9.4 Know your Enemies: Suppression of *Plutella xylostella* and *Crocidolomia pavonana* by Different Predators in West Java, Indonesia

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Plutella xylostella L. (Lepidoptera: Plutellidae) and *Crocidolomia pavonana* F. (Lepidoptera: Crambidae) are serious, co-occurring pests of *Brassica* crops in the highlands of West Java, Indonesia. Prior to the introduction of synthetic pesticides in the region, *C. pavonana* was considered a more serious pest than *P. xylostella* (Ankersmit, 1953), although *P. xylostella* has long been considered the more serious pest at drier times of the year (Vos, 1953). Together, the pests often result in complete crop loss in West Java, particularly during the dry season (Sastrosiswojo and Setiawati, 1992).

Diadegma semiclausum Hellén (Hymenoptera: Ichneumonidae), a *P. xylostella* parasitoid of European origin, was introduced from New Zealand in 1950 (Vos, 1953) and it successfully established in highland regions, including West Java (Sastrosiswojo and Sastrodihardjo, 1986). Parasitoids do not provide effective control of *C. pavonana* anywhere in the world (Uelese *et al*., 2014) and in West Java, two endemic larval parasitoids that attack the pest, *Eriborus argenteopilosus* Cam. (Hymenoptera: Ichneumonidae) and *Sturmia inconspicuoides* Bar. (Diptera: Tachinidae), only occur at very low levels (Sastrosiswojo and Setiawati, 1992).

Despite the lack of effective parasitoids of *C. pavonana* in Indonesia, Shepard & Schellhorn (1997) suggested that if no chemical insecticides were applied to crops then predators would most likely become key mortality factors for *C. pavonana.* However, the empirical evidence to support the claim that predation of this pest is important is lacking. Similarly, despite the extensive studies that have been conducted on biological control of *P. xylostella* worldwide (Furlong *et al.,* 2013; Li *et al.,* 2016), the majority of studies do not consider the impact of predators on pest populations and those that do frequently fail to assess the impact of predators appropriately (Furlong and Zalucki, 2010). Typically, studies of arthropod predation report the abundance and diversity of predator species that are commonly found in *Brassica* crops (Miranda *et al.,* 2011; Sastrosiswojo *et al*., 2004) but they do not progress to develop an understanding of the ecological impact of predators on pest populations so that contributions to biological control can be evaluated.

Quantifying the impact of natural enemies on target pest populations is essential if these ecosystem services are to be used for pest management decision-making (Furlong and Zalucki, 2010). Once the impact of natural enemies on a pest population has been demonstrated, the next step is to determine the key mortality factors through life table construction; this also provides vital information on species interactions and the ecological

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role of different natural enemies. The impact of predators on pest populations is difficult to demonstrate. Predators often leave no remains of their prey and attributing mortality to a given group of predators is difficult without the means to detect evidence of specific predation events; this requires experimental manipulation of both pest and natural enemy populations (Furlong and Zalucki, 2010). These approaches then need to be combined with a reliable method to determine which predators consume target pests to evaluate their importance in pest suppression; for example, visual observation to detect and document incidents of predation directly, or combined with molecular analyses to detect the presence of prey within the predator (Weber and Lundgren, 2009).

Although considerable advances have been made in the development of DNA-based molecular techniques to detect the remains of insect prey within the guts of predatory arthropods, the methods have rarely been applied in conjunction with field experiments that measure the impact of natural enemies on pest/ prey populations (Furlong, 2015). In this study, field experiments used a combination of ecological (natural enemy exclusion techniques and life table construction) and DNA-based molecular methods to quantify the impact of different predatory arthropods on *P. xylostella* and *C. pavonana* populations in *Brassica* vegetable crops in West Java. Prior to these quantitative studies, the specificity of previously designed primer sequences for *P. xylostella* and *C. pavonana* mtCO1 DNA (Furlong *et al.*, 2014) was confirmed by testing them against a wide range of herbivores and predatory arthropods collected from in West Java.

In a series of field studies that simultaneously investigated the impact of the natural enemy complex on *P. xylostella* and *C. pavonana* populations (Fig. 9.4.1), the endemic predator complex and *D. semiclausum* consistently suppressed *P. xylostella* populations, but predators had a greater impact than the parasitoid. The proportion of the original *P. xylostella* cohort recovered from natural enemy exclusion cages (95% and 89%) was significantly greater than the proportion recovered from open cages (2% and 1%) in both the first ($t= 15.40$, $P< 0.001$) and second $t= 10.43$, $P< 0.001$) experiments. No parasitoids were reared from *P. xylostella* that developed in the exclusion cages in either experiment. However, *D. semiclausum* was reared from *P. xylostella* developing in open cages and *D. semiclausum* marginal parasitism rates of 0.33 and 0.63 were recorded in the first and second experiments respectively. In both experiments, the net reproductive rates (R_o) of the *P. xylostella* cohorts in the presence of natural enemies were lower (0.3 and 0.5 respectively) than those in the absence of natural enemies (56.3 and 52.8 respectively).

In the first experiment, the proportion of the original *C. pavonana* cohort recovered from natural enemy exclusion cages (59%) was significantly greater than the proportion recovered from open cages (15%) ($t= 2.67$, $P< 0.014$) but there was no significant difference between recovery rates from exclusion (54%) and open cages (38%) in the second experiment ($t= 1.07$, $P= 0.297$). No parasitoids were reared from any *C. pavonana* larvae. In the first experiment, R_o of the cohort reared in open cages was 14.9, considerably lower than the R_o of the cohort reared in exclusion cages (69.0). However, in the second experiment, R_o of the cohorts reared in open (61.2) and exclusion cages ($R_o = 79.3$) were very similar.

Fig. 9.4.1. Natural enemy exclusion and open cages in an experimental cabbage field at the Indonesian Vegetable Research Institute, Lembang, West Java. Studies simultaneously investigated the impact of the endemic natural enemy complex on experimental cohorts of *Plutella xylostella* and *Crocidolomia pavonana*. Bamboo canes mark the location of pitfall traps.

Most foliar-dwelling predators collected by destructively sampling in-field plants during the natural enemy exclusion studies were predatory insects and they accounted for 58% of all arthropod predators (n = 309) collected from foliage. The most abundant predatory insects found foraging on plants were Syrphidae (50% of 175 predatory insects caught; 10% contained *P. xylostella* mtCO1 DNA and 17% *C. pavonana* mtCO1 DNA). The next most abundant predatory insects collected on foliage were *Menochilus sp.* (n = 36; 8% contained *P. xylostella* mtCO1 DNA, 11% contained *C. pavonana* mtCO1 DNA but none contained mtCO1 DNA of both species;), Staphylinidae (n = 17; 13 *Paederus* sp. (77% contained *C. pavonana* mtCO1 DNA but none contained *P. xylostella* mtCO1 DNA) and 4 unidentified individuals (all contained *P. xylostella* mtCO1 DNA, but none contained *C. pavonana* mtCO1 DNA) and Miridae (n = 11; 1 contained *P. xylostella* mtCO1 DNA and 2 contained *C. pavonana* mtCO1 DNA). The most abundant spiders collected by destructive sampling of plants were Araneidae (57% of the 134 spiders collected), followed by Gnaphosidae (25%) and Clubionidae (≈5%), Linyphiidae (≈5%) and Theridiidae (≈5%). *Plutella xylostella* mtCO1 DNA was found in 50% of the Clubionidae, and 11-17% of the Gnaphosidae, Aranaeidae, Linyphiidae and Theridiidae. Only Araneidae (7%) and Gnaphosidae (3%) contained *C. pavonana* mtCO1 DNA and no spiders contained mtCO1 DNA of both prey species.

Most epigeal predators caught in pitfall traps set to capture predators for gut-content analysis were predatory insects (75% of the 182 captured by this method). Formicidae were the most abundant predatory insects caught in the pitfall traps (80% of 137 predatory insects caught). Four genera of Formicidae were collected, *Pheidole sp., Hypoponera sp., Crematogaster sp.* and *Myrmecina sp. Pheidole sp.* was the most abundant (66% of 109;

54% contained *P. xylostella* mtCO1 DNA, 10% contained *C. pavonana* mtCO1 DNA and 19% contained mtCO1 DNA of both *P. xylostella* and *C. pavonana*. *Hypoponera sp.* was the next most abundant (29% of 109, 47% contained *C. pavonana* mtCO1 DNA but only 3% contained *P. xylostella* mtCO1 DNA).

The most abundant spiders caught in the pitfall traps were Lycosidae (76% of 45 individuals); 29% of these contained *C. pavonana* mtCO1 DNA, 15% contained *P. xylostella* mtCO1 DNA and 3% contained both *P. xylostella* and *C. pavonana* mtCO1 DNA. Araneidae (n = 2), Gnaphosidae (n = 7) and Linyphiidae (n = 1) were also caught in pitfall traps. One Gnaphosidae contained *C. pavonana* mtCO1 DNA, another contained both *C. pavonana* and mtCO1 DNA and the single Linyphiidae caught contained *P. xylostella* mtCO1 DNA; neither of the Araneidae contained prey DNA.

Foliar dwelling spiders appear to be more important predators of *P. xylostella* than of *C. pavonana*, while epigeal Lycosidae are more likely to have preyed upon *C. pavonana*. This possibly reflects the increased likelihood that these predominantly soil surface dwelling predators will encounter *C. pavonana*, which pupates in the soil, over *P. xylostella* which typically completes its lifecycle on its host plant. Similarly, *Paederus* sp. was more likely to have preyed upon *C. pavonana*, while the unidentified species of staphylinid only preyed upon *P. xylostella*. Of the ants, *Hypoponera sp.* was more likely to have preyed upon *C. pavonana* while *Pheidole sp.* was more likely to have preyed upon *P. xylostella*. Whether these differences represent distinct feeding preferences between these species or are simply the result of patchy distributions of the predators within the experimental field, requires further investigation.

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