

Inferring the Origins, Evolution, and Spread of Weed Populations using Molecular Tools

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Population genetic studies using molecular tools can provide information on the origins, evolution, and spread of weeds, and contribute to the design of effective weed management programs. Multiple approaches are currently available, including traditional population-based methods that estimate genetic diversity within populations and assess genetic differentiation and relationships among predefined populations. Newer individual-based Bayesian clustering analyses, such as STRUCTURE and INSTRUCT, use multilocus genotype data to infer population structure and assign individuals to populations. Further analyses allow the testing of competing hypotheses concerning historical or invasion scenarios and the numbers of independent evolutionary events or introductions. Application of these approaches to advance understanding of the processes underlying the introduction, evolution and spread of agricultural weeds and invasive plants in California will be discussed.