

Abstract

Abstract Stem cell niches are microenvironments in which stem cell maintenance and growth are dynamically regulated. Arabidopsis shoot stem cell niche is established early during embryogenesis and maintained throughout the life of a plant. Genetic studies have revealed the role of WUCHEL (WUS), a homeodomain transcription factor, in stem cell specification. Though, WUS is expressed in the organizing center (OC) but WUS protein after being synthesized moves in the cells of the central zone (CZ) and peripheral zone (PZ) to regulate the stem cell homeostasis. To understand the role of WUS mediated gene networks in stem cell specification, we analysed microarray data from an experiment where transnationally fused WUS-glucocorticoid receptor (GR) transgenic plant lines were used to activate WUS conditionally. Plant shoot apices were treated with dexamethasone (DEX) for 4 and 6 hours, respectively and were harvested for RNA isolation followed with microarray experiments. We identified hundreds differentially expressed gene in response to WUS. When WUS responses were superimposed on the shoot cell type-specific genomics data, we found a strong correlation of WUS-responsive transcriptome with the stem cell niche enriched transcriptome. We found that WUS regulates WKRY2, a WRKY family transcription factor. We further analysed WRKY2 to understand its role in shoot stem cell specification.