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Stay at home aphids: comparative spatial and seasonal metapopulation structure and dynamics of two specialist tansy aphid species studied using microsatellite markers

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Two tansy-feeding aphids, *Macrosiphoniella tanacetaria* (MA) and *Metopeurum fuscoviride* (ME), were studied at a small spatial scale in and around Jena (< 80 km^2) using polymorphic microsatellite markers. Both species were found in approximately 60% of sites formerly known to harbour the aphids, although, generally when they did occur, they occurred singly (MA ~50%; ME ~60%) and rarely together on the same plant at the same time (approximately 10%) and then usually only in the early part of the growing season. This difference may be a result of quasi-apparent competition effects elicited by ants farming ME aphids, and preferentially actively eliminating or disturbing MA aphids. In terms of population genetics, both aphids showed extreme genetic heterogeneity within a metapopulation structure, with ME more than MA (i.e. higher F_{ST} values, approximately 0.4 versus 0.15, respectively), and limited levels of interpopulation gene flow. Subpopulations often deviated from Hardy–Weinberg equilibrium and showed linkage disequilibria, as expected in animals with extended parthenogenetic reproduction, and had positive F_{IS} values for most large samples, suggesting inbreeding, and possibly philopatry, certainly in ME. Hierarchical analysis (allele range and number per locus, analysis of molecular variance and F_{ST}) strongly suggested that the plant rather than site governs the level of genetic variation. Bayesian clustering analysis revealed that both species had heterogeneous historical genetic patterning, with K (number of subgroups) in the range 3–7. Evidence is also provided from isolation-by-distance and private allele analyses indicating that, in MA, the presence of winged autumn males, absent in ME where males are wingless, influences comparative population genetic structuring, such that ME subpopulations are comparatively more inbred and genetically differentiated than MA subpopulations. Lastly, additional spatial arrangement (ALLELES-IN-SPACE) analysis showed that, in both species, certain subpopulations were genetically isolated from the remainder, probably as a result of geographical barriers, including intervening buildings and woods. As such, the biology of these tansy aphids living in semi-natural habitats is very different from many pest aphid species examined within agro-ecosystems and infesting ephemeral crops. This is because the former appear to be much more reluctant to fly and hence show contrastingly much higher levels of interpopulation divergence, even at small spatial scales as investigated in the present study. Indeed, the number of genotypic clusters found for tansy aphids using Bayesian approaches is similar to that globally for the major pest, the peach-potato aphid, *Myzus persicae*. *Biological Journal of the Linnean Society*, 2011, **104**, 838–865.

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