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ORIGINAL ARTICLE

Spatial population dynamics of a specialist aphid parasitoid, *Lysiphlebus hirticornis* Mackauer (Hymenoptera: Braconidae: Aphidiinae): evidence for philopatry and restricted dispersal

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Within insect communities, the population ecology of organisms representing higher trophic levels, for example, hymenopterous parasitoids, may be influenced by the structure of their insect hosts. Using microsatellite markers and ecological data, we investigated the population structure of the specialist braconid wasp parasitoid, *Lysiphlebus hirticornis* Mackauer attacking *Metopeurum fuscoviride*, a specialist aphid feeding on tansy, *Tanacetum vulgare*. Previous studies revealed that *M. fuscoviride* has a classic metapopulation structure with high subpopulation turnover. In this study, up to 100% of ramets within a host plant genet colonized by aphids were colonized by the parasitoid, yet plants with aphids but no parasitoids were also observed. Genetic differentiation measured by F_{ST}, actual differentiation (D) and relative differentiation (G_{ST}) indicated highly structured parasitoid population demes, with restricted gene flow among and between parasitoid subpopulations at the various sites. Interestingly, both field data and population assignment analysis showed that the parasitoid is highly philopatric. Thus, despite the frequent local extinctions of the aphid host, the parasitoid continuously exploits its aphid host and contributes to the demise of local aphid subpopulations, rather than spreading its genes over many aphid populations. F_{ST} values for the haplodiploid parasitoid were similar to those found in an independent study of the diploid aphid host, *M. fuscoviride*, hence supporting the view that an insect herbivore's population structure directly influences the ecology and genetics of the higher trophic level, in this case the wasp parasitoid.
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Introduction

In recent years, a number of empirical studies have shown that metapopulation structure influences the genetic makeup of subpopulations of various organisms studied (for example, Bay *et al*., 2008; Orsini *et al*., 2008; Purrenhage *et al*., 2009), including aphids (Massonnet *et al*., 2002). General predictions about the genetic structure of metapopulations are difficult to make because of factors such as the population dynamics of local populations, their extinction rate, and the rate and distance of dispersal of the species under consideration (Harrison and Hastings, 1996; Pannell and Charlesworth, 2000). Broadly speaking, a metapopulation with frequent extinctions is expected to show lower overall genetic variability compared with an unstructured population of a similar organism with similar natural history, and subpopulations (colonies or demes) are more or less genetically differentiated depending on the balance between dispersal, colonization and extinction dynamics (Pannell and Charlesworth, 2000). For example, in insect species with metapopulation dynamics, genetic differentiation between populations range from: (1) significant differences between almost all subpopulation pairs investigated, for example, the tansy aphid, *Macrosiphoniella tanacetaria* Kaltenbach (Hemiptera: Aphididae) (Massonnet *et al*., 2002); to (2) some level of genetic differentiation, such as that found in the wasp parasitoid, *Hyposoter horticola* Gravenhorst (Hymenoptera: Ichneumonidae), which attacks the Glanville fritillary butterfly, *Melitaea cinxia* L. (Lepidoptera: Nymphalidae) (Kankare *et al*., 2005); to (3) no genetic differentiation despite the existence of discrete subpopulations, for example, in the dung beetle, *Aphodius fossor* L. (Coleoptera: Scarabaeidae) (Roslin, 2001).

In spatially structured multitrophic systems such as those formed on plants by insect herbivores and their natural enemies, the population ecology of the higher trophic levels, for example, wasp parasitoids, may be influenced by the metapopulation structure of the host insect. However, few studies have to date estimated dispersal and genetic population structure at one or more trophic levels or analysed the influence of species interactions on metapopulation structure of one or more of the organisms involved (Cronin and Reeve, 2005). The few studies performed (for example, Johannesen and

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