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Seed comparative genomics in three coffee species identify desiccation tolerance mechanisms in intermediate seeds

Anna K. Stavrinides1,2, Stéphane Dussert1, Marie-Christine Combes1, Isabelle Fock-Bastide2,3, Dany Severac3, Jérôme Minier4, Aldecinei Bastos-Siqueira1, Vincent Demolombe5, Sonia Hem5, Philippe Lashermes1,2, and Thierry Joët1,*,

1 IRD, Université Montpellier, UMR DIADE, BP 64501, F-34394 Montpellier, France
2 Université de La Réunion, UMR PVBMT, 7 Chemin de l’IRAT, Ligne Paradis, 97410 Saint Pierre, France
3 MGX-Montpellier GenomiX, c/o Institut de Génomique Fonctionnelle, 141 Rue de la Cardonille, Montpellier Cedex 5 34094, France
4 CIRAD, UMR QUALISUD, 7 Chemin de l’IRAT, Ligne Paradis, Réunion, France
5 BPMP, CNRS, INRA, Montpellier SupAgro, Univ Montpellier, Montpellier, France

* Correspondence: thierry.joet@ird.fr

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Abstract

In contrast to desiccation-tolerant ‘orthodox’ seeds, so-called ‘intermediate’ seeds cannot survive complete drying and are short-lived. All species of the genus Coffea produce intermediate seeds, but they show a considerable variability in seed desiccation tolerance (DT), which may help to decipher the molecular basis of seed DT in plants. We performed a comparative transcriptome analysis of developing seeds in three coffee species with contrasting desiccation tolerance. Seeds of all species shared a major transcriptional switch during late maturation that governs a general slow-down of metabolism. However, numerous key stress-related genes, including those coding for the late embryogenesis abundant protein EM6 and the osmosensitive calcium channel ERD4, were up-regulated during DT acquisition in the two species with high seed DT, C. arabica and C. eugenioides. By contrast, we detected up-regulation of numerous genes involved in the metabolism, transport, and perception of auxin in C. canephora seeds with low DT. Moreover, species with high DT showed a stronger down-regulation of the mitochondrial machinery dedicated to the tricarboxylic acid cycle and oxidative phosphorylation. Accordingly, respiration measurements during seed dehydration demonstrated that intermediate seeds with the highest DT are better prepared to cease respiration and avoid oxidative stresses.

Keywords: Coffea, dehydration, desiccation tolerance, intermediate seeds, late maturation, metabolic quiescence, respiration, seed development, transcriptome.

Introduction

Desiccation tolerance (DT) is the ability of an organism or tissue to withstand removal of intracellular water whilst retaining structural integrity and viability, and then to resume normal metabolism upon rehydration (Crowe et al., 1992; Leprince and Buitink, 2015). The vast majority of flowering plants produce seeds that are desiccation tolerant. In a dry quiescent
state at maturity, these seeds are endowed with an exceptional capacity to endure extreme adverse environmental conditions after dispersal (Sano et al., 2016). These so-called ‘orthodox’ seeds can survive \textit{ex situ} storage for very long periods under conventional gene-bank conditions (Li and Pritchard, 2009).

DT is a complex trait that is mostly genetically determined in the developing seed and is put in place during the late maturation program. This is achieved through the interplay of multiple cellular protectants and repair mechanisms designed to cope with the various desiccation-associated stresses including oxidation, hyperionicity, mechanical strain associated with cell shrinkage, protein misfolding/aggregation and phase transition of lipid membranes (Crowe et al., 1992; Leprince and Buitink, 2015). Coordinated repression of metabolism, stabilization of membranes and proteins against conformational change by chemical and protein chaperones, and the accumulation of efficient antioxidant, detoxication and repair systems appear to be among the essential attributes that contribute to seed DT (Hoekstra et al., 2001; Buitink and Leprince, 2008; Leprince and Buitink, 2010). Some of these protective mechanisms are shared across eukaryotic kingdoms since the accumulation of chemical and protein chaperones such as non-reducing sugars (e.g. trehalose), heat-shock proteins, and intrinsically disordered proteins (e.g. late embryogenesis abundant (LEA) proteins) have been recently confirmed to be of tremendous importance in conferring DT in unicellular yeasts, tardigrades, and nematodes (Erkut et al., 2011; Tapia et al., 2015; Boothby et al., 2017). The repertoire of DT-related genes, including key transcriptional regulators, has been extensively studied in orthodox seeds through transcriptome profiling and co-expression analyses during the acquisition of desiccation tolerance (e.g. Verdier et al., 2013; Righetti et al., 2015; González-Morales et al., 2016; for a review see Leprince et al., 2017).

Estimates suggest that about 8% of the world’s flowering plants (>40,000 species) produce desiccation-sensitive short-lived seeds (Tweddle et al., 2003; Wyse and Dickie, 2017). Two other categories of seeds—intermediate and recalcitrant—have been defined with respect to their storability in gene banks (Roberts, 1973; Ellis et al., 1990) and these terms are now used to describe their sensitivity to drying. Although desiccation tolerance may vary considerably within each of these two seed categories (Dussert et al., 1999; Berjak and Pammenter, 2008), it is commonly acknowledged that recalcitrant seeds are extremely sensitive to dehydration and do not survive if dried to about 90% relative humidity (RH), while intermediate seeds are able to withstand enforced drying to about 30% RH (Black and Pritchard, 2002). Seeds of many major tropical crops are recalcitrant (e.g. cocoa, coconut, rubber tree) or intermediate (e.g. coffee, tea, oil palm, citrus), which represents a major constraint for growers, seed companies, and germplasm repositories (Li and Pritchard, 2009; Walters et al., 2013).

Albuminous seeds of \textit{Coffea} species are the model system for the ‘intermediate seed’ category (Ellis et al., 1990; Dussert et al., 1999). As in all fleshy fruits, coffee seeds are not subjected to dry ambient air during maturation (Dussert et al., 2000). Partial DT is acquired without dehydration \textit{in planta} during the late stage of maturation, well after the onset of reserve deposition in the cellular endosperm, a living tissue that represents more than 98% of the mature coffee seed mass (Dussert et al., 2018). The desiccation-induced loss of seed viability is due to damage to the endosperm only, the embryo being much more tolerant to desiccation (Dussert et al., 2006). Transcriptomic analysis of developing \textit{C. arabica} seeds revealed that the cellular and regulation processes that occur during late maturation in the coffee seed are strikingly similar to those known or thought to be involved in orthodox seed DT (Dussert et al., 2018). Briefly, acquisition of DT coincides with a dramatic transcriptional switch characterized by the repression of genes involved in the cell cycle, DNA processing, and primary metabolism, and the up-regulation of a large number of genes coding for protein involved in cell protection and rescue, including reactive oxygen species (ROS)-scavenging enzymes, LEA proteins and heat-shock protein stress proteins, defense-, cold-, and drought-induced proteins, as well as many components of sugar and nutrient sensing systems. The DT-associated transcriptional switch also had the signature of a coordinated metabolic slow-down, with a marked decrease in the mRNA abundance of genes involved in protein fate and major energy processes such as photosynthesis, the tricarboxylic acid (TCA) cycle, respiratory electron transport, ATP synthase, and glycolysis. With regard to phytohormones, there was an up-regulation of genes for abscisic acid (ABA) synthesis, perception, and signaling during the late maturation and a drastic down-regulation of cytokinin biosynthetic genes associated with a large drop in cytokinin content. Finally, major transcription factors (TFs) homologous to those identified as associated with DT in orthodox seeds have been described as massively up-regulated during DT acquisition in coffee seeds, namely PLATZ, DOGL4, HSFA9, and DREB2G (Prieto-Dapena et al., 2006, 2008; Righetti et al., 2015; González-Morales et al., 2016). The late maturation program described in coffee seed is therefore qualitatively comparable to that of orthodox seeds. This led to the hypothesis that the differences observed in DT between orthodox and intermediate seeds, and between intermediate seeds displaying different DT levels, could be due to a quantitative variation in gene expression and metabolite accumulation. In the present work we therefore compared the seed maturation transcriptomes of three closely related \textit{Coffea} species (Cenci et al., 2012) that were previously shown to differ in their DT (Dussert et al., 1999); \textit{C. arabica}, \textit{C. eugenioides}, and \textit{C. canephora}.

**Material and methods**

**Plant material**

Seeds at three different maturation stages known to span the acquisition of desiccation tolerance in \textit{C. arabica} (ST3, ST6, and ST7, Dussert et al., 2018) were collected from three trees of each species from the Biological Resource Center Coffee, Basin Martin, Reunion Island. The average seed development duration being different for the three studied species, i.e. respectively ca. 7, 8, and 10 months for \textit{C. arabica}, \textit{C. eugenioides}, and \textit{C. canephora}, respectively (Dussert et al., 2000). The developmental stages were selected based on marked anatomical and morphological seed and fruit traits that are shared across coffee species, as defined and described previously for \textit{C. arabica} (Joët et al., 2009; Dussert et al., 2018). Briefly, stage 5 is the peak of reserve deposition and corresponds to endosperm hardening due to massive deposition of galactomannans in cell walls, stage 6 coincides with fruit veraison, and stage 7 corresponds to mature
cherry fruits with red pericarp. After being cross-sectioned, the seed was separated from the pericarp and immediately frozen in liquid nitrogen and stored at −80 °C. The endosperm was separated from the perisperm and the embryo while frozen. To minimize the impact of genotypic effect and facilitate inter-species comparisons, developing seeds were collected (pools of ca. 50 seeds) on different wild accessions for each species (C. arabica accessions AR28-06, AR02-06, AR38b/05; C. eugenioides accessions DA71, DA78, DA78c; C. canephora accessions BD55, BD56, DAF71), and were considered biological replicates.

**Desiccation tolerance assays and respiration measurement during desiccation**

Mature seed lots (50 seeds) of C. arabica, C. canephora, and C. eugenioides were desiccated by equilibration over various saturated salt solutions (K-acetate (23% RH), K2CO3 (45% RH), NH4NO3 (62% RH), and (NH4)2SO4 (81% RH)) for 20 d at 27 °C in the dark, as previously described (Dussert et al., 2000). For germination tests, batches of nine seeds were placed on 18 g of vermiculite fully imbibed with 50 ml of sterile water in closed plastic boxes (Magenta, Chicago, IL, USA). After 6 weeks of culture at 27 °C in the dark, successful seed germination was scored (emergence of the hypocotyl and radicle geotropic growth). Desiccation sensitivity was quantified using the previously developed quantal response model (Dussert et al., 1999). For respiration measurements, fresh ST7 mature seeds were desiccated at 25 °C by equilibration over a saturated K2CO3 solution. During 4 d of desiccation, subsamples of four to five seeds were taken every 12 h for respiration measurement. For each replicate, seeds (the fresh weight was recorded) were placed in individual 10 ml hermetically sealed vials at 25 °C. CO2 release (µmol CO2 min−1 replicate, seeds (the fresh weight was recorded) were placed in individual 10 ml hermetically sealed vials at 25 °C. CO2 release (µmol CO2 min−1)

**Transcriptome analysis**

For each of the 27 samples of the experimental design, a mix of >20 endosperms was ground to a fine powder in an analytical grinder (IKA A10, Staufen, Germany) and total RNA was extracted from 70 mg using the Qiagen RNeasy Lipid Tissue kit (Qiagen, Stanford, CA, USA). cDNA libraries were constructed using the TruSeq™ Stranded mRNA sample preparation kit (Illumina, USA) then sequenced on an Illumina HiSeq 2500 (single reads, 100 nt) on the MGX platform (Montpellier Genomix, http://www.mgx.cnrs.fr/). After quality filtering using Cutadapt (quality score>Q30 and removal of reads shorter than 60 bp or higher than 140 bp), a total of 875 million reads were retained (average of 31.95 million reads per library) (Supplementary Table S1 at JXB online). The entire dataset has been deposited at the European Nucleotide Archive (ENA) under the project number PRJEB32533. Owing to the very low genetic divergence between the three Coffea species (average of 1.3% gene sequence difference; Cenci et al., 2012), the trimmed reads (cutadapt, Genome Analysis Toolkit) of each library were mapped to the C. canephora coding transcriptome DNA reference sequence (25747 CDS) (Denoëud et al., 2014) using BWA MEM (Li, 2013, Preprint) with the default parameters. Reads were counted using IDXstats in SAMtools (Li et al., 2009) and counts normalized (RPKM; Supplementary Table S2). A total of 628 million reads were mapped (average of 23.3 million reads per library). Genes with extremely low expression (<20 counts in total) were removed for subsequent analyses (22 503 retained genes).

**Proteome analysis**

Soluble proteins were extracted from 500 mg of mature coffee endosperms by suspension and stirring in 10 ml buffer (30 mM HEPES pH 8.0, 1 mM EDTA, 5 mM DTT, 4% polyvinylpyrroliodine, 700 units of benzonase endonuclease, and 1% protease inhibitor cocktail) for 40 min at 4 °C. After centrifugation, proteins were precipitated from supernatant at 4 °C with trichloroacetic acid (10% v/v), washed twice with acetone, and air dried. Proteome analysis included protein fractionation by one-dimensional SDS-PAGE sliced into four bands, trypsic digestion, and analysis of samples by nano-LC-MS/MS using a QExactive Plus (ThermoFisher Scientific Inc.), as described by Geiger et al. (2015). Raw files were analysed using Maxquant 1.5.5.1 on the predicted C. canephora peptide database (25 574 peptides, http://coffee-genome.org/) with a protein and peptide false discovery rate <1%, as described in Chen et al. (2019). Difference in protein abundance between species was tested by one-way ANOVA and post hoc Tukey test. Label-free data have been deposited at ProteomeXchange under the project number PXD013806.

### Table 1. Categories of DT-related candidates and the filters used for each category

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Cluster C1 is designed to comprise genes that are up-regulated during late maturation in both C. arabica and C. eugenioides desiccation-tolerant seeds, and whose expression is concomitantly lower in desiccation-sensitive C. canephora seeds (key positive effectors of DT). Cluster C2 groups genes that are down-regulated during late maturation in both C. arabica and C. eugenioides desiccation-tolerant seeds, and whose expression is concomitantly higher in desiccation-sensitive C. canephora seeds (negative effectors of seed DT). Cluster C3 is the opposite of C1; it includes genes that are up-regulated during late maturation in desiccation-sensitive C. canephora seeds, and whose expression is concomitantly lower in both C. arabica and C. eugenioides seeds. C3 thus comprises late maturation genes specific to a desiccation-sensitive context.

a An adjusted P-value cut-off of 0.05 was used during the filtering.

b For these filters a P-value cut-off was not imposed.
Hormone analysis
Hormones in freeze-dried powder of endosperms (50 mg) were analysed by National Research Council, Canada. ABA and ABA metabolites, cytokinins, auxins, and gibberellins were quantified by ultra-performance liquid chromatography–electrospray ionization–tandem mass spectrometry as previously described (Chiwocha et al., 2003).

Promoter cis-element analysis
The 1000 bp sequences upstream of the start codon of the candidate genes and of a random selection of 500 C. canephora genes (control genes) were collected from the Coffee Genome Hub (coffee-genome.org) and submitted to the Genomatix MatInspector tool (Cartharius et al., 2005). The presence of seed and stress-related plant cis-elements was determined using the default parameters of MatInspector. The resulting contingency tables were submitted to enrichment analysis (hypergeometric test in R) by comparing the candidate gene cis-elements by cluster with those found in the control genes.

Results
The transcriptional program associated with late seed maturation shares common essential features among the different coffee species
Mature seeds of C. eugenioides and C. arabica were tolerant to relatively intense dehydration, with almost no loss of viability noticed when dried up to 23% RH (Fig. 1A). For both species, the equilibrium relative humidity at which 50% of the initial viability was lost, RH₅₀, was lower than 10%. By contrast, C. canephora seeds displayed significantly higher desiccation sensitivity. They could only withstand mild drying without noticeable loss of viability, i.e. drying at 62% RH, and did not survive drying at 23% RH. The equilibrium RH₅₀ estimated for C. canephora was around 50%. At stage (ST) 5, most seeds of the three species were already able to germinate and to develop into normal seedlings but displayed high mortality upon drying, at both 45% and 62% RH (Fig. 1B). The seeds of the three studied species acquired most of the capacity to be dried to 62% RH between ST5 and ST6 (Fig. 1B), demonstrating a conserved phenological sequence among the three coffee species for partial DT acquisition.

DT acquisition was concomitant with a major transcriptional switch observed during late maturation in all three species (Fig. 2A). When species were analysed separately, most transcriptional changes appear to occur in the transition between the ST5 and ST6 with 2837, 3622, and 4109 DEGs identified in C. eugenioides, C. arabica, and C. canephora, respectively (11.3–16% of the reference genes). The ST5–ST7 comparison, i.e. taking the whole late maturation phase into account, identified a larger number of DEGs than the ST5–ST6 transition, specifically 6285, 5506, and 5535, in C. canephora, C. arabica, and C. eugenioides, respectively (21.5–24.6% of the reference genes). By contrast, the late maturation stages ST6 and ST7 were transcriptionally similar, with very few DEGs between them (16, 8, and 82 DEGs in C. canephora, C. arabica, and C. eugenioides, respectively). It is worth noting that down-regulated genes represented a slightly higher fraction than the up-regulated genes in these comparisons. Hierarchical clustering analysis of the global expression dataset grouped the vast majority of ST5 samples on one major branch of the dendogram (group I, Fig. 2B), while late stages ST6 and ST7 grouped together, by species, on another branch (group II). This suggests a close transcriptional program between the three species, with 2533 genes being commonly up- or down-regulated in the three coffee species (Fig. 2C; Supplementary Table S4).

Mapman-based DEG enrichment analysis showed a clear overview of molecular processes involved in the late maturation phase, allowing the identification of specific molecular pathways that are associated with the acquisition of desiccation tolerance and with the transition from seedling to plant. These pathways include stress response, energy metabolism, and cell wall modification, among others. The analysis also highlighted the role of transcription factors and signal transduction pathways in regulating the expression of genes involved in seed development and desiccation tolerance.

Fig. 1. Characterization of seed desiccation tolerance in the three coffee species, Coffea arabica, C. canephora, and C. eugenioides. (A) Survival rate of mature (stage 7) coffee seeds after equilibration drying at various relative humidity (RH) conditions. The curves correspond to the fitted patterns using the quantal response model described in Dussert et al. (1999). (B) Changes in viability (%) after equilibration drying at various RH conditions during seed development (stage 5–6).
maturation program, with a total of 94 functional categories detected as significantly enriched at least in one species (Fig. 3; Supplementary Tables S5, S6). More categories (62) were significantly over-represented among the down-regulated genes than among the up-regulated genes (30), and only two categories displayed contrasting behavior among different species (minor CHO metabolism and redox processes, mapman bin codes 3 and 21, respectively, which were enriched in C. canephora up-regulated genes and in C. eugenioides down-regulated genes). Most importantly, 24 functional categories (25.5%) were shared among the three species for at least one of the two comparisons (ST5–6 or ST5–7, labeled by red stars in Fig. 3) while each species also revealed a similar number (14–15) of specific categories. Transcriptional processes associated with C. canephora during the ST5–6 transition appear to be the most dissimilar compared with other stages and species, since only nine out of the 24 shared functional categories are represented during this early transition, whereas 23/24 were identified within the ST5–7 comparison. By contrast, most of these shared functional categories were already detected during the early ST5–6 transition among C. arabica and C. eugenioides. This important result indicates that the late maturation transcriptional program is delayed in the desiccation-sensitive C. canephora compared with species with desiccation-tolerant seeds.

The composition for the 18 common categories shared between species for down-regulated genes strongly suggests a transcriptional co-ordination of metabolic slow-down during late maturation, with a significant decrease in mRNA abundance of genes involved in key energetic processes such as respiration (including the TCA cycle, mitochondrial electron transport and ATP synthase) and photosynthesis (including light reactions and photosystem I components). Genes encoding components of cytoskeleton, membrane transporters, or components of the machinery for cell wall precursors were also found to be significantly down-regulated (Fig. 3). GO enrichment analysis revealed similar features, but also pointed out a general decrease of carbohydrate metabolic process, and
Fig. 3. Mapman functional class enrichment (Fisher enrichment test, adjusted P-value<0.05) for DEGs of ST5–6 and ST5–7 for each Coffea species. Up- and down-regulated genes are colored in shades of orange and blue, respectively; only significant enrichments are colored. Mapman functional classes which are found to be enriched in all three species are indicated by a red star. FDR, false discovery rate.
intracellular trafficking, including endomembrane systems and Golgi apparatus (Supplementary Table S7).

With regard to functional classes associated with late maturation up-regulated genes, only six were found to be shared among the three species. These mostly concerned RNA processing (splicing and RNA binding) and the translational machinery (i.e. ribosome biogenesis, including pre-rRNA processing and modifications). Surprisingly, functional enrichment analysis did not identify any functional class that would be specifically induced during late maturation in desiccation-tolerant seeds only. By contrast, it revealed several specific features of desiccation-sensitive *C. canephora* seeds. Indeed, functional processes such as gluconeogenesis and carbohydrate metabolism, flavonoid metabolism, redox homeostasis, and hormone metabolism (gibberellin synthesis and auxin-regulated genes) were significantly over-represented among the *C. canephora* genes up-regulated during late maturation (Fig. 3).

**DT-related candidate genes and processes identified through inter-specific comparative transcriptomics**

The DEGs between species/stages were filtered by using combinations of Boolean operators to identify candidate genes related to different categories of DT (Table 1; Fig. 4). The first cluster (C1; 150 genes), designed to encompass positive effectors of DT, groups genes that are up-regulated during late maturation in both *C. arabica* and *C. eugenioides* seeds, and whose expression is concomitantly lower in desiccation-sensitive *C. canephora* seeds (Fig. 4; Supplementary Tables S7, S8). Interestingly, the 1000 bp promoter regions of C1 candidate genes were significantly enriched in four *cis*-elements (Supplementary Table S9), including CGCG, which is bound by Calmodulin-binding transcription activator and known to play a key role in plant stress response (Galon et al., 2008; Doherty et al., 2009). Among the 120 genes with expert-assigned putative functions, the most-represented functional classes were transcriptional activities (19.2% of the 120 candidate genes),

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**Fig. 4.** Candidate gene clusters related to desiccation tolerance. The standardized log2 of the gene expression is plotted against the developmental stage of each *Coffea* species. The average gene expression for each cluster is traced in a dark line, while individual gene expressions are plotted in thin gray lines.
cellular communication (14.6%), cell rescue (11.3%), and protein synthesis and fate (11.3%) (Fig. 5A).

The second cluster (C2), designed to comprise negative effectors of seed DT, was composed of genes that are down-regulated during late maturation in both *C. arabica* and *C. eugenioides* seeds, and whose expression is concomitantly higher in desiccation-sensitive *C. canephora* seeds (Fig. 4). Cluster C2 contains 292 genes, including 250 with a putative function assigned, with primary metabolism (12.7% of the candidate genes), cellular communication (12%), cellular organization (11%), transcriptional activities (11.6%), and energetic processes (10.6%) being the most represented functional classes in this group (Fig. 5A; Supplementary Table S7). Generation of precursor metabolites and energy, photosynthesis, and TCA cycle were among the biological processes significantly enriched using GO or Mapman ontologies (Supplementary Table S8). This result suggests that over the course of seed maturation differences in DT between species may be based on quantitative differences at the level of transcriptional control of the metabolic slow-down associated with seed quiescence.

The analysis of the relative size and composition of the different gene functional classes (Fig. 5B) revealed striking differences between DT-associated (C1) and DS-related genes (C2), with some functional classes being almost exclusively represented in one group. Specifically, C1 alone includes representatives of the functional class related to the synthesis and repair of DNA and chromatin structure (Fig 5A). Similarly, the relative size of the functional class related to transcriptional processes was highest for DT-associated genes, with many genes predicted to be implicated in RNA processing or encoding many chromatin remodeling factors involved in regulation of transcription, but with very few TFs (three) including GATA and MADS factors (Fig 5B). In this context, it is worth noting that C1 contains multiple genes encoding putative chromatin remodeling factors/complex subunits, including MRG1 (*Cc07_g06470*), SWC6 (*Cc07_g10850*), SW13A (*Cc07_g20270*), and SWIB

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**Fig. 5.** The percentage of candidate genes in clusters 1 (red) and 2 (blue) that belong to each functional class. Class sizes that are significantly different between the two clusters ($\chi^2$ test, $P$-value<0.05) are indicated with asterisks. (A) The first level of functional terms; (B) the second level of functional terms. Functional terms that are child terms of the first level are separated and numbered for ease of visualization.
complex BAF60b domain-containing protein (Cc02_g18450). In Arabidopsis, MRG1 has been shown to be involved in increasing the transcriptional levels of the flowering time genes FLC and FT (Bu et al., 2014) while SWC6 is a component of the SWR1 complex that mediates transcriptional regulation of selected genes such as FLC (Choi et al., 2007). By contrast, C2 does not contain chromatin remodeling factors; instead it contains many TFs (14) related to key developmental activities and cell differentiation, including homologs of HOX, B3, LOB, MADS, and MYB TFs. This result suggests DT acquisition could be associated with intense chromatin remodeling and repression of specific developmental TFs.

Moreover, C2 displays a higher number of genes involved in redox homeostasis and defense against biotic stress while C1 includes many genes with a direct role in the regulation of abiotic stress response (Fig 5B). C1 genes include key stress proteins such as LEA (EM6, Cc05_g00080), co-chaperone (JAC1, Cc10_g03210; Cc08_g03570), cold-stress (COR28, Cc02_g18840), and drought-stress proteins (ERD4, Cc11_g12570) (Supplementary Table S7). C1 also includes mediators of ABA and jasmonate stress response (AFP2, ABO5, NHL6, MKS1), a regulator of ROS homeostasis (APP1, Cc07_g09130; Yu et al., 2016), a modulator of unfolded protein response (CPR5, Cc07_g16050), and proteins involved in plastid stress response mediated by effector nucleotides (ppGpp synthetase, Cc10_g06010) (Supplementary Table S7).

With regard to cellular communication processes, while C1 presents mainly genes implicated in signal transduction processes (Fig 5B), such as components of receptor-like kinase signaling pathways, protein kinase cascades, and protein phosphatases (subunits of PP2A and PP2C), C2 mostly contains genes implicated in hormone metabolism and signaling, a majority of them being putatively dedicated to the metabolism, transport, and perception of auxin, and, to a lesser extent, cytokinin and gibberellins (Supplementary Table S7).

Finally, functional classes related to energetic processes appear mostly restricted to DS-related genes (Fig 5B). Many C2 genes are associated with key energetic processes such as respiration (including molecular components of the TCA cycle, respiratory electron transfer chain and ATP synthase), photosynthesis, and glycolysis, as well as key enzymes of the pentose phosphate pathway. These candidates point to the existence of a transcriptional orchestration of metabolic quiescence that differs between desiccation-tolerant and desiccation-sensitive seeds. This could lead to different levels of repression of energetic processes and basal cellular processes when entering quiescence during seed desiccation.

**Desiccation-sensitive specific genes expressed during late maturation**

Finally, a third cluster (C3) included 571 genes specific to a desiccation-sensitive context, i.e. genes that are up-regulated during late maturation in C. canephora seeds, and whose expression is concomitantly lower in both C. arabica and C. eugenioides desiccation-tolerant seeds (Fig. 4). The Mapman functional classes over-represented within this cluster are mainly related to nitrogen metabolism, tocopherol biosynthesis, and translational control (Supplementary Table S8). As shown for genes that were up-regulated during C. canephora late seed maturation (Fig. 3), auxin-regulated genes were also enriched in C3. Accordingly, the analysis of promoter regions for C3 candidate genes revealed significant enrichment for three cis-elements (Supplementary Table S9), including the auxin response factor ARF3 cis-element. This motif is bound by auxin-regulated TFs (Chandler, 2016), probably including the ARF homolog gene (Cc08_g16330) detected in C3. The cis-element GCCF (GCC-box bound motif by TF of the AP2/ERF family) was shown to be enriched in both C3 and C1 genes, suggesting this cis-element is an important driver of gene expression at the late maturation stage, independently of the DT level. The most common GCCF cis-element signatures found in these two clusters are those of the AtERF-1 and of the RAP2.6 TF, known to be involved in jasmonate- and ethylene-dependent stress response, and in ABA and salt stress response signaling, respectively (Lorenzo et al., 2003; Pré et al., 2008; Zhu et al., 2010).

A comparison of the functional classes’ relative size between C1 and C3 also highlighted striking differences in late maturation transcripts specific to C. arabica and C. eugenioides compared with the desiccation-sensitive C. canephora seeds (Fig. 6). Interestingly, genes of C1 are enriched in functions related to stress response, chromatin remodeling, and RNA processing when compared with C3, as seen in the C1–C2 comparison. By contrast, C3 contains many genes involved in defense against biotic stress or associated with energetic processes (cytosolic and plastidial glycolysis, control of the redox poise in plastid and mitochondrial respiratory electron transporters), and cell cycle or organelle differentiation (Fig. 6). In addition to many TFs, C3 also contains numerous genes encoding members of the Pentatricopeptide repeat-containing (PPR) protein family. To date, a majority of characterized PPRs are predicted or shown to localize to chloroplasts or mitochondria where they play essential roles in gene expression, mRNA editing, mRNA processing, and protein synthesis (Hayes et al., 2015; Liu et al., 2016).

**Comparative proteomics validates processes and candidate genes inferred from transcriptome analysis**

The soluble proteome of mature coffee seeds was analysed among the three species in order to ascertain the differential functions inferred from transcriptomic analysis (Supplementary Table S10; Supplementary Fig. S1). Among the 1389 proteins accurately detected in at least one species, quantification revealed 95 proteins whose abundance is higher in desiccation-tolerant C. arabica and C. eugenioides seeds compared with C. canephora (Supplementary Table S11). Mapman functional classes over-represented within this group are mainly related to calcium signaling, protein post-translational modification, and synthesis of amino acids of the serine–glycine–cysteine group (Supplementary Table S12). This proteomic analysis also revealed 99 proteins over-accumulated in desiccation-sensitive C. canephora mature seeds. Hormone metabolism related to auxin, secondary metabolism associated with flavonoids, and biotic stress-associated PR proteins were among the biological processes significantly enriched using Mapman ontologies (Supplementary Table S12). All these functional classes were
also detected at the transcriptome. Besides, the expert analysis of the relative size and composition of the different functional classes revealed striking differences between DT- and DS-associated proteins, with some functional classes such as those related to glycolysis, photosynthesis, hormone signaling, and defense against biotic stress being higher in desiccation-sensitive C. canephora seeds as observed with transcriptomic data (Supplementary Fig. S2). Finally, DT candidates detected at both transcript and protein levels included the LEA EM6 in desiccation-tolerant seeds and the glycolytic GAPC2c (Cc07_g00460) or the redox-involved NRX1 (Cc11_g14760) for desiccation-sensitive seeds (Supplementary Table S13).

Hormone sensing and signaling pathways are differentially expressed between desiccation-tolerant and -sensitive coffee species

Phytohormone profiling detected only faint amounts of active molecules in mature seeds and no significant differences among the three species studied (Supplementary Table S14). However, our survey highlighted key genes involved in hormone sensing, predominantly in desiccation-sensitive seeds (Supplementary Table S7). Indeed, in the DT-repressed genes (C2) we found homologs of major hormone transporters (auxin, PIN1, Cc06_g19880; ABA, ABCG40, Cc11_g01420; cytokinin, ABCG14, Cc08_g05640; Zhang et al., 2014; Kang et al., 2015), several predicted auxin response regulators (Phabulosa, Cc09_g08040; LBD16, Cc01_g18520; MIZU-KUSSEI-like protein, Cc04_g07700; Lee et al., 2009; Moriwaki et al., 2011; Müller et al., 2016), and a cytokinin signaling inhibitor that mediates auxin–cytokinin crosstalk (AHP6, Cc04_g04370; Bishopp et al., 2011). Furthermore, C3 (DS-specific late maturation genes) contained predicted hormone receptors (ABA, PYL8, Cc08_g15960; auxin, AFB5, Cc10_g15520; Prigge et al., 2016), and other potential auxin response proteins (ARF9, Cc08_g16330, IAA1, Cc04_g03620). This gene composition fingerprint suggests increased hormone sensitivity in desiccation-sensitive seeds, especially for auxin and cytokinin, while desiccation-tolerant seeds displayed higher expression (C1) for NHL6 (Cc05_g06810), a mediator of ABA signaling in Arabidopsis.
Differentially accumulated proteins associated with auxin signaling were also detected in the proteome. Similar levels of phytohormones in mature seeds do not exclude the possibility that desiccation-tolerant and -sensitive species integrate and respond to the hormone signals differently.

**Desiccation-tolerant and -sensitive coffee seeds display differences in transcriptional and metabolic control of respiratory processes**

The three coffee species shared a transcriptional slow-down for energy metabolism during seed maturation with down-regulation of numerous mitorespiration-related transcripts, such as those encoding several subunits of ATP synthase, many components of the electron transfer chain (NADH dehydrogenase complex I, cytochrome b₆f complex, cytochrome c oxidase), as well as many enzymes of the TCA cycle (isocitrate dehydrogenase, pyruvate dehydrogenase, succinyl-CoA ligase, dihydrodipiolipoyl dehydrogenase) (Supplementary Table S4). However, the interspecific transcriptome comparison revealed fundamental differences in the regulation of mitochondrial energy metabolism between desiccation-tolerant and desiccation-sensitive seeds. First, compared with *C. canephora*, desiccation-tolerant seeds displayed higher expression (C1 genes) of the translocase inner membrane subunit TIM44-2 (Cc01_g18340) and the mitochondrial splicing factor OTP439 (Cc01_g05040, Organelle transcript processing), involved in basal cellular processes such as protein import and organelle post-transcriptional processes, respectively (Murcha et al., 2014; Colas des Francs–Small et al., 2014). Second, there is a down-regulation in desiccation-tolerant seeds (C2 genes) of many genes encoding proteins pivotal for regulation of energetic processes, namely malate dehydrogenase MMDH1 (Cc02_g32320), a central enzyme in the TCA cycle (Sew et al., 2016), the voltage-dependent anion channel VDAC1 (Cc11_g13460), and the ATP synthase delta subunit (Cc02_g04940). VDAC1, an abundant protein of the outer mitochondrial membrane, contributes to the exchange of small metabolites essential for respiration and plays a role in redox control (Tateda et al., 2011; Robert et al., 2012). This transcriptional fingerprint suggests a slow-down of the machinery dedicated to oxidative phosphorylation, i.e. ATP production, without necessarily affecting the electron transfer chain operability. By contrast, desiccation-sensitive *C. canephora* seeds displayed late maturation induction (C3 genes) of several respiratory electron transfer chain complex components or genes involved in their assembly, namely complex I accessory subunits 6 and 7 (Cc02_g25880, Cc08_g10410) and complex I α subcomplex assembly factor 3 (Cc02_g25880), as well as the ubiquinone biosynthesis protein COQ4 (Cc06_g15640) and the cytochrome c-type biogenesis protein CcmH (Cc04_g07670). Desiccation-sensitive *C. canephora* seeds also displayed late maturation induction of genes involved in mitochondrial post-transcriptional and translational activities, such as elongation factors EFTu and EFTs (Cc03_g02960 and Cc05_g09920), and editing factors MEF10 and MEF11 (Cc04_g00410 and Cc11_g07090, respectively), the latter also being involved in ABA signaling (Sechet et al., 2015). The high expression level of these genes corresponds to the signature of organelles capable of maintaining high energy metabolism on demand. In this context, one may note the presence of a mitochondrial phosphate transporter, PMT3 (Cc07_g01200), which plays vital roles in phosphate homeostasis and ATP biosynthesis and whose expression levels modulate salt stress tolerance in Arabidopsis (Zhu et al., 2012). Finally, C3 contains two genes encoding proteins that may play a role in regulating mitochondrial metabolism under stress conditions: formate dehydrogenase (FDH, Cc07_g02270) and prohibitin PHB3 (Cc07_g00470). The mitochondrial FDH is a positive regulator of cell death and defense response, and confers tolerance to hypoxia, metal toxicity and low pH in Arabidopsis (Choi et al., 2014; Lou et al., 2016) while PHB3 functions in nitric oxide-mediated plant stress responses (Wang et al., 2010).

This transcriptional signature for differential energetic processes among desiccation-tolerant and desiccation-sensitive seeds led us to probe their respiratory activity during desiccation. Respiration rates, estimated as CO₂ release, were measured on mature seeds of the three coffee species at various moisture contents upon dehydration (Fig. 7). Within the 0.6–0.8 g H₂O g⁻¹ DM hydration window, all seeds displayed roughly equivalent respiratory activities. Upon desiccation, *C. arabica* and *C. eugenioides* seeds displayed a smooth reduction in respiration rate until ceasing detectable respiration at approximately 0.3 g H₂O g⁻¹ DM. Desiccation-sensitive *C. canephora* seeds, however, had a biphasic mode of respiration, initially displaying rather stable respiration rates between 0.8 and 0.4 g H₂O g⁻¹ DM. Below this threshold *C. canephora* seeds experienced drastic reduction in respiration rate that remained significantly higher than that measured for *C. arabica* and *C. eugenioides* seeds (Fig. 7).

**Discussion**

*A late maturation program also occurs in desiccation-sensitive coffee seeds*

Performed on developing seeds of three coffee species, the present transcriptome survey reveals the shared existence of a major transcriptional switch during the ST5–ST6 transition.
Desiccation-tolerant seeds harbor key stress proteins and integrators of stress response

Analysis of the DEGs identified relatively few DT-specific up-regulated genes (C1, 150 genes) compared with DT-specific down-regulated genes (C2, 292 genes), and identified many genes specifically induced in maturing desiccation-sensitive C. canephora seeds (C3, 571 genes; Fig. 4). Although transcription factors were under-represented among DT candidate genes (Figs 5, 6), three putative TFs were identified, a MADS (Cc09_g07070) and two GATA (Cc02_g34640; Cc01_g21240). These deserve further attention and validation of their potential role in orchestrating the DT-associated transcriptome during late maturation in coffee seeds.

In addition to these TFs, our survey did detect multiple genes related to cell rescue and stress response. Most notably, our survey revealed one LEA protein, EM6 (Cc05_g00080), whose gene expression and protein levels are significantly higher in C. canephora seeds (C3, 571 genes; Fig. 4). Although transcription factors were under-represented among DT candidate genes (Figs 5, 6), three putative TFs were identified, a MADS (Cc09_g07070) and two GATA (Cc02_g34640; Cc01_g21240). These deserve further attention and validation of their potential role in orchestrating the DT-associated transcriptome during late maturation in coffee seeds.

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loss during Arabidopsis seed germination (Maia et al., 2014). Our survey also revealed DT and DS differences in the expression of nuclear-encoded mitochondrial genes dedicated to energetic processes. Recent evidence suggests hormones and the mitochondrial metabolism could be more closely linked than initially thought as ABA was shown to induce typical transcripts of the mitochondrial retrograde response while auxin has the inverse effect (Ivanova et al., 2014; Wagner et al., 2018).

**Metabolic shut-down is better coordinated in desiccation-tolerant seeds**

In coffee seeds, the major transcriptional switch observed during late maturation included several nuclear-encoded mitochondrial proteins that are markers of large reorganization of energy metabolism (Fig. 3), mimicking what is observed in orthodox seeds, such as down-regulation of genes dedicated to the TCA cycle (Logan et al., 2001; Howell et al., 2006). Furthermore, our dataset revealed numerous quantitative differences in transcript accumulation for key mitochondrial proteins between coffee seeds displaying different DT levels. Among them, it is worth noting that desiccation-sensitive C. canephora seeds displayed enhanced accumulation of transcripts for subunits of the complexes I and III (NADH dehydrogenase and cytochrome b6), the major sites of superoxide production through one-electron reduction of molecular oxygen (Wagner et al., 2018). These transcriptomic differences observed between desiccation-tolerant and -sensitive coffee seeds appear to reflect the potential to slow down metabolism and respiration during dehydration rather than an actual slow-down phase during maturation since measured respiration rates in non-dehydrated mature seeds were similar among the three coffee species (Fig. 7). However, during their dehydration we observed striking differences in respiration rates. A better preparation or coordination of down-regulation of metabolism in desiccation-tolerant seeds during drying could play an important role in avoiding or limiting oxidative stress conditions and/or accumulation of by-products of metabolism to toxic levels. Seed respiration is generally detectable around 0.25 g H2O g−1 DM and respiration rates increase with increasing water contents above this threshold (Vertucci and Leopold, 1984; Vertucci, 1989). However, it is considered that at intermediate water contents the metabolism that occurs is unregulated, and there is evidence of damaging reactions that are probably free radical-mediated occurring in this water-content range (Leprince et al., 1990; Hendry et al., 1992; Hendry, 1993; Finch-Savage et al., 1994; Vertucci and Farrant, 1995). Interestingly, differences in the respiratory activities we observed between intermediate coffee seeds displaying different DT levels upon dehydration were similar to those observed between intermediate tea seeds and orthodox pea seeds (Walters et al., 2001), and between different recalcitrant Castanea seed tissues (axes and cotyledons) displaying differences in desiccation sensitivity (Leprince et al., 1999). The lack of coordinated repression of metabolism during drying is thought to play a predominant role in the oxidative burst that triggers lipid oxidation, membrane disruption, and ultimately the death of recalcitrant seeds (Leprince et al., 1999; Bailly, 2004; Kramer and Birtic, 2005). This mechanism could be shared with intermediate seeds displaying relatively low DT levels. Given that ROS-provoked mitochondria-dependent cell death has also been recently described for hydrated orthodox elm seeds under detrimental artificial ageing conditions (Wang et al., 2015), it defines mitochondria and the regulation of respiratory processes as universal targets of seed sensitivity to stress.

**Supplementary data**

Supplementary data are available at JXB online.

**Fig. S1.** Protein abundance variation among mature coffee seeds of the three species.

**Table S1.** RNAseq statistics of samples used.

**Table S2.** Gene expression (RPKM) in each sample.

**Table S3.** Pairwise comparisons of gene expression.

**Table S4.** Genes commonly up- and down-regulated during late maturation.

**Table S5.** Mapman functional enrichment analysis of late seed maturation.

**Table S6.** GO-term enrichment analysis of late maturation.

**Table S7.** DT-related gene candidates of seed late maturation.

**Table S8.** Mapman and GO functional enrichment analysis of DT-related clusters.

**Table S9.** Promoter cis-element enrichment analysis.

**Table S10.** Proteome of mature coffee seeds.

**Table S11.** DT-related protein candidates.

**Table S12.** Mapman functional enrichment analysis of candidate proteins.

**Table S13.** Candidate genes detected at both transcript and protein levels.

**Table S14.** Phytohormone profiling in mature coffee seed.

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