

Genetic Variation Controlling Wrinkled Seed Phenotypes in *Pisum*: How Lucky Was Mendel?

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AAATATAAATTCTAATATGATGCTACCATGATTTATGAAACTCAATCAACCTATCCTATAATCATTAAATGTTGTTTACAAATTTTGCAACAT
GACAAATGACTTCCACATACATCCAAACCCCGCCATCAAATGTGAGATGTAAGCATCCTTAAATCATGAACAGTAATTTTGTGTACATAA
GATAAACTACAAATACTTCCCTTTTAAACAACACTTTATTTTGTAGTGAAGTTCTAACACTTTGTTACATTTTACAACACATTGAAGCA
AATAACACCCGCAAAAGTTACATCAAGTGAAAATGACATTTGTTGTGTAATGAGAATCCCATTACAACCTTGGACTTTTGTGAGTG
AATCATTTTCATCAACCATGTTTCCAAAGGCAACAAATATCAAAAAATATAATAATATTTTGTAGAAATTGAGGTTTCTGAATTCTCTCA
ATAAAGGCAACACTTTTCCCTTCATCACTACTCAATAATAGTTTGTAGATTACATTCTCTCTTTGTTTCTCTAGATTCTATATTTTAGTT
GTGACCTTTCTACTAGCATTGTTTCTCTCTTATTCTCTTGGTCTGAGTTTGAACAACTCAAAAAAAGGCTTAGTTTGTGAGGTTACT
ACAATTGCTTCTGGTTGTGTGAGCTTGAAAACCAACACCCATTTCCTAAATTTCAAAAAAGGTTCTTTTGTGGGAAAGAATCAAGGAAG
CTTGAAAAACAGTTCATGGGTCACTACCCAGAAGAAGATCAAACTGCTTCTTTTCTGCTATTCTTACTTTCAGATGACCCCAAGGTTCC
TGTAAACTCAGTTTCATTCTGGGTTTCACTTTTGTCTTCCAAATCTGAAAAAAGAAAGACTTTTCTCCCATTTATGACATAACT
TTTTATGTTAATTATTTTGTCTACATTTTGTGTTGGTATATGATTATGATTATGATTATGATTATGATTATGATTATGATTATGATTATGATT
CAAGTGCCCTTCATTTCTGAGACTAAGAGCTGATCCAAAAATGTGATTTCATTGTGTTGGGAGGAGGCGCTGGAACACATCTCTATCCTCT
TACCAACGAGCTGCTGTGAGTGAGTGTGATGATGAATTGTTGTCTGAATCTAACATTTTGGTGTGTTGTGTAACCTTGTGCTGTTTGT
GATGAAGATTGTTGTGCTGTGTTTGTGTTGAAAGCTTCTGTTGGAGGATGCTATAGGCTTATAGACATTCCAATGAGCACTGCATCAATAG
TGGCATCAACAGATATTTGTGCTGACTCAGTTCAACTCTGCTTCACTAAATCGTCACATCGCTCGCACCTATTTTCGGAATGGTGTCACT
TTTGGAGATGGATTGTTGGAGCTAATCATGCAATCACCATCATGAAAAATGGATGGAATTAGTACTTTTTTTTCTGCAATTTTATATGGA
ACAATCTTTTAGCATACTTTGTTTATCTTTTGTGCGAATCCGAATAACTAGGATCCGCTCTTTTCTGGGATTTAGAGAGTTAAGAACAAAA
AATATATTTTTCATGCAATGAGTTTGTGAGTGAACATGACAGTTGCCAACAAACAAAAACATAAGTAATTCGGTTTTCGCTAGAGAAATACCGAT
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AGTCACGTTGATAGAAATGCCGATATTACAGTTTTCGTGTGCTGCGCTTGGTGACAAAGTGAATGAGTATTATACCTTTATTTCTAGAAATGGGTG
AATAGAAAGAACTCAACTAAGTGGAACAAAAATACGATTTCATTTGTCTGATTTTCAGCCGCGCATCTGATTATGGATTGGTCAAAGTAGAC
GACAGAGGCAACATCGTACAATTTTCAGAAAAACCGAAGGCGCTGATCTGAAAGCAATGTAAATTCCAAACATAATAACCTAATGTTTGCA
CCTTCTTTCTGTTTCTTGTATCTGGTAAATCCACTGAGATTGTTTCATCTCTCATTTTTCAGCAAGTAGATACTTCTCGTCTTGGGTTGTCA
CCGCAAGACGCATTGAAGTCCGCATATATTGCATCTATGGGAGTTTATGTGTTCAAGAAAGATGTTTACTCAAGCTTCTGAAATGGAGGTA
TCCATCTTCTAATGACTTCGGATCCGAAATCATTTCTTCCGCAATAAGAGAGCACAATGTCCAAATAAGAGGAATTCGGATAAAATATATCAG
CTTACAAATGTTTTTATCCATTTTCAGAAGATTTTATCTGCCATCTATGCTTTTATGCAAGCATATTTTTCGGAGACTACTGGGAAGATAT
TGGAAACGATAAAATCCTTCTACGATGCTAACCTCGCTCTTACTGAAGAGGTAGGTTCAAGAATTTTTCAGTGTCTTGTTCAGTTTAGTTGA
TTGAAACTAAAACTGTCTACATGTTACTCTCTCACAGAGTCCAAAGTTCGAGTTTATGATCCAAAACTCCGATTTTCACATCTCCAGGAT
TCCACCAACCAAGAAATGACAACTCTCGGATACGATAATCTATCTATCTTGTATCATGCTAATAATTCGAAACATCATGTCTTTCTTAT
TCTGTCCGCGTTGCTTTGTTGTTGGTAGGTTGTGGATGCCATTATCTCCCATGGATGTTTCTGAGAGATTGTACAATCCAACACTCCATTG
TAGGTGAAAGGTCGCGTTTAGATTATGGCGTTGAGCTTCAGGTAATTAACCTACCATATATTCTAGACTCGTTACTCCATTAAACGGTTCTCT
CCTAACGAAAAACAGATCAACTTTTACAGGACACTGTAATGATGGGAGCTGACTATTACCAAACTGAATCCGAAATCGCTTCCCTACTTGC
AGAAGGGAAGGTCCTGATTCGGATCCGAAATGACAAATCAAATAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
TGAAACTCATAGTTTGTATTTATTATCTCTGTAAAGGAACTGCATTATTGACAAGAATGCAAAAACTCGGGAAGAAGTTGTATCGCGA
ACAAAGAAATAAGAAATAAAACAAGTTAGTAGTTTTCCTGTTCCAGCATACATTTGTTTACGCGTATAAACTCGAATGCTTTATCTGTAGGGCG
TTCAAGAAGCAGATAGATCGGAAGATGGTTTCTACATCCGATCAGGAATCACCATCATAATGGAGAAAGCAACGATAGAAGACGGAAGTCTC
ATAATAACAGATGATGTTTATTTTACGAGCTGTTTTCGTAAGCGCCGGAAGAAGCATTGCAAGGAACATCCCTCTATCTTTTGGG
ATTGGTACAAATGTTATGTTGAATAGAGAAAGCTGCATGTGTAAATAGGAGAGCTCTTCTACTAGATGTAGAAATAGAAATGAATAAATG
ATGAAAGTGAAGATGCAGAAAAGTTAAATAAATGGAAGGGT

Key:

GCTGCG borders the position of the nine base pair deletion relative to the wild-type gene

INTRON

ATG

TAA predicted by GeneMarker & database comparisons

Ps AGP1L-F1:GCAAGTGCCTTCATTTCTGAG
Ps AGP1L-F2:TGGAGATGGATTTGTGGAGG
Ps AGP1L-F3:GCAAGTAGATACTTCTCGTCTTGGG
Ps AGP1L-F4:ACCGATTTTCACATCTCCTGG
Ps AGP1L-F5:CCTCTTACCAAACGAGCTGC
Ps Agp1l-F6:AGTTTCGTGTGCTGCGG
Ps Agp1l-F7:GAGGTTACTACAATGGCTTCTGG
Ps Agp1l-F8:TTTAGTTGTGACCTTTCACTACTAGC
Ps Agp1l-F9:TTTCTCTCAATAAAGGCAACACC
Ps Agp1l-F10:ACTTCCACATACATCCAAACCC

Ps Agp11-F11:GAATCCGAAATCGCTTCCC
 Ps Agp11-F12:TGGCCGGAGATCATTTATATCG

Ps AGP1L-R1:CTCCTGGTGTGTTGAGTCGC
 Ps AGP1L-R2:TGAACACATAAACTCCCATAGATGC
 Ps AGP1L-R3:CTGAAGCTCAACGCCATAATC
 Ps AGP1L-R4:TGATACCTTCACACACTCAACCC
 Ps AGP1L-R5:GCATCCTCCAACAGGAACC
 Ps Agp11-R6:ACATTGTGCTCTCTTATTGCGG
 Ps Agp11-R7:GGATAGAGATGTGTTCCAGGC
 Ps Agp11-R8:CGAAATAGGTGCGAGCG
 Ps Agp11-R9:GGAACCTTTGGGGTCATCTG
 Ps Agp11-R10:GCAGGTTTGATCTTCTTCTGGG
 Ps Agp11-R11:CGATGACAACTTCTTTCCCG
 Ps Agp11-R12:GCGAGGTTAGCATCGTAGAAGG

Figure S1. The consensus genomic sequence of the naturally occurring *rb* mutant allele for the large subunit of ADP-glucose pyrophosphorylase, present in the pea accession, JI 399. Introns are indicated in yellow highlight; forward and reverse primers are indicated in green and blue font, respectively, and underlined. The position where nine bases are missing relative to the wild-type allele is in pink font. Initiator and stop codons are highlighted in red. The sequences of 12 primer pairs are listed underneath the sequence.

A.

JI281Rfs1	--PPSITKTATPQDVINTVDIGNSPLFSISLDQSRNFLVNGHPFLTQVPPNIITTTTSTP	58
JI2110	--PPSITKTATPQDVINTVDIGNSPLFSISLDQSRNFLVNGHPFLTQVPPNIITTTTSTP	58
DB	MAPPSITKTATQQDVISTVDIGNSPLLSISLDQSRNFLVNGHPFLTQVPPNIITTTTSTP	60
	***** . ***** : *****	
JI281Rfs1	SPFLDFKSNKDTIANNNNTLQQQGC FVG FNTTEAKSHHVPLGKLKGIKFTSIFRFKVWW	118
JI2110	SPFLDFKSNKDTIANNNNTLQQQGC FVG FNTTEAKSHHVPLGKLKGIKFTSIFRFKVWW	118
DB	SPFLDFKSNKDTIANNNNTLQQQGC FVG FNTTEAKSHHVPLGKLKGIKFTSIFRFKVWW	120

JI281Rfs1	TTHWVG TNGHELQHETQILILDKNISLGRPYVLLLPILENSFR TSLQ PGLNDYVDM SVES	178
JI2110	TTHWVG TNGHELQHETQILILDKNISLGRPYVLLLPILENSFR TSLQ PGLNDYVDM SVES	178
DB	TTHWVG TNGHELQHETQILILDKNISLGRPYVLLLPILENSFR TSLQ PGLNDYVDM SVES	180

JI281Rfs1	GSTHVTGSTFKACLYLHLSNDPYRLVKEAVKVIQTQLGTFK TLEEKTPPSIIEKFGWCTW	238
JI2110	GSTHVTGSTFKACLYLHLSNDPYRLVKEAVKVIQTQLGTFK TLEEKTPPSIIEKFGWCTW	238
DB	GSTHVTGSTFKACLYLHLSNDPYRLVKEAVKVIQTQLGTFK TLEEKTPPSIIEKFGWCTW	240
	***** . *****	
JI281Rfs1	DAFYLKVHPKGVREGVKALTDGGCPPGFVIIDDGWQSI SHDDDPVTERDGMNRTSAGEQ	298
JI2110	DAFYLKVHPKGVWEGVKALTDGGCPPGFVIIDDGWQSI SHDDDPVTERDGMNRTSAGEQ	298
DB	DAFYLKVHPKGVWEGVKALTDGGCPPGFVIIDDGWQSI SHDDDPVTERDGMNRTSAGEQ	300

JI281Rfs1	MPCRLIKYEENYKFREYENGDNNGKKGLGVFRDLKEEF RSVESVYVWHALCGYWGGVRP	358
JI2110	MPCRLIKYEENYKFREYENGDNNGKKGLGVFRDLKEEF RSVESVYVWHALCGYWGGVRP	358
DB	MPCRLIKYEENYKFREYENGDNNGKKGLGVFRDLKEEF RSVESVYVWHALCGYWGGVRP	360

JI281Rfs1	KVCGMPEAKVVVPKLSPGMKMTMEDLAVDKIVENG VGLVPPNLAQEMFDGIHSHLESAGI	418
JI2110	KVCGMPEAKVVVPKLSPGVKMTMEDLAVDKIVENG VGLVPPNLAQEMFDGIHSHLESAGI	418
DB	KVCGMPEAKVVVPKLSPGVKMTMEDLAVDKIVENG VGLVPPNLAQEMFDGIHSHLESAGI	420
	***** . *****	
JI281Rfs1	DGVKVDVIHLLLELLSEEYGG RVELAKAYYKALTSSVNKHFKGNGVIASMEHCNDFLLGT	478
JI2110	DGVKVDVIHLLLELLSEEYGG RVELAKAYYKALTSSVNKHFKGNGVIASMEHCNDFLLGT	478
DB	DGVKVDVIHLLLELLSEEYGG RVELAKAYYKALTSSVNKHFKGNGVIASMEHCNDFLLGT	480

JI281Rfs1	EAISLGRVGDDFWCCDPSGDPNGTYWLQGCHMVHCAYNLSLWMGNFIHPDWDMFQSTHPCA	538
JI2110	EAISLGRVGDDFWCCDPSGDPNGTYWLQGCHMVHCAYNLSLWMGNFIHPDWDMFQSTHPCA	538
DB	EAISLGRVGDDFWCCDPSGDPNGTYWLQGCHMVHCAYNLSLWMGNFIHPDWDMFQSTHPCA *****	540
JI281Rfs1	EFHAASRAISGGPVYVSDCVGNHNFKLLKSFVLPDGSILRCQHYALPTRDCLFEDPLHNG	598
JI2110	EFHAASRAISGGPVYVSDCVGNHNFKLLKSFVLPDGSILRCQHYALPTRDCLFEDPLHNG	598
DB	EFHAASRAISGGPVYVSDCVGNHNFKLLKSFVLPDGSILRCQHYALPTRDCLFEDPLHNG *****	600
JI281Rfs1	KTMLKIWNLNKYAGVLGLFNCQGGGWCPEPTRRNKSASEFSRAVTCYASPEDIEWCNGKTP	658
JI2110	KTMLKIWNLNKYAGVLGLFNCQGGGWCPEPTRRNKSASEFSRAVTCYASPEDIEWCNGKTP	658
DB	KTMLKIWNLNKYAGVLGLFNCQGGGWCPEPTRRNKSASEFSRAVTCYASPEDIEWCNGKTP *****:*****	660
JI281Rfs1	MDIKGVDVFAVYFFKEKKLSLMKCSRLEVSLEPFSFELMTVSPLKVFSKRLIQFAPIGL	718
JI2110	MDIKGVDVFAVYFFKEKKLSLMKCSRLEVSLEPFSFELMTVSPLKVFSKRLIQFAPIGL	718
DB	MDIKGVDVFAVYFFKEKKLSLMKCSRLEVSLEPFSFELMTVSPLKVFSKRLIQFAPIGL *****	720
JI281Rfs1	VNMLNSGGAVQSLEFDDASASLVKIGVRGCGELSVFMSEKPVCKIDGVSVEFDYEDKM--	776
JI2110	VNMLNSGGAVQSLEFDDASASLVKIGVRGCGELSVFASEKPVCKIDGVSVEFDYEDKM--	776
DB	VNMLNSGGAVQSLEFDDASASLVKIGVRGCGELSVFASEKPVCKIDGVSVEFDYEDKMVR *****	780
JI281Rfs1	-----	776
JI2110	-----	776
DB	VQILWPGSSTLSLVEFLF	798

B.

JI281AAP1	MVVEKNASKNHHHQTDFDVSIDQQLDSKFFDDDGRVKRTGTSTASAHVITAVIGSGVLSL	60
JI2110AAP1	MVVEKNASKNHHHQTDFDVSIDQQLDSNFFDDDGRVKRTGTSTASAHVITAVIGSGVLSL	60
AAX56951.1	MVVEKNASKNHHHQTDFDVSIDQQLDSKFFDDDGRVKRTGTSTASAHVITAVIGSGVLSL *****:*****	60
JI281AAP1	AWAIAQLGWIAGPVVMILFAVWTTYTSVLLAECYRNGDPVNGKRNITYMEVHNSNLGGLQ	120
JI2110AAP1	AWAIAQLGWIAGPVVMILFAVWTTYTSVLLAECYRNGDPVNGKRNITYMEVHNSNLGGLQ	120
AAX56951.1	AWAIAQLGWIAGPVVMILFAVWTTYTSVLLAECYRNGDPVNGKRNITYMEVHNSNLGGLQ *****	120
JI281AAP1	VQFCGFIQYLNLIQVAIGYTVASAISSMAIERSNICYHRSGGKDPCHMNSNAYMIAFGAVQ	180
JI2110AAP1	VQFCGFIQYLNLIQVAIGYTVASAISSMAIERSNICYHRSGGKDPCHMNSNAYMIAFGAVQ	180
AAX56951.1	VQFCGFIQYLNLIQVAIGYTVASAISSMAIERSNICYHRSGGKDPCHMNSNAYMIAFGAVQ *****	180
JI281AAP1	IIVSQIPDFDQLWWSIVAAVMSFTYSTIGLGLGIGKVIENKKFAGTITGVNDVTKAQKT	240
JI2110AAP1	IIVSQIPDFDQLWWSIVAAVMSFTYSTIGLGLGIGKVIENKKFAGTITGVNDVTKAQKT	240
AAX56951.1	IIVSQIPDFDQLWWSIVAAVMSFTYSTIGLGLGIGKVMENKKFAGTITGVNDVTKAQKT *****:*****	240
JI281AAP1	WGSLLQALGDIAFAYSFSMILIEIQDQTVKAPPPSESKTMMKATLISVIVTTFYMLCGCLG	300
JI2110AAP1	WGSLLQALGDIAFAYSFSMILIEIQDQTVKAPPPSESKTMMKATLISVIVTTFYMLCGCLG	300
AAX56951.1	WGSLLQALGDIAFAYSFSMILIEIQDQTVKAPPPSESKTMMKATLISVIVTTFYMLCGCLG *****	300
JI281AAP1	YAAFGNSSPGNLLTGFGFYNPFWLLDIANAIAIVHLIGAYQVYCQPLYAFVENYMTKKFP	360
JI2110AAP1	YAAFGNSSPGNLLTGFGFYNPFWLLDIANAIAIVHLIGAYQVYCQPLYAFVENYMTKKFP	360
AAX56951.1	YAAFGNSSPGNLLTGFGFYNPFWLLDIANAIAIVHLIGAYQVYCQPLYAFVENYMTKKFP *****.*:**	360
JI281AAP1	DNYFLNKNIKIPIPGLDYKLNLFKLVWRTVFVILTTLVSMLLPFFNDIVGLLGALGFWP	420
JI2110AAP1	DNYFLNKNIKIPIPGLDYKLNLFKLVWRTVFVILTTLVSMLLPFFNDIVGLLGALGFWP	420
AAX56951.1	DNYFLNKNIKIPIPGLDYKLNLFKLVWRTVFVILTTLVSMLLPFFNDIVGLLGALGFWP *****	420

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JI281AAP1   LTVYFPVEMYIIQKKIPKWSTKWICLQLLSGACLIITIAASVGSIAGIYLDLKVFKPFKT   480
JI2110AAP1  LTVYFPVEMYIIQKKIPKWSTKWTCLQLLSGACLIITIAASVGSIAGIYLDLKVFKPFKT   480
AAX56951.1  LTVYFPVEMYIIQKKIPKWSTKWTCLQLLSGACLIITIAASVGSIAGIYLDLKVFKPFKT   480
*****

JI281AAP1   IY   482
JI2110AAP1  IY   482
AAX56951.1  IY   482
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Figure S2. The protein sequences predicted for genes (*Rfs*, *AAP1*) on LG III which map in the region of the testa trait in JI 2110 x JI 281. **A.** Rfs comparison in JI 2110, JI 281 and the NCBI database accession AJ426475 (DB). **B.** AAP1 comparison in JI 2110, JI 281 and the NCBI accession AAX56951. Asterisks or dots underneath the alignments indicate amino acid identity or extent of similarity, respectively.