A Aethionema arabicum plant growth (glasshouse)



Glasshouse conditions: 16h light, 20°C for vegetative growth of all plants

Transfer to distinct temperature regimes during flowering/reproductive growth:

Day/night cycle: 16h / 8h Light intensity: 170 µmol • s⁻¹ • m⁻² Relative humidity: 65% Temperature at night: 20°C

Distinct day temperatures (PT, parental temperature during reproduction): Set 1 (1000 plants): parental temp. 20°C Set 2 (1000 plants): parental temp. 25°C

Harvest of fruits and seeds followed by germination experiments and sampling

M⁺ seeds from 20°C parental temperature (PT) 100 M⁺ seed T_{1%} times: M⁺ seed 24h Oh 9°C °C **PT20 PT25** 24h (T1% 0h 80 14°C 9 50h 35h 50h (T1%) 24h 20°C 14 24h 24h 24h 50h (T1%) 0h 60 ► 24°C 20 50h no germ. 24 no germination 40 Physiological times T_{1%} 20 Sampling times (h) for 20M⁺ seeds as indicated in scheme; comparisons of physical and physiological times possible (grey lines). Germination [%] 175 25 50 75 100 125 150 IND fruits from 20°C parental temperature (PT) 100 IND fruit IND fruit T_{1%} times: 24h 75h 125h (T_{1%}) 0h 9°C °C **PT20 PT25** 24h 75h 100h (T_{1%}) 0h 80 14°C 75h 9 125h 75h 24h)h 20°C 24h 14 100h 75h Dh 60 24°C 20 no germination 24 no germination 40 Sampling times (h) for 20IND fruits as 1% 1% indicated in scheme; note that IND fruits were separated into M⁻ seeds and pericarp 20 (fruit coat); transcriptomes were conducted 0 with M⁻ seeds from imbibed IND fruits and 25 100 50 75 125 150 175 for comparison with imbibed M⁻ seeds; Time [h] hormones were also analysed in pericarps.

B Sampling scheme during seed and fruit imbibition for transcriptome and hormone analyses



Supplemental Figure S1. Large-scale *Aethionema arabicum* diaspore production experiment, example germination curves and sampling scheme for the molecular analyses (Supports Figure 1). A, Plant growth with two distinct maternal temperatures during reproduction. B, Sampling scheme for the transcriptome and hormone analyses during seed and fruit imbibition. A combination of dry (0 h), physical (e.g. 24 h) and physiological ($T_{1\%}$) timepoints was used; $T_{1\%}$ represents the population's onset of germination curves and maximal germination percentages (G_{max}). for *Ae. arabicum* M⁺ seeds, IND fruits and bare M⁻ seeds (with IND pericarp manually removed) at different imbibition temperatures and as affected by distinct maternal temperature environments. Mean ± SEM values of 3 replicates each with 20 seeds or fruits are presented.

Supplemental Data. Chandler et al. (2024). Dimorphic germination control. Plant Cell



Supplemental Data. Chandler et al. (2024). Dimorphic germination control. Plant Cell



Supplemental Figure S2. Aethionema arabicum Gene Expression Atlas tool (https://plantcode.cup.unifreiburg.de/easy_gdb/tools/expression/expression_input.php) (Supports Figures 2, 3, and 4). A, Genes with the highest module membership of the pink co-expressed gene module AA4G00252, AA31G00360, AA60G00187, AA39G00802, AA57G00255, AA102G00141, AA10G00208, AA32G00445, AA89G00051, AA8G00115, which was associated with pericarp removal (more highly expressed in imbibed bare M⁻ seeds, pericarp removed) were used as a query in the Gene Expression Atlas tool using the '03 Morphotype' experiment dataset, the dataset used for this study. B, Expression trends in the atlas (line graph and heatmap) show the strong increase in the imbibed M⁻ seed samples compared to M⁺ and IND. Sample naming scheme used for the atlas is available in Supplementary Data Set S1. C, Separation of replicates across samples and average values as a table can also be visualized using the expression atlas. D, The associated expression comparator tool was used to visualize expression of the top ten yellow module genes AA111G00011, AA32G00335, AA41G00057, AA69G00003, AA32G00709, AA33G00330, AA193G00003, AA28G00037, AA44G00143, AA32G00987 in the experiments of Wilhelmsson *et al.* (2019) on dry seed, Arshad *et al.* (2021) on fruit development and in dry and imbibed seeds from this study. The normalization option was used to normalize the expression to reference genes used for RT-qPCR in this study (AA30G00197, AA255G00007). E, The trends suggest that the yellow module genes are generally most highly expressed in dry seeds, including in Wilhelmsson *et al.* (2019). Expression may be relatively higher in buds, flowers and fruits than in imbibed M^+ and M^- seeds.





Supplemental Figure S3. Principal components analysis (PCA) comparing the seed mRNA transcriptome data (RNA-sequencing analysis) of *Aethionema arabicum* (Supports Figure 2). A, Average PCA coordinates for PC2 versus PC1 (Figure 2) and samples shaded relative to final germination percentages (G_{max}) comparing diaspore morphs, maternal and imbibition temperatures. Icon shape represents morph, lower left bold blue text indicates imbibition temperature, lower right black text indicates time-point, central bold black text indicates maternal temperature, and shading indicated G_{max} . B, Average PCA coordinates for PC3 versus PC1. C, Variance explained by the top 15 PCs. Note that a broad trend was observed following imbibition in that under conditions that are generally germination-permissive, with increasing imbibition time, samples travel positively along PC1 (25% of variance). PC2 (14% of variance) on the other hand appears to generally separate IND and M⁺ from bare M⁻ seed. PC3 (11% of variance) may have some relation to imbibition temperature. PCA plots were drawn in R with the ggplot2 package (v3.3.6; Wickham, 2016).

Supplemental Data. Chandler et al. (2024). Dimorphic germination control. Plant Cell

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Supplemental Figure S4 continued next page...

Supplemental Data. Chandler et al. (2024). Dimorphic germination control. Plant Cell





Supplemental Figure S4. Expression of WGCNA modules over all *Aethionema arabicum* samples (Supports Figure 3), M⁺ and M⁻ seeds and IND fruits from two maternal temperatures (20°C and 25°C), at four imbibition temperatures (9°C, 14°C, 20°C and 24°C), and multiple time-points. Panels show sample means (thick lines) of mean Z-score expression of module member genes as well as sample mean Z-scores of each individual module gene member (thin lines, 'spaghetti plots). Modules are referred to by color (yellow, red, green, brown, black, blue, magenta, purple, turquoise, grey, pink) as detailed in Figure 3. Plots drawn in R with ggplot2 (v3.1.0; Wickham, 2016).





Supplemental Figure S5. Temperature responses and ABA and GA metabolism (Supports Figures 4 and 5). Comparative analysis of germination responses at different temperatures and associated abscisic acid (ABA) and gibberellin (GA) metabolism gene transcript abundance patterns of Aethionema arabicum dimorphic diaspores. A. Dimorphic diaspores (M⁺ seeds, IND fruits) and bare M⁻ seeds (extracted from IND fruits) from two maternal temperature regimes during reproduction (20°C versus 25°C) were compared for their kinetics of germination at four different imbibition temperatures (9, 14, 20 and 24°C). Comparative results were obtained for physical (in hours) and physiological timepoints ($T_{1\%}$, representing the population's onset of germination completion). Mean ± SEM values of 3 replicates each with 20 seeds. B, Normalized transcript abundances in reads per kilobase per million (RPKM) from the transcriptomes (RNA-seq) are presented for the ABA metabolism genes 9-cisepoxycarotenoid dioxygenase (AearNCED), zeaxanthin epoxidase (AearZEP/ABA1), short-chain dehydrogenase/reductase (AearSDR1/ABA2), abscisic aldehyde oxidase (AearAAO), and ABA 8'hydroxylase (AearCYP707A). WGCNA modules (Figure 3) for these genes are indicated by the vertical color lines next to the graphs. Mean ± SEM values of 3 replicates each with 60-80 (RNA-seg) seeds. C. Simplified ABA biosynthesis and degradation pathway. Major metabolites and associated enzymes are indicated; phaseic acid (PA) and dihydrophaseic acid (DPA) are generated non-enzymatically. D, Normalized transcript abundances from the transcriptomes (RNA-seq) for gibberellin GA3-oxidases and GA2-oxidases which catalyze the formation of bioactive GAs from inactive precursors and the inactivation of bioactive GAs, respectively. For Ae. arabicum gene names and IDs see Supplemental Table S2 the Gene Expression Atlas (https://plantcode.cup.unior freiburg.de/easy gdb/tools/expression/expression input.php); for RNAseg single values see the Expression Atlas or Supplemental Data Set S1. For gene IDs from and modules of the presented expression results (individual or as cumulative sum) see Supplemental Table S2.



Supplemental Figure S6 continued next page...



13



Supplemental Figure S6. Comparative analysis of *Aethionema arabicum* dimorphic diaspore germination responses at different temperatures, associated hormone metabolite contents and effects of hormones (Supports Figure 6). A, Dimorphic diaspores (M⁺ seeds, IND fruits) and bare M⁻ seeds (extracted from IND fruits) from two maternal temperature regimes during reproduction (20°C versus 25°C) were compared for their kinetics of germination and hormone metabolite contents at four different imbibition temperatures (9, 14, 20 and 24°C). Comparative results were obtained for physical (in hours) and physiological time-points (T_{1%}, representing the population's onset of germination completion). Hormone metabolites contents in pericarp and in M⁺ and M⁻ seeds presented: abscisic acid (ABA) and ABA degradation products phaseic acid (PA) and dihydrophaseic acid (DPA), and salicylic acid (SA). B, Comparative analysis of indole-3-acetic acid (IAA), 2-oxoindole-3-acetic acid (IAAox), *cis*-(+)-12-oxophytodienoic acid (OPDA), jasmonic acid (JA) and its isoleucine conjugate (JA-IIe) contents in pericarp and in M⁺ and SA optaterns during seed or fruit imbibition at 14°C. D, Effect of OPDA, JA, JA-IIe, and SA on M⁺ seed germination. Mean ± SEM values of 3 (germination) or 5 (metabolites) biological replicate samples each with 20 (germination) or 30-40 (metabolites) are presented.



Supplemental Figure S7. Effects of IND pericarp extract (PE) and abscisic acid (ABA) of *Aethionema arabicum* dimorphic diaspore germination and expression of selected genes representing the WGCNA modules (Supports Figures 6 and 8). A, The effect pf IND PE and ABA on the germination of bare M⁻ seeds (obtained from IND fruits by pericarp removal) from plants grown at 20°C parental termperature (PT). B, The effect of PE and ABA on the expression of selected genes representing the WGCNA modules. Note that the corresponding effect of hypoxia on the expression of these genes is presented in Figure 8B. For *Ae. arabicum* gene names and IDs see Supplemental Table S2 or the Expression Atlas (https://plantcode.cup.uni-freiburg.de/aetar_db/index.php). C, The effect pf IND PE and ABA on the germination of bare M⁻ seeds from plants grown at 20°C PT. D, The effect pf IND PE and ABA on the germination of M⁺ seeds from plants grown at 20°C or 25°C PT. Mean ± SEM values of 3 (germination, RT-qPCR) biological replicate samples are presented.



Supplemental Figure S8. *Aethionema arabicum* pericarp (fruit coat) biomechanics (Supports Figure 6). A, Typical force-displacement curve of a IND fruit pericarp. Fruits have been cut in half, seeds removed and the dry, empty fruits halves have been probed with a rounded 0.3 mm needle. B, pericarp strength of whole IND fruits. Fruit was laid flat on a sample holder and a 0.3 mm steel probe was driven into the sample while force and displacement were measured simultaneously. Dry fruits show no significant difference to re-dried fruits that had been incubated for 9 days at 80% relative humidity. Imbibed fruits (3 h in water) show a significantly lower pericarp resistance.



Supplemental Figure S9. Transcription factor (TF) and target *cis*-regulatory motif analysis of *Aethionema arabicum* gene expression with focus on hypoxia and ABA related genes (Supports Figure 7). A, Transcript abundance patterns (RNA-seq) of the *Ae. arabicum* pyruvate decarboxylase (*AearPDC2* and *AearPDC1*) and lactate dehydrogenase (*AearLDH*) genes in seeds of imbibed dimorphic diaspores (M⁺ seeds, IND fruits) and bare M⁻ seeds (extracted from IND fruits) from two maternal temperature regimes (20°C versus 25°C) at four different imbibition temperatures (9, 14, 20 and 24°C). WGCNA modules (Figure 3) for these genes are indicated by the vertical color lines next to the graphs. Mean ± SEM values of 3 replicates each with 60-80 seeds are presented. C, Addition to working model for the pericarp-mediated hypoxia up-regulation (P[↑]) and ABA signaling (Figure 6C) for

the A. thaliana and Ae. arabicum PDC genes. Motifs indicated include the hypoxia-responsive promoter element HRPE, the G-box and ABA-responsive element (ABRE), the ERF73 cis-regulatory element and HB-motifs for the binding of homeobox TFs. These motifs are the targets for the AearERF71/73 TF and the ABA related ABI5, ABF (ABRE-binding factors), GBF (G-box-binding factors), and AREB3 TFs (blue boxes). For details about the cis-regulatory motif analysis see Supplemental Figure S10. The AearADH1a 5'-regulatory gene region contains ERF73 and HRPE motifs and is distinct from the AtADH1 and AearADH1b 5'-regulatory gene regions in that it does not contain G-box/ABRE and HB binding motifs (Figure 7C). The AearERF71/73 5'-regulatory gene region was also distinct from its A. thaliana homologs by the presence of two ERF73 and one HB13/20 motif, suggesting that the AearERF71/73 gene possibly provides a positive feedback regulation on the pericarp/hypoxia-mediated AearADH1a and AearERF71/73 expression (Figure 7C). Further support for the importance of these motifs is that the pericarp/hypoxia-induced AearPDC2 5'-regulatory gene region also contains these motifs, as well as no G-box/ABRE motifs. In contrast to this, the low expressed AearPDC1 and AearADH1b 5'regulatory regions contain, as the AtPDC2 and AtADH1 gene promoters, in addition G-box/ABRE motifs (Figure 7C; Supplemental Figure S10). Supplemental Figure S10 provides a more detailed comparative analysis of Ae. arabicum and A. thaliana 5'-regulatory gene regions, including for AearDOG1 (Figure 7C). For Ae. arabicum gene names and IDs see Supplemental Table S2 or the Gene Expression (https://plantcode.cup.uni-freiburg.de/easy_gdb/tools/expression/expression input.php); Atlas for RNAseg single values see the Expression Atlas or Supplemental Data Set S1. For gene IDs from and modules of the presented expression results (individual or as cumulative sum) see Supplemental Table S2.



Supplemental Figure S10. Expression patterns of *Aethionema arabicum* genes involved in the seedspecific "Perl's pathway" (Supports Figure 7). A, Transcript abundance patterns (RNA-seq) of *Ae. arabicum* aspartate amino tranferase (*AspAT*), cytosolic malate dehydrogenase (*MDHc*), and NADPdependent malic enzyme (*NADP-ME2*) genes in seeds of imbibed dimorphic diaspores (M⁺ seeds, IND fruits) and bare M⁻ seeds (extracted from IND fruits) from two maternal temperature regimes (20°C versus 25°C) at four different imbibition temperatures (9, 14, 20 and 24°C). WGCNA modules (Figure 3) for these genes are indicated by the vertical color lines next to the graphs. Mean ± SEM values of 3 replicates each with 60-80 seeds are presented. B, Scheme of the "Perl's pathway" in *A. thaliana*, for details about this metabolic shunt pathway see Weitbrecht *et al.* (2011). For gene IDs from and modules of the presented expression results (individual or as cumulative sum) see Supplemental Table 2. For *Ae. arabicum* gene names and IDs see Supplemental Table S2 or the Gene Expression Atlas (https://plantcode.cup.uni-freiburg.de/easy_gdb/tools/expression/expression_input.php); for RNAseq single values see the Expression Atlas or Supplemental Data Set S1.



Supplemental Figure S11. Expression patterns of *Aethionema arabicum* genes known to be regulated by hypoxia in *Arabidopsis thaliana* seedlings (Supports Figure 7). Transcript abundance patterns (RNA-seq) of *Ae. arabicum* genes in seeds of imbibed dimorphic diaspores (M⁺ seeds, IND fruits) and M⁻

seeds (extracted from IND fruits) from two maternal temperature regimes (20°C versus 25°C) at four different imbibition temperatures (9, 14, 20 and 24°C). WGCNA modules (Figure 3) for these genes are indicated by the vertical color lines next to the graphs. Mean ± SEM values of 3 replicates each with 60-80 seeds are presented. Examples presented (references for *A. thaliana* hypoxia experiments): NAC-domain containing TF *AearNAC102* (*NAM* (*no apical meristem*), *ATAF1,2 and CUC2* (*cup-shaped cotyledon*)) (Christianson et al., 2009), Myb-type TF *AearHHO2* (*HRS1* (*hypersensitive to low Pi-elicited primary root shortening*) homolog), *AearHAR1* (receptor kinase), plant cysteine oxidase *AearPCO1/2* (Lee et al., 2019), 1-aminocyclopropane-1-carboxylic acid oxidase *AearACO1*, *AearETR1* (*Ethylene response 1*), *AearJAZ3* (*Jasmonate-zim-domain protein*) (Ju et al., 2019; Gasch et al., 2016). For *Ae. arabicum* gene names and IDs see Supplemental Table S2 or the Gene Expression Atlas or Supplemental Data Set S1. For gene IDs from and modules of the presented expression results (individual or as cumulative sum) see Supplemental Table S2.



Supplemental Figure S12 continued next page...



Supplemental Figure S12. Comparative analysis of germination and gene expression in IND fruits and bare M⁻ seeds as affected by hypoxia and abscisic acid (ABA) and the pericarp (Supports Figure 8). A, The effect of hypoxia (4.5±0.2% oxygen) on the germination of bare M⁻ seeds and M⁺ seeds at 14°C in continuous white light. B, RT-pPCR expression analysis of selected genes during *Aethionema arabicum* bare M⁻ seed imbibition (14°C, continuous light) under hypoxia (4.5±0.2% oxygen) and normoxia (21% oxygen) conditions ± 5 μ M abscisic acid (ABA). The 38 h timepoint (arrow) corresponds to T_{1%} of the control (normoxia without ABA). For additional genes and expression in IND fruits see Figure 8. C, RT-

pPCR expression analysis of selected genes during *Aethionema arabicum* IND fruit and bare M⁻ seed imbibition under control (normoxia) conditions. Bare M⁻ seeds were obtained from dry IND fruits by pericarp removal and imbibed at 14°C in continuous light. The 38 h timepoint (arrow) corresponds to $T_{1\%}$ of the control (normoxia). Mean ± SEM values of 3 (germination, RT-qPCR) biological replicate samples are presented. Differential gene expression was assessed using statistical tests (Supplemental Table S4). For *Ae. arabicum* gene names and IDs see Supplemental Table S2 or the Expression Atlas (https://plantcode.cup.uni-freiburg.de/aetar_db/index.php).

A 5'-regulatory motif analyses - FIMO and AME motif search tool best hits:

MOTIF	WIDTH	BEST POSSIBLE MATCH	TF
AP2EREBP_tnt.ERF73_col_a_m1 AP2EREBP_tnt.ERF73_colamp_a_m1 HRPEGasch2016	21 21 12	CCACCGCCGCCGCCATTTCCG ATGGCGGCGGCGGCGGCGGCG GCCCCTGGTTTT	ERF73 ERF73 HRPE
AP2EREBP_tnt.RAP212_col_a_m1	21	CGGCGGAAAIGGCGGCGGAGG	RAP2.12
bZIP_tnt.ABI5_col_v3h_m1	18	AAATGGTGACGTGGCAGT	ABI5
bZIP_tnt.ABI5_colamp_v3b_m1	15	AATGGTGACGTGGCA	ABI5
bZIP_tnt.AREB3_col_v31_m1	15	AATGGACACGTGGCA	AREB3
bZIP_tnt.AREB3_colamp_a_m1	15	AATGGACACGTGGCA	AREB3
bZIP_tnt.ABF2_col_v3a_m1	18	AAAAATGCCACGTGACCA	ABF2
bZIP_tnt.GBF3_col_m1	15	TGCCACGTCAGCATT	GBF3
bZIP_tnt.GBF3_colamp_m1	15	AATGGTCACGTGGCA	GBF3
bZIP_tnt.GBF5_col_v3a_m1	15	AATGCTGACGTGGCA	GBF5
bZIP_tnt.GBF5_colamp_a_m1	15	AATGCTGACGTGGCA	GBF5
bZIP_tnt.GBF6_col_m1	15	TGCCACGTCAGCATC	GBF6
bZIP_tnt.GBF6_colamp_a_m1	15	AATGCTGACGTGGCA	GBF6
RAV_tnt.RAV1_col_m1	17	CAGATAATTTCTGTTGT	RAV1
RAV_tnt.RAV1_colamp_a_m1	21	TTTTCAGGTGATTTCTGTTGT	RAV1
Homeobox_tnt.ATHB13_col_a_m1	11	ΤCΑΑΤΑΑΤΤΑΑ	HB13
Homeobox_tnt.ATHB13_colamp_a_m1	11	TCAATAATTGA	HB13
Homeobox_tnt.ATHB20_col_a_m1	11	TCAATAATTGA	HB20
Homeobox_tnt.ATHB20_colamp_a_m1	11	TCAATTATTGA	HB20
ZFHD_tnt.ATHB23_col_b_m1	22	ΑΑΤΟΤΤΑΑΤΤΑΑΤΤΑΑΤΑΑΑΤΤ	HB23
ZFHD_tnt.ATHB23_colamp_a_m1	11	CTTAATTAATT	HB23
ZFHD_tnt.ATHB33_col_a_m1	11	ACGTAATTAAT	HB33
ZFHD_tnt.ATHB33_colamp_a_m1	15	AAAAACGTAATTAAT	HB33
ZFHD_tnt.ATHB25_col_a_m1	15	TAATTAATTAAGTTT	HB25
ZFHD_tnt.ATHB25_colamp_a_m1	11	CGTAATTAATG	HB25
ZFHD_tnt.ATHB34_col_a_m1	15	TTTAATCATTAATTA	HB34
ZFHD_tnt.ATHB34_colamp_a_m1	15	TAAAACATGATTAAT	HB34
HB_tnt.ATHB5_col_a_m1	11	TCAATAATTGA	HB5
HB_tnt.ATHB5_colamp_a_m1	10	CAATGATTGA	HB5

²] ERF73 ᡱ'-²]ABI5 ∄' <mark>وني ي</mark> ي ي ال ²]ABI5 ÷1 *** ²]GBF3

) RAP2.12 ERF73 ž1 AREB3 ź,] AREB3 **⊋**C -÷ GBF5 --GGC -

AME - Analysis of Motif Enrichment, Database ArabidopsisDAPv1

ABF2 ÷÷÷ GBF6

Supplemental Figure S13 continued next page...



Motif analyses of Aethionema arabicum and Arabidopsis thaliana ADH1 genes: detail analysis of proximal 1-kb 5'-regulatory regions







Motif analyses of ERF73/71 genes: ERF73 (red triangles) and HRPE (blue triangles) motif analysis of 3.5-kb regions





Motif analyses of PDC genes: ERF73 (red triangles) and HRPE (blue triangles) motif analysis of 3.5-kb regions

AearPDC1	1 1,884,839	200 1,884,640	400 1,884,440	600 1,884,240	800 1,884,040	1,000 1,883,840	1,200 1,883,640	1,400 1,883,440	1,600 1,883,240	1,800 1,883,040	2,000 1,882,840	2,200 1,882,640	2,400 1,882,440	2,600 1,882,240	2,800 1,882,040	3,000 1,881,840	3,200 1,881,640	3,400 1,881,440	3,600 1,881,240
AA 1900000)-н	RPE	AA19 AA19 - HRPE	ERF73 9G00366.Cl G00366.mF	(weak) - DS1 DS1 HRPE - ERF73- ERF73- EF	ERF73	H - ERF73 →- ERF73	RPE-)		HRPE-(H ERF	AA19G00 AA19G003 RPE-((-HF 73-()-ER	0365.CDS5 065.mRNA1 RPE 9F73 E	- 1 RF73
AearPDC2 AA215G00009	1 252,346	200 252 ₁ 545	400 252,745	600 252 ₁ 945	800 253,145	1,000 253,345	1,200 253,545	1,400 253,745	1,600 253,945	1,800 254,145	2,000 254,345	2,200 254,545	2,400 254,745	2,600 254,945	2,800 255,145	3,000 255,345	3,200 255¦545 AA215G000 AA215G000	3,400 255,745 0009.CDS1- 009.mRNA1	3,600 255,945
		HRPE	•	HRPI	F73- E-) HRPE-	4		ERF73- ERF73-	- HRPE						HRPE	-)	ERF73- ERF73- ERF73 HRPE	- ERF73	
<i>AtPDC1</i> AT4G33070	1 15,958,271	200	400 15,957,872	600 15,957,672	800 15,957,472	1,000 15,957,272	1,200 15,957,072	1,400 15,956,872	1,600 15,956,672	1,800 15,956,472	2,000 15,956,272	2,200 15,956,072	2,400 15,955,872	2,600 15,955,672	2,800 15,955,472 HRPE -	3,000 15,955,272	3,200 15,955,072	3,400 15,954,872	3,600
		(- HRPE	E	RF73-			HR	PE-(H	RPE-	ERF73 3-) ((3-) (HRPE- - ERF73 - ERF73	ERF7:	3 E ERF73 1973	ERF	HRPE- 73- ≬	(AT H	'4G33070.1- IRPE - (CDS-
<i>AtPDC2</i> AT5G54960	1 22,316,26	200 i2	400 22,315,863	600 22,315,663	800 22,315,463	1,000 22,315,263	1,200 22,315,063	1,400 22,314,863	1,600 22,314,663	1,800 22,314,463	2,000 22,314,263	2,200 22,314,063	2,400 22,313,863	2,600 22,313,663 HRPE (2,800 22,313,463 fairly strong)	3,000 22,313,263	3,200 22,313,063	3,400 22,312,863	3,600
		AT5G	554980.1 CDS	HRPE	4	•					Þ			HRPE-)	AT5G54970 CDS	HRPE	TA I	5G54960.1 HRPE HRPE	DDS-C
<i>AtPDC3</i> AT5G01330	1 138,362	200 138,163	400 137,963	600 137,763	800 137,563 HRPE (\	1,000 137,363 weak)-	1,200 137,163	1,400 136,963	1,600 136,763	1,800 136,563	2,000 136,363	2,200 136,163 HRPE (wea	2,400 135,963 k)- ERI	2,600 135,763	2,800 135,563	3,000 135,363	3,200 135,163	3,400 134,963	3,600 134,763
	{-+ ∢	IRPE	(- HRPE		HRPE-	HRPE	AT5G	01335.1 01335 (-HRPE 4 5 4	HRPE	↓ -HRPE	HR •	PE-(HRP	E-(1+ HRI IRPÉ	PE (-HRPI	E		TA	CI 5G01330.1	
AtPDC4	1 135,126	200 134,927 ERI	ERF73 (we 400 134,7:7	eak) ERF 600 134, 27	73 (weak) 800 134,327	1,000 134,127	1,200 133,927	1,400 133,727	1,600 133,527	1,800 133, <mark>327</mark>	2,000 133,127	2,200 132,927	2,400 132,727 HRPE (1	2,600 132,527	2,800 132,327	3,000 132,127	3,200 131,927	3,400 131,727 ERI	3,600 131,527
			44.4	CDS			HRPE-	AT50 CDS	501330.1 4					HRPE	-)		ΓA	5G01320.1 CDS	-
						4			,				N A	,					



Motif analyses of Aethionema arabicum and Arabidopsis thaliana LDH genes: detail analysis of proximal 1-kb regions

Promoter analyses of LDH genes: ERF73 (red triangles) and HRPE (blue triangles) motif analysis of 3.5-kb regions

AearLDH	1 200 1,340,952 1,341,151	400 1,341,351	600 1,341,551	800 1,341,751	1,000 1,341,951	1,200 1,342,151	1,400 1,342,351	1,600 1,342,551	1,800 1,342,751	2,000 1,342,951	2,200 1,343,151	2,400 1,343,351	2,600 1,343,551	2,800 1,343,751	3,000 1,343,951	3,200 1,344,151	3,400 3,600 1,344,351 1,344,55
AA57G00289)-HRPE	ERF73-	- EF	RF73												445700	0289 CDS1-
			AA57G0	0288 mRNA	1											AA57G002	89.mRNA1-
	HRPE HRPE	IRPE	RPE	HR	PE, HRPE -)	(HRPE-))-HR	PE		1	HRPE, HRPE	≅-((HRPE
AtLDH	1 200 9,670,491 9,670,690	400 9,670,890	600 9,671,090	800 9,671,290	1,000 9,671,490	1,200 9,671,690	1,400 9,671,890	1,600 9,672,090	1,800 9,672,290	2,000 9,672,490	2,200 9,672,690	2,400 9,672,890	2,600 9,673,090	2,800 9,673,290	3,000 9,673,490	3,200 9,673,690	3,400 3,600 9,673,890 9,674,090
AT4G17260						HRPE	-)					ERF73	(weak)-				
			_				AT	4G17250.2								AT	4G17260.1-
								AT40	G17250.1					-CDS			CDS-C
								C	DS								
			ERF7 ERF7	HRPE-('3-	- ERF73 - ERF73 - ERF73	HRPE- ERF73- ERF73-	- HRPE	4 - €	RF73	ERF73-		E	ERF73-			HRPE-	- HRPE





Supplemental Figure S13. Comparison of Aethionema arabicum and Arabidopsis thaliana ADH, PDC, ERF73/71, LDH and DOG1 gene 5'-regulatory regions for hypoxia and ABA-related *cis*-regulatory motifs (Supports Figure 7). A, Best possible hits for motifs used in FIMO (Grant et al., 2011) scans of promoter sequences. All motifs except one (HRPE) were from the ArabidopsisDAPv1 database (O'Malley et al., 2016) obtained from The MEME Suite (https://meme-suite.org/meme/doc/download.html) (Bailey et al., 2015). HRPE (also known as C9-motif from Gasch et al., 2016, Supplemental Data Set 2) was converted to MEME motif format. Sequence logos show similarity of ERF73 and RAP2.12 motifs, and similarity of the ABI5, AREB3, ABF2, and GBF motifs. FIMO was used to scan for all above motifs in the start codon -1000 bp to +100 bp ('1kb') and for HRPE and ERF73 motifs in -3.5 kb (-3.4 kb for A. thaliana) to +100 bp regions ('3.5kb') of: B, ADH1 homologs AearADH1a (AA39G00353) and AearADH1b (AA31G00264) and AtADH1 (AT1G77120); C, AtERF71 (AT2G47520), AtERF73 (AT1G72360) and homolog AearERF73/71 (AA21G00481); PDC homologs AearPDC1 (AA19G00365), AearPDC2 (AA215G00009), AtPDC1 (AT4G33070), AtPDC2 (AT5G54960), AtPDC3 (AT5G01330) and AtPDC4 (AT5G01320) for D, 1kb regions and E, 3.5kb regions; F, LDH homologs AearLDH (AA57G00289), AtLDH (AT4G17260) and G, DOG1 homologs AearDOG1 (AA6G00020) and AtDOG1 (AT5G45830). Identified motifs were shaded and annotated according to their p-value. Strong hits are shaded darker and weak hits shaded lighter. Hits subjectively determined to be weaker relative to other hits for a given sequence were labelled as such. p-values of <1E-4 and <1E-3 were considered as hits for the 1kb and 3.5 kb FIMO scans, respectively. Detailed output for hits is given in Supplemental Data Set S4.



Supplemental Figure S14 continued next page...



Supplemental Figure S14 continued next page...

Time [h] or physiological time $T_{1\%}$



Supplemental Figure S14. Expression patterns of *Aethionema arabicum* ABA-related genes (This supports Figure 9). Transcript abundance patterns (RNA-seq) of *Ae. arabicum* genes in seeds of imbibed dimorphic diaspores (M⁺ seeds, IND fruits) and bare M⁻ seeds (extracted from IND fruits) from two maternal temperature regimes (20°C versus 25°C) at four different imbibition temperatures (9, 14,

20 and 24°C). WGCNA modules (Figure 3) for these genes are indicated by the vertical color lines next to the graphs. Mean ± SEM values of 3 replicates each with 60-80 seeds are presented. A, ABA-related bZIP TF TFs binding to G-box and ABA-responsive element (ABRE) motifs, including ABF (ABREbinding factors), AREB3 (ABRE-binding proteins), and GBF (G-box-binding factors). B, ABA and hypoxia related AP2/EREBP and homeobox (HB) TFs including RAV (Related to ABI3/VP1), RAP (HRPE-binding ERF-VII TF). In contrast to AearABI5, AearGBF1-4, and AearAREB/ABF TF genes, which were higher expressed in IND fruits, the AearGBF5, AearHB13, AearHB20, AearHB23, AearHB25, AearHB33, AearRAP2.2, AearRAP2.12, and AearRAV2 TF genes were generally higher expressed in bare M⁻ seeds and in M⁺ seeds. In A. thaliana, the HB13 and HB20 TFs constitute noderegulators within the co-expression network controlling seed-to-seedling phase transition (Silva et al., 2016) while other HB TFs control seed ABA sensitivity, dormancy, longevity and embryo growth (Barrero et al., 2010; Wang et al., 2011; Bueso et al., 2014; Stamm et al., 2017; Renard et al., 2021). The RAV (Related to ABI3/VP1) TFs are involved in ABA and stress responses of seeds, and the ERF-VII RAP2 TFs are known to be involved in sustaining ABA responses during hypoxia of A. thaliana seedlings (Papdi et al., 2015; Gasch et al., 2016). C; ABA receptors (PYR1/RCAR11, PYR/PLY/RCAR) and signaling components including protein phosphatase 2C proteins (e.g., HAB1 and AGH3) and SNF1related protein kinase subfamily 2 (SnRK2) which has ABI5 and other ABA-related TFs as targets (Nambara et al., 2010). Transcript abundance patterns of these ABA signaling components also exhibit pericarp-affected expression patterns in the Ae. arabicum morphs. D, Simplified scheme of ABA perception and signaling, for details see Nambara et al. (2010). For Ae. arabicum gene names and IDs or the Gene Expression Atlas Supplemental Table S2 (https://plantcode.cup.unisee freiburg.de/easy gdb/tools/expression/expression input.php); for RNAseg single values see the Expression Atlas or Supplemental Data Set 1. For gene IDs from and modules of the presented expression results (individual or as cumulative sum) see Supplemental Table S2; included PYR/PYL/RCAR genes and modules are listed here: AA57G00057 (PYR1/RCAR11, turquoise), AA11G00152 (grey), AA1G00061, AA29G00245 (turquoise), AA31G00648, AA31G00648, AA32G00133, AA32G01060 (purple), AA35G00054 (grey), AA56G00008 (turquoise), AA57G00145, AA61G00520, AA6G00016 (yellow), AA805G00002 (turquoise).



Supplemental Figure S15. Expression patterns of Aethionema arabicum general transcription and translation related genes (Supports Figure 9). This includes the general RNA polymerase II transcription elongation complex (Antosz et al., 2017), ribosomal proteins (RPs) and 20S proteasome subunits. For details see Wilhelmsson et al. (2019). Transcript abundance patterns (RNA-seq) of Ae. arabicum genes in seeds of imbibed dimorphic diaspores (M⁺ seeds, IND fruits) and M⁻ seeds (extracted from IND fruits) from two maternal temperature regimes (20°C versus 25°C) at four different imbibition temperatures (9, 14, 20 and 24°C). WGCNA modules (Figure 3) for these genes are indicated by the vertical color lines next to the graphs. Mean ± SEM values of 3 replicates each with 60-80 seeds are presented. For Ae. arabicum gene names and IDs see the Gene Expression Atlas (https://plantcode.cup.uni-freiburg.de/ easy gdb/tools/expression/expression input.php) for: NRBP2 (DNA-directed RNA polymerase protein, AA57G00370), cumulative TAF sum (TBP-associated factors: AA19G00069, AA46G00184, AA7G00014, AA93G00180, AA31G00549, AA3G00252, AA6G00143, AA102G00330, AA12G00070, AA15G00183, AA118G00072, AA15G00168, AA2G00137, AA33G00098), cumulative TFIIS sum (AA139G00004, AA44G00247, AA35G00003, AA93G00180, AA53G00202, AA9G00120, AA53G00203), TFIID/EER2 (AA31G00674), PAF-C/VIP5 (vernalization independence5, AA53G00526), cumulative 20S proteasome subunits sum (AA32G00927, AA326G00002, AA3G00223, AA87G00203, AA37G00101, AA31G00785, AA17G00024, AA26G00153, AA87G00239), cumulative RP sum (ribosomal proteins of the turquoise (*RPs) and grey/pink/blue/purple modules (**RPs):

*RPs: AA101G00012, AA102G00014, AA102G00094, AA102G00243, AA10G00061, AA10G00080, AA10G00130, AA10G00137, AA10G00174, AA10G00246, AA10G00354, AA10G00397, AA116G00015, AA1312G00001, AA157G00010, AA15G00029, AA15G00304, AA162G00004, AA1679G00001, AA17G00034, AA17G00041, AA18G00038, AA18G00042, AA18G00170, AA19G00027, AA19G00104, AA19G00122, AA19G00206, AA19G00268, AA19G00272, AA19G00282, AA19G00299, AA19G00300, AA1G00040, AA20G00024, AA21G00117, AA21G00126, AA21G00142, AA21G00422. AA21G00486, AA21G00490, AA226G00005, AA22G00082, AA23G00037, AA23G00103, AA252G00005, AA25G00051, AA26G00029, AA26G00105, AA26G00107, AA26G00174, AA26G00228, AA26G00313, AA26G00402, AA26G00541, AA279G00004, AA29G00062, AA29G00097, AA29G00120, AA29G00136, AA29G00278, AA2G00051, AA2G00074, AA30G00077, AA30G00151, AA30G00277, AA30G00351, AA311G00008, AA3165G00002, AA31G00179, AA31G00196, AA31G00518, AA31G00537, AA31G00545, AA31G00733, AA31G00868, AA32G00184, AA32G00418, AA32G00452, AA32G00474, AA32G00577, AA32G00856, AA32G00913, AA32G01182, AA337G00005, AA33G00214, AA33G00250, AA33G00253, AA34G00018, AA34G00041, AA35G00035, AA35G00079, AA36G00021, AA36G00061, AA37G00154, AA38G00037, AA38G00038, AA39G00034, AA39G00138, AA39G00156, AA39G00380, AA39G00525, AA39G00536, AA39G00618, AA39G00628, AA39G00709, AA39G00764, AA3G00049, AA3G00100, AA3G00155, AA3G00197, AA40G00110, AA40G00119, AA40G00120, AA40G00125, AA40G00138, AA40G00490, AA40G00566, AA40G00048, AA40G00643, AA41G00015, AA44G00144, AA44G00294, AA44G00425, AA44G00509, AA44G00549, AA44G00550, AA44G00659, AA45G00025, AA46G00082, AA48G00034, AA4G00202, AA4G00258, AA52G00021, AA53G00041, AA53G00289, AA53G00416, AA53G00609, AA53G00917, AA53G00945, AA53G01026, AA53G01078, AA53G01298, AA53G01346, AA54G00080, AA54G00146, AA54G00200, AA54G00208, AA54G00274, AA54G00294, AA54G00404, AA57G00082, AA57G00225, AA58G00014, AA598G00001, AA5G00068, AA5G00080, AA5G00081, AA56G00034, AA5G00168, AA5G00254, AA60G00122, AA60G00131, AA60G00190, AA60G00274, AA61G00059, AA61G00106. AA61G00154, AA61G00286, AA61G00291, AA61G00341, AA61G00453, AA61G00469, AA61G00604, AA634G00006, AA63G00010, AA63G00014, AA63G00040, AA64G00014, AA69G00034, AA6G00024, AA6G00038, AA70G00001, AA71G00017, AA77G00006, AA7G00019, AA7G00025, AA87G00051, AA87G00166, AA87G00216, AA87G00291, AA89G00010, AA8G00038, AA8G00132, AA8G00148, AA8G00265, AA8G00319, AA90G00024, AA90G00045, AA93G00112, AA93G00120, AA93G00125, AA96G00014, AA96G00070, AA96G00143, AA96G00153, AA9G00044, AA9G00101, AA9G00158, AA9G00170. ****RPs:** AA10G00010. AA10G00387. AA11G00002. AA11G00055. AA14G00024. AA16G00060. AA16G00071. AA21G00173. AA21G00221, AA21G00348, AA21G00412, AA25G00056, AA26G00495, AA26G00566, AA26G00692, AA31G00860, AA32G00227, AA33G00249, AA33G00251, AA33G00279, AA40G00523, AA40G00524, AA44G00242, AA44G00717, AA44G00719, AA45G00019, AA4G00198, AA52G00039, AA53G01352, AA56G00064, AA61G00345, AA65G00313. AA78G00023, AA87G00117, AA88G00003, AA93G00183, AA9G00203, AA104G00013, AA123G00016, AA18G00076, AA18G00235, AA1976G00001, AA21G00091, AA21G00273, AA29G00007, AA31G00096, AA31G00455, AA32G00110, AA32G00256, AA32G00442, AA32G00581, AA32G00921, AA32G01176, AA33G00107, AA33G00137, AA34G00040, AA37G00047, AA37G00051, AA38G00113, AA40G00013, AA447G00006, AA44G00057, AA4G00096, AA53G00830, AA54G00092, AA60G00009, AA60G00061, AA61G00683, AA72G00011, AA78G00038, AA7G00077, AA87G00075, AA10G00188, AA119G00004, AA131G00038, AA14G00034, AA18G00011, AA19G00483, AA24G00028, AA26G00426, AA30G00072, AA30G00134, AA31G00420, AA31G00703, AA31G00855, AA32G00542, AA32G00843, AA32G01181, AA33G00099, AA37G00041, AA38G00070, AA39G00471, AA40G00277, AA44G00379, AA45G00031, AA4G00252, AA53G00417, AA57G00013, AA60G00181, AA65G00020, AA6G00134, AA87G00134, AA94G00008, AA39G00366.



Supplemental Figure S16 continued next page...



Supplemental Figure S16. Expression patterns of *Aethionema arabicum* cell wall remodeling protein genes with focus on expansins and enzymes modifying xyloglucan (supports Figure 10). Transcript

abundance patterns (RNA-seq) in seeds of imbibed dimorphic diaspores (M⁺ seeds, IND fruits) and bare M⁻ seeds (extracted from IND fruits) from two maternal temperature regimes (20°C versus 25°C) at four different imbibition temperatures (9, 14, 20 and 24°C). WGCNA modules (Figure 3) for these genes are indicated by the vertical color lines next to the graphs. Mean ± SEM values of 3 replicates each with 60-80 seeds are presented. A and B, Effect of the pericarp on the expression ratios of expansin and xyloglucan-related cell-wall remodeling protein genes in the M⁻ seeds of imbibed IND fruits and isolated M⁻ seeds at T1% (A) and at 24 h (B). C, Transcript abundance patterns of *Ae. arabicum* expansins (EXP) and xyloglucan modifying enzymes: α -xylosyltransferase (XXT), α -fucosidase (FUC), α -fucosyltransferase (FUT), β -galactosidase (β GAL), α -galactosyltransferase (GAT), glucan synthase (CSCL), β -glucosidase (β GLU). For *Ae. arabicum* gene names/IDs see lists or the Expression Atlas or Supplemental Data Set S1. Symbols, gene IDs and modules of these genes are listed below:

AA31G00510	purple	βGAL	AA18G00007	
AA32G00279	grey	βGAL	AA26G00093	
AA39G00160		βGAL	AA30G00144	
AA61G00614		βGAL	AA31G00649	
AA65G00104		βGAL	AA32G00498	green
AA118G00010	turquoise	βGAL	AA32G00867	grey
AA118G00011	turquoise	βGAL	AA44G00698	
AA118G00012	blue	βGAL	AA4G00117	
AA19G00339		βGAL	AA4G00118	blue
AA32G00891	grey	GAT	AA21G00082	
AA901G00001	turquoise	GAT	AA57G00452	turquoise
AA93G00092		GAT	AA5G00089	grey
AA10G00221	magenta	GAT	AA87G00320	turquoise
AA14G00009	blue	CSCL	AA102G00313	
AA15G00140		CSCL	AA29G00116	blue
AA19G00061	grey	CSCL	AA53G01041	turquoise
AA21G00205	turquoise	CSCL	AA627G00001	brown
AA26G00281	blue	βGLU	AA10G00241	yellow
AA26G00769	turquoise	βGLU	AA11G00006	black
AA2G00219	turquoise	βGLU	AA12G00212	turquoise
AA31G00030	red	βGLU	AA26G00479	red
AA39G00026	turquoise	βGLU	AA26G00787	yellow
AA39G00435		βGLU	AA44G00262	
AA40G00525		βGLU	AA45G00011	green
AA43G00095		βGLU	AA61G00378	
AA4G00195	red	βGLU	AA62G00052	
AA4G00273	brown	βGLU	AA78G00002	purple
AA53G00296	grey	βGLU	AA78G00006	green
AA53G00630	brown	βGLU	AA8G00196	blue
AA53G00855	grey	βXYL	AA44G00238	
AA53G01435	yellow	βXYL	AA44G00321	grey
AA54G00100		βXYL	AA58G00011	turquoise
AA54G00344		βXYL	AA7G00012	turquoise
AA57G00016	black	EXPA2	AA35G00022	turquoise
AA586G00001	magenta	EXPA9	AA19G00314	turquoise
AA946G00002	grey	EXP3	AA228G00009	turquoise
AA9G00083		XTH4	AA110G00001	turquoise
AA32G01046	turquoise	XTH16a	AA78G00036	turquoise
	AA31G00510 AA32G00279 AA39G00160 AA61G00614 AA65G00104 AA118G00010 AA118G00011 AA118G00012 AA19G00339 AA32G00891 AA901G00001 AA93G0092 AA10G00221 AA19G00092 AA10G00221 AA19G00061 AA26G00281 AA26G00281 AA26G00219 AA31G00030 AA39G00435 AA40G00525 AA43G0095 AA43G0095 AA4600195 AA43G00195 AA43G000435 AA43G00435 AA40G01525 AA43G00195 AA43G00195 AA43G00195 AA43G00195 AA43G00195 AA43G00195 AA43G00195 AA43G00195 AA43G00100 AA53G01435 AA53G01435 AA54G00100 AA54G000016 AA54G00002 AA946G00002 AA946G00002 <	AA31G00510 purple AA32G00279 grey AA39G00160	AA31G00510purpleβGALAA32G00279greyβGALAA39G00160βGALAA61G00614βGALAA65G00104βGALAA61G00010turquoiseβGALAA118G00011turquoiseβGALAA118G00012blueβGALAA19G00339βGALAA32G00891greyGATAA901G00001turquoiseGATAA901G00001turquoiseGATAA901G00001turquoiseGATAA10G00221magentaGATAA14G0009blueCSCLAA16G00265turquoiseCSCLAA21G00205turquoiseGGLUAA26G00281blueβGLUAA36G00769turquoiseβGLUAA39G00026turquoiseβGLUAA39G0027βGLUAA39G0026AA40000525βGLUAA400095AA4000195redβGLUAA4600195redβGLUAA4600195greyβGLUAA53G00435greyβCLUAA53G00435greyβCLUAA4600195redβCLUAA53G00435greyβXYLAA53G00435greyβXYLAA53G00435greyβXYLAA54G00100βXYLAA54G00101magentaEXPA9AA946G00002greyEXP3AA960083XTH4AA32G01046turquoiseXTH16a	AA31G00510 purple βGAL AA18G0007 AA32G00279 grey βGAL AA26G00093 AA39G00160 βGAL AA30G00144 AA61G00614 βGAL AA31G00649 AA65G00104 βGAL AA32G00867 AA118G00010 turquoise βGAL AA32G00887 AA118G00012 blue βGAL AA44600698 AA118G00012 blue βGAL AA44600117 AA392G00891 grey GAT AA21G00082 AA93000092 GAT AA21G00082 AA93G00092 AA11600001 turquoise GAT AA5G00089 AA1460009 blue CSCL AA2000116 AA19600021 magenta GAT AA32G000116 AA19G00061 grey CSCL AA26000116 AA2600025 turquoise GGLU AA1060021 AA2600026 turquoise βGLU AA16000212 AA26600769 turquoise βGLU AA26600787 AA39000026 turquoi

Supplemental Table S1. Aethionema arabicum seed and fruit harvest results: seed and fruit mass, amounts and ratios of each harvested from plants grown at two temperatures.

Maternal temperature _(°C)	Seed/ fruit	mass (mg) ¹	Harvested (g)	Seed number	Fruit number ²	Seed mass (%)	Diaspore mass (%)	Diaspore number (%)	Fruit number (%)
	M+	0.3355	72.0	214605	N/A	69.6	37.3	65.1	N/A
20	M-	0.273	31.4	114938	N/A	30.4	N/A	N/A	N/A
20	DEH	-	-	N/A	53651	N/A	N/A	N/A	31.8
	IND	1.0535	121.1	N/A	114938	N/A	62.7	34.9	68.2
	M+	0.378	50.0	132275	N/A	87.0	67.9	83.7	N/A
25	M-	0.2894	7.5	25847	N/A	13.0	N/A	N/A	N/A
25	DEH	-	-	N/A	33069	N/A	N/A	N/A	56.1
	IND	0.9161	23.7	N/A	25847	N/A	32.1	16.3	43.9

¹ Seed mass based on 8 × 100 seed / fruit weights ² Fruit number for DEH fruits based on approximation of an average of 4 M^+ seeds per DEH fruit.

Supplemental Table S2. *Aethionema arabicum* gene names and IDs and modules (Figure 3) for the presented expression results in Figures 5, 7, 8, 9, 10 and Supplemental Figures S5, S8, S10, S11, and S12. For further details about individual genes and gene IDs and link to the v3.1 genome (Fernandez-Pozo et al., 2021) see the Gene Expression Atlas (<u>https://plantcode.cup.uni-freiburg.de/easy_gdb/tools/expression/expression_input.php</u>).

		Aethionema arabicum	
Figure	Symbol	gene ID (v2.5 genome)	Module
5, 8, S5	NCED6	AA78G00012	green
5, 8, S5	CYP707A3a	AA6G00060	blue
5, 8	ABCG40	AA37G00179	brown
5, 8	DOG1	AA6G00020	
S5	ZEP/ABA1	AA8G00025	brown
S5	NCED2	AA57G00116	
S5	NCED3a	AA26G00165	
S5	NCED3b	AA15G00127	
S5	NCED5	AA54G00417	grey
S5	NCED9	AA31G00716	grey
S5	ABA2/SDR1	AA32G01008	grey
S5	AAO	AA8G00200	yellow
S5	AAO	AA8G00197	
S5	AAO	AA19G00094	
S5	AAO	AA32G00943	brown
S5	CYP707A3b	AA57G00196	
S5	CYP707A2	AA32G00787	grey
S5	CYP707A4	AA26G00741	
S5	CYP707A4	AA26G00600	
S5	GA3OX1	AA37G00176	turqoiuse
S5	GA3OX2	AA31G00895	purple
S5	GA3OX4	AA31G00896	
S5	GA2OX1	AA31G00720	
S5	GA2OX2	AA54G00411	grey
S5	GA2OX3	AA18G00108	
S5	GA2OX4	AA18G00203	
S5	GA2OX6	AA7G00001	
S5	GA2OX7	AA2G00197	
S5	GA2OX8	AA57G00320	
7, 8	ERF71/73 (HRE1/2)	AA21G00481	grey
7, 8	ADH1a	AA39G00353	brown
7	ADH1b	AA31G00264	green
S9	PDC1	AA19G00365	
8, S9	PDC2	AA215G00009	yellow
S9	LDH	AA57G00289	yellow
S11	AspAT	AA46G00122	red
S11	AspAT-ASP1	AA32G00623	turquoise
S11	AspAT-ASP2	AA7G00130	grey

S11	AspAT-ASP3	AA44G00406	blue
S11	MDHc	AA19G00113	grey
S11	MDHc	AA32G00436	grey
S11	NADP-ME2	AA44G00419	grey
S12	NAC102	AA4G00115	brown
S12	HHO2	AA1304G00001	green
8, S12	HRA1	AA93G00176	grey
S12	PCO1	AA40G00576	grey
S12	PCO2	AA87G00177	grey
S12	ACO1	AA33G00241	turquoise
8, S12	ETR2	AA17G00111	blue
8, S12	JAZ3	AA26G00461	brown
9	ABI5	AA60G00170	green
9	AREB3a (ABF)	AA93G00015	green
S14	AREB3b (ABF)	AA61G00149	yellow
9	ABF1	AA2G00098	red
S14	ABF2	AA210G00005	
S14	ABF3	AA118G00053	
8, S14	ABF4	AA26G00601	
S14	GBF1	AA30G00183	red
8, 9	GBF3	AA21G00361	red
S14	GBF2	AA32G00122	red
S14	GBF4	AA19G00150	grey
S14	GBF5	AA33G00153	turquoise
S14	GBF6	AA45G00023	grey
S14	RAV2	AA39G00678	turquoise
S14	RAP2.2	AA26G00147	purple
S14	RAP2.12	AA15G00147	turquoise
8, S14	HAB1	AA31G00661	red
S14	AHG3	AA52G00006	yellow
S14	SNRK2.10/2B	AA53G00514	red
S14	SNRK2.3	AA8G00036	brown
S14	SNRK2.4	AA65G00151	yellow
S14	SNRK2.5	AA46G00035	red
S14	SNRK2.5	AA4G00103	turquoise
S14	SNRK2.7	AA44G00187	blue
9	HB13	AA38G00103	turquoise
S14	HB20	AA10G00418	turquoise
S14	HB23	AA9G00043	turquoise
S14	HB25	AA4G00267	purple
S14	HB33	AA31G00431	purple
10	αXYL	AA32G01046	turquoise

Supplemental Table S3. RT-qPCR primers targeting *Aethionema arabicum* genes. Primers were designed using Primer3 2.3.4 (Untergasser et al., 2012).

Gene	ID	Direction	Sequence (5´ to 3´)
CTU2	A A 20 C 00 10 7	Forward	GTTGGCTCGTCCTCCTCAAG
CTUZ	AA30G00197	Reverse	CCGTACAATTGTGCACTCCC
DECT4		Forward	AGAAGGAGTTTCCAGCACCG
PECIT	AA255G00007	Reverse	TGTGAGACTCGAACACTGGC
	A A 1 1 1 C 0 0 0 1 1	Forward	GTGAGCAGGGTGACAGGTAC
DANFZ	AATTIGUUUTI	Reverse	CCCAACCCAAAGCATGTGTG
		Forward	GAAACCTCAGCTCCCTTCGG
DREZ	AA40G00275	Reverse	TCCTCGATCTCAGCCCTACC
EVDAO	AA10C00214	Forward	CTGAATGGTGTCTCCCAGGG
EXFAS	AA 19000314	Reverse	CATCTCCTGCTCCAGCTACG
GST	AA3C00170	Forward	CTAAATGGCGCAAGTGGGTG
	AA3000170	Reverse	TCAACCCATGTTTCAGCAGC
ΙΕΔ1Λ	AA1C00071	Forward	CTGGCCGGGAAATTGCAAAG
		Reverse	ACAACGGGAAGGTCAACGAC
NCED6	AA78G00012	Forward	TCGTACGAGTCGGCTTGTTC
	7470000012	Reverse	GGAGTGACCGTGTAGCTCAC
RK29	AA4G00252	Forward	TGCTCCGTCTCCAGAAATCG
	AA+000232	Reverse	TCTGCTGCTGCTTCTTCCTC
SGR2	AA6G00349	Forward	GGACCTGCGATATTCGAAGC
00//2	////0000040	Reverse	TGCCCATCCCTGTAACTGAG
ХТН А	AA110G00001	Forward	CAGCCACCGATTTTGCAGAC
	74110000001	Reverse	TCTCTAAACCGCCACGTGTC
нно2	AA1304G00001	Forward	TCCTTCTCCGGATTCACAACC
	/ (100100001	Reverse	CGTGTCACTTTTAGCACCGC
RAP2 12	AA15G00147	Forward	TCACTTCCACTCCGAAACCC
	///////////////////////////////////////	Reverse	ATCTCAGCTGCCCATTTCCC
FTR2	AA17G00111	Forward	ATGGGCTGCTTGGAGATCAC
		Reverse	ACGACTGAGATGTTCCCGTG
GBE3	AA21G00361	Forward	TGCTCCTCCTGAAACTTGGC
	, , , , , , , , , , , , , , , , , , , ,	Reverse	AGCTCTTCAGTTTCCGCCTG
PDC2	AA215G00009	Forward	TCACTCAGGAGCTTAGGTGC
	,	Reverse	AGTCGGGTGAGGAATTGCAG
JAZ3	AA26G00461	Forward	GCTTGCCGTCAACATACCAC
		Reverse	TTGTGACCCTTTCTTTGCGC
ABF4*	AA26G00601	Forward	GCAGGCTTACACCTTGGAAC
		Reverse	AGCATTGCCTTTTGTTCCCC
HAB1*	AA31G00661	Forward	TTCGGTGTTCTTGCCATGTC
		Reverse	GCCACACCAAGATCCTCCTC
α ΧΥΙ 1	AA32G01046	Forward	CACTATCCTCCGCCTCTTCG
		Reverse	ACCAGAAATCTCCTGCACGG

Supplemental Data. Chandler et al. (2024). Dimorphic germination control. Plant Cell

CRE5*	AA33C00153	Forward	AAATCTGCTCTCCGCCGTAG
GBFJ	AA33G00133	Reverse	AGCTCCGGTAAGTACTGCTTG
EVDAD	A A 25C 00022	Forward	GAGGCCACGCTACCTTCTAC
EXFAZ	AASSGUUUZZ	Reverse	GCAAGCTCCACATGTTGCTC
ABCC40	A A 27C 00170	Forward	CCTTACTCGGGACCATCGTG
ADCG40	AA37G00179	Reverse	TCTCCATCACTTGCAGGCTC
	A A 20C 00252	Forward	AGAATCTCTGGTGCGTCGAG
АДПТА	AA39G00355	Reverse	CACACTCCTGTCCACTCCAC
NAC102	A A 4 C 00 1 1 E	Forward	GGAGCTTGATTTACCGGCG
NACTUZ	AA4G00115	Reverse	CTTTCTCACCGTATAATGCCAAAT
		Forward	ACCGGCGAATACATCCACTG
PIRI/RCARII	AA57 G00057	Reverse	AACCACCGTCCAGATCTGTG
A DIS	A A 60 C 00 1 70	Forward	TCAAGAACCTACCTTCCCTACAC
ADIJ	AA00G00170	Reverse	CCACCATAACAAACACCGGC
DOC1	A A 6 C 0 0 0 2 0	Forward	GGTGGATGCAGACCGTCTTC
DOGT	AA0G00020	Reverse	AGTTGCTCCGCCGTTAGATC
CVD70742a*	A A 6 C 00060	Forward	AAAACTCCCTCTTCCTCCGG
CIFIUIASa	AA0G00000	Reverse	GGGTTTTGAACACCGATCCG
VTU16a	A A 79 C 00026	Forward	ACGAGACAGGGAAGCCTTATG
ATTIVA	AA70G00030	Reverse	GGACACCAAGATGTTCTGCG
	A A 02 C 00015	Forward	AGAATCTGCAGCACGTTCAC
AREDJa	AA93G00015	Reverse	CTGGAGGTGGTGTACTTGGG
	AA03C00176	Forward	ATGACCGTGGTTCAGGTTCC
		Reverse	TTTCTTCCCGTCGGTTCCTG
	AA118C00053	Forward	TGGAAAATCATGCTCCACTTGC
ADFJ	AAT 10000000	Reverse	CTTCCGGGAGATACTGCAGC
EDE71/79	AA21G00481	Forward	GTGGGCAAGAGGAGAAGGAG
ERF/1//3	MAZ 1000401	Reverse	ACCAAGCCAGAGACGAACAC

[†]Reference genes used for normalization. *Annealing temperature 65°C.

Supplemental Table S4. 2-way ANOVA of RT-qPCR analyses presented in Figure 8 and Supplemental Figure S12. P values and significance rating (<0.0001 ****, <0.001 ***, <0.01 **, <0.05 *, >0.05 ns = not significant) are indicated for treatment and time.

Aethionema arabicum gene	M- seed hy versus M- seed no	vpoxia ormoxia	M- seed AE versus M- seed AE	3A/hypoxia 3A/normoxia	IND fruit versus M- seed no	rmoxia	M- seed n versus M- seed A	ormoxia BA/normoxia	M- seed h versus M- seed A	ypoxia BA/hypoxia
	Hypoxia	Time	Hypoxia	Time	Pericarp	Time	ABA	Time	ABA	Time
AearERF71/73	<0.0001	<0.0001	<0.0001	<0.0001	0.0049	<0.0001	0.4833	<0.0001	0.0781	<0.0001
	****	****	****	****	**	****	ns	****	ns	****
AearADH1a	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	0.3751	0.0466	<0.0001	0.0857	<0.0001
	****	****	****	****	****	ns	*	****	ns	****
AearPDC2	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	0.0024	0.1228	<0.0001	0.9791	<0.0001
	****	****	****	****	****	**	ns	****	ns	****
AearHRA1	<0.0001	<0.0001	<0.0001	<0.0001	0.2059	0.1666	0.5774	0.6086	0.3470	<0.0001
	****	****	****	****	ns	ns	ns	ns	ns	****
AearETR2	<0.0001	<0.0001	<0.0001	<0.0001	0.1347	0.0328	0.7348	0.2084	0.0047	<0.0001
	****	****	****	****	ns	*	ns	ns	**	****
AearJAZ3	0.0014	<0.0001	<0.0001	<0.0001	0.0101	<0.0001	0.3652	<0.0001	0.2757	0.0043
	**	****	****	****	*	****	ns	****	ns	**
AearDOG1	<0.0001 ****	0.0006	<0.0001 ****	0.0024 **	<0.0001 ****	0.0200 *	0.2546 ns	0.0155 *	0.7241 ns	<0.0001 ****
AearNCED6	<0.0001	0.2729	<0.0001	0.1153	0.0075	0.0187	0.2160	0.0007	0.2821	0.0016
	****	ns	****	ns	**	*	ns	***	ns	**
AearCYP707A3a	0.1700	<0.0001	0.6986	<0.0001	<0.0001	<0.0001	0.0428	<0.0001	0.4023	<0.0001
	ns	****	ns	****	****	****	*	****	ns	****
AearABCG40	0.0002	0.1377	0.0006	0.0974	0.0319	0.5958	0.8296	0.1442	0.8372	0.0029
	***	ns	***	ns	*	ns	ns	ns	ns	**
AearAREB3a	<0.0001	0.8502	0.0001	0.7501	0.0064	0.0006	0.5384	<0.0001	0.4647	0.0200
	****	ns	***	ns	**	***	ns	****	ns	*
AearABF4	<0.0001	<0.0001	0.0013	<0.0001	0.7507	0.0234	0.1887	0.0116	0.5542	<0.0001
	****	****	**	****	ns	*	ns	*	ns	****
AearGBF3	<0.0001	0.0009	<0.0001	<0.0001	0.0274	0.3455	0.0431	0.2008	0.1645	<0.0001
	****	***	****	****	*	ns	*	ns	ns	****
AearHAB1	<0.0001 ****	0.0002	0.0036 **	<0.0001 ****	0.1373 ns	0.0085 **	0.0423 *	0.0123 *	0.8956 ns	<0.0001 ****
AearEXPA2	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	0.0582	<0.0001	0.1439	0.2364
	****	****	****	****	****	****	ns	****	ns	ns

Supplemental Data. Chandler et al. (2024). Dimorphic germination control. Plant Cell

AearEXPA9	<0.0001	<0.0001	<0.0001	0.0003	<0.0001	<0.0001	0.0065	<0.0001	0.0014	<0.0001
	****	****	****	***	****	****	**	****	**	****
AearXTH4	<0.0001	<0.0001	<0.0001	0.0002	<0.0001	<0.0001	0.0434	<0.0001	0.2153	0.0003
	****	****	****	***	****	****	*	****	ns	***
AearXTH16a	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	0.0017	<0.0001	0.0561	0.0002
	****	****	****	****	****	****	ns	****	ns	***
AearaXYL1	<0.0001	0.0033	<0.0001	0.0002	0.0001	0.0010	0.4687	<0.0001	0.4576	0.0831
	****	**	****	***	***	**	ns	****	ns	ns
AearLEA14	<0.0001	0.0366	<0.0001	0.0080	0.0621	0.0028	0.0488	0.0122	0.0356	<0.0001
	****	*	****	**	ns	**	*	*	*	****
AearDAHP2	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	0.7507	<0.0001	0.0164	<0.0001
	****	****	****	****	****	****	ns	****	*	****
AearGST	0.3703	0.0015	0.0022	0.0002	<0.0001	0.3631	0.9376	0.0005	0.1178	0.0002
	ns	**	**	***	****	ns	ns	***	ns	***
AearNAC102	<0.0001	0.0062	<0.0001	0.0017	0.2084	0.0011	0.2400	<0.0001	0.3277	<0.0001
	****	**	****	**	ns	**	ns	****	ns	****
AearHHO2	0.0016	<0.0001	0.0517	<0.0001	0.0002	<0.0001	0.3151	<0.0001	0.3017	0.0001
	**	****	ns	****	***	****	ns	****	ns	***
AearRAP2.12	0.9204	0.0011	0.0137	0.0007	0.1206	0.0191	0.6362	0.0061	0.0260	<0.0001
	ns	**	*	***	ns	*	ns	**	*	****
AearABI5	0.2944	0.0459	0.3405	0.0081	0.3051	0.7289	0.0456	0.3181	0.4720	<0.0001
	ns	*	ns	**	ns	ns	*	ns	ns	****
AearABF3	0.0031	0.5402	0.0457	0.1557	0.9786	0.1721	0.3885	0.2669	0.6744	0.0234
	**	ns	*	ns	ns	ns	ns	ns	ns	*
AearGBF5	0.1957	<0.0001	0.8175	<0.0001	0.0028	0.0004	0.3555	<0.0001	0.0178	<0.0001
	ns	****	ns	****	**	***	ns	****	*	****
AearPYR1/RCAR11	0.5352	0.0010	0.0106	0.0002	0.3721	0.0135	0.8969	0.0670	0.0036	<0.0001
	ns	***	*	***	ns	*	ns	ns	**	****
AearSGR2	0.5242 ns	0.0014 **	0.6165 ns	0.0044 **	0.2945 ns	0.0025 **	0.3554 ns	0.0028	0.8572 ns	0.0021 **
AearDRE2	0.0315 *	0.0006	0.3487 ns	<0.0001 ****	0.8865 ns	0.0096 **	0.1848 ns	0.0044 **	0.2321 ns	<0.0001 ****
AearRK29	0.3184	0.1106	0.1325	0.0303	0.2511	0.0880	0.8494	0.3435	0.8404	0.0121
	ns	ns	ns	*	ns	ns	ns	ns	ns	*