IN BRIEF

From the archives: Polar auxin transport in nodule development, DNA replication timing, and developmentally light-regulated genes

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September 2021: Polar auxin transport in nodule development

Local accumulation of the phytohormone auxin is a well-known prerequisite in the proper formation of many plant organs (Benkova et al., 2003), including nodule organogenesis in legume plants. Nodules are subdivided into two types, determinate and indeterminate, depending on their meristematic activity. The two types have differences in their underlying molecular regulation as well as polar auxin transport (PAT; Ng and Mathesius, 2018). Main research on PAT comes from indeterminate nodule primordia formation, leaving a gap of knowledge in the role of PAT in determinate nodules. Zhen Gao and colleagues (Gao et al., 2021) investigated PIN-dependent auxin transport in determinate soybean nodules by studying five soybean GmPIN1 (GmPIN1a, b, c, d, and e) orthologs of AtPIN1, and the specific non-canonical GmPIN9 subgroup orthologs of AtPIN2. Besides a change in auxin levels and transport, the triple Gmpin1abc mutants had fewer but similar-sized nodules and developed fewer nodule primordia than the wildtype, whereas overexpression of GmPIN1abc resulted in smaller nodules and almost no nodule primordia. Together, these phenotypes demonstrate the involvement of the GmPIN1s in determinate nodule primordium formation. Moreover, by investigating their polarity and studying auxin flow, the authors showed that the GmPIN1s determine auxin levels in nodule founder cells, whereas GmPIN9d and GmPIN1s act together at later stages to determine auxin transport and accumulation during nodule enlargement (see Figure).

September 2017: DNA replication timing in maize

Duplication of genetic material during mitosis happens in the strictly controlled process of replication during the S phase of the cell cycle. Interestingly, not all parts of the genome are replicated at the same time, and whole-genome replication timing analyses have revealed a spreading of different origins of activation during the S phase. Replication programs in plants, the focus of work by Emily Wear and colleagues (Wear et al., 2017), have not received as much attention as in animals. The authors extended their previous research on the replication timing program of the complex maize genome (Bass et al., 2015) with an in-depth examination of the genome combined with measurements of gene expression and chromatin...
accessibility in mitotic cells of maize root tips. By means of a modified “Repli-seq” protocol (Zynda et al., 2017) making use of the previously established in vivo EdU labeling system of intact root tips, the authors generated whole-genome profiles based on the intensity of replication occurring in early, mid, or late S phase, and profiled the replication timing for each chromosome. They demonstrated that there is clear coordination in the replication timing for some regions of the genome, while other regions exhibit significant replication activity in both early and mid or both mid and late S phase. Regions undergoing early replication were generally enriched for highly expressed genes in open chromatin (euchromatin) active regions, whereas less transcriptionally active chromatin and centromere cores replicated mainly in the mid-S phase, and heterochromatin regions were mainly enriched in late replication regions.

September 1997: Developmentally light-regulated genes in anthocyanin biosynthesis

In maize, increased kernel seed pigmentation due to anthocyanin accumulation can have beneficial effects on human health, including increased antioxidant activity. Environmental factors including light can affect the pigmentation patterns in plants. Color in the seed pericarp and aleurone layers is regulated by anthocyanin biosynthesis and regulatory genes of the R/B and C1/Pl gene families, encoding basic helix-loop-helix and myb transcription factors, respectively. R/B genes include R and related genes Sn and Lc. Antonia Procissi and colleagues (Procissi et al. 1997) studied mutant seed phenotypes exhibiting different combinations of colored and colorless pericarp and aleurone tissue, together with an analysis of the expression patterns of anthocyanin regulatory and structural genes in these tissues in immature developing seeds and kernels close to maturity. The authors demonstrated tissue-specific expression of the regulatory genes and differential light-inducible expression. The light-induced expression of C1 and pl was found to be the limiting factor for conferring the developmental competence of the pericarp and the aleurone layers to respond to light. Five years later, another study of the same research group investigated the regulation of these anthocyanin genes in more detail and demonstrated that they respond to different light qualities and hormone treatments (Piazza et al., 2002). Moreover, numerous new studies based on the work of Procissi et al., (1997) revealed additional levels of control of the R and C1 regulators (e.g., Irani and Grotewold 2005), as well as identifying orthologous regulators in other plant species.

References


