

This file is part of the supplemental information provided with the following article.

The KnownLeaf literature curation system captures knowledge about Arabidopsis leaf growth and development and facilitates integrated data mining^[1]

Dóra Szakonyi*, Sofie Van Landeghem*, Katja Baerenfaller, Lieven Baeyens, Jonas Blomme, Rubén Casanova-Sáez, Stefanie De Bodt, David Esteve-Bruna, Fabio Fiorani², Nathalie Gonzalez, Jesper Grønlund, Richard G.H. Immink, Sara Jover-Gil, Asuka Kuwabara, Tamara Muñoz-Nortes, Aalt D.J. van Dijk, David Wilson-Sánchez, Vicky Buchanan-Wollaston, Gerco C. Angenent, Yves Van de Peer, Dirk Inzé, José Luis Micol, Wilhelm Gruissem, Sean Walsh*, Pierre Hilson*

Department of Plant Systems Biology, VIB, B-9052 Ghent, Belgium (D.S., S.V.L., L.B., J.B., S.D.B., F.F., N.G., Y.V.d.P., D.I., P.H.); Department of Plant Biotechnology and Bioinformatics, Ghent University, B-9052 Ghent, Belgium (D.S., S.V.L., S.D.B., J.B., F.F., N.G., Y.V.d.P., D.I., P.H.); Department of Biology, ETH Zurich, CH-8093 Zurich, Switzerland (K.B., A.K., W.G., S.W.); División de Genética and Instituto de Bioingeniería, Universidad Miguel Hernández, 03202 Elche, Alicante, Spain (R.C.S., D.E.B., S.J-G., T.M.N, D.W.S., J.L.M.); Warwick Systems Biology Centre, University of Warwick, Coventry CV4 7AL, United Kingdom (J.G., V.B.-W.); School of Life Sciences, University of Warwick, Coventry CV4 7AL, United Kingdom (J.G., V.B.-W.); Plant Research International, Bioscience, 6708 PB Wageningen, The Netherlands (R.G.H.I., A.D.J.v.D., G.C.A.); Genomics Research Institute (GRI), University of Pretoria, Private bag X20, Pretoria, 0028, South Africa (Y.V.d.P.); INRA, UMR1318, Institut Jean-Pierre Bourgin, RD10, F-78000 Versailles, France (P.H.); AgroParisTech, Institut Jean-Pierre Bourgin, RD10, F-78000 Versailles, France (P.H.)

Phenotype examples

1. The rot3-2 allele causes enlarged leaf blades

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Genotype ID	rot3-2	mutated gene_MI:0804
Gene ID	rot3	ROT3_AT4G36380
Genotype Zygoty		homozygous diploid_APO:0000229
Mutant LOF_GOF ID		loss of function_APO:0000011
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID	leaf blades	leaf lamina_PO:0020039
Process ID		
Property Slot		size_PATO:0000117
Value ID	enlarged	increased size_PATO:0000586

2. The rot3-2 allele causes ... short petioles

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Genotype ID	rot3-2	mutated gene_MI:0804
Gene ID	rot3	ROT3_AT4G36380
Genotype Zygoty		homozygous diploid_APO:0000229
Mutant LOF_GOF ID		loss of function_APO:0000011
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID	petioles	petiole_PO:0020038
Process ID		
Property Slot		length_PATO:0000122
Value ID	short	decreased length_PATO:0000574

3. 35S-ICK1 plants ... there was a range of changes in leaf shape

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Genotype ID	35S-ICK1	over expressed level_MI:0506
Gene ID	ICK1	ICK1 KRP1_AT2G23430
Growth Condition Slot		
Localisation ID		

Methodology ID		
Plant part ID	leaf	leaf_PO:0025034
Process ID		
Property Slot	shape	shape_PATO:0000052
Value ID	changes	abnormal_PATO:0000460

4. double mutants between se and as1 ... showed dramatic lobing of leaves

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Genotype ID	double mutants between se and as1	mutated gene_MI:0804
Gene ID	se	SE_AT2G27100
	as1	ATPHAN AS1 ATMYB91 MYB91_AT2G37630
Genotype Zygosity		homozygous diploid _APO:0000229
Mutant LOF_GOF ID		loss of function_APO:0000011
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID	leaves	leaf_PO:0025034
Process ID		
Property Slot		shape_PATO:0000052
Value ID	lobing	lobed_PATO:0001979

5. 35S::KNAT1 leaves are ... folded upwards

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Genotype ID	35S::KNAT1	over expressed level_MI:0506
Gene ID	KNAT1	KNAT1 BP BP1_AT4G08150
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID	leaves	leaf_PO:0025034
Process ID		
Property Slot		shape_PATO:0000052
Value ID	folded upwards	involute_PATO:0001962

6. The serrate (se) mutant (Fig. 1B) showed strong serration of the leaves

Information type/Slots	Original text	Ontologies attached
Developmental stage		

Factuality ID		
Genotype ID	se	mutated gene_MI:0804
Gene ID	se	SE_AT2G27100
Genotype Zygosity		homozygous diploid_APO:0000229
Mutant LOF_GOF ID		loss of function_APO:0000011
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID	leaves	leaf_PO:0025034
Process ID		
Property Slot		shape_PATO:0000052
Value ID	serration	serrated_PATO:0001206

7. Fresh weight ... of exo shoots were diminished in comparison to the wild-type

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Genotype ID	exo	mutated gene_MI:0804
Gene ID	exo	EXO_AT4G08950
Genotype Zygosity		homozygous diploid_APO:0000229
Mutant LOF_GOF ID		loss of function_APO:0000011
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID	shoots	shoot system_PO:0009006
Process ID		
Property Slot	Fresh weight	shoot fresh weight_TO:0000571
Value ID	diminished	decreased weight_PATO:0000583

8. Transgenic 35S-ICK1 plants were smaller than control plants

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Genotype ID	35S-ICK1	over expressed level_MI:0506
Gene ID	ICK1	ICK1 KRP1_AT2G23430
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID	plants	whole plant_PO:0000003
Process ID		
Property Slot		size_PATO:0000117
Value ID	smaller	decreased size_PATO:0000587

9. The complexity of venation in as2-1 cotyledons was lower than that in the wild type

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Genotype ID	as2-1	mutated gene_MI:0804
Gene ID	as2	AS2_AT1G65620
Genotype Zygosity		homozygous diploid_APO:0000229
Mutant LOF_GOF ID		loss of function_APO:0000011
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID	venation in ... cotyledons	cotyledon vascular system_PO:0000035
Process ID		
Property Slot	complexity	complexity_PATO:0001502
Value ID	complexity ... lower	simple_PATO:0001503

10. Epidermal leaf cells of 3-week-old gpa1 mutants are significantly larger

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Genotype ID	gpa1	mutated gene_MI:0804
Gene ID	gpa1	GPA1 GP ALPHA 1 ATGPA1_AT2G26300
Genotype Zygosity		homozygous diploid_APO:0000229
Mutant LOF_GOF ID		loss of function_APO:0000011
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID	Epidermal leaf cells	leaf epidermis_PO:0006016
Process ID		
Property Slot		cell size_MESH:68048429
Value ID	larger	increased size_PATO:0000586

11. kan1 kan2 plants ... Leaves are ... dark green

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Genotype ID	kan1 kan2	mutated gene_MI:0804
Gene ID	kan1	KAN KAN1_AT5G16560
	kan2	KAN2_AT1G32240
Genotype Zygosity		homozygous diploid_APO:0000229
Mutant LOF_GOF ID		loss of function_APO:0000011
Growth Condition Slot		

Localisation ID		
Methodology ID		
Plant part ID	Leaves	leaf_PO:0025034
Process ID		
Property Slot		color_PATO:0000014
Value ID	dark green	dark green_PATO:0001249

12. treatment with GA3 increased ... the length of wild-type leaf blades by 17%

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Genotype ID	wild-type	Wild type_SO:0000817
Growth Condition Slot	treatment with GA3	gibberellic acid regimen_EO:0007069
Localisation ID		
Methodology ID		
Plant part ID	leaf blades	leaf lamina_PO:0020039
Process ID		
Property Slot	length	length_PATO:0000122
Value ID	increased	increased length_PATO:0000573

13. swp leaves ... some of the mesophyll cells contained larger nuclei

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Genotype ID	swp	mutated gene_MI:0804
Gene ID	swp	SWP MED14 ATMED14_AT3G04740
Genotype Zygoty		homozygous diploid_APO:0000229
Mutant LOF_GOF ID		loss of function_APO:0000011
Growth Condition Slot		
Localisation ID	mesophyll cells	mesophyll cell_PO:0004006
Methodology ID		
Plant part ID	nuclei	nucleus_GO:0005634
Process ID		
Property Slot		size_PATO:0000117
Value ID	larger	increased size_PATO:0000586

14. AS1>>KAN2 plants, the leaves that developed were radialized

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Genotype ID	AS1>>KAN2	Complex genotype
Gene ID	AS1	ATPHAN AS1 ATMYB91

	KAN2	MYB91_AT2G37630 KAN2_AT1G32240
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID	leaves	leaf_PO:0025034
Process ID		
Property Slot		shape_PATO:0000052
Value ID	radialized	cylindrical_PATO:0001873

15. AS1>>KAN2 plants, the leaves that developed were ... abaxialized

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Genotype ID	AS1>>KAN2	Complex genotype
Gene ID	AS1	ATPHAN AS1 ATMYB91
	KAN2	MYB91_AT2G37630 KAN2_AT1G32240
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID	leaves	leaf_PO:0025034
Process ID		
Property Slot		dorsal-ventral polarity_PATO:0001775
Value ID	abaxialized	ventralized_PATO:0000636

16. smp2-1 homozygous plants ... looked wild-type

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Genotype ID	smp2-1	mutated gene_MI:0804
Gene ID	smp2	SMP2_AT4G37120
Genotype Zygosity	homozygous	homozygous diploid_APO:0000229
Mutant LOF_GOF ID		loss of function_APO:0000011
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID	plants	whole plant_PO:0000003
Process ID		
Property Slot		morphology_PATO:0000051
Value ID	wild-type	normal_PATO:0000461

17. fil-8 yab3-2 ant-4 ... decreased leaf area

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Genotype ID	fil-8 yab3-2 ant-4	mutated gene_MI:0804
Gene ID	fil	AFO FIL YAB1_AT2G45190 YAB3_AT4G00180
	ant	ANT DRG CKC CKC1_AT4G37750
Genotype Zygosity		homozygous diploid_APO:0000229
Mutant LOF_GOF ID		loss of function_APO:0000011
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID	leaf	leaf_PO:0025034
Process ID		
Property Slot	area	area_PATO:0001323
Value ID	decreased	decreased area_PATO:0002058

18. Atofp1-1D mutants mainly have defects in cell elongation

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Genotype ID	Atofp1-1D	mutated gene_MI:0804
Gene ID	Atofp1	ATOFP1 OFP1_AT5G01840
Genotype Zygosity		homozygous diploid_APO:0000229
Mutant LOF_GOF ID		gain of function
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID		
Process ID	cell elongation	cell growth_GO:0016049
Property Slot		
Value ID	defects	abnormal_PATO:0000460

19. the leaf index (the ratio of the leaf length to the leaf width) was increased from 2.3 ± 0.2 in control plants to 2.7 ± 0.2 ... in transgenic 35S:MIR396a ... plants

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Genotype ID	35S:MIR396a	over expressed level_MI:0506
Gene ID	MIR396a	AT5G35407
Growth Condition Slot		
Localisation ID		
Methodology ID		

Plant part ID	leaf	leaf_PO:0025034
Process ID		
Property Slot	leaf index	leaf length to width ratio_TO:0000542
Value ID	increased	present in greater numbers in organism_PATO:0000470

20. 35S::ANT leaves had slightly higher rates of cell proliferation than wild-type at Day 0

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Genotype ID	35S::ANT	over expressed level_MI:0506
Gene ID	ANT	ANT DRG CKC CKC1_AT4G37750
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID	leaves	leaf_PO:0025034
Process ID	cell proliferation	cell division_GO:0051301
Property Slot	rates	rate_PATO:0000161
Value ID	higher	increased rate_PATO:0000912

Gene expression examples

1. ROT3P::GUS ... we observed ... in leaves (GUS staining)

Information type/Slots	Original text	String entry	Ontologies attached
Developmental stage			
Factuality ID			
Gene expression ID	observed		present_PATO:0000467
Gene studied	ROT3		ROT3_AT4G36380
Genotype ID			Wild type_SO:0000817
Growth Condition Slot			
Localisation ID			
Methodology ID			
Plant part ID	leaves		leaf_PO:0025034
Property Slot		GUS staining	spatial pattern_PATO:0000060

2. FIL ... No signal is detected in differentiated leaves (in situ hybridization, WT background)

Information type/Slots	Original text	String entry	Ontologies attached
Developmental	differentiated leaves		3 leaf fully expanded_PO:0001053

stage		
Factuality ID		
Gene expression ID	No signal is detected	absent_PATO:0000462
Gene studied	FIL	AFO FIL YAB1_AT2G45190
Genotype ID		Wild type_SO:0000817
Growth Condition Slot		
Localisation ID		
Methodology ID		in situ hybridization
Plant part ID	leaves	leaf_PO:0025034
Property Slot		spatial pattern_PATO:0000060

3. In differentiating leaves FIL mRNA can be detected in the abaxial epidermis (in situ hybridization, WT background)

Information type/Slots	Original text	String entry	Ontologies attached
Developmental stage	differentiating leaves FIL		2 leaf expansion stage_PO:0001052
Factuality ID			
Gene expression ID	detected		present_PATO:0000467
Gene studied	FIL		AFO FIL YAB1_AT2G45190
Genotype ID			Wild type_SO:0000817
Growth Condition Slot			
Localisation ID			
Methodology ID		in situ hybridization	
Plant part ID	leaves... abaxial epidermis		leaf abaxial epidermis_PO:0006019
Property Slot			spatial pattern_PATO:0000060

4. ANT mRNA accumulated in leaf (RT-PCR, WT background)

Information type/Slots	Original text	String entry	Ontologies attached
Developmental stage			
Factuality ID			
Gene expression ID	accumulated		present_PATO:0000467
Gene studied	ANT		ANT DRG CKC CKC1_AT4G37750
Genotype ID			Wild type_SO:0000817
Growth Condition Slot			

Localisation ID			
Methodology ID	RT-PCR		
Plant part ID	leaf	leaf_PO:0025034	
Property Slot	transcript expression level evidence_ECO:0000048		

5. LEP expression was significantly increased in let compared to wild type (Northern blot)

Information type/Slots	Original text	String entry	Ontologies attached
Developmental stage			
Factuality ID			
Gene expression ID	increased		over expressed level_MI:0506
Gene studied	LEP		LEP_AT5G13910
Genotype ID	let		mutated gene_MI:0804
Gene ID	let		LEP_AT5G13910
Genotype Zygoty			homozygous diploid_APO:0000229
Mutant LOF_GOF ID			gain of function_APO:0000010
Growth Condition Slot			
Localisation ID			
Methodology ID	Northern blot		
Plant part ID			
Property Slot	transcript expression level evidence_ECO:0000048		

6. mRNA of REV ... restricted to the adaxial domain ... developing primordia (in situ hybridization WT background)

Information type/Slots	Original text	String entry	Ontologies attached
Developmental stage			
Factuality ID			
Gene expression ID	restricted		present_PATO:0000467
Gene studied	REV		REV IFL IFL1_AT5G60690
Genotype ID			Wild type_SO:0000817
Growth Condition Slot			
Localisation ID			
Methodology ID	in situ hybridization		
Plant part ID	adaxial domain ... primordia		adaxial side of leaf primordium_PO:0004726

Property Slot	spatial pattern_PATO:0000060
----------------------	------------------------------

7. prolonged expression of CycD3;1 also was detected in 35S-ARGOS leaves (RT-PCR)

Information type/Slots	Original text	String entry	Ontologies attached
Developmental stage			
Factuality ID			
Gene expression ID	detected		over expressed level_MI:0506
Gene studied	CycD3;1		CYCD3;1 CYCD3_AT4G34160
Genotype ID	35S-ARGOS		over expressed level_MI:0506
Gene ID	ARGOS		ARGOS_AT3G59900
Growth Condition Slot			
Localisation ID			
Methodology ID		RT-PCR	
Plant part ID	leaves		leaf_PO:0025034
Property Slot			transcript expression level evidence_ECO:0000048

8. In kan1 kan2 double mutants, AS2 transcripts were detected at wild-type levels (RT-PCR)

Information type/Slots	Original text	String entry	Ontologies attached
Developmental stage			
Factuality ID			
Gene expression ID	detected at wild-type levels		normal_PATO:0000461
Gene studied	AS2		AS2_AT1G65620
Genotype ID	kan1 kan2		mutated gene_MI:0804
Gene ID	kan1		KAN KAN1_AT5G16560
	kan2		KAN2_AT1G32240
Genotype Zygoty			homozygous diploid_APO:0000229
Mutant LOF_GOF ID			loss of function_APO:0000011
Growth Condition Slot			
Localisation ID			
Methodology ID		RT-PCR	
Plant part ID			
Property Slot	transcripts... levels		transcript expression level evidence_ECO:0000048

9. AS2 transcripts were detected in rosette leaves, where they were more abundant in the petiole than in the blade (RT-PCR, WT background)

Information type/Slots	Original text	String entry	Ontologies attached
Developmental stage			
Factuality ID			
Gene expression ID	detected		present_PATO:0000467
Gene studied	AS2		AS2_AT1G65620
Genotype ID			Wild type_SO:0000817
Growth Condition Slot			
Localisation ID			
Methodology ID		RT-PCR	
Plant part ID	rosette leaves		rosette leaf_PO:0000014
Property Slot			transcript expression level evidence_ECO:0000048

10. 1-h BR treatments resulted in increased EXO transcript levels in ... wild-type ... plants (microarray on shoot)

Information type/Slots	Original text	String entry	Ontologies attached
Developmental stage			
Factuality ID			
Gene expression ID	increased		over expressed level_MI:0506
Gene studied	EXO		EXO_AT4G08950
Genotype ID	wild-type		Wild type_SO:0000817
Growth Condition Slot	BR treatments		brassinosteroid_EO:0007409
Localisation ID			
Methodology ID		microarray	
Plant part ID			shoot system_PO:0009006
Property Slot	transcript levels		transcript expression level evidence_ECO:0000048

11. In young seedlings, however, the expression of ROT4 was clearly detected in shoots (RT-PCR, WT background)

Information type/Slots	Original text	String entry	Ontologies attached
Developmental stage			
Factuality ID			
Gene expression ID	detected		present_PATO:0000467
Gene studied	ROT4		ROT4 DVL16_AT2G36985
Genotype ID			Wild type_SO:0000817

Growth Condition Slot		
Localisation ID		
Methodology ID		RT-PCR
Plant part ID	shoots	shoot system_PO:0009006
Property Slot		transcript expression level evidence_ECO:0000048

12. ATAF2 ... In mature leaves, strong expression was observed in the hydathodes (GUS staining, WT background)

Information type/Slots	Original text	String entry	Ontologies attached
Developmental stage	mature leaves		3 leaf fully expanded_PO:0001053
Factuality ID			
Gene expression ID	observed		present_PATO:0000467
Gene studied	ATAF2		ATAF2 anac081_AT5G08790
Genotype ID			Wild type_SO:0000817
Growth Condition Slot			
Localisation ID			
Methodology ID		GUS staining	
Plant part ID	hydathodes		hydathode_PO:0005660
Property Slot			spatial pattern_PATO:0000060

13. KNAT1 was ectopically expressed in as1 leaves (RT-PCR)

Information type/Slots	Original text	String entry	Ontologies attached
Developmental stage			
Factuality ID			
Gene expression ID	ectopically		mislocalised_PATO:0000628
Gene studied	KNAT1		KNAT1 BP BP1_AT4G08150
Genotype ID	as1		mutated gene_MI:0804
Gene ID	as1		ATPHAN AS1 ATMYB91 MYB91_AT2G37630
Genotype Zygoty			homozygous diploid_APO:0000229
Mutant LOF_GOF ID			loss of function_APO:0000011
Growth Condition Slot			
Localisation ID			
Methodology ID		RT-PCR	
Plant part ID	leaves		leaf_PO:0025034
Property Slot			transcript expression level evidence_ECO:0000048

14. The level of FIL transcripts increased in as2-1 (RT-PCR on shoot apex)

Information type/Slots	Original text	String entry	Ontologies attached
Developmental stage			
Factuality ID			
Gene expression ID	increased		over expressed level_MI:0506
Gene studied	FIL		AFO FIL YAB1_AT2G45190
Genotype ID	as2-1		mutated gene_MI:0804
Gene ID			Gene ID=AS2_AT1G65620
Genotype Zygoty			homozygous diploid_APO:0000229
Mutant LOF_GOF ID			loss of function_APO:0000011
Growth Condition			
Slot			
Localisation ID			
Methodology ID		RT-PCR	
Plant part ID			shoot apex_PO:0000037
Property Slot	level of ... transcripts		transcript expression level evidence_ECO:0000048

15. level of HLS1 protein was increased in response to ethylene treatment (Western blot on seedlings, WT background)

Information type/Slots	Original text	String entry	Ontologies attached
Developmental stage			
Factuality ID			
Gene expression ID	increased		over expressed level_MI:0506
Gene studied	HLS1		HLS1 COP3 UNS2_AT4G37580
Genotype ID			Wild type_SO:0000817
Growth Condition	ethylene treatment		ethylene regimen_EO:0007068
Slot			
Localisation ID			
Methodology ID		Western blot	
Plant part ID			seedling_BTO:0001228
Property Slot	level of ...protein		protein expression level evidence_ECO:0000046

Feature examples

1. AtCPL2 contains one dsRNA-binding domain

Information type/Slots	Original text	String entry	Ontologies attached
Factuality ID			

Molecular feature ID		one dsRNA-binding domain	
Protein	AtCPL2		CPL2 ATCPL2_AT5G01270

2. SWP protein ... two putative nuclear localization signals

Information type/Slots	Original text	String entry	Ontologies attached
Factuality ID	Putative		speculation
Molecular feature ID		two putative nuclear localization signals	
Protein	SWP		SWP MED14 ATMED14_AT3G04740

3. BOP1 protein ... ankyrin repeat domain is located in the C-terminal region from residues 242 to 368

Information type/Slots	Original text	String entry	Ontologies attached
Factuality ID			
Molecular feature ID		ankyrin repeat domain is located in the C-terminal region from residues 242 to 368	
Protein	BOP1		BOP1_AT3G57130

4. ARF2 has one tasiR-ARF recognition site

Information type/Slots	Original text	String entry	Ontologies attached
Factuality ID			
Molecular feature ID		one tasiR-ARF recognition site	
Protein	ARF2		ARF2 ARF1-BP HSS ORE14_AT5G62000

5. One class-II TCP box was also found in the AtCDT1b promoter

Information type/Slots	Original text	String entry	Ontologies attached
Factuality ID			
Molecular feature ID		One class-II TCP box	
Protein	AtCDT1b		ATCDT1B CDT1B

CDT1_AT3G54710

6. indicating that the R358K mutation in DA1 is responsible for increased seed and organ size

Information type/Slots	Original text	String entry	Ontologies attached
Factuality ID	Indicating (as speculation)		
Molecular feature ID		the R358K mutation in DA1 is responsible for increased seed and organ size	
Protein	DA1		DA1_AT1G19270

Genetic interaction examples

1. se quantitatively and qualitatively enhanced the lobing of ... as2 leaves

Information type/Slots	Original text	Ontologies attached
Factuality ID		
Genetic interactor Gene ID	se	mutated gene_MI:0804 SE_AT2G27100
Genotype Zygotity Mutant LOF_GOF ID		homozygous diploid _APO:0000229 loss of function_APO:0000011
Genotype ID Gene ID	as2	mutated gene_MI:0804 AS2_AT1G65620
Genotype Zygotity Mutant LOF_GOF ID	as2	homozygous diploid _APO:0000229 loss of function_APO:0000011
Growth Condition Slot		
Interaction type	enhanced	negative genetic interaction_MI:0933
Methodology ID		
Plant part ID	leaves	leaf_PO:0025034
Property Slot		
Process ID		shape_PATO:0000052
Value ID	lobing	lobed_PATO:0001979

2. as1 can rescue the stm phenotype in ... vegetative meristems

Information type/Slots	Original text	Ontologies attached
Factuality ID		
Genetic interactor Gene ID	as1	mutated gene_MI:0804 ATPHAN AS1 ATMYB91 MYB91_AT2G37630
Genotype Zygotity		homozygous diploid _APO:0000229

Mutant LOF_GOF ID		loss of function_APO:0000011
Genotype ID	stm	mutated gene_MI:0804
Gene ID	stm	STM BUM1 SHL WAM1 BUM WAM_AT1G62360
Genotype Zygoty		homozygous diploid _APO:0000229
Mutant LOF_GOF ID		loss of function_APO:0000011
Growth Condition Slot		
Interaction type	rescue	positive genetic interaction_MI:0935
Methodology ID		
Plant part ID	vegetative meristems	vegetative shoot apical meristem_PO:0008016
Property Slot		
Process ID		
Value ID		

3. hyl1 ... appeared to suppress the as2 phenotypes

Information type/Slots	Original text	Ontologies attached
Factuality ID		
Genetic interactor	hyl1	mutated gene_MI:0804
Gene ID	hyl1	HYL1 DRB1_AT1G09700
Genotype Zygoty		homozygous diploid _APO:0000229
Mutant LOF_GOF ID		loss of function_APO:0000011
Genotype ID	as2	mutated gene_MI:0804
Gene ID	as2	AS2_AT1G65620
Genotype Zygoty		homozygous diploid _APO:0000229
Mutant LOF_GOF ID		loss of function_APO:0000011
Growth Condition Slot		
Interaction type	suppress	suppressive genetic interaction defined by inequality_MI:0796
Methodology ID		
Plant part ID		
Property Slot		
Process ID		
Value ID		

4. The two kanadi mutants display a strong synergistic interaction: while kan2 has no visible aberrant phenotype on its own, it has a dramatic effect in kan1 background, even when heterozygous

Information type/Slots	Original text	Ontologies attached
Factuality ID		
Genetic interactor	kan2	mutated gene_MI:0804
Gene ID	kan2	KAN2_AT1G32240
Genotype Zygoty		homozygous diploid _APO:0000229
Mutant LOF_GOF ID		loss of function_APO:0000011
Genotype ID	kan1	mutated gene_MI:0804
Gene ID	kan1	KAN KAN1_AT5G16560

Genotype Zygoty	homozygous diploid _APO:0000229	
Mutant LOF_GOF ID	loss of function _APO:0000011	
Growth Condition Slot		
Interaction type	synergistic interaction	negative genetic interaction_MI:0933
Methodology ID		
Plant part ID		
Property Slot		
Process ID		
Value ID		

- If TTL functions as a negative regulator in BR-mediated cell growth, its overexpression could suppress the BRI1-overexpressing phenotype. Indeed, the resulting F2 transgenic plants homozygous for both transgenes displayed wider and shorter rosette leaves than the BRI1-overexpressing transgenic plants

Information type/Slots	Original text	Ontologies attached
Factuality ID		
Genetic interactor	TTL... overexpression	over expressed level_MI:0506
Gene ID	TTL	TTL_AT5G58220
Genotype ID	BRI1-overexpressing	over expressed level_MI:0506
Gene ID	BRI1	BRI1 CBB2 DWF2 BIN1 ATBRI1_AT4G39400
Growth Condition Slot		
Interaction type	suppress	suppressive genetic interaction defined by inequality_MI:0796
Methodology ID		
Plant part ID	rosette leaves	rosette leaf_PO:0000014
Property Slot		
Process ID		
Value ID		

Protein-protein interaction examples

- molecular interaction of AN and ZWI ... using the ... yeast two-hybrid system

Information type/Slots	Original text	String entry	Ontologies attached
Factuality ID			
Interaction type	interaction		direct interaction_MI:0407
Interactor protein	ZWI		ZWI_AT5G65930
Methodology ID		yeast two-hybrid assay	
Protein studied	AN		AN_AT1G01510

- AN was able to form dimers in yeast cells

Information type/Slots	Original text	String entry	Ontologies attached
Factuality ID			
Interaction type	dimers		direct interaction_MI:0407
Interactor protein	AN		AN_AT1G01510
Methodology ID		yeast two-hybrid assay	
Protein studied	AN		AN_AT1G01510

3. BIN2 phosphorylation of BES1 reduced BES1 binding to the promoter of SAUR-15

Information type/Slots	Original text	String entry	Ontologies attached
Factuality ID			
Interaction type	phosphorylation		phosphorylation reaction_MI:0217
Interactor protein	BIN2		BIN2 DWF12 UCU1 ATSK21 SK21_AT4G18710
Methodology ID			
Protein studied	BES1		BES1 BZR2_AT1G19350

4. To investigate NINJA function in JA signalling, we set up a new TAP experiment with NINJA as bait. NINJA was present in a complex with ... the group-II TIFY proteins ... PPD2

Information type/Slots	Original text	String entry	Ontologies attached
Factuality ID			
Interaction type	present in a complex with		physical association_MI:0915
Interactor protein	PPD2		PPD2 TIFY4B_AT4G14720
Methodology ID			
Protein studied	NINJA		NINJA_AT4G28910

DNA-protein interaction examples

1. ARF2 could bind to the SAUR-15 promoter, and preincubation with BIN2 greatly reduced DNA binding activity

Information type/Slots	Original text	String entry	Ontologies attached
DNA target ID	SAUR-15		SAUR_AC1 ATSAUR15 SAUR15 SAUR-AC1_AT4G38850
DNA target			

sequence			
Factuality ID			
Methodology ID			
Plant part ID			
Protein	ARF2		ARF2 ARF1-BP HSS ORE14_AT5G62000
Regulation ID	bind		direct interaction_MI:0407

2. Using double-stranded oligonucleotides covering the potential TCP binding sites in the context of the LOX2 promoter, we performed EMSAs. The in vitro studies confirmed that TCP4 can bind strongly to at least two of the consensus motifs

Information type/Slots	Original text	String entry	Ontologies attached
DNA target ID	LOX2		LOX2 ATLOX2_AT3G45140
DNA target sequence			
Factuality ID			
Methodology ID			
Plant part ID			
Protein	TCP4		TCP4_AT3G15030
Regulation ID	bind		direct interaction_MI:0407

3. We expressed the GST fused with the DNA-binding domain in N-terminus (ARF2-N1-470) in Escherichia coli and purified the fused protein with the help of the GST tag ... ARF2 N-terminal DNA binding domain binds to AuxREs in the promoter of HB33

Information type/Slots	Original text	String entry	Ontologies attached
DNA target ID	HB33		AtHB33 HB33 ZHD5_AT1G75240
DNA target sequence			
Factuality ID			
Methodology ID			
Plant part ID			
Protein	ARF2		ARF2 ARF1-BP HSS ORE14_AT5G62000
Regulation ID	bind		direct interaction_MI:0407

4. Using surface plasmon resonance (SPR), we found that RHL1 binds to DNA in a concentration- and salt- dependent manner

Information	Original text	String entry	Ontologies attached
-------------	---------------	--------------	---------------------

type/Slots		
DNA target ID		
DNA target sequence		
Factuality ID		
Methodology ID		plasmon resonance
Plant part ID		
Protein	RHL1	RHL1 HYP7_AT1G48380
Regulation ID	binds	direct interaction_MI:0407

Process examples

1. RHL2 ... involved during endocycles

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Gene studied	RHL2	RHL2 BIN5_AT5G02820
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID		
Process ID	endocycles	DNA endoreduplication_GO:0042023
Property Slot		
Value ID		

2. These results indicate that ATHB16 affects rosette leaf growth

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID	indicate	speculation
Gene studied	ATHB16	ATHB16 ATHB-16 HB16_AT4G40060
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID	rosette leaf	rosette leaf_PO:0000014
Process ID	growth	growth_GO:0040007
Property Slot		
Value ID		

3. KCS1 protein is involved in wax biosynthesis

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		

Gene studied	KCS1	KCS1_AT1G01120
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID		
Process ID	wax biosynthesis	wax biosynthetic process_GO:0010025
Property Slot		
Value ID		

4. THE1 ... is a ... receptor kinase

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Gene studied	THE1	THE1_AT5G54380
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID		
Process ID	receptor kinase	kinase activity_GO:0016301
Property Slot		
Value ID		

5. KNAT7 ... role in secondary wall formation

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Gene studied	KNAT7	KNAT7 IXR11_AT1G62990
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID		
Process ID	secondary wall formation	secondary cell wall biogenesis_GO:0009834
Property Slot		
Value ID		

Regulation of gene expression examples

1. In stem cells STM negatively regulates AS1

Information type/Slots	Original text	Ontologies attached
-------------------------------	----------------------	----------------------------

Developmental stage		
Factuality ID		
Gene studied	STM	STM BUM1 SHL WAM1 BUM WAM_AT1G62360
Gene target	AS1	ATPHAN AS1 ATMYB91 MYB91_AT2G37630
Methodology ID		
Plant part ID	stem cells	meristematic cell_PO:0004010
Regulation ID	negatively regulates	negative regulation of gene expression_GO:0010629

2. role for AS1 ... in keeping KNAT1 off in leaves post-initiation

Information type/Slots	Original text	Ontologies attached
Developmental stage	leaves post-initiation	2 leaf expansion stage_PO:0001052
Factuality ID		
Gene studied	AS1	ATPHAN AS1 ATMYB91 MYB91_AT2G37630
Gene target	KNAT1	KNAT1 BP BP1_AT4G08150
Methodology ID		
Plant part ID	leaves	leaf_PO:0025034
Regulation ID	keeping off	negative regulation of gene expression_GO:0010629

3. TCP4 ... positively regulate LOX2 promoter activity

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Gene studied	TCP4	TCP4_AT3G15030
Gene target	LOX2	LOX2 ATLOX2_AT3G45140
Methodology ID		
Plant part ID		
Regulation ID	positively regulate	positive regulation of gene expression_GO:0010628

4. ARF4 transcripts are subjected to negative regulation by cleavage and is consistent with potential regulation of these mRNAs by tasiR-ARF

Information type/Slots	Original text	Ontologies attached
Developmental stage		
Factuality ID		
Gene studied		
Gene target	ARF4	ARF4_AT5G60450

Methodology ID		
Plant part ID		
Regulation ID	negative regulation	negative regulation of gene expression_GO:0010629

Regulation of process examples

1. KLU gene is ... promoting growth

Information type/Slots	Original text	Ontologies attached
Factuality ID		
Gene studied	KLU	CYP78A5 KLU_AT1G13710
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID		
Process ID	growth	growth_GO:0040007
Property Slot		
Regulation ID	promoting	positive regulation of biological process_GO:0048518
Value ID		

2. KAN promotes abaxial identity

Information type/Slots	Original text	Ontologies attached
Factuality ID		
Gene studied	KAN	KAN KAN1_AT5G16560
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID		
Process ID	abaxial identity	determination of dorsal identity_GO:0048263
Property Slot		
Regulation ID	promotes	positive regulation of biological process_GO:0048518
Value ID		

3. AtTOR activity is needed to restrain senescence and nutrient recycling

Information type/Slots	Original text	Ontologies attached
Factuality ID		

Gene studied	AtTOR	TOR_AT1G50030
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID		
Process ID	senescence	leaf senescence_GO:0010150
Property Slot		
Regulation ID	restrain	negative regulation of biological process_GO:0048519
Value ID		

4. HERK1 ... promoting cell elongation during vegetative growth

Information type/Slots	Original text	Ontologies attached
Factuality ID		
Gene studied	HERK1	HERK1_AT3G46290
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID		
Process ID	cell elongation	cell growth_GO:0016049
Property Slot		
Regulation ID	promoting	positive regulation of biological process_GO:0048518
Value ID		

Regulation of phenotype examples

1. PHABULOSA ... influence leaf shape

Information type/Slots	Original text	Ontologies attached
Factuality ID		
Gene studied	PHABULOSA	PHB ATHB14 ATHB-14 PHB-1D_AT2G34710
Growth Condition Slot		
Localisation ID		
Methodology ID		
Plant part ID	leaf	leaf_PO:0025034
Property Slot	shape	shape_PATO:0000052
Regulation ID	influence	regulation of developmental process_GO:0050793