

Supplementary Material

Dissecting the genetic basis for seed coat mucilage heteroxylan biosynthesis in *Plantago ovata* using gamma irradiation and infrared spectroscopy

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1 Supplementary Figures and Tables

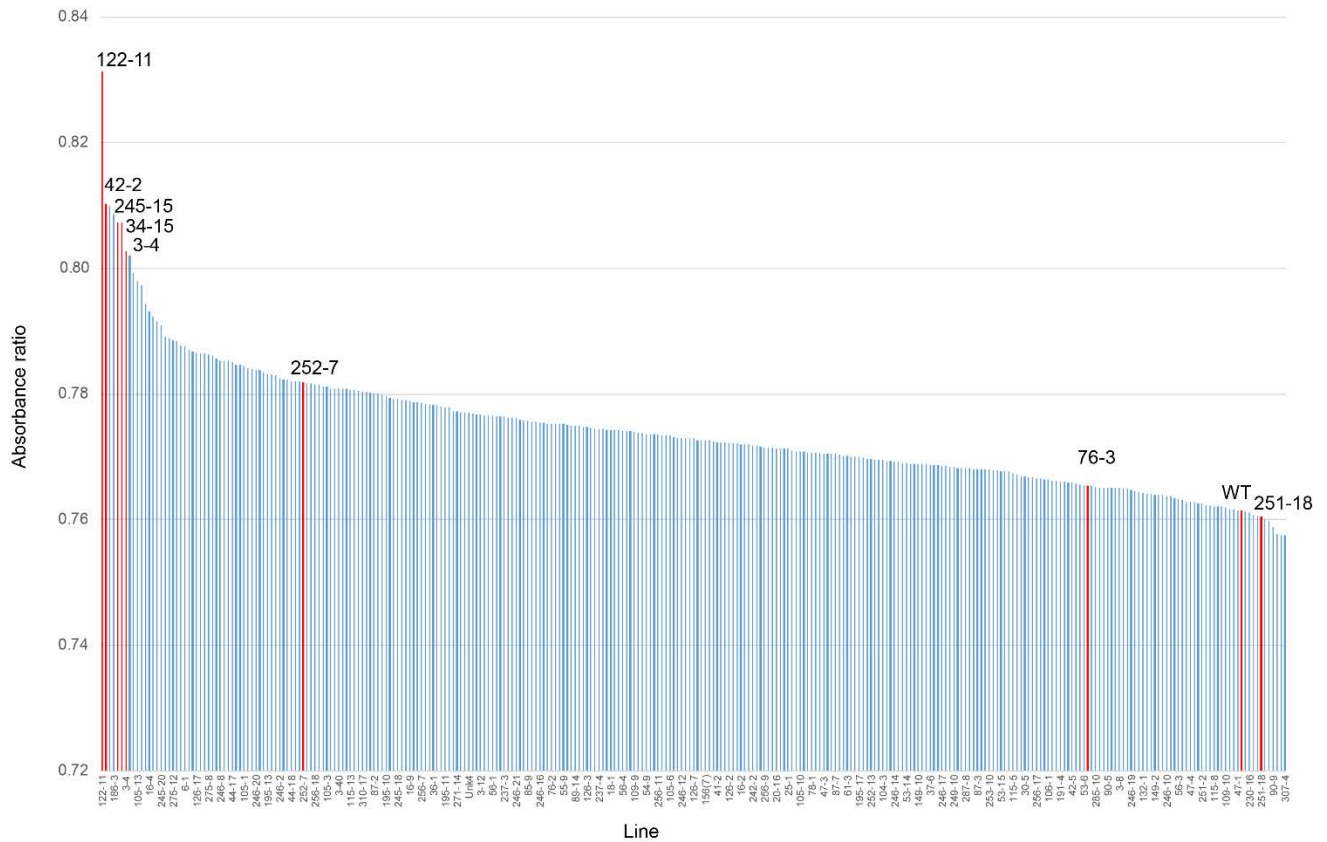
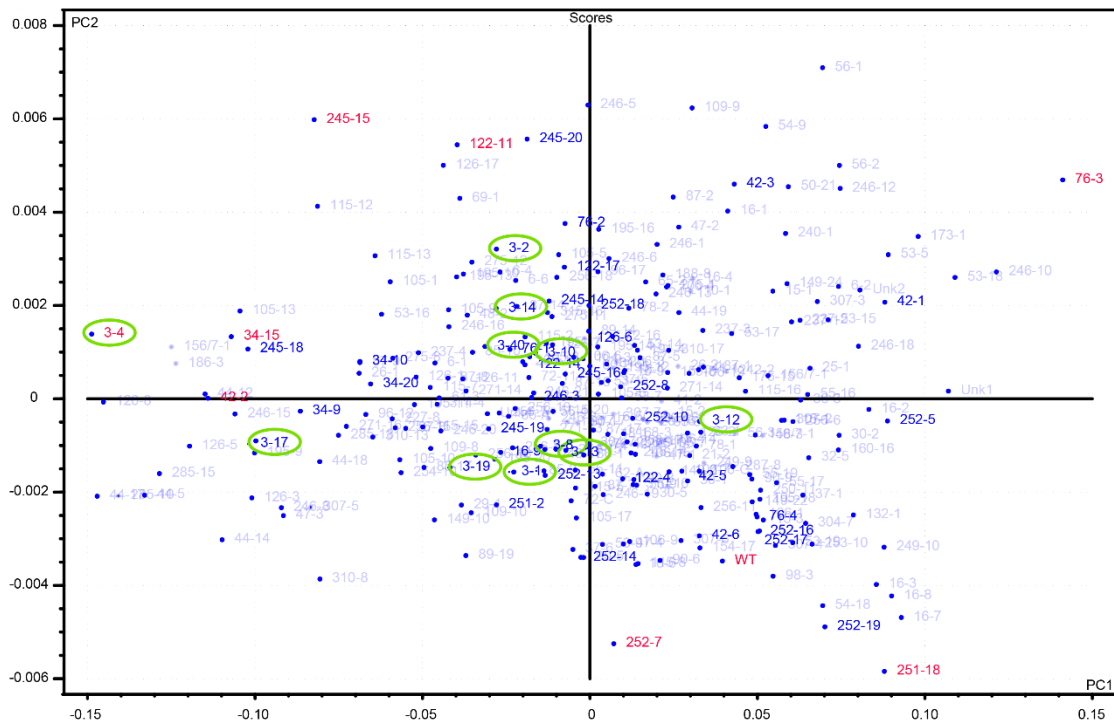


Figure S2: Absorbance ratio values of 1070cm⁻¹/1040cm⁻¹ from 300 *P.ovata* M3 lines and WT, sorted from largest to smallest. The same analysis was carried out for multiple xylan-associated ratios based on the normalised FTMIR data, with the aim of identifying lines showing distinct differences in heteroxylyan composition/structure compared to WT. This data is shown as an example; other wavelength ratios showed distinct distribution patterns, but outlier lines were often conserved (See Table S1). The red bars indicate putative mutant candidates based on PCA analysis (see Fig S1 and S3).

A



B

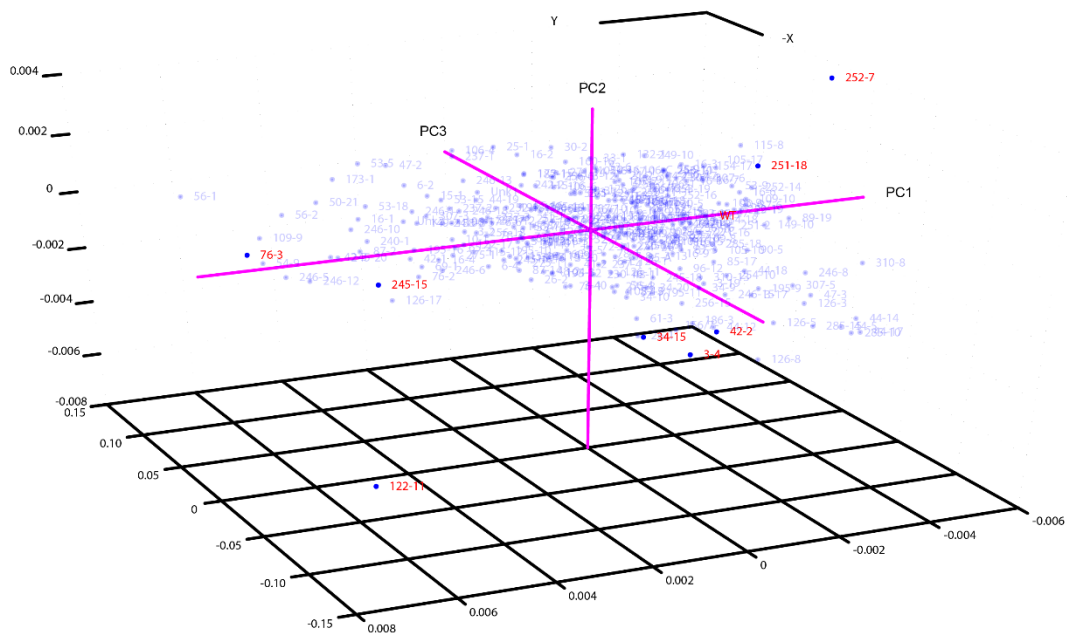


Figure S3: Principal Component Analysis of FTIR absorbance readings derived from xylan-associated wavelengths of *P. ovata* seed samples. The upper panel shows the 2D PCA plot of normalised spectral data from 300 M3 lines including a wild-type (WT) control. Lines that were analysed in greater detail in this study are highlighted in red. Sister plants of line 3-4 are indicated with a green ring. The lower panel shows the 3D PCA plot of the same data.

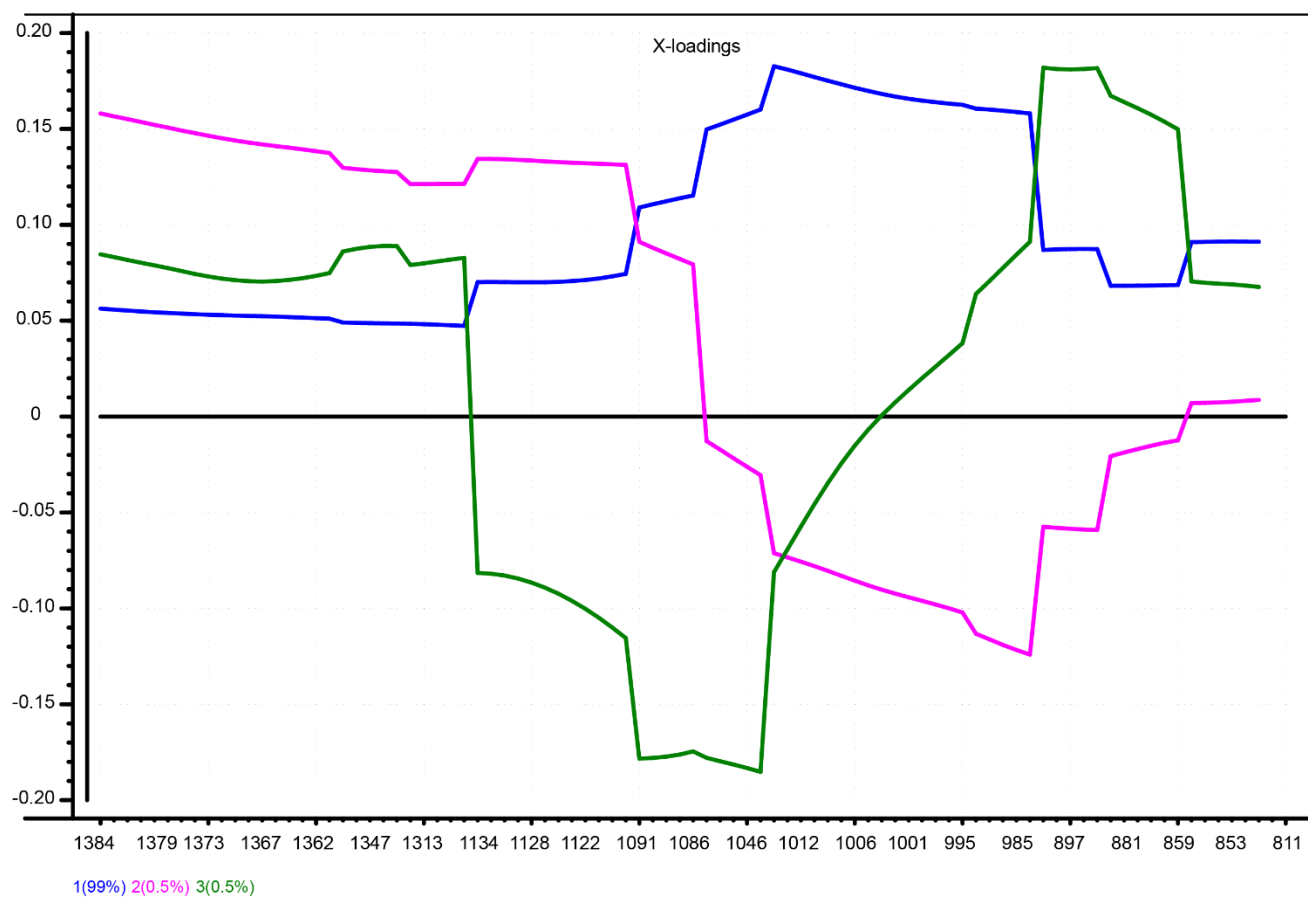


Figure S4: PCA loadings derived from xylan-associated wavelengths of *P. ovata* seed samples. The PCA plots are shown in Fig S3.

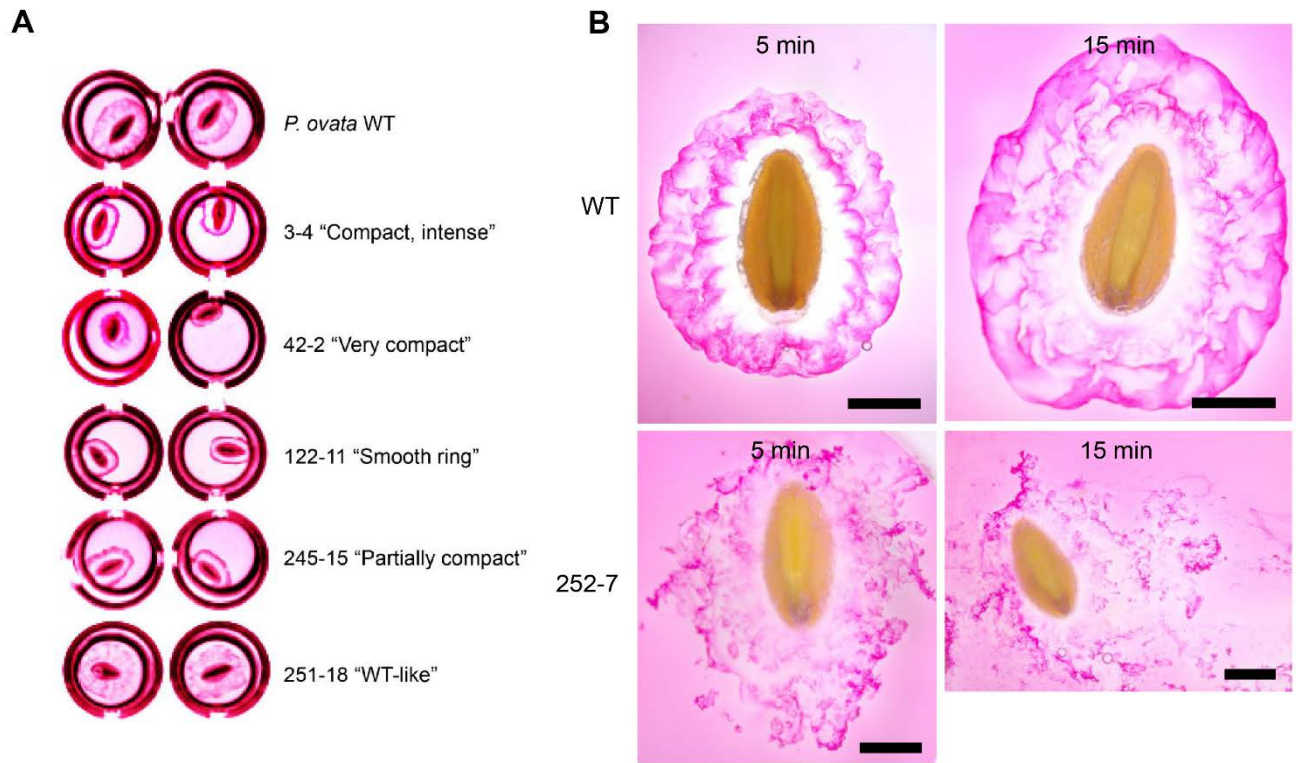


Figure S5: Ruthenium red staining of *P. ovata* seeds from different phenotypic classes. **(A)** Distinct mucilage phenotypes as they appear in microtitre plate assays. **(B)** Comparison of mucilage release and adhesion in *P. ovata* WT and 252-7 over time after RR-staining on slides. Scale bar = 1mm.

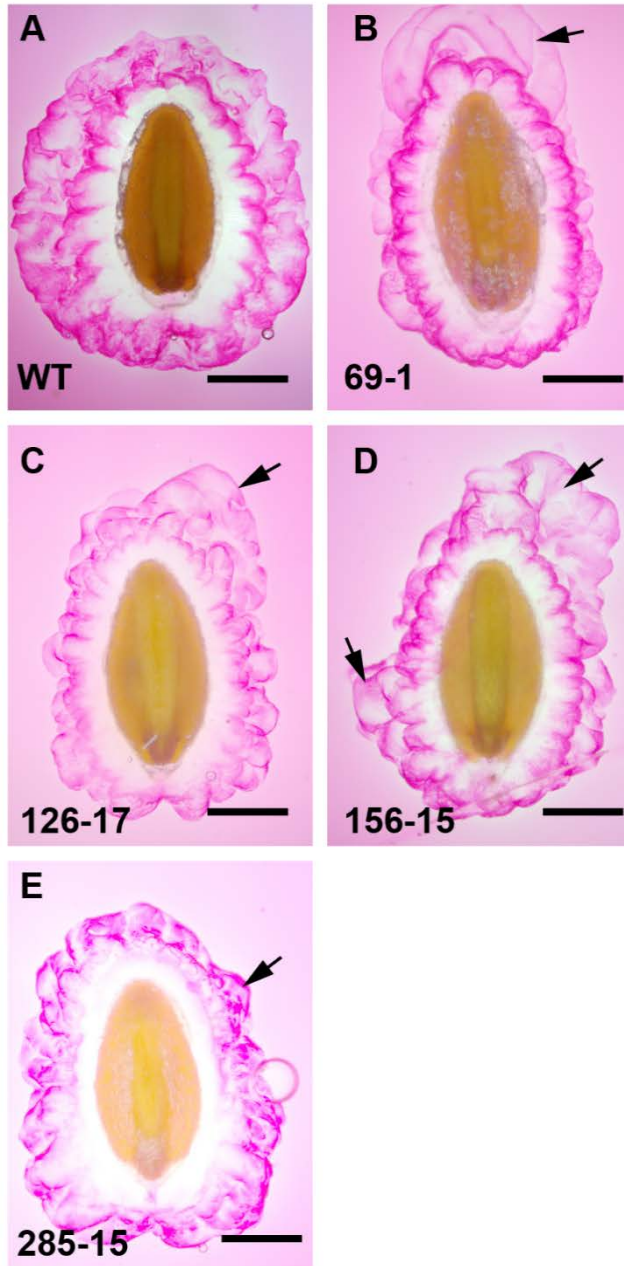


Figure S6: Ruthenium red staining of *P. ovata* seeds from M3 lines showing an “irregular bump” phenotype, as indicated by arrows. Bar = 1mm.

Table S1: Primers used for semi-quantitative PCR in this study

Name	Fwd Primer	Rev Primer	Product Size
<i>PoGAP</i>	TGCCTTGAGCAAGAACTTTGT	AACTGAGTGCATGTGGACGAT	100
<i>PoHisH4</i>	GCTGTCACCTATACCGAGCAC	TCAGCAGAAACAGAAATCCAGA	208
<i>PoAGO1</i>	TAGGTTTACTGGTGCCACGTC	CAACACAACACAGGCATTTGA	131
<i>PoAGO5</i>	GAACATACGCATTGAGGCACT	AAACACAACCTCGCCAAAACAT	152
<i>PoCesA3</i>	GGAAATCCTAGACGACCGAGT	ACAAAAGACACGACCGACAAC	102
<i>PoCesA4</i>	GCAAACCTGGTCCAATTCTCAA	TCAAACACAGACTTCGAGCAA	107
<i>PoCesA1</i>	CCTTATGAACAGTGGGGGAAT	TCATACACATCAAGGCCAACA	101
<i>PoCesA9</i>	TTGCTGTGGGTTTCGTATCAA	CAGCAATACCCTCGGTTTGT	178
<i>PoCslA</i>	TTTGTTCCTCCGGCTAAGGAAT	CAGCAGTAGGAAGGAGTCACG	139
<i>PoCslG2</i>	ATCCTGAAAGCCATGTTTCT	GGAATAAGGACAAGCCCGTAG	223
<i>PoUXS_1</i>	TCTGTGCGCCTTGGTGATATT	AGCTCGCTGAGACTGTGAAAG	112
<i>PoUXS_2</i>	TTCTCCTGGATTTCCGAGATT	TTGATGACGGTCGTGTTGTTA	182
<i>PoUXS_3</i>	TACAACAGATGGGATGCAGTG	GGACTTCCTCTCATGGTGACA	140
<i>PoUAM</i>	CAGTTGACCCCTACTTCACCA	AACAATCCCTATCCCGTTCAC	214
<i>PoGT61_2</i>	CGTGCTTTCTTCTCGACTCAC	CCAACATGGTCTTCTTCCAA	146
<i>PoGT61_8</i>	GGGCAAACCTGTATCCAAGTGA	TCCATGGCCTTAACCTAACGTG	153
<i>PoGT61_7</i>	TGGCTTTCAGAATGGTTTCTC	GGGAAGTACCCAATGGACAGT	139
<i>PoGT61_6</i>	GAATATGAAAGGGGTGCATCA	TTCCTGGCCACTTGTGAAAT	295
<i>PoGT61_1</i>	AAACTAATTGGGGGCAATGAC	AATGTACCTCCCGTTGGAAC	179
<i>PoXylT</i>	TTCCAGGCAGAGCTGAAACTA	CACGGCTTAGCAATGAAGAAG	202
<i>PoIRX10_3</i>	TTCCAAATTAGCAGCCACATC	TTCCAAATTAGCAGCCACATC	275
<i>PoIRX10_4</i>	TATTTCCCGATTAGGTCTGG	AAAATTTGAACGGACCTGGAT	160

Table S2: Absorbance ratio ranking of selected putative *P. ovata* mutants. The top row shows the absorbance ratios. Red coloration indicates the wild-type and internal mutant controls

Line	1164/1048	1110/1040	1070/1040	990/1380	895/1460
<i>P. ovata</i>	238	294	290	19	64
3-4	1	3	7	301	298
3-12	181	79	97	78	57
6-4	108	19	14	268	231
6-6	293	82	57	211	139
10-1	11	50	125	251	284
16-4	71	22	13	153	132
34-15	77	12	6	271	174
34-9	121	14	15	259	242
42-2	47	5	2	250	196
42-3	6	20	30	276	291
44-12	8	9	3	297	294
44-14	182	107	50	3	2
44-17	41	17	34	269	4
44-5	117	37	54	158	125
50-21	4	13	47	280	295
55-9	73	165	118	73	175
56-1	7	42	100	281	293
56-2	14	26	21	239	287
65-2	30	93	171	240	290
69-1	26	27	33	292	296
105-13	13	8	10	296	272
105-17	195	213	203	57	30
105-5	110	10	9	107	203
109-9	5	64	136	290	299
115-12	18	16	72	294	230
115-7	144	61	86	147	9
122-11	9	1	1	137	137
126-11	258	54	44	222	130
126-17	66	18	25	286	228
126-5	12	21	11	260	269
126-7	261	110	151	167	106
126-8	2	2	20	299	301
156-15	3	6	12	298	300
156-16	299	270	154	37	39
186-3	48	72	4	291	128
195-12	281	174	122	101	164
195-13	17	15	43	287	283
230-16	298	223	292	107	144
245-15	15	4	5	300	292
245-18	28	31	76	295	248
245-20	20	23	16	293	289
246-15	59	141	111	288	285
246-20	127	191	40	149	179
246-5	16	11	8	289	297
246-8	234	53	31	44	8
252-7	125	98	52	4	192
275-1	270	146	83	230	146
275-12	10	7	19	285	288
285-15	35	29	24	261	98
304-7	72	63	48	118	226
307-5	206	194	101	22	5
310-8	229	216	138	5	1
U-4	106	60	94	146	77

Table S3 FTMIR absorbance ratios for 37 putative *P.ovata* mucilage mutants representing 22 M1-derived families

Name	Line	RR Phenotype	1164/1048	1110/1040	1070/1040	990/1380	895/1460
<i>rxm1</i>	3-4	Compact, intense	0.435	0.610	0.803	1.818	1.840
	16-3	WT-like, less	0.347	0.518	0.767	2.292	2.244
	16-7	WT-like, less	0.337	0.513	0.761	2.423	2.413
	16-8	WT-like, less	0.328	0.518	0.764	2.419	2.395
	34-9	Compact, intense	0.345	0.557	0.792	2.187	2.216
<i>rxm4</i>	34-15	Compact, intense	0.351	0.559	0.807	2.169	2.324
	42-2	Very compact	0.359	0.576	0.810	2.198	2.294
	42-3	Very compact	0.393	0.553	0.786	2.153	1.977
	44-5	Smooth ring	0.346	0.543	0.782	2.278	2.373
	44-12	Smooth ring	0.389	0.567	0.810	1.996	1.926
	44-14	Smooth ring	0.341	0.532	0.782	2.456	2.632
	44-17	Smooth ring	0.361	0.555	0.785	2.170	2.602
	54-9	WT-like	0.347	0.542	0.774	2.194	2.141
	54-18	WT-like	0.336	0.515	0.765	2.456	2.511
	56-1	WT-like	0.390	0.542	0.777	2.128	1.940
	56-2	WT-like	0.378	0.548	0.788	2.208	2.056
	69-1	WT-like, bumpy	0.370	0.546	0.785	2.048	1.880
	76-3	WT-like	0.347	0.526	0.765	2.270	2.117
	105-13	Compact	0.379	0.567	0.798	2.012	2.129
	109-9	WT-like	0.398	0.539	0.774	2.056	1.834
	115-12	Compact	0.377	0.556	0.780	2.027	2.241
<i>rxm2</i>	122-11	Smooth ring	0.387	0.654	0.831	2.293	2.363
	126-5	WT-like, bumpy	0.386	0.553	0.797	2.187	2.142
	126-8	WT-like, bumpy	0.423	0.620	0.789	1.916	1.762
	126-17	WT-like, bumpy	0.354	0.555	0.787	2.109	2.245
	156-15	WT-like, bumpy	0.422	0.571	0.794	1.950	1.818
<i>rxm3</i>	245-15	Partially compact	0.378	0.582	0.807	1.913	1.966
	245-18	Partially compact	0.368	0.545	0.779	2.016	2.208
	245-20	Partially compact	0.373	0.551	0.791	2.043	2.043
	246-5	Compact, slow	0.378	0.562	0.802	2.071	1.873
	246-8	Compact, slow	0.336	0.540	0.785	2.369	2.553
	246-15	Compact, slow	0.356	0.528	0.776	2.078	2.074
	251-18	WT-like	0.354	0.519	0.760	2.426	2.400

252-7	Dispersed	0.345	0.533	0.782	2.445	2.298
285-15	WT-like, bumpy	0.364	0.546	0.787	2.185	2.399
307-5	Compact	0.338	0.522	0.776	2.391	2.589
310-8	Compact	0.336	0.520	0.774	2.448	2.712
WT	WT-like	0.335	0.509	0.761	2.393	2.433

RR- ruthenium red stain after 10 min imbibition, **WT** - wild-type, **compact** – RR-stained mucilage did not extend as far as WT, **intense** – appeared more heavily stained at the periphery of the mucilage compared to WT, **WT-like** – similar in appearance to WT, **WT-like, less** – similar to WT in plates and slides, but mucilage did not stain as intensely, **partially compact** – appeared compact in plates but only slightly reduced compared to WT on slides, **smooth ring** – the outer layer of mucilage stained in a perfectly smooth ring, **bumpy** – similar to WT but sporadic bumps appeared at the periphery where mucilage appears to spread faster, **dispersed** – appears punctate and disconnected from the seed, **rxm** – putative *reduced xylan in mucilage* mutant.