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Paul, M. J., Watson, A. and Griffiths, C. A. 2020. Trehalose 6-phosphate signalling and impact on crop yield. *Biochemical Society Transactions*.
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Wheat

Grain size
and number

Recovery
from
drought

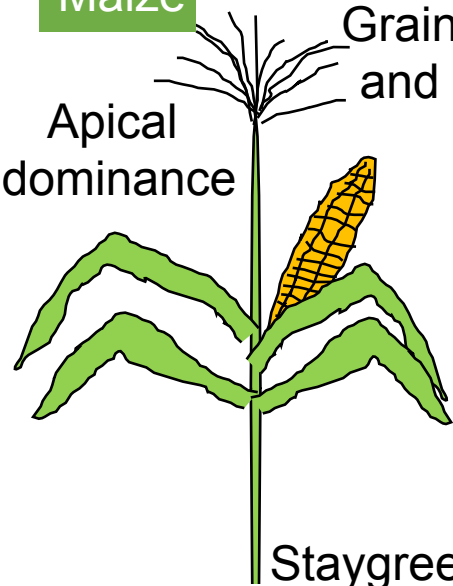
Height
Biomass



Maize

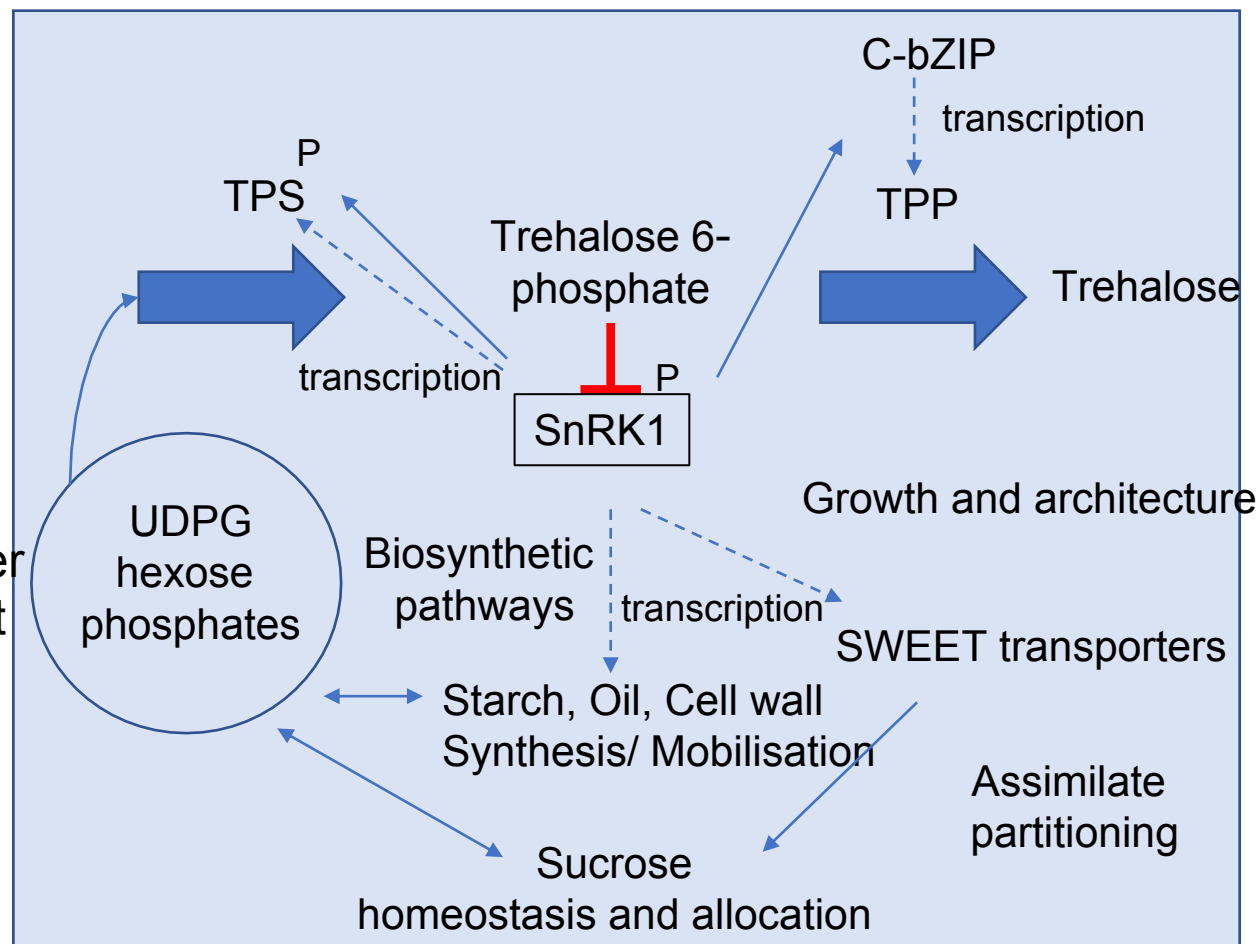
Grain number
and drought

Apical
dominance



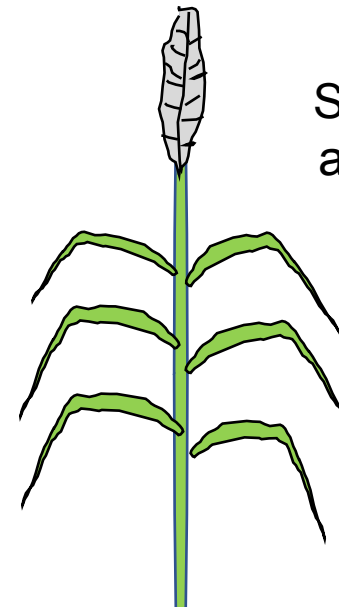
Staygreen
and photosynthesis

**A unifying mechanism for the regulation of resource allocation,
assimilate partitioning and crop yield traits by T6P**



Sorghum

Height
Stem sucrose
accumulation
Assimilate
partitioning



Rice

Anaerobic germination
Salt and drought tolerance



SWEET SORGHUM GRAIN SORGHUM

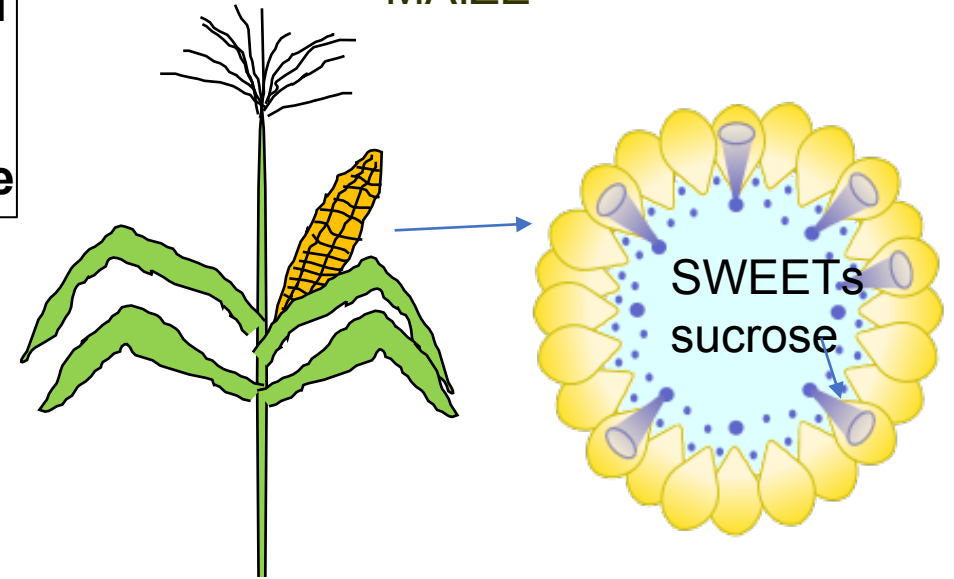
Active TPPs and bzip
= attenuated T6P signal
Down regulated starch,
sucrose, cell wall
metabolism

metabolism

Elevated T6P
Active starch, sucrose,
cell wall metabolism

**Traits affected
by TPPs
in sorghum,
maize and rice**

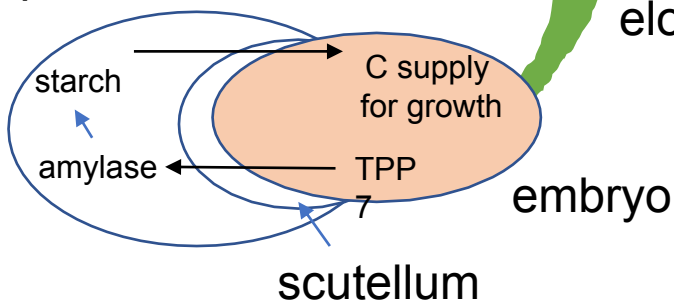
MAIZE



Expression of TPP in phloem and companion cells
Pith - less T6P, elevated SWEET expression, less sucrose
Kernels - less T6P, elevated SWEET expression, more sucrose
More kernels and yield at harvest
particularly under drought at flowering

endosperm

RICE



Coleoptile
elongation

TPP7 activity in embryo enables starch mobilisation under
anaerobic flooding to support better rice germination

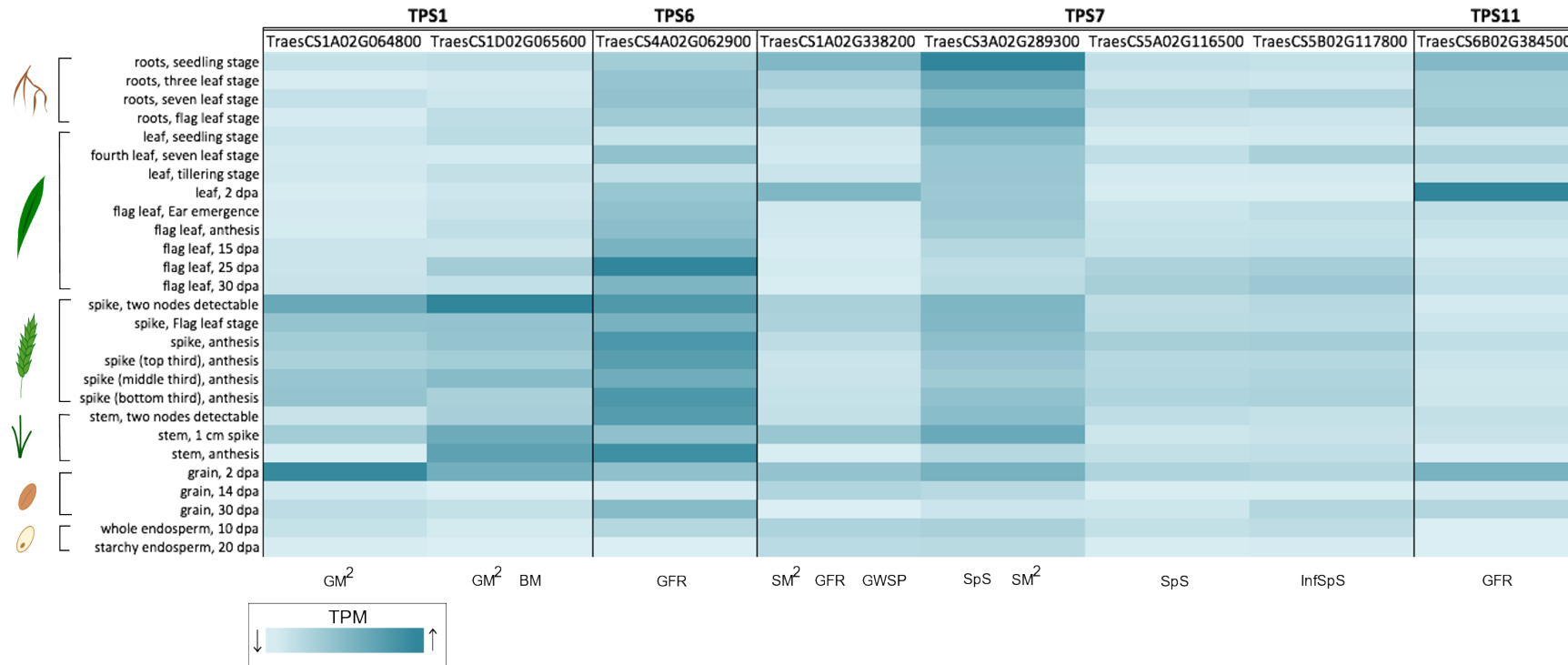


Figure 3. Developmental expression of key TPS genes associated with yield components in the spring wheat HiBAP panel [45]

Transcripts per million (TPM) reads for each gene of interest were extracted from the wheat exvip server from the listed plant organs [50, 51]. All genes chosen were associated with SNPs related to GM2 (grain number per m²), BM (biomass), GFR (grain filling rate), SM2 (spikes per m²), GWSP (grain

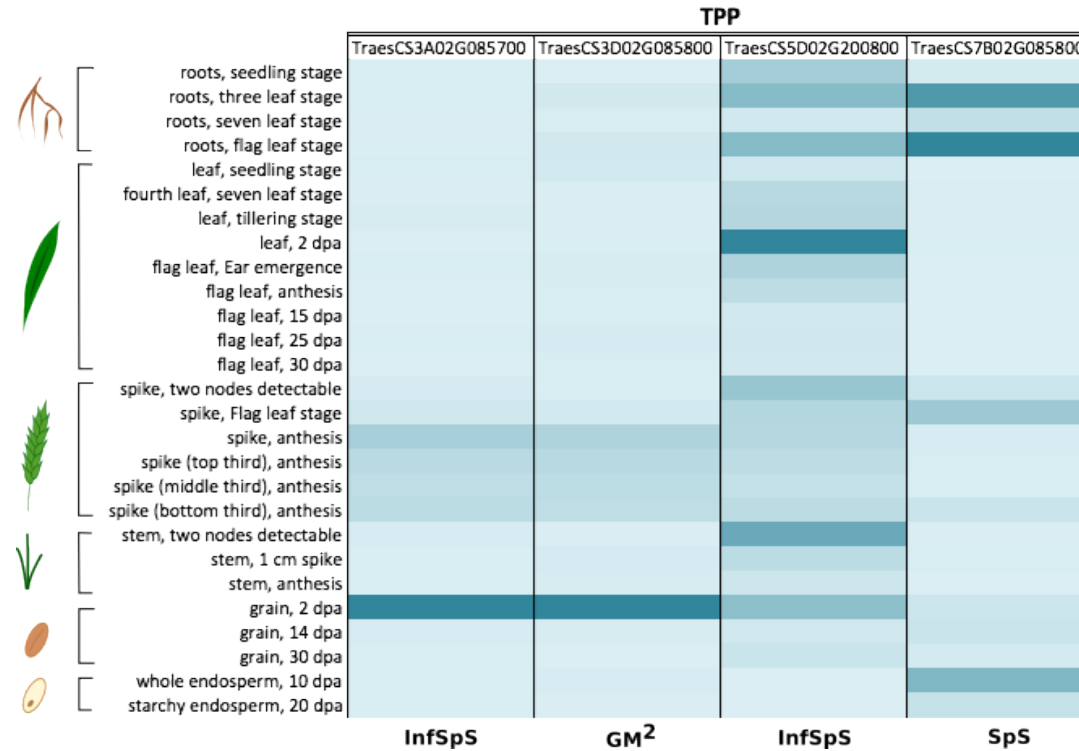


Figure 4. Developmental expression of key TPP genes associated with yield components in the spring wheat HiBAP panel [45]

Transcripts per million (TPM) reads for each gene of interest were extracted from the wheat exvip server from the listed plant organs [50, 51]. All genes