

Zusammenfassungen der Vorträge

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Molecular phylogeny of the bees – preparing of methods and material for diploma thesis

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The author presents his planned phylogeny project on bees. Because this project has only been started recently, no own data can be presented yet. Project leader is Mrs. Jitka Vilímová from the Entomological Department of the Charles University, Prague.

Research is focussed on the higher phylogeny of bees, in particular on the phylogeny of the cleptoparasitic lineages within the “long-tongued bees”. In current morphological studies cleptoparasitic bees are probably the most problematic group. Due to their adaptation for a similar lifestyle, they show many reductions, convergences and apomorphic characters, which contradistinguish them from other bees; and this causes problems in cladistic morphological analyses. It is not clear yet, which group of bees is the sister group of the subfamily Nomadinae, and which is the correct position of the other nomadiform tribes (as two paraphyletic groups next to the Nomadinae). The main purpose of the study is to resolve the phylogenetical tree of this group, or rather to try to find molecular characters for support. The second purpose is to confirm the molecular phylogeny of the basal lineages of the bees – mainly short-tongued bees –, a research which is presently carried out by Mr. Danforth (Cornell University, Ithaca, New York, USA). The author will use different molecular characters. Other objectives are dependent on the availability of material which in some groups is still missing.

The molecular methods are (1) conservation of the beespecimens and isolation of their DNA; (2) choosing the gene(s) for sequencing; (3) PCR – Polymerase Chain Reaction – multiplication of the gene; and (4) sequencing reaction and sequencing by an automatic sequenator.

The best method of conservation and storing of bees for this purpose is the usage of absolute 96 - 100 % alcohol, because the DNA is kept in good condition. It is also possible to isolate DNA from dried material, killed with ethylacetate, but the DNA remains in useful condition only for a few months. The DNA is isolated from dissected flying muscles.

For research on the higher phylogeny the sequencing of conservative genes is the most appropriate method. Mitochondrial genes are not as conservative as nuclear genes, but their use is simple. For the planned research, one mitochondrial gene (Cytochrom oxydase I) and one nuclear gene (Dopa Decarboxylase), which are used in Noctuoidea (Lepidoptera) phylogeny as well, have been chosen. A second nuclear gene will be chosen later.

Using a single gene for presenting a phylogeny of bees would show the phylogeny of that single gene among bees only, and not the phylogeny of bees. Therefore it is necessary to analyse several distinct genes. Morphological data in a combined analysis can support the result.

PCR is the basic method for the sequencing of genes. This method allows multiplication of the gene for sequencing and subsequent work with pure DNA of one gene. The sequencing reaction is based on the principles of polymerase reaction as well.

Advantages of molecular characters in comparison with morphological characters are: neutral characters – characters are rarely adaptive; descriptions of character are single valued – A, C, T, G; evolving of mutations is an independent process – characters are not dependent on each other; quantity – it is usual to have 1000 characters and more; weighting of characters is more objective; comparing of far taxa or different stages (larvae with adults etc.) is possible; information about population structure in the past.

Disadvantages of molecular characters are: there is no information on important adaptive changes in molecular characters, for instance it is not possible to observe the evolving of the abdominal scopa from DNA; molecular methods are expensive and depend on the laboratory equipment; sometimes it is necessary to dissect (and destroy) the whole bee which means a loss of important skeletal information.

Anyone can do molecular work on bees regardless whether she or he has seen a bee in his life before.

Almost all important Palaearctic taxa have been collected, but material of Allodapini, Ctenoplectrini, Pararhophitini and Fideliini is still missing. It seems most difficult to get beetaxa from South America and partly from North America as well.

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Die Hummelfauna Österreichs, Stand der Datenerhebung – erste Ergebnisse

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Hummeln zählen zu jenen Insektengruppen in Mitteleuropa, über die das umfangreichste Sammlungsmaterial vorliegt. Dieses ist jedoch zumeist nur unzureichend oder überhaupt nicht aufgearbeitet. Damit wird die Chance vertan, Erkenntnisse zur Biogeografie, insbesondere zu Wanderungsbewegungen von Arten, zur Biodiversität und Parametern der Nischendifferenzierung (Höhenverbreitung, Phänologie, Blütenbesuch, ...) und zum Naturschutz zu gewinnen. Der Bestand an österreichischen Hummeln in Museen dürfte sich auf ca. 60.000 - 70.000 Individuen belaufen, davon wurden vom Verfasser bisher deutlich über 50 % erfasst. Auch sind wissenschaftliche Publikationen und graue Literatur ausgewertet

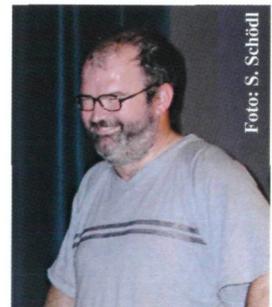


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