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Transcriptional control of the endosperm maturation program and galactomannan cell wall deposition in *Coffea* species

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Rationale:
Seeds of *Coffea*species are albuminous, comprising a tiny embryo encapsulated in a copious living cellular endosperm. As in most albuminous seed species, the main storage carbohydrate of coffee seeds is not starch but polysaccharides of the mannan family that are deposited in the cell walls of the endosperm. To date, little information is available regarding the specific regulatory mechanisms that govern galactomannan biosynthesis and cell wall deposition in albuminous seeds.
Methods:
To gain insight in the coffee seed maturation program, we built a gene coexpression network using a large RNA-seq dataset (14 *Coffea* species × 5 endosperm developmental stages) and a pathway-guided strategy.
Results:
The network revealed tight transcriptional coordination of the core galactomannan biosynthetic machinery with sucrose import and cleavage, glycolysis, fatty acid synthesis, and cellulose biosynthesis. It also showed a concerted regulation of the transfer of nucleotide sugars to the Golgi apparatus, where galactomannan assembly occurs, the trans-Golgi network machinery for delivery of polysaccharides to the cell wall, and enzymes required for their post-deposition modification. The transcription factors FUS3, WRI1, SHN2 and DREB2D appeared as the major regulators of the coffee endosperm maturation program. DREB2D was the only direct partner of the core-galactomannan biosynthetic genes. Molecular genetics approaches further confirmed that DREB2D plays a critical role in nucleotide sugar homeostasis and cell wall polysaccharide metabolism, and triggers part of the seed maturation program when overexpressed in *Coffea arabica* somatic embryos.
Conclusions & Perspectives:
These findings shed light into the specific regulatory mechanisms that govern cell wall storage polysaccharides synthesis and regulate the coffee seed maturation program.