est are other members of the Fabaceae, which includes legumes grown commercially in New Zealand (for timber, food, animal fodder, and as nitrogen-fixing cover crops) and several New Zealand natives. Of eight species of plantation trees and cover crop plants tested to date, those within the same subtribe or tribe as gorse and broom have shown the greatest susceptibility to *F. tumidum*. A further thirteen species of native plants and commercially important legumes will be tested in the next few months. The results from these host range tests will be used to prepare advice on the appropriate use of the bioherbicide.

---

**Potential Evolution of Host Range in Herbivorous Insects†**

DOUG FUTUYMA

Dept. of Ecology and Evolution, State University of New York, Stony Brook, New York 11794-5245, USA

Managers who introduce insects for weed control want to know if the species might adapt to nontarget plants. Such host-plant association expansions would follow from natural selection on genetic variation in insect characteristics such as the insect’s phenology, its feeding and oviposition responses to plant features, and its postingestive processing of nutrients or toxins. Knowledge of these characteristics and their genetics is rudimentary. But, phylogenetic studies confirm that herbivorous insects generally expand their host associations to plants closely related to their ancestral host. Therefore, the genetic variation found in herbivorous insects may be constrained so that evolutionary shifts to closely related plants are more likely than to distantly related species. *Ophraella* leaf beetles (Galerucinae) are host-specific to four tribes of Asteraceae. A phylogeny based on mtDNA sequence data indicates that most host shifts have been among plants in the same tribe. Using a half-sib breeding design, we screened four species for responses to Asteraceae that are hosts of other *Ophraella*. In 16 combinations in which larval survival on periodically replenished foliage was scored, genetic variation in survival was documented in two cases, both on test plants closely related to the insect’s normal host. In 39 larval or adult feeding tests, we found evidence of genetic variation in feeding in 21 cases. There were more cases of genetically variable feeding responses to plants in the same tribe as the insect’s normal host than to plants in different tribes. These data are consistent with the hypothesis that not only mean responses but also the genetic variation required for adaptation to a novel plant are more likely if the plant is closely related to the insect species’ normal host than if it is distantly related. Screening for host specificity of proposed biocontrol agents might profitably be based on large samples, with special attention paid to rare variants.

---

**FOOTNOTE:** Full paper in