The Reduviidae (Hemiptera: Heteroptera) of Ipassa Reserve (Makokou, Gabon)

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The Congo Basin forests are the world's second largest dense humid tropical forests after the Amazon. Gabon's forests are part of this extensive tropical forest. It is not considered as a hot spot like the Guinean Western African forests, but it is also under human pressure, particularly due to logging and slash-and-burn agriculture. Gabon is one of the few African countries where the forest is quite well preserved. The forest actually covers 80% of the country, and 10% of it is included in one of the thirteen protected areas. The Natural Reserve of Ipassa is one of them. It is located along Ivindo River, between Makokou and Ovan in the North-East of Gabon (around 0°30'N and 12°48' E). It is a large area (3,000 km²) of dense evergreen forest, protected since 1971. The Natural Reserve of Ipassa where created in 2002. Several surveys of entomologists were made in the past and occasional collecting was carried out also by other scientists. However, no study provides a global view or collects data to present an overview of the insect fauna of the reserve.

The aim of our work is to provide a first inventory of the species of Reduviidae (Hemiptera: Heteroptera) in a threatened area, the Ipassa Reserve in Gabon, as a first step for evaluating the value of this area. Most of the known fauna of Reduviidae of Gabon and especially from the Ipassa Reserve was recorded by André Villiers. We here assemble recent surveys, publications and collections resulting in the first overview of this fauna.

Auchenorrhyncha (Hemiptera) assemblages of loess habitat islands in Hungary

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The largest alkali habitat complex of the Danube-Tisza interfluve region belongs to the territory of the Kiskunság National Park, Hungary. The area near Miklapuszta is a mosaic complex of the patches of diverse halophytic habitats, consisting of alkaline grassland, temporary and permanent wetlands, and plateaus formed of loess. The 0.5–4 m high loess plateaus are habitat islands in a flat alkaline grassland "sea" covered with shallow water in the spring period. The vegetation of the habitat islands is a species-rich, dry, slightly salt affected pasture dominated by *Festuca pseudovina*, *Achillea setacea*, *Galium verum*, *Thymus glabrescens*, *Koeleria cristata*, *Medicago falcata*, and *Potentilla arenaria*.

Auchenorrhyncha assemblages of 19 different size loess patches were sampled by Barber and plate traps in spring, summer, and autumn. The more than 20,000 adults belonged to 71 species. Only 9% of the species were found in 85–100% of the patches, while 24% were sampled only in one patch. The correlation between species number and island size is positive (p<0.001), the isolation of assemblages living in the islands can be shown (z=0.19 or 0.21). According to the saturation model, we can find 90% of species in an island of 3,500 m^2. The degree of isolation increased dramatically over 250 meter

distance between islands. Assemblages of larger islands are more different than of smaller ones, perhaps because the common species form the Auchenorrhyncha faunas of small islands. The rate of brachypterous individuals increases with the size of islands up to 2000 m^2. As the isolation increases, the rate of brachypters decreases from 60% to 20%. In case of high degree of isolaton, the small mobility is more advantageous in the small islands.

The development status of populations living in different patches are not in syncron according to the head and thorax width of larvae of different populations. The largest differences in size distributions were between the populations of small and large islands. The populations in the large and medium-sized patches are more stable, while in the small patches the immigrants dominate.

Comparative and phylogenomic studies on the mitochondrial genomes of Pentatomomorpha (Hemiptera: Heteroptera)

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Nucleotide sequences and the gene arrangements of mitochondrial genomes are effective tools for resolving phylogenetic problems. Hemipteroid insects are known to possess highly reorganized mitochondrial genomes, but in the suborder Heteroptera (Insecta: Hemiptera) there was only one complete mitochondrial genome sequenced without gene rearrangement, and the phylogeny of infraorder Pentatomomorpha in Heteroptera is still uncertain.

Fifteen mitochondrial genomes of the suborder Heteroptera were sequenced. Gene rearrangements were found as follows: 1) *tRNA-I* and *tRNA-Q* switched positions in Aradidae, 2) *tRNA-T* and *tRNA-P* switched positions in Largidae and Pyrrhocoridae. Two recombination events were found in Alydidae and Malcidae. The other mt-genomes were organized in the same way as observed in *Drosophila yakuba*. The phylogenetic analyses of infraorder Pentatomomorpha based on the nucleotide sequence raised the hypothesis of (Aradoidea + (Pentatomoidea + (Pyrrhocoroidea + (Lygaeoidea + Coreoidea)))). The re-arrangement of *tRNA-T* and *tRNA-P* also linked Largidae and Pyrrhocoridae together. Furthermore, the conserved sequence block in the unusual intergenic spacers between *tRNA-H* and *ND4* favored the monophyly of Lygaeoidea. Tetranucleotide ATCA was inferred to be the initiation codon of *ND2* in Cydnidae. No correlation was found between the rates of nucleotide substitution and gene rearrangement. CG content was significantly correlated with the nucleotide substitution rate of each gene. For ND1, there was a positive correlation ($P<0.01$) between amino acids variations and hydrophobicity, but a negative correlation ($P<0.01$) for ND6. No conserved sequence was found among the control regions and these regions were not always the most AT-rich region of the mt-genome.

Heteropteran insects is an extremely complex group worth of further study because of the unusual tetranucleotide initiation codon and their great mt-genomic diversity, including gene rearrangements and recombinations. The mt-genome is a powerful molecular marker for resolving phylogeny at the level of the superfamily and family. Gene rearrangements were not correlated with nucleotide substitution rates. CG content variation caused the different evolutionary patterns among genes. For ND1, in many polar or nonpolar regions the specific identity of the amino acid residues might be more important than maintaining the polarity of these regions, while the opposite is true for ND6. Most sequences of the control regions did not appear to be important for regulatory functions. Finally, we suggest that the term “AT-rich regions” should not be used.