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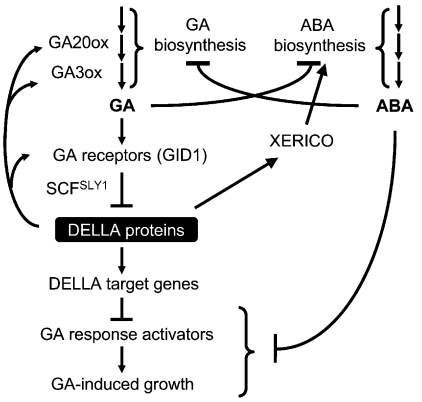
IN BRIEF

GA Signaling: Direct Targets of DELLA Proteins



DELLA inhibits GA-promoted processes by modulating both GA and ABA pathways.

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DELLA proteins are negative regulators of gibberellin (GA) signaling that act immediately downstream of the GA receptor. Binding of GA to its soluble receptor, GID1, causes binding of GID1-GA to DELLAs and leads to their degradation via the ubiquitin-proteasome pathway. DELLAs are nuclear localized and are hypothesized to function as transcriptional regulators, but little is known about their direct targets or even whether they bind DNA directly. **Zentella et al. (pages 3037–3057)** used microarray gene expression analysis to identify direct targets of DELLA proteins in *Arabidopsis* seedlings. The authors compared gene expression in the GA-deficient mutant *ga1-3* in the presence and absence of GA treatment to identify early GA-regulated genes and examined downstream gene expression affected by induced expression of a dominant DELLA mutant protein in a dexamethasone-inducible system to identify DELLA-regulated genes. These experiments led to the identification of 14 early GA-responsive genes that are also early DELLA responsive. These included genes encoding GA biosynthesis components and GA receptors, ubiquitin E2/E3 enzymes, and putative transcription factors/regulators. Chromatin immunoprecipitation experiments provided evidence for in vivo association of DELLA proteins with promoters of eight of these genes. Surprisingly, the expression of all 14 genes was downregulated by GA and upregulated by DELLA. This suggests that DELLA proteins promote the expression of downstream negative components of GA signaling and provide a direct feedback mechanism for regulating GA homeostasis. DELLA may also mediate interaction between GA and ABA pathways because one of its targets (XERICO) regulates ABA metabolism.

MIDGET and the Function of Topoisomerase VI in *Arabidopsis*

DNA topoisomerase VI (topo VI) is found only in archaeabacteria and plants, and in plants, it is required for the progression of endoreduplication cycles. Archaea topo VI is a heterotetramer containing two A subunits required for DNA cleavage and two B subunits that perform ATP hydrolysis. Functional topo VI A and B subunits were previously identified in *Arabidopsis* as TOP6B and RHL2/SPO11-3, respectively. **Kirik et al. (pages 3100–3110)** show that *MIDGET* (*MID*) encodes a novel plant-specific component of topo VI in *Arabidopsis*. *mid* mutants show a range of phenotypic abnormalities associated with effects on endoreduplication, such as a reduction in cell size (and plant size) and abnormal differentiation of root hairs and seed columella cells. Yeast two-hybrid assays, protein coimmunoprecipitation, and analyses of *mid top6b* and *mid rhl2* double mutants demonstrate that MID is a component of the topo VI complex. Analysis of *mid* mutant plants reveals that topo VI is involved in chromatin organization and transcriptional silencing. Genetic evidence for the misregulated cell cycle suggests that a G2-specific checkpoint is activated in *mid* plants, which prevents progression of endoreduplication cycles.

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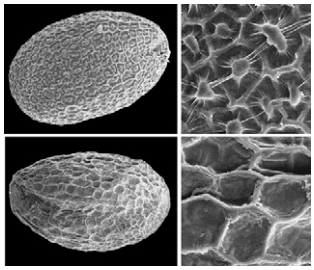

MID is required for seed epidermal differentiation. *mid* seed (bottom panels) do not develop the distinctive columella of wild-type seed (top panels) and fail to release seed coat mucilage after hydration.

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