

Molecular gut-content analysis of a predator assemblage reveals the effect of habitat manipulation on biological control in the field

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Abstract

Habitat manipulation in agroecosystems can influence predator–prey interactions. In this study, we collected foliar predators from field potato plots with different mulch treatments and assayed them for DNA of the target prey, *Leptinotarsa decemlineata* (Say), using species-specific primers. Concurrently, *L. decemlineata* larval abundance and plant damage were recorded from the same plots. Predator species abundance and diversity were not influenced by habitat manipulation, while prey density was highest in plots without mulch. Gut-content analysis revealed that the highest incidence of predators positive for *L. decemlineata* DNA was in plots without mulch, where target prey abundance was highest. Therefore, the lower prey abundance in mulched plots was not due to predation. The most abundant species in the predator assemblage was *Coleomegilla maculata*, which had the lowest proportion of *L. decemlineata* DNA in the gut. *Podisus maculiventris*, *Perillus bioculatus*, and *Lebia grandis* were less abundant but had a higher incidence of target prey DNA in the gut. DNA detectability half-lives were used to adjust for inter-specific variation in DNA digestive rates of the four predator species. Using this information to adjust actual number of positives for prey DNA, we compared proportions positive for *L. decemlineata* and found that *P. maculiventris* is the most effective predator species in the complex.

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Zusammenfassung

Die Veränderung der Habitate in Agrarökosystemen kann die Räuber-Beute-Beziehungen verändern. In dieser Untersuchung sammelten wir Blattprädatoren aus dem Freiland von Kartoffelprobestellen unterschiedlicher Mulchbehandlung und untersuchten sie auf die DNA der Zielbeuteart, *Leptinotarsa decemlineata* (Say), indem wir artspezifische Primer verwendeten. Gleichzeitig wurden auf denselben Probestellen die Abundanzen der Larven von *L. decemlineata* und die Schäden an den Pflanzen registriert. Die Abundanzen und Diversitäten der Prädatorenarten wurden durch die Habitatveränderung nicht beeinflusst, während die Beutedichte auf den Flächen ohne Mulch am größten war. Die Analyse der Darminhalte ließ erkennen, dass das größte Vorkommen von Prädatoren mit einem Nachweis von *L. decemlineata* in den Flächen ohne Mulch auftrat, wo die Beuteabundanz am größten war. Deshalb war die geringere Beuteabundanz in den gemulchten Flächen nicht auf die Prädation zurückzuführen. Die häufigste Art

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in den Prädatorengemeinschaften war *Coleomegilla maculata*, die gleichzeitig den geringsten Anteil von *L. decemlineata* DNA im Darm besaß. *Podisus maculiventris*, *Perillus bioculatus* und *Lebia grandis* waren weniger häufig, hatten aber einen höheren Anteil an Zielbeute-DNA im Darm. Die Halbwertszeiten der DNA-Nachweisbarkeit wurde benutzt, um die interspezifische Variation in den DNA-Verdauungsraten bei den vier Prädatorarten anzugleichen. Diese Informationen wurden verwendet, um die tatsächlichen Anzahlen der positiven Nachweise der Beute-DNA anzugleichen. Wir verglichen die Anteile der positiven Nachweise für *L. decemlineata* und fanden heraus, dass *P. maculiventris* der effektivste Prädator in dem Komplex ist.

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Introduction

Habitat structural complexity is thought to increase the accumulation and conservation of natural enemies in managed ecosystems through a reduction in predator interference by competition and intra-guild predation, and via increased availability of alternative food, shelter, and favourable microclimate (Andow 1991; Landis, Wratten, & Gurr 2000; Sunderland & Samu 2000). On the other hand, predator foraging efficiency may vary inversely with habitat heterogeneity, because of the negative effects of structural complexity, such as a decrease in predator–prey encounter rates due to increased surface area for searching (Hughes & Grabowski 2006; O’Neil 1997). Visually searching predators may be more successful in locating herbivores in less complex habitats (Uetz 1979). Measuring prey suppression by an indigenous predator assemblage in field experiments is further complicated by the fact that prey abundances vary with changes in biotic and abiotic features of their environment (e.g. Baggen & Gurr 1998), thus modifying the net outcome of biological control.

Information on predation rates can be gathered by direct observation (Brust 1994; Chang & Snyder 2004; Nyffeler, Sterling, & Dean 1994), but molecular gut-content analysis of specimens from the field is a more effective way of collecting accurate information on predation rates without altering the environment with experimental equipment or investigator intrusion (Harwood & Greenstone 2008). This method is also able to provide meaningful information on predation without manipulating prey abundance in the field (e.g. Kuusk, Cassel-Lundhagen, Kvarnheden, & Ekblom 2008). Molecular gut-content analysis relies on species-specific markers for fragments of prey DNA that are able to reliably detect the presence of prey remains in the predator’s gut. Since predator species may differ in digestive physiology, a prior knowledge of the prey DNA detectability time-course is required to compare and rank predator species (Greenstone, Rowley, Weber, Payton, & Hawthorne 2007). These rankings could then

be used to inform manipulations of the predator assemblage so as to increase the abundance of the most effective predator species.

The objective of this study was to determine if habitat management might enhance the ability of the indigenous predator assemblage to lower *Leptinotarsa decemlineata* populations. We investigated the effect of two types of mulches on the resident predator complex in experimental potato fields and measured *L. decemlineata* predation with molecular gut-content analysis. Using information on differential *L. decemlineata* DNA digestion rates to normalize raw data from molecular gut content analysis, we compared the relative impact of four predator species on this pest. In addition, we measured changes in two biotic factors, plant damage and *L. decemlineata* abundance. This research aims to advance our knowledge of the impact of native predator assemblages to improve the outcome of biological control.

Methods

Field experiments were conducted in 2006 and 2007 at the Beltsville Agricultural Research Center in Beltsville, MD, USA. Potatoes were grown in rotation; the fields used in the 2 years were ca. 1 km apart. Three treatments were randomized in two blocks in 2006 and three in 2007. Two were mulch treatments of winter rye (*Secale cereale* L., 100 kg/ha) and hairy vetch (*Vicia villosa* Roth, 56 kg/ha). The third treatment was a tilled control, where *S. cereale* L. was also seeded as a winter cover crop, but plots in this treatment were tilled prior to potato seeding; potatoes were then grown without mulch. Plants to create the mulch treatments were seeded on 2 September 2005 and 21 September 2006. Potatoes (*Solanum tuberosum* L. ‘Kennebec,’ 2027 kg/ha, 76 cm × 30 cm spacing) were seeded on 27 April 2006 and 25 April 2007, in 1 ha fields divided into 12 m × 30 m plots for each treatment. Pre-emergent herbicides (*S*-metolachlor at 1.78 kg AI/ha, linuron at 981 g AI/ha, and paraquat dichloride at 1.71 kg AI/ha)

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