

PHYLOGENETIC ANALYSIS OF THE CHENOPODIUM COMPLEX. Sukhvinder Singh, Patrick J. Tranel, and A. Lane Rayburn, Graduate Research Assistant, Professor, and Professor, Department of Crop Sciences, University of Illinois, Urbana, IL 61801.

A key step to efficient weed management is to correctly identify the weed species. Researchers have tried to systematically investigate common weed species, which has helped in proper weed identification and management. The *Chenopodium* genus is not a well-understood complex as there is considerable genetic and morphological variation within the species. The taxonomy of *Chenopodium* has been a major point of controversy, which mainly arises due to the phenotypic plasticity, parallel evolution, and hybridization within the genus. We used a phylogenetic approach to understand this complex genus, which includes some of the worst weeds of the Midwest. Our previous research indicated that some of the common weed species in *Chenopodium* not only have a close resemblance at the morphological level, but also at the level of DNA sequence. For example, *C. album*, *C. strictum*, and *C. berlandieri* accessions could not be consistently distinguished using sequence data from the internal transcribed spacer region of ribosomal DNA: these species were grouped within a common clade in the phylogenetic tree. In an effort to further resolve the phylogenetic tree, we used a cytogenetic approach. Our results from DNA content analysis suggest that *C. berlandieri* and *C. album* have significantly different genome sizes. Additionally, *C. strictum* has half the genome size of *C. album*. Thus, even though *C. strictum*, *C. berlandieri* and *C. album* share highly similar sequences among homologous genes, they can be differentiated based on genome size. These differences may be partially attributed to differences in ploidy levels, which currently is under further investigation.