Invertebrate biodiversity; comparison and identification of Tokoriro (cave weta) taxa at three locations in the North Island, New Zealand

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Eligible for student prize

New Zealand cave weta or Tokoriro, are diverse. Understanding the full diversity and taxonomy of this family has been hampered by problems including synonyms, poor descriptions, lack of diagnostic characters, sexual dimorphism, poor characterization of juvenile stage, under sampling and a general deficiency in our knowledge of cave weta ecology. Our recent work using high density sampling has confirmed high levels of sympatric diversity among Tokoriro living in North Island forest systems. We routinely find 5-10 taxa per site. It is therefore not surprising that historically, attempts to describe this biodiversity have faltered when sampling has consisted of one or few individuals per location. We examined Tokoriro from three locations, Taranaki, Manawatu and Hawke's Bay. We started with two simplistic hypothesis: 1) Each taxon (judged by morpho-type and DNA) is unique to each of the three locations, 2) taxa are shared across all three locations. This approach helps in understanding how visible characters such as spine morphology and sub-genital plate shape of each specimen informs diagnosis of taxa and diversity. Comparison of DNA sequence data enabled us to match males with females and assess the relative difference between similar and dissimilar morphs. What we find is, not surprisingly, a mix of the two hypothesis where some morphological identical species are shared in two or more locations and some morphological species are unique to a location in the current sampling. DNA sequencing shows us how the different morphological units are related and whether the morphological characters are reliable as a tool for species diagnosis. This work supported by a scholarship from MSI supports a related TFBIS project to develop online weta identification and recording tools.