**Identifying the function of sorghum’s drought tolerance stay-green QTL**

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The goal of this research is to understand the function of allelic variation of genes underpinning the stay-green drought adaptation trait in sorghum in order to enhance yield in water-limited environments. Stay-green, a delayed leaf senescence phenotype in sorghum, is primarily an emergent consequence of the improved balance between the supply and demand of water. Positional and functional fine-mapping of candidate genes associated with stay-green in sorghum is the focus of an international research partnership between Australian (UQ/DAFFQ) and US (Texas A&M University) scientists. Stay-green was initially mapped to four chromosomal regions (*Stg1*, *Stg2*, *Stg3*, and *Stg4*) by a number of research groups in the US and Australia. Physiological dissection of near-isolines containing single introgressions of *Stg* QTL (*Stg1-4*) indicate that these QTL reduce water demand before flowering by constricting the size of the canopy, thereby increasing water availability during grain filling and, ultimately, grain yield. *Stg* and root angle QTL are also co-located and, together with crop water use data, suggest the role of roots in the stay-green phenomenon. Candidate genes have been identified in *Stg1-4*, including genes from the PIN family of auxin efflux carriers in *Stg1* and *Stg2*, with 10 of 11 PIN genes in sorghum co-locating with *Stg* QTL. Modified gene expression in some of these PIN candidates in the stay-green compared with the senescent types has been found in preliminary RNA expression profiling studies. Further proof-of-function studies are underway, including comparative genomics, SNP analysis to assess diversity at candidate genes, reverse genetics and transformation.