

Metabolic Profiling: A New Tool in the Prediction of Host-Specificity in Classical Biological Control of Weeds?

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Abstract

Current host-specificity testing for the selection of environmentally safe weed biological control agents is based on the molecular phylogeny of the weed. According to the centrifugal phylogenetic theory, non-target species closely related to a target weed should be at greatest risk of attack by a biological control agent, as they are biochemically and morphologically more similar to the target, and therefore more likely to share the cues used by specialists to select their host. However, a molecular phylogeny is not always a suitable surrogate for phenotypic traits at the species level. For example, the potential weed biological control agent *Ceutorhynchus cardariae* Korotyaev (Coleoptera: Curculionidae) investigated for the invasive Brassicaceae plant *Lepidium draba* L., attacks plant species distantly related to *L. draba* under no-choice conditions, revealing a disjunct fundamental host range. The aim of this study is to compare the reliability of a phenotypic phylogram with a genetically based one for predicting host use by *C. cardariae*. We used data of feeding and oviposition trials for 23 test plant species/populations, differing in susceptibility to *C. cardariae* attack. Host preference of *C. cardariae* was assessed using different phylograms based either on genetic distance between test plant species or various combinations of phenotypic traits, such as chemical profile and physical attributes. Patterns of susceptibility to *C. cardariae* among the different trees were compared using different measures of phylogenetic correlation. Principles discovered could be used to explain and potentially predict the host range of other biological control agents.