

ALLOZYME VARIATION AND POPULATION GENETIC STRUCTURE OF NEW WORLD AND OLD WORLD POPULATIONS OF JOHNSONGRASS, *SORGHUM HALEPENSE*, Paul E. Arriola and Lesley Blancas, Department of Biology, Elmhurst College, 190 Prospect Ave., Elmhurst, IL 60126-3296 and Department of Botany and Plant Sciences, University of California, Riverside, Riverside, CA 92521-0124

It has been suggested that analysis of genetic variation and the population genetic structure of widespread weedy plant groups can provide insight into their evolutionary dynamics and reasons for success. Allozyme diversity in johnsongrass, *Sorghum halepense*, one of the World's most noxious and successful weed species, is surveyed over 46 populations and accessions collected from North America, Central America, northern Africa, India and the Near East. The relative genetic diversity of johnsongrass was low when compared to plants which share many of the same life history characters, with the mean fraction of polymorphic loci in the populations and accessions surveyed at about 23%. The allozyme variation existing in johnsongrass was evaluated using *F*-statistics and *Structure* and was determined to be partitioned within and among populations, but some patterns were apparent. New World populations of johnsongrass tend to have higher genetic identities with other New World populations than with Old World populations. We present evidence that evolutionary and genetic factors which could be affecting the genetic variation and population structure include founder events, polyploidy, genetic drift, and perhaps most significantly gene flow from crop relatives.