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Genetic Mapping of Monoecy and Dioecy in *Amaranthus*

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Amaranthus is a genus of 75 species that display diverse mating strategies. Cultivar species (e.g. *A. hypochondriacus*) are monoecious and weedy species (e.g. *A. palmeri*) are dioecious. These mating strategies are influenced by genes that control the expression of sex determination and floral morphology. Sex-determining loci are highly conserved across species and often the first of genes to be mapped when constructing linkage maps of species. Here I will perform a genome-wide association studies (GWAS) to identify candidate loci of sex determination in monoecious and dioecious species of *Amaranthus*. The monoecious species studied include *A. hypochondriacus*, *A. caudatus*, *A. cruentus*, and *A. retroflexus*. The dioecious species studied include *A. palmeri*, *A. tuberculatus*, *A. arenicola* and *A. cannabinus*. The experiment includes growing, sampling, and sequencing the genome of 800 (400 monoecious and 400 dioecious) individuals of *Amaranthus*. I will perform whole-genome sequencing at 1x coverage of all individuals then use a k-mer based bioinformatic approach to identify sex determination sequences. Assays will be compared across all individuals to confirm the conservation of the identified sex-specific markers. Monoecious species of *Amaranthus* are economically important cereal crops of interest to plant breeders for its rich nutritional content and resilience to arid environments. Dioecious *Amaranthus* species are aggressive weeds with successful outcrossing and adoption of herbicide resistance that is of interest to farmers. There is a hazard for selective breeding and genome editing in grain amaranths because of their potential to interbreed with wild-dioecious relatives, many of which are major yield-affecting agricultural weeds. Thus, hybridization of monoecious and dioecious species pose a threat to both breeders and farmers. Identification of sex sequences in *Amaranthus* provides foundational information to bioengineer sex-selective populations and understand the evolution of monoecy and dioecy in this genus.