ABSTRACT

The shoot apical meristems (SAMs) consist of a small population of stem cells surrounded by proliferating cells that differentiate into distinct cell types to generate aerial parts of the plant. The specification of these cell-types and fates involves complex gene regulatory networks that are primarily regulated by transcription factors (TFs). Despite four decades of intensive genetic research, our understanding of transcriptional gene networks remains poor and deciphering them is vital for understating SAM development in plants. In this study, I identified the TFs that are enriched in stem cells and surrounding cell types and generated a high-resolution protein-protein interaction (PPI) map using high throughput yeast- two-hybrid (Y2H) assay. I checked more than 3000 interactions among 71 TFs enriched in the shoot apical meristem. I found 413 positive interactions, which are supported both by co-expression and co-occurrence, allowing me to produce a highly robust and reproducible protein interaction map of cell-type enriched TFs. I also tried to dissect the genetic roles of these TFs in plant development by looking at the knockout and overexpression. I found out that the plants overexpressing the previously uncharacterized gene AT4G16610 exhibit dwarfism along with petite flowers, showing abnormalities in most floral organs. The carpels had a tendency to protrude out from developing buds and resembled the shape of a “whirligig,” and hence, I gave the name WHIRLIGIG to this locus. Based on the PPI network, I identified AtMYB4 as a hub. It is known as one of the key regulators of anthocyanin production during UV-B stress, and it is enriched in the epidermal layer of SAM. A screen conducted on the SAM epidermal cell-type enriched TF mutants revealed the role of DEWAX in UV-B tolerance. The dewax mutants were highly tolerant to UV-B stress while the plants overexpressing DEWAX showed enhanced sensitivity to UV-B stress and exhibited 100% mortality. I found that DEWAX negatively regulates the biosynthesis of anthocyanins, which quench free radicals generated upon UV-B exposure. In day time HY5 negatively regulates DEWAX to prevent UV-B mediated damage to the cells. This finding is also supported by natural variation studies undertaken in different accessions of Arabidopsis. Arabidopsis natural variants having high DEWAX transcript levels succumb to UV-B stress more rapidly than those which have low DEWAX. Taken together, I found the role of DEWAX in UV-B stress tolerance and established that high levels of DEWAX repress anthocyanin biosynthesis..