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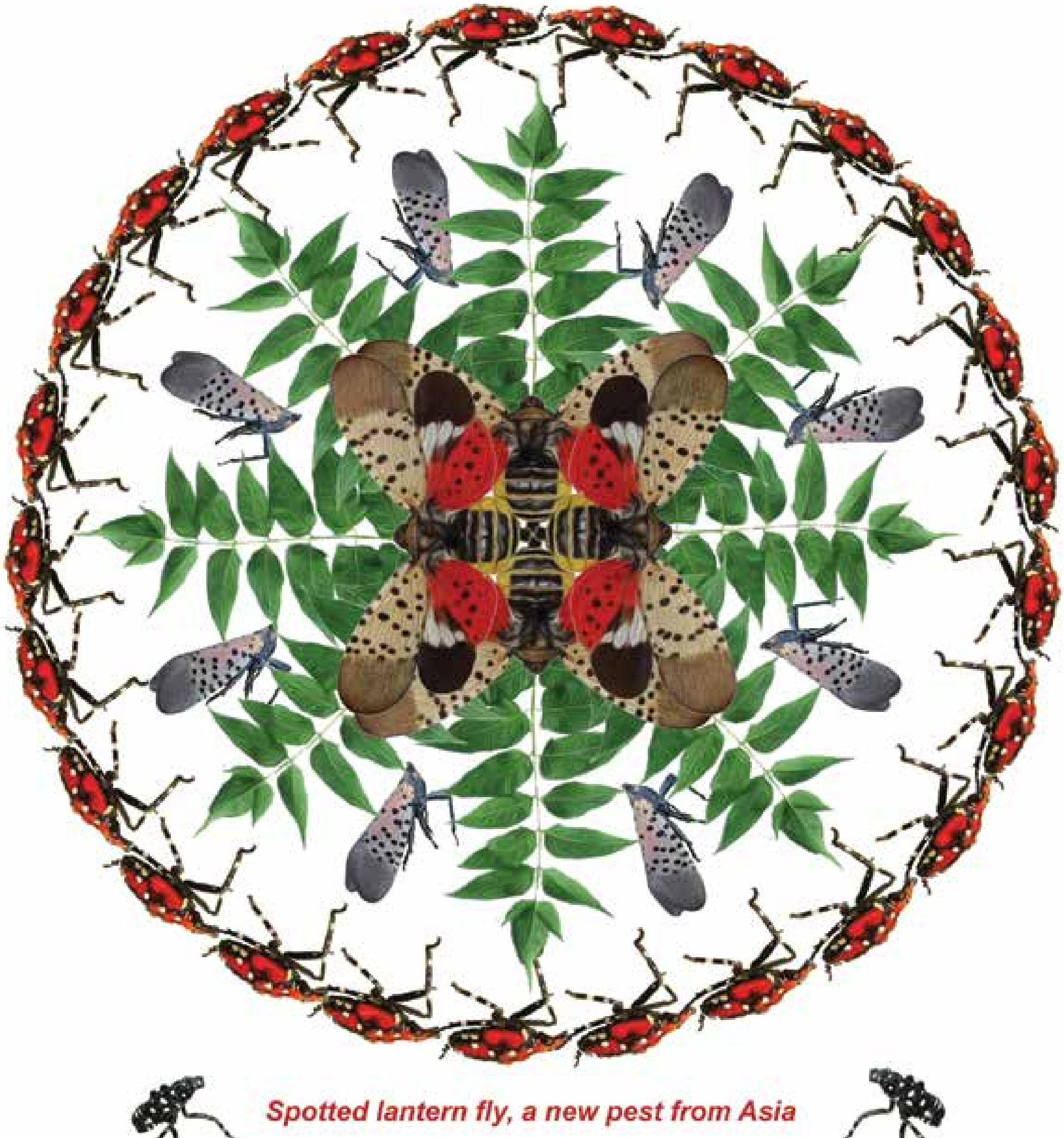

Spotted lantern fly, a new pest from Asia

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DNA-BASED INVESTIGATIONS OF THE SPOTTED LANTERNFLY, *LYCORMA DELICATULA* (WHITE)

Julie M. Urban[1]

[1]Pennsylvania State University, Department of Entomology, 501 ASI Building, University Park, PA 16802

ABSTRACT

To better understand the origin of the Spotted Lanternfly, *Lycorma delicatula* (White) in Pennsylvania, and to characterize its potential impact, three subprojects were conducted as summarized below.

1. Identification of the origin of *L. delicatula* in Pennsylvania using microsatellite sequencing: Six microsatellite loci were sequenced for 32 individuals from the Pennsylvania population of *L. delicatula*, 25 individuals from each of three Korean populations, 19 individuals from China, and 2 individuals from Vietnam. Results indicate 1) the Pennsylvania population appears to represent a single introduction, and 2) the Pennsylvania population is strongly differentiated from all of the other sampled populations, and as such, the origin of this invasion is not yet known. Novel microsatellite loci are currently being developed in order to provide more informative genetic loci that show greater variation within the Pennsylvania population, in order to allow for tracking of population structuring and detection of subsequent introductions. The novel microsatellite loci will also be used to genotype a more extensive sampling of *L. delicatula* within its native range, and hence, serve to better estimate the origin of the current invasion.

2. Characterization of the microbial associates harbored by *L. delicatula*: A region of the bacterial 16S rRNA gene was amplified and deep sequenced on the Illumina MiSeq platform to characterize the bacterial communities harbored in the abdomen and proboscis of 10 *L. delicatula* individuals from the Pennsylvania population. Bacteria from the proboscis did not amplify for any individuals. Abdominal bacterial communities were dominated by three obligate endosymbionts, *Sulcia muelleri, Vidania fulgoroideae*, and an uncharacterized Gammaproteobacterium, consistent with other sampled outgroup species of Fulgoridae. However, principal components analysis indicated *L. delicatula* was distinctly different from other sampled Fulgoridae and Dictyopharidae. In order to determine whether these results perhaps reflect a unique bacterial community within the gut due to feeding on *Ailanthus altissima* (Miller) Swingle, bacterial communities harbored by *L. delicatula* nymphs feeding on grape were sequenced. The composition of the bacterial communities harbored by grape-feeding nymphs was nearly identical to that of adults. To test the hypothesis that the bacterial communities harbored by *L. delicatula* are distinctive in being less diverse due to a founder effect (i.e., genetic bottleneck), bacterial communities were compared for *L. delicatula* individuals sampled from the species' native range (China) to those sampled from two invasive ranges (Pennsylvania and Korea). Preliminary results are consistent with this hypothesis as the bacterial communities harbored by *L. delicatula* in China were significantly more diverse than those sampled from Pennsylvania and Korean populations.

3. Characterization of changes in microbial communities on plants associated with *L. delicatula* feeding and honeydew deposition: A region of the bacterial 16S rRNA gene and a region of the eukaryotic 26S rRNA gene were amplified and deep sequenced to characterize the bacterial and fungal communities harbored in a frothy substance collected from *A. altissima* trees heavily infested with *L. delicatula*

in Pennsylvania. Bacterial communities from six froth samples were dominated by two bacterial genera, *Acetobacter* and *Leuconostoc*, both of which are aerobic fermenting bacteria capable of converting sugars to acetic acid and lactic acid, respectively. Analysis of fungal communities indicated that the most abundant species detected was *Geotrichum candidum*, a ubiquitous yeast, also capable of aerobic fermentation. These microbes may be feeding upon sugars present in *L. delicatula* honeydew and/or seeping tree sap. Further investigation is underway to examine a broader range of tree species for evidence of froth production in order to better understand the potential scope and impact of this unusual phenomenon.