WATERHEMP GENOMICS FOR HERBICIDE RESISTANCE RESEARCH. Chance W. Riggins, Patrick J. Tranel, Yanhui Peng, and C. Neal Stewart Jr., Postdoctoral Research Associate and Professor, Department of Crop Sciences, University of Illinois, Urbana, IL 61801, Postdoctoral Research Associate and Professor, Department of Plant Sciences, University of Tennessee, Knoxville, TN 37996.

Genomic resources for waterhemp have been expanded as a result of Roche 454 pyrosequencing technology. Whole genome and transcriptome pyrosequencing produced 158,015 (43 Mbp) and 483,225 (114.8 Mbp) raw reads, respectively, which have enabled us to develop new marker-based assays to address important questions related to the genetics, molecular mechanisms, and spread of herbicide resistance in waterhemp. For example, of the 44,469 assembled transcriptome reads (contigs + singletons), forty-nine percent displayed highly significant similarities to *Arabidopsis* proteins and were subsequently grouped into gene ontology categories. These initial hits combined with further BLAST searches against custom databases have helped us identify and obtain preliminary sequence data for all of the major target-site genes for which waterhemp has documented resistance. Moreover, sequence data for two other targets where resistance has not yet been reported in any plant were also investigated in waterhemp and six related weedy *Amaranthus* species. These preliminary experimental results demonstrate the enormous value of 454 sequencing for gene discovery and mutation detection in a major weed species and its relatives. Additional examples of current and potential applications of this valuable resource are also highlighted.

2009 North Central Weed Science Society Proceedings 64:39.