

PRODUCTION AND TESTING OF TRANSGENIC COTTON THAT EXPRESSES TRANSCRIPTION FACTORS FOR ENHANCED SEED TRAITS AND PRODUCTIVITY UNDER DROUGHT STRESS**Aman Mittal****Qingjun Luo****Dept. Biological Sciences****Lubbock, TX****Craig Bednarz****Texas Tech University****Lubbock, TX****John J. Burke****USDA-ARS****Lubbock, TX****Chris Rock****Dept. Biological Sciences****Lubbock, TX****Abstract**

Abscissic acid (ABA) is a plant hormone involved in abiotic and biotic stress adaptation and seed development. We have previously shown that Basic3 (B3) domain-containing and basic leucine zipper (b-ZIP) transcription factors from the model plant species *Arabidopsis thaliana* can transactivate monocot and dicot gene promoters containing ABA response elements (ABREs) and some of these effectors can synergize as positive effectors of ABA responses. We have shown that the re-generable line Coker 312 responds to ABA in a dose-dependent manner for inhibition of seed germination. Preliminary data suggests exogenous ABA treatment of leaves, similar to drought stress, results in altered carbon metabolism manifest as relatively higher chlorophyll fluorescence yields under respiratory demand in the dark (measured by metabolic fitness bioassay). It is hypothesized that stress- and ABA-mediated photosynthetic adaptation protects sink tissues such as developing bolls and meristems from stress-induced growth cessation. We have generated transgenic cotton and *Arabidopsis* plants over-expressing *Arabidopsis* B3 domain effectors RELATED TO ABA-INSENSITIVE3/VIVIPAROUS1 (RAV1, RAV2, RAV2-Like) and b-ZIPs ABA-INSENSITIVE5 and ABRE-BINDING FACTOR1 (ABF1) and are in process of crossing these lines together to test for effector synergy. It is hypothesized that these ABA effectors can render transgenic crops, including cotton, metabolically fit in terms of yields, reduced transpiration under drought stress, with improved water use efficiencies and value-added seed qualities. Results of physiological and molecular studies on green house-grown transgenic cotton and *Arabidopsis* lines over-expressing RAV and bZIP transcription factors will be presented.