A new method to produce phylogenetic trees applied to the phylogeny of bumble bees (Hymenoptera: Apidae).

Following the cladistic paradigm, classification must be based on the phylogenetic relationships among taxa. Presently, all the available reconstruction methods are based on discrete characters. However, morphometric data are very useful to characterize some taxonomic groups. Numerical taxonomy has developed a powerful methodology for the processing of such continuous data. The authors propose here a new method for using morphometric measurements to obtain phylogenetic hypotheses. It leads to the integration of some numerical taxonomy tools and fundamentals of cladistics. These tools are principal component analysis, Manhattan’s distance and Neighbor-joining tree. As a test-case, we have studied the phylogenetic relationships among bumble bees (Hymenoptera: Apidae). In the unique phenogram obtained, *Psithyrus* Lepeletier are monophyletic and included in the resulting tree at the same level as subgenera of *Bombus* Latreille. It must be synonymised. The *Anodontobombus* and *Odontobombus* groups are both monophyletic, this last including *Psithyrus* at the subgeneric level. Noticeable morphological, ethological and biogeographical evidence supports the present hypothesis and the new method.