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Abstract-Volume

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Sexual dimorphisms impose difficulties for allocating conspecifics in many animals, such as in asellote isopods. Adult males are often characterized by pronounced morphological differences after final moult compared to females and juvenile males. These are potentially related to pre-copulatory dispersal and/or search for mating partners. In several families, females tend to show great morphological similarity, while the males bear aberrant character states. In the deep-sea isopod family Macrostylidae Hansen, 1916, for example, sexual dimorphism is regarded to be amongst the relevant explanations for why of 50 % of the described species only one sex is known. Thanks to molecular evidence, such problems can be avoided. Above that the rising awareness of sexual dimorphisms and DNA-based allocation provides the possibility to apply dimorphism-related characters in taxonomy, systematics and phylogeny. This poster presents a preliminary approach to identify, characterize and apply sexual-dimorphism based morphological information in the understudied Macrostylidae. Using "DNA barcodes" amongst other markers, extremely dimorphic sexes could be allocated. The morphological information obtained will be valuable to infer a phylogeny of the Macrostylidae.

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Not only better sampling but also better modelling [Talk]

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Most, if not all, of the sites in a sequence do not evolve according to the same pattern; this is because each residue is characterised by specific biophysical environments and different evolutionary constraints. Homogenous models of sequence evolution fail to account for this assumption and may, for example, misinterpret the non-phylogenetic signal embedded in highly saturated positions; indeed, the deeper the nodes in the phylogeny, the higher the risk of falling in such type of systematic error. An effecting way of overcoming this problem is the employment of among-site heterogeneous models of sequence evolution. Here we outline various examples of how these models, most of which belongs to the "CAT-family", have helped producing phylogenies that significantly differs to those obtained using homogenous models. Examples span from arthropods to rodents, and from large phylogenomic to mitogenomic and classical rRNA datasets. Not only heterogeneous models are clear improvement in term of fit to the datasets, but notably recover phylogenies more congruent with morphology and other sources of evidence. We also show that the use of among-site heterogeneous models also affects molecular clock estimates, which are typically older when using homogeneous models in nodes describing radiations of fast evolving species. Although both an adequate taxon and gene sampling are needed to address many phylogenetic problems, we advocate that more importance should be given to the accurate modelling of sequences rather than to massive harvesting of data, except if this allows to break long branches.

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