACT

This special issue comprises seven papers: one review, one opinion and five experimental papers. Together, these articles illustrate how molecular tools and isotope analyses are improving our understanding of food-web structure and dynamics in agricultural systems. The papers collated here make use of the PCR-based DNA barcoding approach, protein-marking ELISA and the analysis of isotopic ratios to investigate a wide range of ecological questions. These studies advance our understanding of biodiversity and food-web dynamics in agroecosystems, provide direction on how to improve biological control of pests, detail the movement of energy and nutrient fluxes in soil food webs, and quantify anthropogenic disturbances in agroecosystems.

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1. Introduction

Agricultural landscapes are often regarded as highly simplified ecosystems with few species. Because of this apparent simplicity, species interactions have often been treated as linear. For example, in all forms of biological control of pests (classical, augmentative and even conservation biological control) most studies focus on one pest species and one natural enemy or at least one predator guild. However, recent studies using molecular tools have shown that surprisingly complex food webs can occur in supposedly simplified communities (Wirta et al., 2014). Even in so-called monocultures, natural enemy species interact with each other through competition, predation or parasitism, and indirectly when initiating trophic cascades which impact plants (Casula et al., 2006; Thomas et al., 1992). This special issue explores food webs in agroecosystems through the lens of molecular ecology and isotopes, with seven contributions illustrating how molecular tools are improving our understanding of trophic interactions and food-web dynamics, which are difficult to observe, quantify and explain using other methods.

2. DNA barcoding vs ELISA

A variety of molecular methods have been used to study trophic interactions. In this special issue, a review by Gonzalez-Chang et al. (2016)

reveals that the DNA barcoding approach, in particular using the COI gene, has become the method of choice for most molecular trophic interaction studies in agroecosystems. This method has the advantage of being a standardized method with the possibility of designing species-specific primers to detect predation of a variety of prey. In addition, a large and ever-growing library of sequences exists, to which results can be compared for species-level identification. However, an important limitation of this species-specific PCR approach lies in the fact that it cannot differentiate between predation on live prey and scavenging (the feeding on dead organisms) or identify instances of cannibalism (the feeding on conspecifics) (Traugott et al., 2013). Overlooking these two phenomena is problematic, because mistaking scavenging for predation will overestimate predator impacts on prey, while failing to quantify cannibalism will underestimate the true strength of predator–predator interference. Although it has been less utilized in recent years, the protein-marking ELISA approach offers a solution to distinguish scavenging from predation. For example, in a study presented here, Mansfield & Hagler (2016) assess scavenging in three common predatory species of cotton plantations by marking live prey with chicken IgG and dead prey with rabbit IgG. Their results demonstrate that all three predators were also facultative scavenger and that scavenging was often more prevalent than predation.

3. A food-web approach

Using PCR-based DNA barcoding and a collection of specific primers, Gomez-Polo et al. (2016) reconstructed a food web comprising seven species over two trophic levels in a Mediterranean lettuce crop. This

* Corresponding author at: Applied Molecular Solutions Research Group, Environmental and Animal Sciences, Unitec Institute of Technology, Private Bag 92025, Victoria Street West, Auckland 1142, New Zealand
 E-mail address: Stephane.Boyer@gmail.com (S. Boyer).

method is particularly suited to agricultural studies where the focus is often on the predation of one pest species by several potential predator species. In their review, [Gonzalez-Chang et al. \(2016\)](#) show that over the last 15 years, biological control studies investigating interactions with 3 or more species are becoming more important and the focus is changing from a 'food chain' to a food web approach. Using multiplex PCR, predation on several different prey species can be simultaneously examined to measure predation on alternative (non-pest) prey as well as intraguild predation ([Staudacher et al., 2016](#)), both of which can weaken pest suppression.

4. Temporal shifts

Agroecosystems are often characterized by dramatic seasonal variations in resource availability. To deal with this, species can either disperse, endure the food shortage through a dormancy or quiescence state or shift to alternative (possibly less preferred) food sources. In addition to target pest species, [Gomez-Polo et al. \(2016\)](#) demonstrate that alternative non-pest prey (Collembola in this case) provide key sustenance for predators in their system. The presence of such species can lead to a decrease of pest suppression by diverting predation by natural enemies, but they can also sustain predator populations at times when the pest species are rare. This is often the case early in the crop growing season ([Welch and Harwood, 2014](#)). Being able to predict how and when natural enemies of pests may shift to alternative food is essential for the timely implementation of floral subsidies to provide supplemental food to predators ([Lu et al., 2014](#); [Tylanakis et al., 2004](#)) or of trap crops to mitigate pest damage ([Shelton and Badenes-Perez, 2006](#)). In their opinion paper, [Athey et al. \(2016\)](#) discuss how early season predation can influence the outcome of pest suppression, suggesting that this is a strategic time to manipulate agricultural food webs because the predator:prey ratio is very high. Their analysis of existing literature indicates that ESP can maintain pests below economic thresholds, however, accurately measuring ESP requires a decoupling of abundance data and direct levels of consumption, which can only be obtained through molecular gut content analysis.

5. Below-ground processes

Most of the biodiversity in agricultural landscapes (as in any landscape) is below ground. However, soil remains a 'black box' at many levels, including our understanding of how soil biodiversity loss may impact ecosystem functioning ([Bardgett and van der Putten, 2014](#)). The difficulty in observing soil organisms and their feeding behaviour has been alleviated by the rise of new molecular approaches, but these tools remain limited when it comes to studying the flux of energy and the trajectory of essential nutrients in the soil food web. This can however be achieved using isotope pulse labelling. After labelling plant shoots with $^{14}\text{CO}_2$, [Pausch et al. \(2016\)](#) trace organic C released from living roots into communities of bacterial, fungal and plant-feeding nematodes. Their study illustrates how the C share in the herbivore and detritivore food chains can be distinguished, to quantify root C fluxes into different food web compartments and measure their respective contribution to C and energy transfers within soil food webs. Using a similar approach, [Scheunemann et al. \(2016\)](#) investigate the incorporation of root-derived ^{13}C and fertilizer-derived ^{15}N into the soil food web and found that C is channelled to higher trophic levels concurrently with fertilizer-derived N, predominantly via saprotrophic fungi. Their results also suggest that in arable systems the incorporation of root-derived C and fertilizer-derived N decreases at higher trophic levels, and the majority of root-derived C remains locked up at the base of the soil food web.

6. Impact of anthropogenic disturbances

The population dynamics of many species are highly influenced by agricultural practices, which directly and indirectly affect species interactions. For example, crop harvest corresponds to the removal of resources and habitat for many species. This in turn, leads to a dramatic drop in animal population sizes, thereby affecting the food webs of which they are part. Other agricultural practices potentially affecting food webs include soil cultivation, the delivery of agrochemical inputs and other disturbances ([Jonsson et al., 2012](#)). Which parts of the food web are more affected by these disruptions may give clues about how to preserve food web stability and ecosystem function in the face of agricultural intensification ([Garnett et al., 2013](#)). Important ecosystem functions such as nutrient cycling and pest suppression can be difficult to quantify holistically, and the selection of appropriate indicator species is therefore essential to understand the impacts of disruptive farming practices. In this special issue, [Welch and Lundgren \(2016\)](#) propose a framework to select indicator species for insecticidal risk assessment based on their ecology and trophic linkages as revealed by molecular gut-content analyses. In a maize crop system, they selected species that were widespread, trophically linked to maize, and highly connected within ecological networks as optimal indicators for monitoring risks of modern insecticidal products.

7. Conclusion

Molecular ecological approaches and stable isotope analyses have greatly enhanced our capacity to describe and study food webs in agricultural systems. The applications of these tools are far-reaching and span from a better knowledge of biodiversity, to the potential manipulation of food webs to conserve and promote ecosystem services. This special issue captures the current state of the art and highlights the complementarity of these techniques as well as the diversity of questions they can address. Future developments, including a wider utilization of high-throughput DNA sequencing and genomic tools, will continue to improve our capacity to understand and manage these landscapes in a rapidly changing world.

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