

Public Abstract

First Name:Huong

Middle Name:Nguyen Thanh

Last Name:Tran

Adviser's First Name:Henry

Adviser's Last Name:Nguyen

Co-Adviser's First Name:

Co-Adviser's Last Name:

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Title:HIGH THROUGHPUT PROFILING OF TRANSCRIPTION FACTORS INVOLVED IN SOYBEAN ROOT GROWTH UNDER WATER DEFICIT

Drought is the major abiotic stress factor limiting crop productivity worldwide. Plant root and shoot systems respond to environmental changes by altering the expression of complex gene networks through sensing environmental stresses and modifying signaling and metabolic pathways. Previous work (Yamaguchi et al., 2009) showed that the soybean primary root adapts to low water potential (-1.6 MPa) by maintaining longitudinal expansion in the apical 4 mm (region 1), whereas in the adjacent 4 mm (region 2), longitudinal expansion reaches a maximum in well-watered roots but is progressively inhibited at low water potential. To identify the key transcription factors (TFs) that determine these responses to low water potential, we have conducted high-throughput profiling of root-related TF expression in regions 1 and 2 of water-stressed and well-watered roots using quantitative real-time PCR. 186 root- and stress-related TFs were selected to identify their specific expression patterns in root regions 1 and 2 of well-watered and water-stressed soybean seedlings at four time points (5h, 12h, 24h, and 48h) after transplanting. Several stress-specific and root-region-specific transcripts were identified which may contribute to root responses to water deficits. Among these were zinc-finger protein, MYB-related protein, GmNAC3, GmNAC4, and bZIP transcription factors. These TFs were differentially expressed in distinct root regions, and therefore they can be targeted for functional characterization and further genetic engineering for enhanced drought resistance in soybean.