

**PHYLOGENY AND MORPHOMETRIC VARIATION OF SEVERAL WEEVILS SPECIES (COLEOPTERA: CURCULIONIDAE) FROM MALAYSIA**

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**ABSTRACT**

The phylogeny of 43 species under 20 genera of seven subfamilies of weevils' species (Coleoptera: Curculionidae) from Malaysia were successfully inferred based on 34 morphological characters, of which combined the qualitative and quantitative inputs. The monophyletic clade of the Curculionidae was supported by Neighbor Joining (NJ) and Maximum Parsimony (MP) trees with bootstraps values of 79% and 76%, respectively. Although the arrangement and placement among the 19 species of Dryophthorinae were not fully resolved, however the phylogenies were able to elucidate the relationships of the other curculionids from the Curculioninae, Entiminae, Lixinae and Molytinae subfamilies. Therefore, further multivariate analyses were conducted on 17 selected species of Curculionidae, which has been successful to discriminate the examined species. From the principal component analysis (PCA; eigenvalues of PC1 for cluster 1 = 7.4650; eigenvalues of PC1 for cluster 2 = 5.1874) and canonical variate analysis (CVA; cluster 1 with  $p < 0.0001$ ; cluster 2 with  $p < 0.0001$ ), the diagnostic morphological characters were resulted from the elytron, pronotum, total length of body, and femur length. As a conclusion, the morphometrics has proven to be reliable and informative as another alternative to subfamilies classification and to show the relationships within the examined insect's species. However, it is also recommended that further studies should include more diagnostic and informative characters to represent up to the tribes or genus levels in future.

**Keywords:** Curculionidae, phylogeny, morphometrics, multivariate, weevils