

An integrated approach to use genetic resources for resurrection plants to enhance drought tolerance in breeding-extension programs

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The ultimate goals of this project are to gain a basic understanding of the unique gene and gene regulatory networks that are necessary and sufficient for vegetative tissues to withstand dehydration and then rapidly recover upon rehydration and to use the knowledge gained to develop crops, maize and forage grasses that maintain biomass production under drought condition. Our approach is to combine comparative genomics and phylogenetics to identify genes and gene networks that are adaptive and central to the tolerance of cellular dehydration. This involves the use of resurrection species as models for dehydration tolerance coupled with a suite of comparative bioinformatic tools that allows for the phylogenetic assessment of gene expression patterns in response to dehydration and rehydration. Once the key genetic elements have been identified and assessed we will use a transgenic functional assessment of their involvement in the phenotype, both at a molecular and physiological level, of drought tolerance. One of our key resurrection species is the South African grass *Sporobolus stapfianus*, which is capable of surviving -240 MPa of water deficit (a hundred times lower than most crop plants). This plant not only serves as a model for monocot crops such as maize and switchgrass, our major targets for crop improvement, but also serves as a direct possibility for an alternate forage grass and biomass source. The improvement of biomass production under drought conditions is not only important for sustainable biofuel production but also for food and energy security. Funded by a CSREES-NRI Grant of \$450,000 over three years to PI Mel Oliver USDA-ARS-PGRU Columbia, CoPIs Robert Sharp, University of Missouri; John Cushman, University of Nevada, Reno; Paxton Payton, USDA-ARS-PSRU Lubbock.