

Selection of Test Plant Lists for Weed Biological Control with Molecular and Biochemical Data

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Abstract

The initial steps of weed biological control programs involve the determination of the host range of a prospective agent prior to consideration for release. Accurately predicting the host range of a potential agent is fundamental to this process. This may be conducted first in the country of origin in open field testing (Briese et al., 2002) and later under controlled environmental conditions in quarantine (Zwölfer and Harris, 1971; McFadyen, 1998). Initially a plant test list is established composed of species that are taxonomically related to the weed and species of economic and ecologic importance from the area where the weed is a problem (Wapshere, 1974). This centrifugal / phylogenetic testing procedure involves “testing plants of increasingly distant relationship to the host until the host is circumscribed” (Wapshere, 1974) and is based upon the assumption that host shifts occur to plants of similar taxa (Ehrlich and Raven, 1964; Mitter and Farrell, 1991). Typically rare species are also included in the plants tested. As useful as this process is it potentially overlooks unrelated plant taxa that share similar secondary plant metabolites. Recent evidence indicates that chemical similarity may be a better predictor of host use than are phylogenetic relationships (Becerra, 1997; Wahlberg, 2001). Although little evidence may exist from weed biological control projects (Schaffner, 2001), species with secondary metabolites similar to the target weed should be included in the test list as they may contain the behavioral cues used by these specialized herbivore species to locate hosts and initiate feeding (Wheeler, 2005). As useful as the centrifugal / phylogenetic testing procedure may be, it potentially overlooks distantly unrelated plant taxa that share similar secondary plant metabolites.

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