

***Diabrotica virgifera virgifera* LeConte wing shape variation reveals multiple populations across the European expansion front**

Unterschiedliche Flügelausprägungen bei Diabrotica virgifera virgifera LeConte offenbaren das Vorhandensein multipler Populationen entlang der europäischen Ausbreitungsfrent

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The western corn rootworm (WCR), *Diabrotica virgifera virgifera* LeConte (Coleoptera: Chrysomelidae) is subject to much research because of the economic damage it causes to maize crops in the USA and recently in Europe. Understanding levels of genetic variability of introduced populations is important for investigating the adaptive potential of such populations in their new invaded environments e.g. WCR in Europe. To enhance the management and control of the WCR, an understanding of the temporal and spatial genetic structure, number of genetic clusters and pattern of gene flow is required. Croatia was the country economically affected first by the range expansion of the WCR from Serbia (where the beetle was detected for the first time in Europe) and it is an important part of the invasion puzzle in central Europe. The WCR core set of microsatellite markers was used to investigate populations from Croatia collected in 1996 (introduction) and again in 2009 (expansion). Using the program STRUCTURE, low to no genetic differentiation was found between populations by pairwise comparisons in 1996, with a greater level of differentiation found between populations sampled in 2009. A single genetic cluster was found for putative populations sampled in 1996 ($\Delta K_{1996}=1$) and in 2009 ($\Delta K_{2009}=1$). However, two genetic clusters were detected when the 1996 and 2009 data were combined ($\Delta K=2$), suggesting that the genetic structure and thus pattern of alleles changed over time either in response to genetic drift, increased gene flow or a single or multiple admixture event(s). Although the use of classical population genetic analyses has provided much needed information on the population genetic structure and gene flow of WCR in Croatia, its use to completely understand how populations have changed over time is limited. Thus, further population and diagnostic markers were investigated that could provide a more complete understanding of how WCR populations had changed over time and during the invasion of Croatia. Specifically 14 wing venation landmarks were used to assess the variation in wing shape and size for WCR populations shown to be genetically homogenous using microsatellites. The results showed that asymmetry and allometry did not occur in WCR, however sexual dimorphism was significant for both size and shape. Sexual dimorphism in wing morphology was found to be the result of females having generally larger and longer wings, a result consistent with a greater capacity for migratory flight, probably reflecting the role that gravid females play in range expansion. Significant pairwise differences in 2011 were noted between all sampled sites. Otok had the largest pairwise Mahalanobis distances with all sites investigated and was thus recognized as a distinct population. In addition, an isolation by distance pattern in the population structure was found throughout the sites investigated. This study found that a significant amount of variation in wing morphology exists in WCR across their invaded range in Croatia. The results indicate that the use of wing morphology can provide valuable additional information on population structure when used with microsatellite markers especially in suspected genetically homogenous geographic locations.