PRODUCTION AND TESTING OF TRANSGENIC COTTON THAT EXPRESSES TRANSCRIPTION FACTORS FOR ENHANCED SEED AND FIBER TRAITS AND PRODUCTIVITY UNDER DROUGHT STRESS

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Abstract

Abscisic acid (ABA) is a plant hormone involved in abiotic and biotic stress adaptation and seed development. We have previously shown that Basic3 (B3) domain and basic leucine zipper (b-ZIP) transcription factors from the model plant species maize and *Arabidopsis thaliana* can transactivate monocot and dicot gene promoters containing ABA response elements (ABREs) and some of these transcription factors can synergize as positive effectors of ABA responses. We have shown that the re-generable line Coker 312 responds to ABA, NaCl and the non-penetrating osmolyte mannitol in a dose-dependent manner for inhibition of seed germination and root growth. We are assessing the effect of applied drought and ABA on fiber quality of Coker 312 in the field. We have generated transgenic cotton over-expressing Arabidopsis B3 domain transcription factors ***R***ELATED TO ***A***BA-INSENSITIVE3/***V***IVIPAROUS1 (RAV1, RAV2, RAV2-Like) and b-ZIP transcription factor ABA-INSENSITIVE5, which have enhanced vegetative growth phenotypes of increased leaf area, photosynthetic parameters, and internode length. In the future we will cross these lines together and test for synergy. Our data demonstrate that under greenhouse conditions, ABI5-, RAV1- and RAV2-Like transgenic cotton have significantly longer fibers, whereas RAV2 lines have increased seed size. It is hypothesized that stress- and ABA-mediated photosynthetic adaptation protects sink tissues such as developing bolls and meristems from stress-induced growth cessation and 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 and fiber qualities. Coker lint and seed qualities in the field in response to drought- and ABA-treatments, and physiological and molecular characterization of transgenic cotton over-expressing RAV and bZIP transcription factors will be presented.