

Of lice and Men(*acanthus*): supercoloniser or host-race complex?

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Menacanthus eurysternus (Burmeister, 1838), is the most widely distributed louse species being found on at least 176 host species throughout the Passeriformes. The cosmopolitan nature of *M. eurysternus* is all the more interesting given that mean number of host species sharing louse species for passerines is 1.9. *Menacanthus* species are not generally widespread with most species found on only a few host species. *M. eurysternus*, therefore, represents an interesting anomaly amongst lice. There are several hypotheses that may account for the pattern observed. *M. eurysternus* may represent: [1] a true multi-host species that has exploited an as yet unknown mechanism to move easily between different host species at a level that maintains high levels of gene-flow; [2] a species that was found on a group of European passerines, e.g. blackbirds, sparrows and starlings, which have been extensively introduced around the world and from which endemic passerine species have been recently colonised; [3] a morphologically conservative group which forms a cryptic species complex, e.g. '*M. eurysternus*' from some hosts in a given area may be genetically distinct from lice of other hosts or areas. We have collected *M. eurysternus* samples from New Zealand, Australia and England and from several common species of passerines. We have examined molecular markers (COI and EF1alpha) and they imply a complex level of genetic variation that suggests hidden diversity among the lice and some structures that match the phylogeny of host species.

