DIFFICULTIES IN USING CONTINUOUS CHARACTERS IN SPECIMEN-LEVEL OSTEOLOGICAL PHYLOGENETIC ANALYSES OF LACERTID LIZARDS

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Morphological phylogenetic analyses are mostly based on discrete characters or continuous characters that have been coded as discrete ones. However, the discretisation of a continuous character leads to a certain loss of information. Even though methods for analysing continuous character states have been developed, relatively little effort to estimate the contribution of those characters to the tree accuracy has been made until recently. In this study, we carried out specimen-level phylogenetic analyses of lacertid lizards with maximum parsimony. We sampled 34 ingroup and 4 outgroup species with up to 10 specimens scored per species. Our character matrix contained 250 characters describing osteological features only. 33 of the characters were continuous. We compared the tree topologies when treating all 250 characters as discrete, and when analysing the 33 continuous characters as such together with the 217 discrete ones. Tree accuracy was evaluated counting the number of specimens of a known biological species forming a clade. The overall tree resolution and recognition of species as clades seemed to be better for the combination of continuous and discrete characters than for discrete characters only. In addition, our results show that an increase in specimen sampling correlates with increasing tree accuracy. This is possibly due to better coverage of intraspecific variation which makes the individual variation carry less weight. However, phylogenetic relationships on higher taxonomic levels remained questionable when using continuous characters indicating that further modification is needed to have the complete analysis benefit from the extra bit of information gained from continuous characters.