

The utility of molecular marker approaches to understanding plant invasions

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Summary Genetic characterisation of plant populations can increase our underlying knowledge of species evolutionary histories and present day movement patterns within and across landscapes. Such information provides insights to traits which may increase invasiveness as well as providing background information applicable to opportunities for biological control. We know that alien or weedy species impact the composition, function, and structure of native plant populations in numerous ways including disruption of mutualisms, alteration of microsite conditions and shifts in species compositions. By combining data from field-based control and/or eradication efforts of invasive plant species with potential insights that can be gained by applying molecular marker approaches, we can improve our understanding both of weed spread across the landscape and of the dispersal processes that give rise to the patterns of recruitment we observe. We discuss insights that may be gained from molecular markers in the context of invasive plant species.

It is generally presumed that increased genetic diversity promotes invasion success (Kolbe *et al.* 2004), although there are few tests of this in the tropical plant literature. Within the last decade researchers have increasingly applied molecular approaches to address questions about patterns and processes that drive species invasions with a goal of increasing our success at managing, eradicating and controlling invasions. Due to short times since introduction for many plant species, however, some molecular approaches may be more or less appropriate given the biology and evolutionary history of the target species in question and their underlying genetic diversity. For recently introduced species, sufficient genetic variation may or may not be present to understand exact movement pathways, even if the general pattern of invasion or the site of origin is discernible. This is especially the case in instances of single introductions when genetic diversity is reduced and/or a population bottleneck may be expected to occur.

For direct management application, the straightforward benefit of molecular markers is the opportunity to potentially determine the site of origin, to provide information as to whether single or multiple

introductions have occurred, and to understand whether hybridisation or other genetic changes which may increase the possibility of invasion success have occurred. Genetic approaches also can inform us about net movement pathways as seeds are dispersed through landscapes. Specifically, we can use molecular markers to directly match parents and offspring, to identify genetic variability within and among populations, and to detect levels of outcrossing and inbreeding.

In instances where morphological traits cannot clearly elucidate taxonomic relationships, a phylogenetic approach can aid understanding of plant species relatedness which may in turn provide insight to the evolution of host choice for control agents and/or to the most likely region of origin. Identifying site(s) of origin as revealed through intraspecific genetic variation can be particularly important if the goal is to identify potential host-specific enemies for biological control. Phylogenetic approaches may also be useful for teasing apart cases of cryptic speciation. Whether managers are targeting a single species or a species complex can have impacts for on the ground control or eradication efforts, particularly if there is species-specific variability in phenology/timing of reproduction.

Overall, combined ground-based and molecular approaches can underpin management efficiency by improving our understanding of the underlying processes that drive plant invasions, as well as by potentially detecting the source and number of invasion events. Choosing the appropriate marker system is critical and hinges upon clear research and management questions and ascertaining which tool is most appropriate.

Keywords Genetic diversity, molecular markers, phylogenetic analysis, rain forest invasion.

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REFERENCE

Kolbe, J.J., Glor, E.E., Schettino, L.R., Lara, A.C., Larson, A. and Losos, J.B. (2004). Genetic variation increases during biological invasion by a Cuban lizard. *Nature* 431, 177-81.