Genetic Characterization of the Bat and Human Lineages of the Common Bed Bug (Cimex lectularius) at a Local Scale

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Résumé

After its near eradication in the 1940's, the common bed bug (*Cimex lectularius*) experienced a global resurgence with some populations displaying insecticide resistance. Two distinct lineages of bed bugs have been identified, one of which is associated with humans and the other with bats. A strong genetic differentiation between the two host-associated bugs has been identified between European sites. However, how and whether gene flow can occur at the local level is poorly known. In this study, we compared the genetic composition of human and bat-associated bed bugs in western Switzerland. We first conducted a median-joining analysis based on COI and 16S rRNA mitochondrial genes and compared it to European sequences to detect any local scale host-specific separation of haplotypes. Then, using 10 microsatellites, we estimated the genetic diversity and structure between and within the two hosts-associated bed bugs. Finally, we carried out an analysis of knock-down insecticide resistance gene variants (V419L, L925I and I936F) to assess the difference in resistance of the host-associated common bed bugs to pyrethroid insecticides. The median-joining analysis shows a clear separation of all haplotypes that are host-specific with no effect of the locality. Consistently, the analysis of genetic structure reveals two genetic clusters associated with bats and humans with some structure among human-associated sites. Human-associated bed bugs might have settled from multiple colonisation events or undergone bottlenecks. This separation is also supported by the analysis of knock-down insecticide resistance gene variants which shows that bed bugs infecting humans have evolved insecticide resistance in contrast to the ones infecting bats. Taken together, our results show that bed bugs seem to have evolved into genetically differentiated lineages specialised on different hosts, at local and global scale, thus supporting the hypothesis of host specialisation in the common bed bugs.

Mots-Clés: Cimex lectularius, local scale, genetic differentiation, insecticide resistance

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