

Eigth International Meeting of the Orthopterists' Society

International Conference on Orthopteroid Insects

Montpellier, France

August 19-22, 2001

Organised by the Orthopterists'Society and CIRAD (Centre de coopération internationale en recherche agronomique pour le développement)







The representatives of some cladistic schools consider that usage of some "logical" principles (principles of parsimony and outgroup comparison) allows an objective basis for the phylogenetic reconstruction. They postulate that these principles follow from the philosophical principle of economy. But the favourite principle of parsimony is not in conformity with the logic of the economy principle as the latter principle is possible for usage only in case of the absence of any contradictory facts. We cannot reject these facts only because of their minority in comparison with the number of non-contradictory facts, but we can remove these contradictions with help of the method of analogy. The use of the analogy method inevitably leads to a certain subjective component in the phylogenetic study.

The presence of subjective (intuitive) elements in taxonomy is not a defect in taxonomical work, but it is the evidence of insufficiency of our knowledge and methodology when investigating the complex systems.

Key words: classification, phylogeny, methodology, problems.

The Most Interesting Finds of Orthopteroid Insects in the End of Twentieth Century. Poster 29

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During the 20 final years of the twentieth century, numerous very interesting finds of Polyneoptera have been made. They include the discoveries of representatives of a new high taxon (subfamily or family) of recent Ensifera, new genera of most relict recent Ensiferan groups, new genera and species of recent Orthoptera and Dictyoptera with remarkable morphological characteristics, and a series of paleontological finds including the new highest taxa, most ancient representatives of some other highest taxa, several interesting problematic and enigmatic fossils. Some of these finds clarify the difficult problems of classification and evolution of Polyneoptera (the origin of Hagloidea and Tettigonioidea, the fossil history of Grylloblattida, the peculiarities of phylogeny of main branches of Dictyoptera, and so on).

Key words: Polyneoptera, discoveries, significance.

Possible Phylogenetic Relations of Some Holarctic Acridids as Derived from Mitochondrial Ribosomal RNA Sequences. Poster 22

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The fragments of 16S mitochondrial ribosomal RNA gene of 30 species (representing 3 subfamilies of the Acrididae family) were sequenced. Standard insect mDNA primers were used for the amplification: 5'-CCGGTCTGAACTCAGATCACGT-3' and 5'-CGCCTGTTTATCAAAAACAT-3'. The PCR amplification products were sequenced by Sanger dideoxy method (Sanger et al., 1977). The sequences of 7 species of the Acrididae family and cricket (*Gryllus fultoni*) were taken from NCNI. Phylogenetic analysis was performed using a variety of different computer programs (PAUP v3.11, PHYLIP v3.57). Bootstrap replicates were generated for the maximum likelihood program using the SEQBOOT program.

The species belongs to Catantopinae s.l. (Cyrthacanthacridini, Melanoplini), Acridinae s.l. (Aulacobothrini, Hypernephiini, Arcypterini, Gomphocerini, Chrysochraontini, Dociostaurini), and Locustinae s.str. (=Oedipodinae) (Locustini, Oedipodini, Bryodemini, Sphingonotini, Arphiini).

Different methods of analysis indicated several general trends. All trees have usually two main branches. One of them includes the locustine grasshoppers. Another one unites catantopines and acridines. This result is surprising because now taxonomists prefer to decrease a taxonomic level of Locustinae in comparison with Catantopinae s.l. and Acridinae s.l.

In some cases the studied species of one genus are very similar (*Arphia*, *Eremippus*, *Stenobothrus*). However, the members of several genera are extremely different (*Celes*, *Bryodema*, *Chorthippus*). Thus, they can be divided into some separate groups. It is interesting that *Dociostaurus* and *Eremippus* belong to extremely different branches of the Acridinae-Catantopinae stem. This supports an idea about excluding *Eremippus* from the tribe Dociostaurini. Another intriguing branch unites *Euchorthippus* (Gompocerini) and two typical members of Chrysochraontini. These studies were partly supported by the Russian Federal Programs "Integration" and "Universities of Russia".

Key words: grasshopper, taxonomy, biogeography.

The Phylogeography of Rainforest Grasshoppers, a Comparison of Molecular and Morphological Markers. Poster 1

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The Eastern Arc Mountains in Tanzania are a hot spot of biodiversity in Africa. The number of endemic taxa is particularly high for flightless species, such as forest grasshoppers. The grasshopper genus Afrophlaeoba contains four species, each of which is endemic to one single mountain block. A. usambarica occurs in the East Usambara Mts., A. nguru in the Nguru Mts., A. euthynota in the Uluguru Mts. and A. longicornis in the Rubeho Mts. Those species are believed to have evolved due to separation of the forested areas in Eastern Africa during periods of drought, since they are not able to cross larger forest gaps. A phylogenetic analysis was performed to reconstruct the former connections for gene flow between them. Three mitochondrial gene fragments (ND1, ND5, 12S rRNA) have been sequenced for a phylogenetic inference of a gene tree. The most parsimonious tree proved to be very stable, as the branches are supported by high bootstrap values. The phylogenetic inference with distance methods or different weighting schemes did not influence the tree as well. A low skewness and a high proportion of transitions suggests a low homoplastic content. Within the genus the genetic distances are extremely low, especially between A. nguru and A. longicornis. This assumes a young phylogenetic origin of the species or at least a recent gene flow of the mitochondria studied. For both events a connection between the populations has to be assumed. The close relationships are also supported by a discriminant analysis of 27 morphometric characters and an examination of 52 nonmetric characters. A former or even still existing connection between the species is proposed along the river Wami and along the coastal forests, since the species seem to survive in riverine forests.