EXPANDED EXPLORATIONS FOR EMERALD ASH BORER IN ASIA AND IMPLICATIONS FOR GENETIC ANALYSIS

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ABSTRACT

Emerald ash borer (EAB) is considered native to northeast China, Korea, Japan, Taiwan, Mongolia, and eastern Russia. We are using genetic analyses to determine the origin of North America's EAB infestations; however, acquiring samples from countries other than China has proven difficult. To increase the diversity of EAB populations sampled in Asia, an expanded survey was conducted in areas of South Korea, Japan, and China from June-August 2006.

Live ash trees (*Fraxinus* spp.) were visually observed for EAB exit holes and/or crown dieback. If symptoms were observed, bark was peeled at breast height to inspect the trees for larvae. Leaves and branches were sampled using an aerial net to sweep for adult beetles. In South Korea, six new field sites were evaluated for EAB at the end of June to mid-July. *Fraxinus rhynchophylla* was the primary tree species at our sites. Larvae were collected at five of the six field sites (Mt. Juri, Mt. Muju, Mt. Sangju, Mt. Wolak, and Jurisan National Park), while two adults were collected at the Suwon site. A single adult was also collected at Mt. Sangju. The majority of larvae collected in South Korea were early instars. Six field sites were evaluated in two provinces in China (Jilin and Tianjin) from mid-July to mid-August with Roger Fuester (USDA-ARS). Live larvae were collected at three of the six field sites

(Dagong in Tianjin province and JingYueTan Park and Jiang Nan Forest in Jilin province). All live larvae were placed on artificial media developed by Dr. Leah Bauer (USDA-FS), shipped to her containment room at Michigan State University to rear any parasitoids, and healthy raised EAB will be used for genetic evaluation. Finally, eight field sites were evaluated in Japan throughout the remainder of August 2006. No evidence of EAB was detected at seven of the eight sites (Otsuki, Morioka, Iwaki-san, Aomori, Odate, and the University of Tokyo Tanashi and Chiba stations), while two larvae were collected from *F. lanuginosa* at Mt. Zao near Shirioshi City. These larvae, however, cannot be distinguished as EAB or *A. koyoi* , another *Agrilus* specie attacking *F. lanuginosa* in this area of Japan. Therefore, these larvae were placed on artificial media to rear to the adult stage.

Healthy EAB specimens will be used for genetic analysis to determine 1) the geographic origin of North American EAB populations; 2) the number of EAB introductions; 3) invasion history; 4) possible changes in EAB biology; and 5) sites in Asia for discovery of potential EAB biological control agents. Specimens will be evaluated by a variety of genetic techniques, including mitochondrial cytochrome oxidase I (COI) gene sequencing, amplified fragment length polymorphisms (AFLP), nuclear gene sequencing (wingless (*Wg*), phosphoenolpyruvate carboxykinase (*Pep*CK), cytochrome c (*Cytc*), elongation factor-1 (EF-1)), and microsatellite analysis. Preliminary data from samples collected before the summer of 2006 observed COI haplotype diversity in South Korea, while the common haplotypes shared by all Chinese and North American EAB individuals exists in each of the Korean populations sampled, and a single Japanese specimen had a 3.7% divergence from the common haplotype (Bray et al. 2006).

We expect that genetic analyses of our expanded data set will improve resolution of the EAB populations, allow us to determine which populations are most closely related to each other, and see if the North American infestations resulted from single or multiple introductions of this pest. Knowledge of EAB genetics will be useful in understanding the invasion dynamics of the beetle and to help identify geographic localities of potential biocontrol agents.

REFERENCES

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