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**Genetic Analysis of Bed Bug (*Cimex lectularius* L.) Populations Reveals Small  
Propagule Size within Individual Infestations but High Genetic Diversity  
across Infestations from the Eastern U.S.**

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**ABSTRACT**

Bed bugs (*Cimex lectularius* L.) are a resurgent pest worldwide and infestations within the U.S. are increasing at a rapid rate. Due to the physical and psychological discomfort inflicted by their blood feeding habits, and allergies and even secondary infections associated with bites, bed bugs are recognized as a significant public health problem. Although bed bug infestations are spreading and becoming more prevalent, we have a poor understanding of their dispersal patterns and sources of infestation. To help fill this gap, we conducted a genetic study of 21 bed bug infestations from Eastern U.S., nearly all of which came from single rooms within homes. We genotyped samples comprised of 8-10 individuals per infestation at nine polymorphic microsatellite loci. Despite high genetic diversity across all infestations, with 5 to 17 alleles per locus (mean = 10.3 alleles per locus), we found low genetic diversity (1 to 4 alleles per locus) within all but one of the infestations. These results suggest that nearly all the studied infestations were started by a small propagule possibly consisting of a singly mated female and/or her progeny, or a female mated with multiple males that were highly related to her. All infestations were strongly genetically differentiated from each other (mean pairwise  $F_{ST}$  between populations = 0.68) and we did not find strong evidence of a geographic pattern of genetic structure, indicating infestations located in closer proximity to each other were nearly as genetically differentiated as those located hundreds of kilometers away. The high level of genetic diversity across infestations from the eastern U.S. together with the lack of geographically organized structure is consistent with multiple introductions into the U.S. from foreign sources.

**KEY WORDS:** *Cimex lectularius*, bed bug, gene flow, introduced species, microsatellite, population genetic structure