

Assessing the invasive potential of different source populations of ragweed (*Ambrosia artemisiifolia* L.) through genomically-informed species distribution modelling

Andhika Putra¹, Kathryn Hodgins², and ALEXANDRE FOURNIER-LEVEL¹

¹The University of Melbourne

²Monash University

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Abstract

The genetic composition of founding populations plays a key role in determining invasion success. Despite this fact, the role of genetic variation on the potential distribution of invaders has rarely been investigated. Here, we integrate genomic data into ecological niche models (ENMs) to predict the distribution of globally invasive common ragweed (*Ambrosia artemisiifolia*) to Australia. We identified three genetic clusters of ragweed and used these clusters to construct separate ENMs. The predicted distribution of ragweed in Australia changed depending on the genetic composition and continent of origin of the source population. By quantifying this change, we identified source populations most likely to expand the ragweed distribution. As prevention remains the most effective method of invasive species management, our work provides a valuable way of ranking the threat posed by different populations to better inform management decisions.

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