Characterizing the Expression of Candidate Genes for Herbicide Resistance in the Agricultural Weed Hairy Fleabane (*Erigeron bonariensis*). Priyanka Chaudhari*[1], Diana Camarena[2], and Katherine Waselkov[2].[1] Biotechnology Department, California State University, Fresno, CA, USA, [2] Plant Physiology Department, California State University, Fresno, CA, USA, [2] Biology Department, California State University, Fresno, CA, USA.[*2] Diana Camarena (sweetdc@mail.fresnostate.edu), [*2] Katherine Waselkov (kwaselkov@csufresno.edu)

Herbicide resistance is the heritable ability of weeds to survive and reproduce in the presence of herbicide doses that are lethal to the wild type of the species. *Erigeron bonariensis* is an agricultural weed that infests orchards and crop fields in California's Central Valley, and has become resistant to the herbicide chemical glyphosate (RoundUp®), through an unknown genetic mechanism. One mechanism of glyphosate resistance demonstrated in *E. canadensis*, a close relative of *E. bonariensis*, is non-target site reduced translocation of the herbicide, in which vacuolar sequestration prevents the chemical from spreading around the plant. Resistance of *Erigeron canadensis* to glyphosate is believed to involve upregulation of the target gene *EPSPS* in combination with the ABC transporter genes *M10* and *M11*. This study aims to determining through quantitative PCR (qPCR) and RNA-Seq if these genes provide the mechanism for glyphosate resistance in wild populations of *Erigeron bonariensis*, and/or if there are other genes responsible for the observed glyphosate resistance. Sample leaves of the weed were collected before and after glyphosate spraying in plants from 10 different populations wild-collected from the Central Valley and two control populations of *Erigeron bonariensis*. Response to glyphosate was used to characterize percent resistance for each wild-collected population. RNA was extracted from the leaves of glyphosate-treated and untreated individuals, and used for cDNA synthesis. Quantitative PCR primers were designed for the *E. bonariensis* orthologues of the *E. canadensis* genes *EPSPS*, ABC *M10*, and ABC *M11*, and pre- and post-spraying expression levels of each gene (relative to the housekeeping gene actin) are currently being analyzed through qPCR. This experiment will establish whether the same candidate genes are involved in the glyphosate resistance response in *E. bonariensis* compared to its relative, and among *E. bonariensis* populations. Future RNA-Seq analysis via Illumina HiSeq may reveal other genes that are differentially up- or down-regulated in resistant populations of *E. bonariensis* after glyphosate exposure. Determination of the genetic basis of herbicide resistance will provide fundamental data about parallel evolution in response to strong selection pressures, and help suggest alternative mechanisms for field control of this weed.