



E-sove 2012

From biology
to integrated
control in a
changing world

European Society for Vector Ecology
www.esove2012.eu



cirad

EID MÉDITERRANÉE

IRD
Institut de recherche
pour le développement

poster
1.17

Recognition on independent evolutionary units within *Aedimorphus vexans* (MEIGEN, 1830) (Diptera, Culicidae)

► B. Krtinac¹, L. Francuski², D. Petric³, V. Milanov²

¹ Ekolozicija, Novi Sad, Serbia

² Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad, Serbia

³ Department of Phytomedicine and Environmental Protection, Faculty of Agriculture, University of Novi Sad, Novi Sad, Serbia

Aedimorphus vexans is a polycyclic species predominantly breeding in inundated areas such as flood-
ing of rivers and lakes with fluctuating water level, and distributed almost worldwide. The species has
secondary and public health importance as competent vector of more than 30 viruses and nematodes.
In need for a more comprehensive understanding of population structure of this species, as an integral
part of vector control programs motivated us to examine genetic diversity of populations of *Ae. vexans*
(two populations: one Nearctic - USA and two Palearctic - Serbia and Germany) through protein elec-
trophoresis. Variability of 17 allozyme loci was evaluated. Species-specific alleles at the diagnostic *Ao*,
Idh-1, *Idh-2*, *Idh-3*, *Idh-4*, *Idh-1* and *Idh-2* loci were used for identification and separation of Nearctic (USA) and
Palearctic (SER, GER) populations. The population from Serbia was the most polymorphic ($P = 35\%$)
with the highest observed heterozygosity ($H_o = 0,031$). The lowest observed heterozygosity ($H_o = 0,000$)
was obtained for Nearctic population. Wright's *F* statistics showed an *F*st values from 0,017 bet-
ween Palearctic populations to 0,754 and 0,762 between USA and GER and USA and SER, respectively.
Diagram of genetic relationships points out independent evolution of Nearctic and Palearctic popu-
lations of *Ae. vexans*. STRUCTURE statistical analysis shows structuring on two genetic clusters, which
supported population genetic results of likely presence of cryptic taxa within *Ae. vexans*.