PREDICTING THE FEMALE FLIGHT CAPABILITY OF GYPSY MOTHS BY USING DNA MARKERS

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ABSTRACT

Gypsy moths (*Lymantria dispar* L.) from different geographic origins have different biological and behavioral traits that can affect the risk of establishment and spread in new areas. One behavioral trait of major concern is the capacity of females from some geographic origins to fly, thus increasing the potential rate of spread and making detection and delimitation more difficult. Gypsy moths from some areas where females are capable of flight also possess traits that make them more threatening to North American forests than the established Western European strain: the ability of larvae to use hosts that are only marginally acceptable to gypsy moths from other areas, shortened egg chill requirements, and reduced susceptibility to some available biopesticides, all of which could influence the effectiveness of eradication or control programs. The flight-capable females are attracted to lights and will lay their egg masses on nearby vehicles or cargo, giving them an easy pathway around the world. Multiple introductions into North America of gypsy moth strains with flight-capable females have occurred and prompted major eradication programs, the largest occurring in 1992 and 1994. For regulatory purposes, USDA APHIS refers to any biotype of *Lymantria dispar* possessing female flight capability as the Asian gypsy moth. Individuals from populations with and without flight-capable females cannot reliably be distinguished morphologically so molecular techniques were developed to determine the origin of males caught in pheromone traps. There had been no previous attempt to compare the world variation in all of these markers, and they had never been used on the same populations in which female flight capability had been specifically determined. Understanding the relationship between marker results for intercepted males and female flight capability of different world populations would help in assessing the risk that an introduction contains flight-capable females.

We documented the female flight capability and the traits that affect it (wing length and muscle strength) from 46 strains of gypsy moth from throughout its range. For 31 of the strains, we determined the mtDNA haplotype based on two polymorphic COI mtDNA restriction sites, the nuclear FS1 genotype and four microsatellite loci for males from the same generation as the flight-tested females. We discuss the relationship between the marker results and female flight capability as well as implications for management programs.

Females capable of strong directed flight were found in strains that originated from Asia, Siberia, and northeastern Europe, but flight capability was not fixed in most strains (Fig. 1). One strain from Siberia (RS) was the only one in which 100 percent of the females flew. Far Eastern strains exhibited >64 percent female flight while European strains exhibited lower percentages. No flight-capable females were found in strains from the United States or Europe south of the Carpathian Mountains and Alps, most of France, or further west in northern Europe. Wing size and musculature were shown to correlate with flight capability and could potentially be used in predicting female flight capability.

The mtDNA haplotypes broadly separated the gypsy moth strains into three groups: North American, European/Siberian, and Asian. All Far East strains (except for JS) had the N+B+ mtDNA haplotype, the strains from Siberia and Europe all had the N+B- haplotype, and the strains from the United States had the N-B- haplotype. The AA FS1 nuclear DNA genotype occurred in 100 percent of the males sampled from the Asian and Siberian strains, except for the CS and RB strains. Males from three of the four United States strains and the PP strain all had the NN genotype. Across Europe, both alleles are present and the percentage of the A allele tended to decrease from east to west. Up to 70 percent of the males from strains

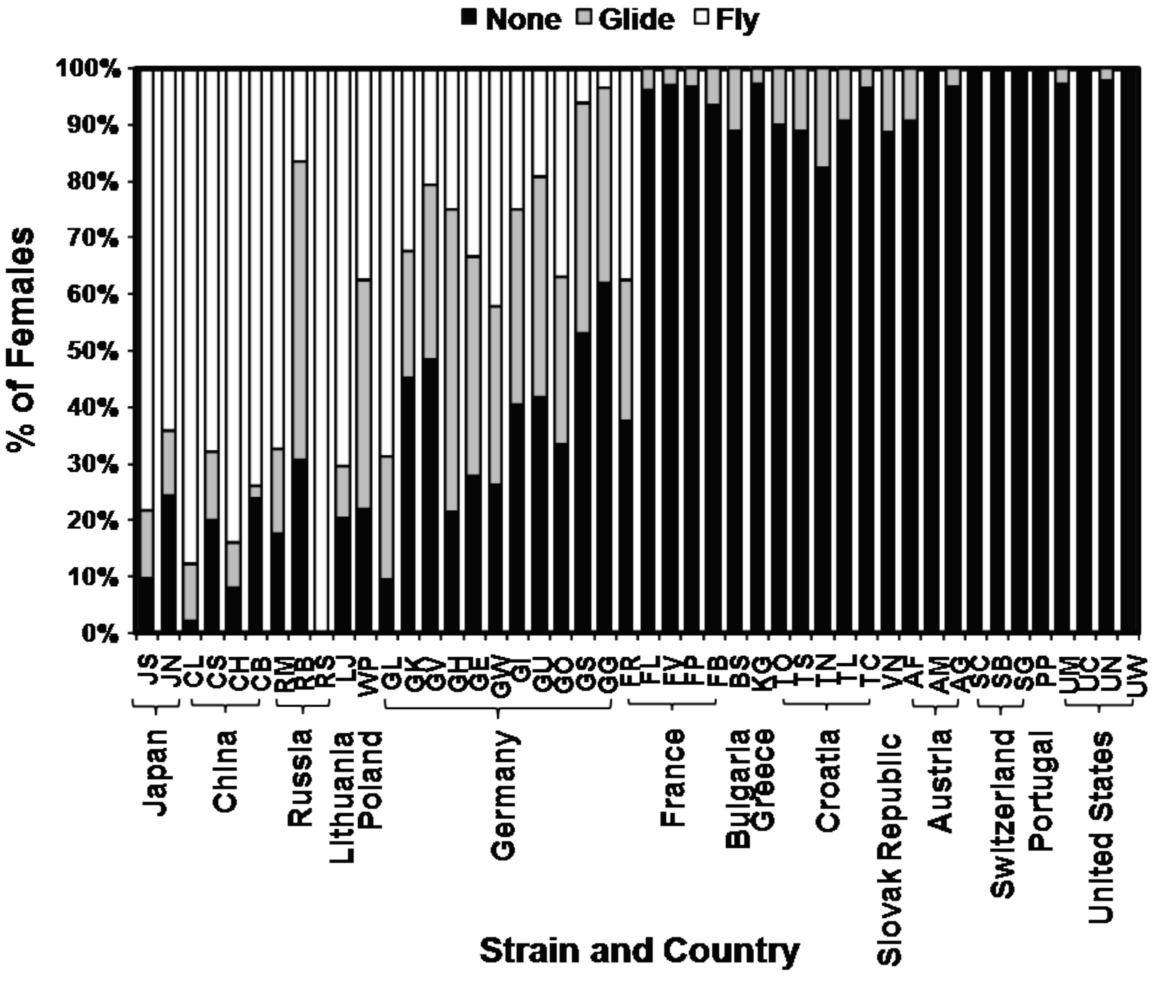

Figure 1.—World variation in female flight capability.

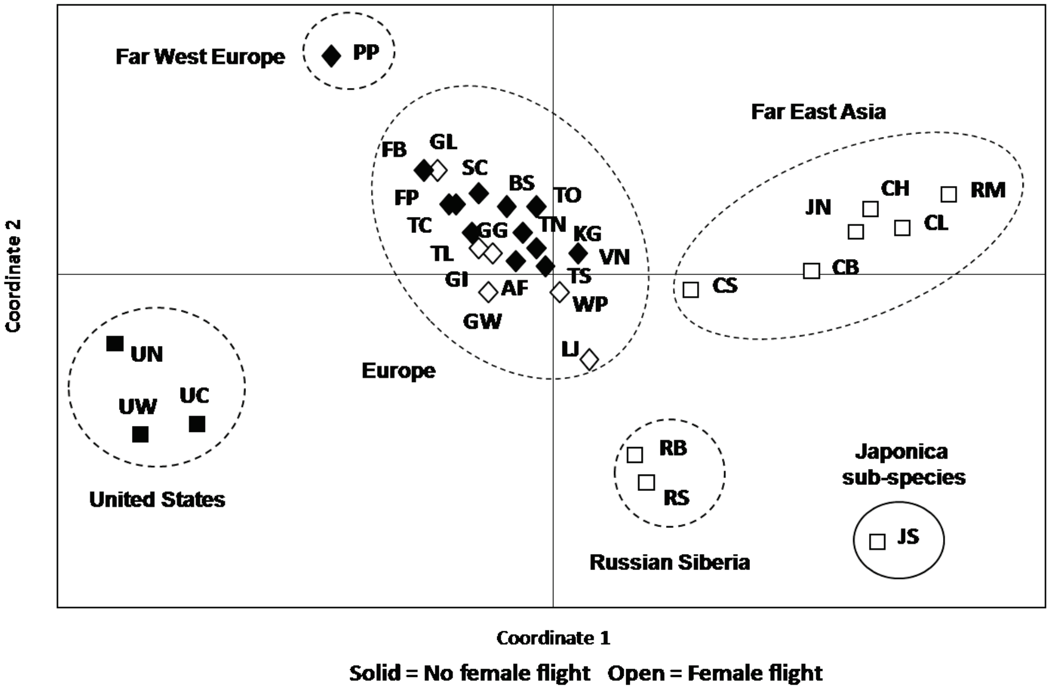

Figure 2.—Principle Coordinate Analysis based on Nei Genetic Distances (all markers).

with no flight-capable females had the AA genotype. Specific microsatellite or FS1 alleles were fixed only in a few strains, and there was a gradual increase in the frequency of alleles dominant in Asia at both the nuclear and microsatellite loci moving geographically from west to east. The U.S. strains had only two to three alleles per microsatellite locus, and in general these were the most common worldwide. There were only nine private (i.e., occurred in only one strain) alleles, seven of which were found only in single Far East Asian strains and none were found in U.S. strains. An additional seven alleles were found only in Asian strains (Fig. 2). The average number of total alleles was highest in the Asian strains (18.3), intermediate in the European/Siberian strains (14.8), and lowest in the U.S. strains (9.0). When all the genetic marker information was used, 94 percent of the individuals were accurately assigned to their broad geographic group of origin (North American, European, Siberian, and Asian), but female flight capability could not be predicted accurately. This suggests that gene flow or barriers to it are important in determining the current distribution of flight-capable females and demonstrates the need for added markers when trying to predict female flight capability in introduced populations, especially when a European origin is suspected. For a complete discussion of these data, see Keena et al. (2008).

Literature Cited

Keena, M.A.; Coté, M.-J.; Grinberg, P.S.; Wallner, W.E. 2008. **World distribution of female flight and genetic variation in *Lymantria dispar* (Lepidoptera: Lymantriidae).** Environmental Entomolology. 37: 636-649.