



Characterising the invasive *Lantana camara* complex using a population genomic approach.

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The *Lantana camara* species complex is one of the world's worst weeds, with serious economic and environmental impacts globally. The management of invasive lantana is hindered by its complicated taxonomy and wide range of morphological variation. Biological control efforts spanning over a century have yielded limited success in Australia, in part due to the diverse nature of the complex, with several agents failing to establish on some or all lantana varieties present. There is a clear need to characterise the variation within invasive lantana and to unravel the genetic and biogeographic patterns which underlie it. Using geographically extensive sampling and trait data combined with genome-wide marker sequencing, this study reveals unprecedented insight into the genetic composition and ancestry of invasive lantana. Several highly divergent lineages are present across Australia, New Zealand, South Africa, and Hawaii, consistent with the notion that the complex comprises multiple species and their hybrids. The results from this study can inform a worldwide taxonomic treatment of *Lantana camara sensu lato*, with accurate identification of invasive populations expected to enable better management.

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