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Genetic diversity of the leafy spurge chloroplast genome

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DNA markers from the chloroplast genome of leafy spurge have been used to assess the amount of genetic variation within leafy spurge populations in North America. DNA samples from 124 individuals in five North American populations were analyzed. Mung bean chloroplast DNA probes were used to detect restriction fragment length polymorphisms from EcoRI, EcoRV, and HindIII digests of the DNA. Genotypes were determined by scoring individuals for the presence or absence of each restriction fragment. Twenty-two chloroplast genotypes were identified among the samples. Three of these genotypes included 68% of the individuals and could be used to distinguish four out of the five populations. One population did not have a predominant genotype, but was a mix of several types. Band difference and principle component analysis were used to describe the degree of difference between each genotype. This study indicates that large sample sizes are required to adequately describe the genetic makeup of leafy spurge populations, and that it is possible to distinguish genetically different populations. Correct assessment of the amount of genetic variability in a population of leafy spurge may be an important factor in the development of an effective biocontrol strategy.