

GEPHE SUMMARY

	Gephebase Gene		GepheID
KAl2 paralogs (<a +kal2+paralogs+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+KAl2+paralogs+"#gephebase-summary-title)		GP00000509	
	Entry Status	Courtier	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology+"#gephebase-summary-title)			
	Trait		
Seed dormancy (strigolactone responsiveness) (<a +seed+dormancy+(strigolactone+responsiveness)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Seed+dormancy+(strigolactone+responsiveness)+"#gephebase-summary-title)			
	Trait State in Taxon A		
non-parasitic Orobanchaceae			
	Trait State in Taxon B		
Orobanche spp.; Conopholis americana			
	Ancestral State		
Taxon A			
	Taxonomic Status		
Intergeneric or Higher (<a +intergeneric+or+higher+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Intergeneric+or+Higher+"#gephebase-summary-title)			
	Taxon A	Taxon B	
	Latin Name		Latin Name
Orobanchaceae (<a +orobanchaceae+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Orobanchaceae+"#gephebase-summary-title)		Orobancheae (<a +orobancheae+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Orobancheae+"#gephebase-summary-title)	
	Common Name		Common Name
-		-	
	Synonyms		Synonyms
Cyclocheilaceae Marais, 1981; Nesogenaceae Marais, 1981; Orobanchaceae Vent., 1799; Rehmanniaceae Reveal, 2011		Orobancheae Lam. & DC., 1806	
	Rank		Rank
family		tribe	
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Lamiales		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Lamiales; Orobanchaceae	
	Parent		Parent
Lamiales () - (Rank: order) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4143)		Orobanchaceae () - (Rank: family) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=91896)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
91896 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=91896)		216770 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=216770)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Oryza sativa subsp. japonica
D14		Q10QA5 (http://www.uniprot.org/uniprot/Q10QA5)	
	Synonyms		GenebankID or UniProtKB
D14; D88; HTD2; Os03g0203200; LOC_Os03g10620		()	
	String		
39947.LOC_Os03g10620.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=39947.LOC_Os03g10620.1)			
	Sequence Similarities		
Belongs to the AB hydrolase superfamily.			
	GO - Molecular Function		
GO:0016787 : hydrolase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016787)			
	GO - Biological Process		
GO:0010223 : secondary shoot formation (https://www.ebi.ac.uk/QuickGO/term/GO:0010223)			
GO:1901601 : strigolactone biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:1901601)			

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

No (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=~No~#gephebase-summary-title>)

Coding (<https://www.gephebase.org/search-criteria?/and+Molecular+Type=~Coding~#gephebase-summary-title>)

Unknown (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Unknown~#gephebase-summary-title>)

Ligand-binding pocket tuning in duplicated gene

Candidate Gene (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Candidate+Gene~#gephebase-summary-title>)

PLANT EVOLUTION. Convergent evolution of strigolactone perception enabled host detection in parasitic plants. (2015) (<https://pubmed.ncbi.nlm.nih.gov/26228149>)

Conn CE; Bythell-Douglas R; Neumann D; Yoshida S; Whittington B; Westwood JH; Shirasu K; Bond CS; Dyer KA; Nelson DC

Obligate parasitic plants in the Orobanchaceae germinate after sensing plant hormones, strigolactones, exuded from host roots. In *Arabidopsis thaliana*, the \hat{I}^{\pm}/\hat{I}^2 -hydrolase D14 acts as a strigolactone receptor that controls shoot branching, whereas its ancestral paralog, KAI2, mediates karrikin-specific germination responses. We observed that KAI2, but not D14, is present at higher copy numbers in parasitic species than in nonparasitic relatives. KAI2 paralogs in parasites are distributed into three phylogenetic clades. The fastest-evolving clade, KAI2d, contains the majority of KAI2 paralogs. Homology models predict that the ligand-binding pockets of KAI2d resemble D14. KAI2d transgenes confer strigolactone-specific germination responses to *Arabidopsis thaliana*. Thus, the KAI2 paralogs D14 and KAI2d underwent convergent evolution of strigolactone recognition, respectively enabling developmental responses to strigolactones in angiosperms and host detection in parasites.

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Presumptive Null

Molecular Type

Aberration Type

Molecular Details of the Mutation

Experimental Evidence

Main Reference

Authors

Abstract

Additional References

RELATED GEPHE

No matches found.

No matches found.

Related Genes

Related Haplotypes

EXTERNAL LINKS

COMMENTS

@GeneDuplication and divergence