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Tracking aphid predation by lycosid spiders in spring-sown cereals using PCR-based gut-content analysis

A.-K. Kuusk[a,*], A. Cassel-Lundhagen[a], A. Kvarnheden[b], B. Ekbom[a]

[a]*Department of Ecology, Swedish University of Agricultural Sciences (SLU), Box 7044, SE-750 07 Uppsala, Sweden*
[b]*Department of Plant Biology and Forest Genetics, Swedish University of Agricultural Sciences (SLU), Box 7080, SE-750 07 Uppsala, Sweden*

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Abstract

Detection of prey DNA-remains in arthropod predators by polymerase chain reaction (PCR) is useful when investigating food webs. In this study we estimated how long after a feeding event it was possible to detect mitochondrial COII DNA (331 bp) from an important aphid pest, *Rhopalosiphum padi* (Homoptera: Aphididae), in spiders of the genus *Pardosa* (Araneae: Lycosidae). Following laboratory evaluations we tested spiders collected in spring-sown cereals for aphid predation during two seasons. Aphids were digested rapidly in laboratory-fed predators and the time point when prey DNA could be amplified from 50% of the spiders was estimated to be 3.7 h. A total of 372 field- collected predators were analyzed by PCR and despite low aphid densities many spiders (26% in 2004 and 19% in 2005) tested positive for *R. padi*, indicating consumption of at least one aphid within a few hours before capture. The percentage of spiders that tested positive for *R. padi* DNA varied considerably between fields and logistic regression analysis revealed that the probability of detecting aphid DNA was significantly influenced by location and year. We conclude that *Pardosa* spiders, under certain conditions, frequently feed on *R. padi* and deserve special attention in conservation biological control.

Zusammenfassung

Der Nachweis von Beute-DNA bei räuberischen Arthropoden durch Polymerase-Kettenreaktion (PCR) ist eine nützliche Methode bei der Erforschung von Nahrungsnetzen. Hier untersuchten wir an Spinnen der Gattung *Pardosa* (Araneae: Lycosidae), wie lange nach der Nahrungsaufnahme DNA der schädlichen Blattlaus *Rhopalosiphum padi* (Homoptera: Aphididae) noch nachzuweisen war. Wir benutzten PCR-Primer, die ein 331 bp langes Bruchstück des mitochondrialen COII-Gens von *R. padi* vervielfältigen sollten. Nach Vorversuchen im Labor testeten wir in zwei Jahren Spinnen aus Sommergetreidefeldern auf Blattlausspuren. Die Blattlaus-DNA wurde nach Fütterung im Labor schnell verdaut, und der Zeitraum, nach dem noch 50% der Spinnen positiv auf Blattlaus-DNA getestet werden konnten, wurde rechnerisch zu 3.7 Stunden bestimmt. Von den Getreidefeldern sammelten wir 372 Räuber, die mit PCR analysiert wurden. Trotz geringer Blattlausdichten in beiden Jahren wurden viele Spinnen (2004: 26%; 2005: 19%) positiv auf *R. padi*-DNA getestet, was den Verzehr von mindestens einer Blattlaus innerhalb weniger Stunden vor dem Einfangen anzeigt. Der Anteil der Spinnen,

*Corresponding author. Tel.: +46 18672367; fax: +46 18672890.
E-mail address: Anna-Karin.Kuusk@ekol.slu.se (A.-K. Kuusk).

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die positiv auf *R. padi*-DNA getestet wurden, variierte beträchtlich zwischen den Feldern, und eine logistische Regressionsanalyse zeigte, dass die Wahrscheinlichkeit Blattlaus-DNA nachzuweisen signifikant von der Örtlichkeit (Betrieb) und dem Jahr beeinflusst wurde. Wir schließen, dass die Spinnen der Gattung *Pardosa* unter bestimmten Umständen häufig an *R. padi* fressen und daher besondere Beachtung bei der Nützlingsförderung verdienen.

Keywords: Biological control; Generalist predators; *Pardosa*; Prey DNA detection success; *Rhopalosiphum padi*

Introduction

Conservation biological control of arthropod pests aims to increase the numbers of local natural enemies and to enhance their pest suppression efficacy (Van Driesche & Bellows, 1996). Careful timing and selective use of agrochemicals, mulching, and provision of refuge areas are possible approaches (Riechert & Bishop, 1990; Thorbek & Bilde, 2004). To conserve and promote the most important natural enemies it is essential to obtain information about their prey range under natural conditions (Symondson, Sunderland, & Greenstone, 2002).

Arthropod predation is generally difficult to observe and estimate directly for obvious reasons: predators and prey are often small, mobile or live under dense vegetation. One way to overcome these obstacles is analysis of gut-content of field-collected predators. This approach not only reveals predation events that occurred without any experimental disturbance, but also provides consumption data at the species level. Traditionally, gut-content analyses have primarily been performed by dissection or detection of prey protein remains with serological and electrophoretic methods (reviewed by Harwood & Obrycki, 2005). A recent approach is analysis using the polymerase chain reaction (PCR) in which prey-specific DNA sequences are detected within the gut-contents of predators.

Numerous studies have demonstrated the possibility of detecting semi-digested arthropod prey DNA in laboratory-fed predators (reviewed by Sheppard & Harwood, 2005). Laboratory evaluations have, to a considerably lesser extent, been accompanied by PCR-analysis of predators feeding under natural conditions (but see e.g. Agustí, Shayler, et al., 2003; Juen & Traugott, 2007). To interpret PCR data obtained from field-collected predators it is essential to estimate the length of time after a feeding event that it is possible to detect the target prey in the predator of interest (Greenstone & Hunt, 1993; Greenstone, Rowley, Weber, Payton, & Hawthorne, 2007). This can be achieved by investigating the detection success of prey DNA in laboratory-fed predators (e.g. Agustí, Unruh, & Welter, 2003; Chen, Giles, Payton, & Greenstone, 2000).

Here, we focus on predation of the bird cherry-oat aphid (*Rhopalosiphum padi,* Homoptera: Aphididae), an important pest in spring-sown cereals in Northern Europe (Wiktelius & Ekbom, 1985; reviewed by Leather, Walters, & Dixon, 1989). During the aphids' establishment phase, over 75% of the pest population occurs on the bases of plants, at or even slightly below soil level (Wiktelius, 1986). Consequently, aphids are exposed to attack by ground-dwelling predators. Both modeling (Ekbom, Wiktelius, & Chiverton, 1992) and experimental manipulation of predator and prey densities (Chiverton, 1986; Edwards, Sunderland, & George, 1979; Östman, Ekbom, & Bengtsson, 2001) have shown that assemblages of ground-living generalist predators (mainly spiders, carabid and staphylinid beetles) can suppress aphid populations in cereals. When aphids arrive, the predators can potentially start feeding immediately, ideally suppressing the pest population below economic thresholds. In manipulative field experiments, however, consumption data at the genus or species level are rarely collected (Toft, 1995). For such specific dietary evaluations, the strength of a gut-content analysis becomes apparent.

Over 100 studies have utilized some kind of gut-content analysis to assess aphid predation (Harwood & Obrycki, 2005). In more than 70 cases carabid beetles were studied, clearly demonstrating a need for more data on other taxa. Spiders have received little attention despite their high abundance in cereal fields in Europe (reviewed by Sunderland, 1987). Several species from the diurnal genus *Pardosa* (Araneae: Lycosidae) are well adapted to agroecosystems and often found in very high numbers (Samu & Szinetár, 2002; Schmidt, Roschewitz, Thies, & Tscharntke, 2005). The most common *Pardosa* species around Uppsala, Sweden, is *P. agrestis* which is not only numerous but also present and uniformly distributed in spring-sown cereals early in the season (Öberg & Ekbom, 2006). The temporal and spatial synchronization with *R. padi* together with high activity densities suggest a high conservation biological control potential for *Pardosa* and we argue that special attention to the diet of this genus is well justified. Our aims were to use PCR-technology to (1) investigate the detection success of *R. padi* DNA in laboratory-fed *Pardosa* and (2) to track *R. padi* predation by *Pardosa* spiders feeding under natural conditions.