metopleures in Aculeata, has not been found in other groups. Such abrupt morphological rearrangements appear owing to reversions of plesiomorphic characters and are naturally not taken into account in formalized cladistic schemes. In particular, F. Ronquist (1999) regards Palaeocynipidae as well as Charipidae, Eucoelidae, Emarginidae and Thrasoridae as subfamilies and places them in an artificial group «Figitidae», which he placed in a separate family. However, all generations of families of archaecynipoids discovered by us in Cretaceous deposits stratigraphically precede and are an ancestral group to the superfamily Cynipoidea, the first representatives of which appeared in the Upper Cretaceous. Therefore the assumption of F. Ronquist (1999) that «Macrocynipoids ... presumably go back to the Jurassic or possibly the Late Triassic» should be regarded as erroneous. Cynipomorphs have no relations with the primitive family of proctotrupoforms. Structural plan and the role of laterally flattened body in the evolution of cynipomorphs were responsible for different scenarios in the evolution of these to infraorders. Evolution of wing in cynipomorphs has no analogies among Hymenoptera. Reduction of wing venation occurs not along but across the anterior wing margin.

PARASITOIDS OF XYLOPHAGOUS AND PHLOEOPHAGOUS INSECTS OF THE HUNGARIAN CONIFEROUS TREE SPECIES

Lakatos, Ferenc & Csaba Thuróczy (Hungary)

In Hungary besides the most important broad leaves tree species (Quercus spp., Robinia, Populus, Fagus and Carpinus) 15.1 % of forested land is covered by coniferous tree species. The three most important ones are Pinus sylvestris (9.1 %), Pinus nigra (4.2 %) and Picea abies (1.5 %). Both genus are either economically or ecologically important. In the last years the mass outbreak of different bark and wood boring insects caused enormous economic losses in these stands. In our study, made in 1998-99, through field investigations and labour experiments we assessed the phloephagus and xylophagous insect species and further the parasitoid complex on them. Twenty three study plots were chosen, P. sylvestris: 14; P. nigra: 4 and P. abies: 5. The use of felled trap trees allowed us to determine the species abundance: P. sylvestris – 34 Scolitidae, 2 Curculionidae and 5 Cerambicidae species; P. nigra – 22 Scolytidae, 2 Curculionidae and 2 Cerambicidae; P. abies – 28 Scolytidae, 1 Curculionidae and 7 Cerambicidae species were found.

High number of various parasitoid species could be determined. For example the family Pteromalidae (Chalcidoidea) were presented with 9 species (Catolaccus ater, Dinotiscus colon, D. eupterus, Heydenia pretiosa, Metacolus unifasciatus, Rhopalicus brevicornis, Rh. guttatus, Rh. tutela and Raptocerus xylophagorum). Further species of the families Eurytomidae, Mymaridae (Chalcidoidea) and Platygastridae (Proctotrupoidea) were presented.

PRELIMINARY MOLECULAR PHYLOGENY OF CRYPTINE ICHNEUMONIDAE

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The tribal classification of the large, cosmopolitan ichneumonid subfamily is widely regarded as being artificial and based on either symplesiomorphies or potentially highly homoplastic characters. I have sequenced representative taxa from throughout the subfamily, together with a number of potential outgroups, for an approximately 1000 base pair region of the cytochrome oxidase I gene. The results of parsimony analysis of this data set as well as explorations of various weighting schemes will be presented, and the implications for tribe level classification discussed.

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