Tables

Supplemental Table S1. CESA expression in seed coat cells during seed development (Le et al., 2010).

	Pre-globular	Globular (~3 DPA)	Heart	Linear embryo (~6 DPA)	Mature green (~10 DPA)
CESA1	268 (20)	260 (20)	201 (52)	275 (35)	**294 (48)**
CESA2	543 (85)	611 (91)	**1024 (38)**	435 (86)	192 (109.48)
CESA3	811 (101)	677 (12)	1094 (58)	**1765 (185)***	1115 (192)
CESA4	8 (7.31)	2 (0.47)	8.21 (7.22)	5 (4.49)	**34 (19.84)**
CESA5	101 (20)	74 (16)	51 (1)	**362 (123)**	239 (52)
CESA6	**168 (86)**	80 (33)	140 (58)	123 (24)	121 (12)
CESA7	5 (1.77)	13 (0.97)	1 (0.31)	17 (8.1)	**22 (9.53)**
CESA8	1 (0.41)	21 (10)	33 (16.69)	**80 (27.23)**	62 (5.67)
CESA9	12 (1.52)	15 (1.55)	10 (7.65)	26 (6.83)	**45 (0.06)**
CESA10	62 (7.15)	59 (21.19)	303 (53.98)	**887 (376.26)**	420 (2.89)
MUM4	547.9 (131)	787 (196.81)	1018.76(33.19)	7764 (503)	**7937 (610)**

Values in parenthesis indicate standard deviation. Values in bold indicate the highest expression level of each *CESA* throughout seed development. Asterisks indicate highest expression level of all *CESA*s in seeds. http://bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi?dataSource=Seed

Supplemental Table S2. *CESA* expression in the seed coat during development (Dean et al., 2011).

Seed stage	**3 DPA**	**7 DPA**	**11 DPA**
Gene			
CESA1	380 (105.88)	**620.78 (256.58)**	467.66 (175.3)
CESA2	**5321.52 (7049.24)**	1440.8 (846.67)	2620.3 (1453.59)
CESA3	9692.38 (6893.56)	**13475.48 (9182.12)***	9165.4 (4859.99)
CESA4	**151.76 (114.61)**	127.24 (49.46)	122.34 (54.39)
CESA5	149.13 (92.44)	159.94 (45.2)	**165.48 (37.39)**
CESA6	10656.71 (4871.29)	7786.39 (4196.9)	**12414.76 (7440.4)**
CESA7	**622.9 (1148.5)**	142.11 (30.75)	163.67 (46.87)
CESA8	203.64 (76.79)	**293.03 (65.99)**	216.49 (52.6)
CESA9	155.9 (29.18)	152.34 (41.39)	**184.3 (93.18)**
CESA10	1021.04 (719.53)	**2207.19 (3105.38)**	416.8 (203.13)
MUM4	380 (105.88)	**620.78 (256.58)**	209.31 (89.37)

Values in parenthesis indicate standard deviation. Values in bold indicate the highest expression level of each *CESA* throughout seed development. Asterisks indicate highest expression level of all *CESA*s in seeds. http://bar.utoronto.ca/efp_seedcoat/cgi-bin/efpWeb.cgi

Supplemental Table S3. CESA expression in whole seeds during development (Winter et al., 2007).

Embryo stage		**Globular**	**Heart**	**Torpedo**	**Bent cotyledon**			**Mature green**
Seed stage	**Seed stage 3**	**Seed stage 4**	**Seed stage 5**	**Seed stage 6**	**Seed stage 7**	**Seed stage 8**	**Seed stage 9**	**Seed stage 10**
Silique	+	+	+	-	-	-	-	-
Gene								
CESA1	348 (10.79)	359 (26.4)	385 (57.16)	377 (11.58)	**410 (19.78)**	321 (15.7)	295 (13.53)	256 (11.47)
CESA2	327 (7.43)	573 (18.27)	507 (3.58)	561 (3.15)	**605 (14.84)**	379 (23.14)	294 (5.31)	246 (16.25)
CESA3	912 (29.81)	1222 (65.07)	**1197 (26.17)***	987 (29.18)	930 (16.47)	798 (11.64)	630 (25.65)	624 (24.53)
CESA4	98 (19.69)	**1141 (22.18)**	664 (30.6)	23 (3.35)	27 (2.51)	12 (7.22)	21 (7.61)	30 (2.17)
CESA5	195 (5.18)	385 (3.87)	**352 (3.54)**	269 (19.43)	292 (9.41)	132 (9.55)	120 (4.57)	99 (4.59)
CESA6	460 (32.77)	429 (9.91)	439 (6.43)	483 (11.76)	**505 (33.26)**	416 (3.34)	326 (18.24)	316 (23.76)
CESA7	41 (4.87)	**489 (53.28)**	224 (7.06)	19 (0.53)	24 (0.73)	21 (5.85)	31 (3.63)	38 (2.03)
CESA8	81 (5.62)	**669 (46.14)**	328 (7.12)	4 (0.8)	2 (1.46)	2 (0.53)	1 (0.37)	2 (0.45)
CESA9	22 (4.3)	40 (5.08)	56 (1.64)	**135 (11.66)**	125 (4.15)	85 (7.01)	65 (2.54)	61 (7.11)
CESA10	94 (1.87)	**1327 (92.07)**	1058 (48.6)	547 (11.27)	490 (6.18)	151 (8.87)	119 (3.75)	98 (2.92)
MUM4	192 (10.81)	**1097 (21.88)**	1075 (21.88)	410 (18.43)	326 (5.57)	65 (7.01)	66 (3.04)	81 (16.55)

Values in parenthesis indicate standard deviation. Values in bold indicate the highest expression level of each *CESA* throughout seed development. Asterisks indicate highest expression level of all *CESA*s in seeds. The “+” and “-“ indicate presence or absence, respectively, of silique tissue used for RNA extraction. http://bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi

Supplemental Table S4. List of the top 30 genes coexpressed with CESA5 in seeds (http://bbc.botany.utoronto.ca/ntools/cgi-bin/ntools_expression_angler.cgi). The r-value represents the Pearson's correlation coefficient of the expression pattern of CESA5 with all other genes (Toufighi et al., 2005).

Locus	Gene	r-value
AT5G09870	***CESA5***	**1**
AT2G04780	*FLA7*	0.742
AT5G05170	***CESA3***	**0.733**
AT1G75680	*GH9B7*	0.713
AT3G11700	*FLA18*	0.709
AT3G25780	*AOC3*	0.696
AT2G25220	N/A	0.691
AT1G28600	N/A	0.681
AT5G49720	*GH9A1/KOR1*	0.676
AT1G33800	N/A	0.674
AT3G28340	*GATL10*	0.671
AT1G23200	N/A	0.669
AT4G30440	*GAE1*	0.668
AT1G28590	N/A	0.659
AT1G08280	N/A	0.656
AT5G45770	*RLP55*	0.656
AT5G50750	*RGP4*	0.652
AT5G15180	N/A	0.649
AT4G32410	***CESA1***	**0.648**
AT2G24550	N/A	0.642
AT5G04530	*KCS19*	0.641
AT3G54810	*BME3*	0.639
AT3G11600	N/A	0.638
AT2G23570	*MES19*	0.637
AT4G35060	*HIPP25*	0.637
AT2G24240	N/A	0.636
AT2G25450	N/A	0.636
AT2G25540	***CESA10***	**0.633**
AT5G06530	*ABCG22*	0.631
AT5G03170	*FLA11*	0.63

*Genes in bold denote cellulose synthases

Supplemental Table S5. Pearson correlations and Manders coefficients for GFP-CESA10 (M1) colocalization with RFP-VHA-1a (M2) in seed coat epidermal cells.

Replicate	Pearson Correlation	Manders coefficients	
1	0.503	M1	0.319
		M2	0.342
2	0.391	M1	0.101
		M2	0.608
3	0.5	M1	0.324
		M2	0.597
4	0.396	M1	0.283
		M2	0.699
5	0.404	M1	0.139
		M2	0.281
Average	0.4388	M1	0.2332
		M2	0.5054

Supplemental Table S6. Genes, accession numbers, and mutant lines used in this study.

Gene	Accession	Mutant line	T-DNA line/TAIR accession	Reference
CESA1	AT4G32410	*any1-1*		Fujita et al., 2013
CESA3	AT5G05170	*ixr1-1*	CS6201	Scheible et al., 2001
		ixr1-2	CS6202	Scheible et al., 2001
CESA5	AT5G09870	*cesa5-1*	SALK_118491	Mendu et al., 2011
CESA6	AT5G64740	*prc1-1*	CS297	Fagard et al., 2000
CESA10	AT2G25540	*cesa10-1*	SALK_150533	
		cesa10-2	SALK_052533	
BXL1	AT5G49360	*bxl1-1*	CS16299	Arsovski et al., 2009
FLY1	AT4G28370	*fly1-1*	CS67936	Voiniciuc et al., 2013

Supplemental Table S7: Monosaccharide composition and whole seed acid insoluble cellulose amounts.

	Col	*cesa5-1*	*ixr1-1*	*ixr1-2*
Soluble mucilage				
Fucose	0.037 +/- 0.01	0.043 +/- 0.01	0.033 +/- 0.01	0.05 +/- 0.01
Arabinose	0.27 +/- 0.023	0.49 +/- 0.04*	0.38 +/- 0.02*	0.45 +/- 0.03*
Rhamnose	36.40 +/- 0.58	45.48 +/- 0.38*	35.31 +/- 0.25	30.53 +/- 0.69*
Galactose	2.02 +/- 0.152	1.57 +/- 0.12	1.70 +/- 0.06	1.62 +/- 0.174
Glucose	0.98 +/- 0.061	1.58 +/- 0.385	2.80 +/- 0.98	2.63 +/- 1.16
Xylose	2.77 +/- 0.15	3.46 +/- 0.05*	2.97 +/- 0.08	2.34 +/- 0.08
Galacturonic acid	44.08 +/- 7.42	50.33 +/- 1.15	36.92 +/- 0.54	31.19 +/- 0.92
Whole seed AIR				
Fucose	7.68 +/- 0.23	4.71 +/- 0.21*	8.26 +/- 0.34	7.41 +/- 0.11
Arabinose	236.91 +/- 4.25	230.91 +/- 3.80	257.34 +/- 7.34	245.76 +/- 4.03
Rhamnose	228.63 +/- 3.91	214.66 +/- 2.31*	216.24 +/- 3.95	226.85 +/- 5.04
Galactose	154.14 +/- 3.37	134.94 +/- 5.04*	153.03 +/-5.58	165.45 +/- 3.97*
Glucose	197.65 +/- 23.29	102.47 +/- 26.74*	225.44 +/- 29.39	182.66 +/- 20.23
Xylose	78.54 +/- 5.60	64.78 +/- 3.43*	89.29 +/- 1.66	81.88 +/- 1.77
Galacturonic acid	323.13 +/- 10.13	300.81 +/- 10.11	286.34 +/- 11.81	315.87 +/- 10.49
Acid insoluble cellulose				
Cellulose	110.06 +/- 12.15	76.04 +/- 5.57*	81.76 +/- 5.17*	88.7 +/- 6.54

Values are the mean +/- SE of four samples, and are expressed as nmol sugar/mg seed. Cellulose amounts are expressed as mg cellulose/g seed. Results were similar for three independent biological replicates. Asterisks indicate significantly different from wild type based on a Student's t-test, $p < 0.05$.

Supplemental Table S8. Sequences of primers used in this study.

Gene	Purpose	Primer name	Sequence (5′-3′)
CESA3	*ixr1-1* identification	*ixr1-1* MseI F	CAATCATGGGGACCACTCTTTA
		ixr1-1 MseI R	GACTCGGCTAGTGAAGGGATCA
CESA10	GFP-CESA10 construction	CESA10-attB1	AAAAAGCAGGCTtaATGGTTGCGGGATCTTACCGGAGAT
		CESA10-attB2	AGAAAGCTGGGTaTCACTCACCCATGAAACTGTTGCTCA
		HindIII_CESA10p F	TGTAAGCTTTGAATCATAAAGCAATCAAACCCCTAA
		XbaI_CESA10p R	ATATCTAGAGCCGGCGTTTTGCTGCAA
	cesa10-2 and RT-PCR	CESA10-1R	AAAGGAGCTTTCCCATGAGAGG
		CESA10-2F	CCAATTACATCCATCCCGCTCC
		CESA10-4F	CCTGAAGATGGTTGGACAATGG
		CESA10-3R	TGGCTTCCTTAATCGCCTTGC
	cesa10-2 genotyping	052533-LP	AACCCCTTCAAGTTGATCTCG
		052533-RP	TACCCAGTGGATAAAGTTGCG
CESA5	Genotyping	CESA5-1 LP	GCTGATCCTTTAAAGGCCGG
		CESA5-1 RP	CCCGGATTTGACCATCACAAG
	N-Terminal cloning	NCESA5 HindIII F	CCCAAGCTTGGGATGAATACTGGTGGTCGGCTCATCG
		NCESA5 XhoI R	CCGCTCGAGCGGCGGATTTATTTTGCTCGACTTTATCG
	Site Directed Mutagenesis	CESA5C39	GAACTAAGTGGACAAACAGCTCAAATCTGTGGAGATGAG
		CESA5C84	GGAAACCAATCTTGTCCTCAGGCCAAAACTCGTTACAAGCGC
	Phage sequencing	T7 F	GGAGCTGTCGTATTCCAGTC
		T7 R	AACCCCTCAAGACCCGTTTA
	Yeast two-hybrid	CESA5 pGADT7-F	GCCGGAATTCATGAATACTGGTGGTCGGCTC
		CESA5 pGADT7-R	GCGCGGATCCCGGATTTATTTTGCTCGAC
		CESA3 pGBKT7-F	GCCGGAATTCATGGAATCCGAAGGAGAAACC
		CESA3 pGBKT7-R	GATCCACTACCTTTGAGCCTCTTG