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Regulation of aquaporin expression in maize: proximal and distal eQTLs

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Plasma membrane intrinsic proteins (PIPs) are aquaporins that facilitate the passive movement of water through biological membranes. These channels are involved in numerous physiological and cellular processes such as hydraulic conductivity, transpiration, photosynthesis and osmoregulation in plants. In a context of climatic changes, they could turn out to be key targets for selection of crop varieties optimized for water use efficiency.

Whereas *PIP* mRNA levels in maize tissues vary according to the developmental stages and under varying environmental conditions, the molecular actors and mechanisms regulating the transcription of these genes remain largely unknown. Relying on the genetic material (254 maize genotypes and ~1000 K SNPs collection) and expertise of the European DROPS (DROught tolerant yielding PlantS) project, we performed GWAS (genome-wide association study) analyses in order to identify promising eQTLs (expression quantitative trait loci) associated with variation in the expression of five *PIP* genes in the mature and elongation zones of the leaf. In most cases, highly significant eQTLs were identified close to the *PIP* genes themselves suggesting the large impact of *cis*-regulation, as well as numerous promising distal eQTLs that appear to be mainly zone-specific. Conditional GWAS, avoiding the *cis*-eQTLs effects, allowed the identification of even more proximal and distal eQTLs, highlighting the complex regulation of the *PIP* gene expression. Deeper analyses and functional validation of several eQTLs are currently ongoing.

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