ASIAN VERSUS EUROPEAN *ENTOMOPHAGA MAIMAIGA*/GYPSY MOTH RELATIONS

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Abstract

The European biotype of gypsy moth, *Lymantria dispar* (L.) [Lepidoptera: Lymantriidae], was introduced in the eastern United States from France in 1868 and has since become one of the most important defoliators of broadleaved trees in North America. In addition, the Asian biotype of gypsy moth has been accidentally introduced in North America several times, but so far eradication programs appear to have been successful in preventing establishment of this strain.

Entomophaga maimaiga Humber, Shimazu & Soper [Zygomycotina: Entomophthoraceae] is a naturally occurring fungal pathogen specific to gypsy moth larvae. *E. maimaiga* was originally described from Japan and is thought to be native to Asia where it causes epizootics in gypsy moth populations, suppressing outbreak populations. *E. maimaiga* was released twice in the U.S. in an effort to control gypsy moths; an isolate originating from Tokyo, Japan was released in Massachusetts in 1910-1911 and then an isolate from Ishikawa, Japan was released in New York and Virginia in 1985-1986 (Speare & Colley 1912, Hajek et al. 1995). Despite many years of intensive surveys by insect pathologists in North America, *E. maimaiga* was not observed in the field until 1989, but since then, it has spread across the distribution of gypsy moth (Andreadis & Weseloh 1990, Hajek et al. 1995). Several hypotheses for the origin and establishment of *E. maimaiga* in the U.S. have been proposed. One hypothesis proposes that the fungus originated from one of the deliberate introductions and was present at undetectable levels until 1989; another hypothesis proposes that *E. maimaiga* was successfully introduced to the U.S. by accident (see Hajek et al. 1995). However, no matter how and when *E. maimaiga* was introduced into North America it is likely that the population experienced a restriction in size (a bottleneck) resulting in reduced genetic variability compared to the source population.

The objectives for our studies were (1) to determine whether non-North American gypsy moth strains are susceptible to North American strains of *E. maimaiga*; (2) to compare the genetic diversity of North American and Asian populations of *E. maimaiga*; and (3) to determine the origin of the North American *E. maimaiga* population.

We used bioassays to assess the variability in susceptibility, measured as time to death for gypsy moth larvae challenged with *E. maimaiga*. Cross-inoculations with host strains originating from far eastern Russia, Japan, Greece and the U.S., and pathogen originating from China, far eastern Russia, Japan and the U.S. were accomplished by injecting fungal protoplasts into larvae or by subjecting larvae to showers of conidia. We found that all *E. maimaiga* isolates tested were pathogenic to all strains of *L. dispar*, regardless of the geographical origin of the fungal isolate or inoculation method; percent mortality varied between 87 % and 100%. Fungal isolates differed significantly with regard to virulence; times from inoculation to death varied between averages of 4.1 days for one of the Japanese isolates (03JP5-1-2) to 5.4 days for a Russian isolate (99RU-1-1-1). In contrast, gypsy moth strain seemed to have little effect on time to death after inoculation with *E. maimaiga*. Based on these results we therefore expect that the populations of *E. maimaiga* already present in North America would be able to help control the Asian gypsy moth if it becomes established in North America. This does not mean that introductions of Asian gypsy moth strains into North America should be ignored, since the dynamics and behavior of the Asian and North American populations are extremely different, e.g., the gypsy moth strains from Asia have a broader host range (Baranchikov 1988), shortened egg chill requirements (Keena 1996), female flight and attractions to lights that result in egg deposition on vehicles or cargo (Wallner 1996).

These attributes could influence the effectiveness of *E. maimaiga* on gypsy moth populations since it is a well-known fact that larval behavior affects the impact and dynamics of *E. maimaiga* infections (Hajek et al. 1996, Hajek 2001, Hajek et al. 2004).

We used AFLPs to assay the genetic diversity among 30 *E. maimaiga* isolates originating from seven states in the U.S., five prefectures in Japan, one province of China and one region of far eastern Russia. Among the 14 U.S. isolates, only 10 polymorphic AFLP loci were found, whereas 56 polymorphic loci were found among the 16 Asian isolates; 29 loci were polymorphic among the 12 isolates from Japan alone. Average gene diversity for the polymorphic loci was 0.223 ± 0.005 for Asia (including Japan), 0.131 ± 0.006 for Japan only, and 0.041 ± 0.004 for the US. Thus, native populations from Asia were more diverse than the U.S. populations. These results are consistent with the expectation of a population founded from a source population by a small number of individuals. Distance and parsimony analyses of AFLP data showed that the isolates from the U.S. formed one distinct clade that was not closely related to Japanese isolates collected near the Tokyo area. The closest relative to the North American isolates was the isolate released in New York State and Virginia in 1985 and 1986. However, the released isolate is in a clade distinct from the U.S. clade. These results, plus further analysis, support the hypothesis of an undocumented introduction of *E. maimaiga* into North America from Japan are the source of the current *E. maimaiga* population that is suppressing gypsy moth populations in the U.S.

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