

# Forest Macrolepidopteran Parasitoid Host Range and Richness in the Central Appalachian Range

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## Abstract

In a long-term nontarget study initiated in 1995 on the effects of *Lymantria dispar* (L.) and its control with applications of *Bacillus thuringiensis* var. *kurstaki* Berliner (Btk), parasitoids were sampled by Malaise traps and through rearing of macrolepidopterous larvae. Sampling was performed on 18 200-ha study plots located in the George Washington National Forest (GWNF) in Virginia and Monongahela National Forest (MNF) in West Virginia in the central Appalachians.

During 1995 and 1996, a total of 13,310 larvae were collected on foliage and under canvas bands with 5,213 of these reared for parasites and disease symptoms. Gypsy moth accounted for 6,856 larvae collected and 2,202 larvae reared. The caterpillars reared represented 114 species in 12 families, with each family having species parasitized. Tachinid flies, Hymenoptera or nematodes parasitized a total of 69 species of caterpillars. The tachinids had the widest host range, attacking 52 caterpillar species in eight families. The other two commonly encountered parasitic families, Braconidae and Ichneumonidae, parasitized 28 and 33 host species, respectively, with a combined total of 47 species parasitized in seven families. Of the 24 species of reared tachinids, 60 new hosts associations were determined, including first-known hosts for seven tachinids. This is a significant increase to our knowledge of tachinid associations and supports the possibility that Tachinidae and Ichneumonidae may be equally important in regulating macrolepidopteran larval populations in forest environments.

Reared species of tachinids were represented in Malaise samples as well, where 186 species have been identified in the first four years of sampling. Species richness is similar between the two forests with 158 species collected in the GWNF and 138 species in the MNF, with 103 (55%) shared between the two forests. The majority of all reported tachinid host relationships are with lepidopteran larvae, and this was true in our tachinid collections in these forest environments as well with 133 species represented: 112 on the GWNF, 91 on the MNF, and 70 shared between the forests. Temporal patterns of species richness and abundance of tachinids and their caterpillar hosts were similar.

The most diverse tachinid subfamily, Goniinae, made up 66% of the species richness and 67% of the abundance in the Malaise samples. Most Goniinae, Tachininae, and Dexiinae are parasitoids of lepidopterous larvae, and combined make up 96% of the species richness and 95% of the sampled abundance. Nearly all Phasiinae host associations known are with Hemiptera. The same 10 tachinid species were most abundant on both the GWNF and MNF, making up approximately 50% of the total sampled abundance on each forest. The most abundant tachinid on the MNF, *Compsilura concinnata* (Meigen), quickly increased with the movement of gypsy moth into the study plots in 1995. It has since declined in abundance with the decline of gypsy moth following the impact of the gypsy moth fungus, *Entomophaga maimaiga* (Humber, Shimazu & Soper).

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