Developing a benchmark invertebrate group for biodiversity modelling: phylogenetics and databasing of the dung beetle (Scarabaeidae) genus Lepanus

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Biodiversity modelling methods such as Generalised Dissimilarity Modelling (GDM) are increasingly incorporating phylogenetic as well as species distribution data to more effectively model biodiversity. Developing and testing these methods rely on the existence of benchmark groups for which the taxonomy, phylogenetic relationships and distributional databasing are complete. Few groups of Australian organisms are so well known and at present no invertebrate examples are available. A native dung beetle genus Lepanus Balthasar which consists of 24 described species and 22 undescribed provisional species seemed like an ideal candidate for biodiversity modelling due to its distribution, having both widespread species and narrow range endemics. Almost 5,500 specimens were databased, providing complete distributional records for all pinned specimens at the Australian National Insect Collection and Queensland Museum. The examination of material for databasing prompted a revision of morphological diversity in the group and lead to the recognition of a further 34 undescribed species. Lepanus species are most reliably characterised by the distinctive shape of the pygidium. Based on this as a primary character, the species can be divided up into 12 assemblages. There are variations within the groupings and some groupings are more homogeneous than others, but pygidium structure provides a hypothesis to investigate genetic relationships within the genus. Phylogenetic analysis of species with both COI and 28S sequence data was preformed on 27 Lepanus spp. (131 specimens) representing 10 of the 12 species assemblages. Species assemblages were generally well supported including monophyletic clades for species assemblages 1, 4, 5, 8 and 11. Associations between all species in assemblages 3 and 12 currently remain unsupported due to limited resolution of the tree; however clades containing multiple species in both complexes are supported. The only relationship which is supported that does not correspond to species assemblage is that of CYP3 and CYP5 (Assemblages 6 & 9), however assemblage 6 is only represented by a single specimen. Further taxon or gene sampling is likely to resolve these relationships.