

EVALUATING COMMON DANDELION POPULATION DIVERSITY USING RAPD MARKERS.
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The increased adoption of no-tillage cropping practices has contributed to the widespread occurrence of common dandelion (*Taraxacum officinale*) in Michigan and the Midwest. Inconsistent control of common dandelion with common postemergence herbicides has been observed and has led to the hypothesis that distinct biotypes of common dandelion exist and respond differently to herbicides. To evaluate common dandelion genetic diversity, mature seeds were collected from selected field populations in Michigan and several other states. Individual plants were selected from field populations to represent the population. Common dandelion plants were established in the greenhouse and transplanted to a field nursery.

Genomic DNA was extracted from the youngest leaf tissue and screened with 10 base pair RAPD primers. Polymorphic fragments were scored as either present (+) or absent (-). Only those fragments which were repeatable and intensely amplified were scored. Genetic distances between biotypes were determined using Nei's distance formula. Dendograms were created using the unweighted pair group method with arithmetic averages (UPGMA) cluster analysis. Genetic distance calculations and dendograms were made using NTSYSpc version 2.11L software. The amount of diversity observed from the RAPD analysis indicated that common dandelion is highly variable and the genetic distance and geographical distance between biotypes did not appear to be highly correlated.