

GEPHE SUMMARY

KUK (https://www.gephebase.org/search-criteria/?and+Gene Gephebase=^KUK^#gephebase-summary-title)	Gephebase Gene GP00001233	GepheID Main curator
Published	Entry Status Courtier	

PHENOTYPIC CHANGE

	Trait Category
Morphology (https://www.gephebase.org/search-criteria/?and+Trait Category="Morphology">#gephebase-summary-title)	Trait
Root development (https://www.gephebase.org/search-criteria/?and+Trait=^Root development="#gephebase-summary-title")	Trait State in Taxon A
Arabidopsis thaliana - long meristem and long mature cells	Trait State in Taxon B
Arabidopsis thaliana - short meristem and short mature cells	Ancestral State
Data not curated	Taxonomic Status
Intraspecific (https://www.gephebase.org/search-criteria/?and+Taxonomic Status="Intraspecific">#gephebase-summary-title)	

Taxon A		Taxon B	
	Latin Name		Latin Name
Arabidopsis thaliana (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Arabidopsis+thaliana #gephebase-summary-title)	Common Name	Arabidopsis thaliana (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Arabidopsis+thaliana #gephebase-summary-title)	Common Name
thale cress	Synonyms	thale cress	Synonyms
thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress		thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress	
species	Rank	species	Rank
	Lineage		Lineage
cellular organisms; Eukaryota; Viriplantae; Streptophytina; Streptophytina; Embryophytina; Tracheophytina; Euphylophyta; Spermatophytina; Magnoliophytina; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelinae; Arabidopsis		cellular organisms; Eukaryota; Viriplantae; Streptophytina; Streptophytina; Embryophytina; Tracheophytina; Euphylophyta; Spermatophytina; Magnoliophytina; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelinae; Arabidopsis	
Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701)	Parent	Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701)	Parent
3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702)	NCBI Taxonomy ID	3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702)	NCBI Taxonomy ID
is Taxon A an Infraspecies?		is Taxon B an Infraspecies?	
Yes	Taxon A Description	Yes	Taxon B Description
Wa-1	Uk-1		

GENOTYPIC CHANGE

	Generic Gene Name		
At1g60370	Synonyms	O80758 (http://www.uniprot.org/uniprot/O80758)	UniProtKB Arabidopsis thaliana
KUK; KURZ UND KLEIN; T13D8.24; T13D8_24; At1g60370	String	842332 (https://www.ncbi.nlm.nih.gov/nucleotide/842332)	GenebankID or UniProtKB
3702.AT1G60370.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=3702.AT1G60370.1)	Sequence Similarities		
-	GO - Molecular Function		
-	GO - Biological Process		
-	GO - Cellular Component		

Mutation #1

No (https://www.gephebase.org/search-criteria/?and+Presumptive+Null=%No%gephebase-summary-title)	Presumptive Null
Coding (https://www.gephebase.org/search-criteria/?and+Molecular+Type=%Coding%gephebase-summary-title)	Molecular Type
Unknown (https://www.gephebase.org/search-criteria/?and+Aberration+Type=%Unknown%gephebase-summary-title)	Aberration Type
exact causing mutation(s) unknown	Molecular Details of the Mutation
Association Mapping (https://www.gephebase.org/search-criteria/?and+Experimental+Evidence=%Association+Mapping%gephebase-summary-title)	Experimental Evidence
Genome-wide association study using cellular traits identifies a new regulator of root development in <i>Arabidopsis</i> . (2014) (https://pubmed.ncbi.nlm.nih.gov/24212884)	Main Reference
MeijÃ³n M; Satbhai SB; Tsuchimatsu T; Busch W	Authors
With the increased availability of high-resolution sequence information, genome-wide association (GWA) studies have become feasible in a number of species. The vast majority of these studies are conducted in human populations, where it is difficult to provide strong evidence for the functional involvement of unknown genes that are identified using GWA. Here we used the model organism <i>Arabidopsis thaliana</i> to combine high-throughput confocal microscopy imaging of traits at the cellular level, GWA and expression analyses to identify genomic regions that are associated with developmental cell-type traits. We identify and characterize a new F-box gene, KUK, that regulates meristem and cell length. We further show that polymorphisms in the coding sequence are the major causes of KUK allele-dependent natural variation in root development. This work demonstrates the feasibility of GWA using cellular traits to identify causal genes for basic biological processes such as development.	Abstract
	Additional References

Mutation #2

No (https://www.gephebase.org/search-criteria/?and+Presumptive+Null=%No%gephebase-summary-title)	Presumptive Null
Cis-regulatory (https://www.gephebase.org/search-criteria/?and+Molecular+Type=%Cis-regulatory%gephebase-summary-title)	Molecular Type
Unknown (https://www.gephebase.org/search-criteria/?and+Aberration+Type=%Unknown%gephebase-summary-title)	Aberration Type
role of the upstream cis-regulatory region on phenotypic trait shown by various chimeric constructs rescuing a <i>kuk1</i> mutant - exact causing cis-regulatory mutation(s) unknown	Molecular Details of the Mutation
Association Mapping (https://www.gephebase.org/search-criteria/?and+Experimental+Evidence=%Association+Mapping%gephebase-summary-title)	Experimental Evidence
Genome-wide association study using cellular traits identifies a new regulator of root development in <i>Arabidopsis</i> . (2014) (https://pubmed.ncbi.nlm.nih.gov/24212884)	Main Reference
MeijÃ³n M; Satbhai SB; Tsuchimatsu T; Busch W	Authors
With the increased availability of high-resolution sequence information, genome-wide association (GWA) studies have become feasible in a number of species. The vast majority of these studies are conducted in human populations, where it is difficult to provide strong evidence for the functional involvement of unknown genes that are identified using GWA. Here we used the model organism <i>Arabidopsis thaliana</i> to combine high-throughput confocal microscopy imaging of traits at the cellular level, GWA and expression analyses to identify genomic regions that are associated with developmental cell-type traits. We identify and characterize a new F-box gene, KUK, that regulates meristem and cell length. We further show that polymorphisms in the coding sequence are the major causes of KUK allele-dependent natural variation in root development. This work demonstrates the feasibility of GWA using cellular traits to identify causal genes for basic biological processes such as development.	Abstract
	Additional References

RELATED GEPHE

No matches found.	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

Strong experimental evidence through comparison of KUK gene expression in root of different lines. KUK mutant displaying small meristem and reduced mature cell length.

