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## Presence Of Russian Honey Bee Genotypes In Swarms In Louisiana Notes

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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

(Ru) or Non-Russian (NRu). The mean of the four individual bee probabilities was calculated to estimate the overall probability of group membership for each swarm. Data for the correlation of genotype and mite infestation were analyzed with ANOVA using SAS proc corr (SAS 2008).

Of the 80 swarms analyzed, 10 were Russian ( $Ru P > 0.60$ ), 15 hybrid ( $0.60 > Ru P > 0.40$ ) and 55 non-Russian ( $Ru P < 0.40$ ). Thus, Russian genotypes were detected in 25 of 80 swarms. Possible sources of the Russian genotypes sampled are the Russian colonies in the ARS apiaries, feral Russian colonies from previous swarms, and Russian drones mating with feral virgin queens. While these colonies are intensively managed to reduce swarming and to maintain the Russian queens in the colonies for ongoing research, Russian colonies have been maintained in these apiaries for several years. Villa (2004) suggested an average swarm movement distance of 3 km for Louisiana, in the absence of swarm traps. Here, distance from the apiaries was positively correlated ( $R = 0.224, P = 0.045$ ) with probability a swarm was Russian. However, the presence of traps alters the distance preferences of swarms (Villa 1993) so it is impossible to determine the origin of the swarms.

All swarms had either no comb or only early stages of brood which was unsuitable for *Varroa* mite invasion. Hence, all mites were phoretic on adult bees and mite infestation levels were low for most swarms, regardless of genotype (overall mean =  $3.63 \pm 0.45\%$ ; Russian =  $2.20 \pm 0.45\%$ ; hybrid =  $2.57 \pm 0.60\%$ ; non-Russian =  $4.18 \pm 0.62\%$ ) and showed no correlation with probability of Russian assignment ( $r = -0.077, P = 0.5$ ; Figure 1). Only five swarms had mite infestation levels greater than 10%, all of which were non-Russian. *Varroa* mites have been present in this area for many years. It is possible that some of these non-Russian swarms may have come from ARS and other managed colonies that had been managed with treatments to control mites. The non-Russian swarms could also have originated from surviving feral colonies that had been naturally selected for *varroa* mite resistance, as was hypothesized by Villa *et al.* (2008). The incidence of Russian genotypes found here indicates that Russian honey bees are contributing to regenerating the feral population of honey bees. Harris and Rinderer (2004) reported that

SMR-Russian hybrids had lower growth of mite populations than Russian bees, suggesting mite resistance may be an additive trait. Similarly, Russian swarms entering the feral population could be contributing an additive increase in mite resistance and increasing the genetic heterogeneity of the feral honey bee population. The contribution of Russian genotypes and a concomitant increase in mite resistance in feral populations is expected in areas surrounding Russian apiaries throughout the U.S. A regenerated feral population will be of benefit to growers depending on feral bees to pollinate their plants as well as contributing mite-resistant drones to mate with virgin queens from managed colonies.

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Figure 1 - Correlation between the probability a swarm is Russian and its mite infestation percentage.

