An emerging picture of the seed desiccome: confirmed regulators and newcomers identified using transcriptome comparison

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Résumé en anglais	Desiccation tolerance (DT) is the capacity to withstand total loss of cellular water. It is acquired during seed filling and lost just after germination. However, in many species, a germinated seed can regain DT under adverse conditions such as osmotic stress. The genes, proteins and metabolites that are required to establish this DT is referred to as the desiccome. It includes both a range of protective mechanisms and underlying regulatory pathways that remain poorly understood. As a first step toward the identification of the seed desiccome of Medicago truncatula, using updated microarrays we characterized the overlapping transcriptomes associated with acquisition of DT in developing seeds and the re-establishment of DT in germinated seeds using a polyethylene glycol treatment (−1.7 MPa). The resulting list contained 740 and 2829 transcripts whose levels, respectively, increased and decreased with DT. Fourty-eight transcription factors (TF) were identified including MtABI3, MtABI5 and many genes regulating flowering transition and cell identity. A promoter enrichment analysis revealed a strong over-representation of ABRE elements together with light-responsive cis-acting elements. In Mtabi5 Tnt1 insertion mutants, DT could no longer be re-established by an osmotic stress. Transcriptome analysis on Mtabi5 radicles during osmotic stress revealed that 13 and 15% of the up-regulated and down-regulated genes, respectively, are mis-regulated in the mutants and might be putative downstream targets of MtABI5 implicated in the re-establishment of DT. Likewise, transcriptome comparisons of the desiccation sensitive Mtabi3 mutants and hairy roots ectopically expressing MtABI3 revealed that 35 and 23% of the up-regulated and down-regulated genes are acting downstream of MtABI3. Our data suggest that ABI3 and ABI5 have complementary roles in DT. Whether DT evolved by co-opting existing pathways regulating flowering and cellular phase transition and cell identity is discussed.
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