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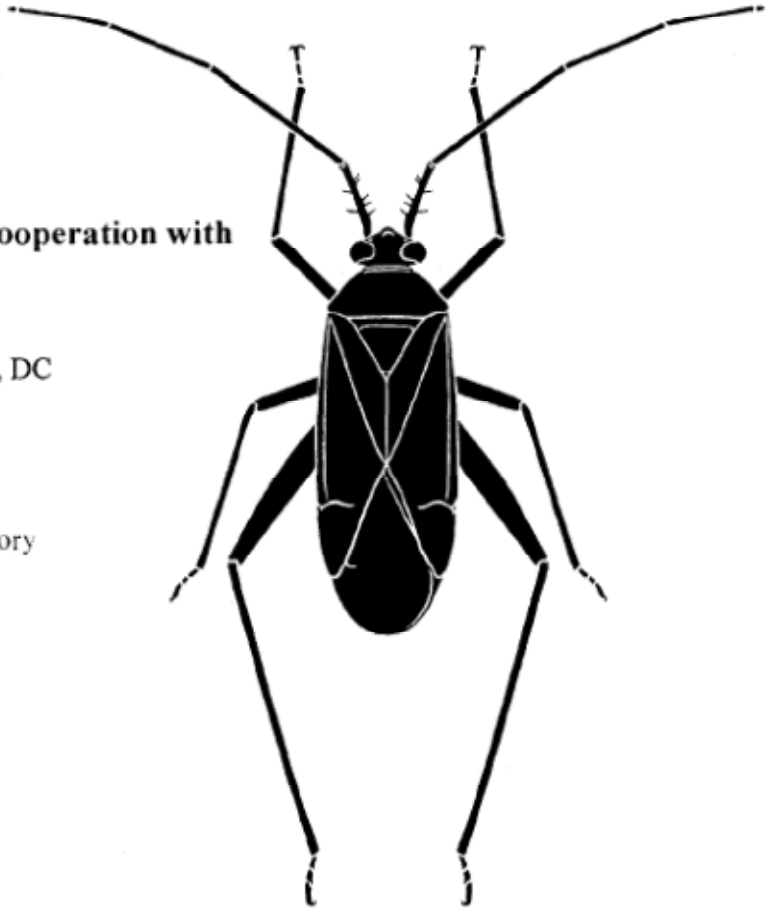
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PROCEEDINGS OF THE FIFTH QUADRENNIAL MEETING OF THE INTERNATIONAL HETEROPTERISTS' SOCIETY

National Museum of Natural History, Smithsonian Institution, Washington, DC

21-25 July 2014



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fold increase of the subfamily diversity on the island. The first Ectrichodiinae molecular dataset (COI mtDNA, 28S D2-D5 rDNA) is assembled to test generic concepts. Phylogenetic results indicate that the Malagasy Ectrichodiinae do not form a clade but consists of four distinct lineages. Subjecting the molecular dataset to divergence dating analysis reveals that Malagasy ectrichodiines diverged from Afrotropical and Oriental sister taxa after the island split from Africa (~160 mya) and India (~80-90 mya). Thus, dispersal is responsible for the endemic fauna we see today. Arrival of the Malagasy Ectrichodiinae correlate with the emergence of islands between India and Madagascar within the last 65 my, which would have facilitated long-range dispersal, whereas dispersal between Madagascar and Africa would have been facilitated by their close proximity. The results of this study will contribute to conservation efforts and our knowledge on the evolutionary history of the Malagasy biota.

Halyomorpha halys (Hemiptera, Pentatomidae): Ten Years After in Europe

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Abstract: We describe the situation of the invasion of *Halyomorpha halys* (Stal, 1855) (Hemiptera, Pentatomidae), the brown marmorated stink bug in Europe, since its discovery in Switzerland in 2007, but with effective presence since 2004. After a relative stagnation for many years, the dispersal of *H. halys* seems to increase, probably due to growing populations and passive transport by human activities. We suppose that it is not possible to stop the invasion of this species in Europe due to global warming but mostly to ecological characteristics such as high dispersal capability especially with human assistance, a broad host spectrum, a high female fecundity, and a high overwintering survival. The particularly mild winter 2013-2014 in France and Western Europe may further contribute to its progressive dispersal. It is likely that *H. halys* is already much wider distributed than previously assumed because it is easily confused with the native species, *Raphigaster nebulosa* Poda, 1761. Most recently *H. halys* was recorded from Hungary, which is nearly 1,000km east of its centre of distribution in Switzerland. In France, *H. halys* was first recorded in the Alsace in 2012, but in fall 2013 it was also discovered 400km further west in Paris and Ile de France (Essonne). The ongoing dispersal in western France will be monitored. After the first occurrence in 2012, a "citizen-science" type of survey allowed to detect many specimens of *H. halys* in different areas of Northern Italy, with a bigger nucleus centred in the territory of first detection, in the Emilia Romagna region. As this region has extended areas

cultivated with high value fruit crops, field monitoring is currently being performed to verify *H. halys* presence and damage. One of the problems of this invasion is the absence of preventive method that needs to be primarily investigated.

Evolution of the Termite Assassin Bugs: Salyavatinae and Sphaeridopinae (Hemiptera: Reduviidae)

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Abstract: Salyavatinae is a moderately diverse subfamily of Reduviidae with just over 100 described species. Many species of Salyavatinae have been documented in close association with termites and some exhibit a unique strategy of "fishing" for additional prey using carcasses of recently-predated termites. Morphology indicates that Salyavatinae may be paraphyletic; the only Neotropical genus of Salyavatinae shares several features with the small Neotropical subfamily, Sphaeridopinae, which is also suspected to feed on termites. The first molecular phylogeny of Salyavatinae is here constructed using 4 ribosomal gene loci (28S D2 region, 28S D3-D5 region, 18S, and 16S) and 2 nuclear protein-encoding genes (Wingless [Wg] and Deformed [Dfd]) from 25 species in six genera. In order to test the monophyly of Salyavatinae and the placement of Sphaeridopinae within Reduviidae, molecular data from Sphaeridopinae and two representatives from each major clade of higher Reduviidae are included in the analysis. DNA extracted from gut contents of suspected-termite feeders was run in PCR with termite-specific primers. The resulting molecular phylogeny corroborates the close relationship of these two subfamilies. Enigmatic expanded structures on the fore-tibiae of several genera of termite-specialist assassin bugs are shown to have evolved once. A BEAST dating analysis indicates that colonization of the Neotropics from this primarily old world clade could not have been due to vicariance. Analysis of gut contents provides unequivocal evidence of the specialist nature of this clade of termite predators. Finally, some notes on the tortuous taxonomy and the pending revision of this group are provided.

True Bugs (Heteroptera) of the Neotropics: The Book

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Abstract: A review of the forthcoming book on the Neotropical Heteroptera to be