//

Presence Of Russian Honey Bee Genotypes In Swarms In Louisiana
Notes

H. Allen Sylvester, Lelania Bourgeois, Lilia I. de Guzman, Thomas E. Rinderer

United States Department of Agriculture, Agricultural Research Service, Honey-Bee Breeding, Genetics & Physiology Laboratory, 1157 Ben Hur Road, Baton Rouge, LA 70820, USA

In addition to the problems they have brought to the beekeeping industry, *Varroa* mites have, at least temporarily, devastated feral honey bee colonies. Russian honey bees were collected by this laboratory, evaluated, selected and bred for resistance to varroa mites, while still maintaining resistance to tracheal mites, good honey production, manageability and other desirable beekeeping characteristics (Tubbs *et al.* 2003). We were interested in determining if Russian bees are contributing mite-resistant genotypes to the feral honey bee population.

Two hundred pheromone-lured paper pulp swarm traps as reported by Schmidt and Thoenes (1987) were placed in locations near Baton Rouge, Louisiana, in March 2004. We placed traps in trees at varying distances around three apiaries containing ARS Russian and Italian honey bee colonies. The sampling area was 5.7 km x 1.7 km in a low-lying, somewhat forested area that was recently part of the flood plain of the Mississippi River. Sampling sites were chosen based on access and the presence of trees in which to hang the traps. These sites were generally along the edge of forested areas or along fence lines. Each week, for 28 weeks, traps were sampled, emptied, and then replaced. Samples (Mean = 617 ± 31 bees per swarm) were stored at -20°C until processing. A total of 147 swarms were sampled, 80 of which were used for this analysis. Clustering of captured swarms was observed in the traps around the ARS apiaries, but a more uniform distribution of analyzed swarms was desired to evaluate effect of distance on probability a swarm was Russian. Therefore, 80 swarms that were evenly distributed within the sampling area were selected for further analysis. Mite infestation levels were determined by washing, using detergent solution following Rinderer *et al.* (2004). Honey bee genotypes were generated from microsatellite and single nucleotide polymorphism (SNP) markers following Bourgeois *et al.* (2010). Four bees per swarm were analyzed individually for genetic stock identification, i.e., probability that they are Russian