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P102

Genome-wide analysis of small RNA-controlled gene networks in leaf development

(submitted by Xiaoli Ma <xiaoli.ma@uni-tuebingen.de>)

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In plants, stem cell niches serve as a stable source of cells for postembryonic growth and development. The shoot apical meristem (SAM) gives rise to all aerial organs of a plant, and its activity throughout the plant's lifetime therefore has to be tightly controlled in a spatiotemporal manner. To gain insight into gene regulatory networks behind stem cell maintenance and organogenesis, we generated a high-resolution gene expression atlas of 12 distinct domains within the vegetative maize shoot apex using laser microdissection and RNA deep sequencing. We also generated small RNA sequencing data that informs on the role of miRNAs in the maize shoot apex. Together these data reveal a subfunctionalization of miRNA family members across the SAM subdomains, and the regulation of miRNA accumulation in the stem cell containing SAM tip and vasculature. In addition, miRNA degradome sequencing data, combined with information from the SAM atlas, predicts the presence of mechanisms that further fine-tune the accumulation and activity of select small RNAs to regulate key meristem genes.

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P103 

Grain abortion under drought in maize: expansive growth and hydraulics also matter

(submitted by Claude Welcker <claude.welcker@inra.fr>)

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Yield maintenance under drought in maize (*Zea mays*) requires the rapid extension of styles and stigma (silks) that collect pollen. We have shown that the control of grain set under moderate water deficits similar to those in the field result from a developmental process linked to the timing of silk growth, in opposition to the common view that abortion is linked to the sugar metabolism in ovaries. A switch to abortion occurs 2-3d after first silk emergence in water-stressed plants, when silk growth stops simultaneously for all ovary cohorts, and explains abortion rates in different treatments and positions on the ear. Analyses of transcripts and metabolites indicate that the first molecular events occur in silks rather than in ovaries, and involve genes affecting expansive growth rather than sugar metabolism. Sugar availability is preserved in ovaries until the switch to abortion, and the disruption of carbon metabolism only occurs afterwards. Hence, changes in metabolite contents, transcript amounts and enzyme activities involved in ovary sugar metabolism would be a consequence rather than a cause of the beginning of ovary abortion. Patterns of silk growth responses to environment share common features with those of leaf growth with both kinetic and genetic evidences. These findings have large consequences for breeding drought tolerant maize and for modelling grain yields under drought.

Oury et al (2016) *Plant Physiology* 171: 986-996 and 171: 997-1008

Turc et al (2016) *New Phytologist* 212: 377-388

Dignat G et al (2013) *Plant Cell and Environment* 36: 1105-1119.

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