

UNDERSTANDING THE *CHENOPODIUM* COMPLEX USING DNA-BASED MARKERS.  
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The genus *Chenopodium* is a complex group as it includes several species that have considerable genetic and morphological variation, sometimes even within the species as is the case of *C. album*, known as common lambsquarters. Several species of *Chenopodium* (e.g. *C. album*, *C. berlandieri* and *C. bushianum*) resemble each other due to similar morphology. There have been several reports suggesting populations of common lambsquarters are not being controlled by commercial herbicides. A question that arises is whether these are really populations of *C. album*, or if they may be some other *Chenopodium* species. Thus, a study was initiated to identify the prevalent *Chenopodium* species found in the North Central States. *Chenopodium* species were obtained from the North Central Regional Plant Introduction Station, Ames, IA. These species were utilized as a test case to determine if they could be differentiated based on DNA sequence of the internal transcribed spacer (ITS) region of the ribosomal DNA (rDNA). ITS sequence data are commonly used for plant phylogeny studies. Hierarchical clustering of 18 plants of 12 species, based on ITS sequence data, grouped *Chenopodium* species into four main clusters. Each cluster had more than two species and in one case a species was grouped in two different clusters. To aid in species identification, we will further develop markers for the ITS region based on restriction site polymorphisms. These markers may be used to help distinguish among the weedy *Chenopodium* species; however additional molecular markers likely will also be needed for positive *Chenopodium* species identification.