

GEPHE SUMMARY

	Gephebase Gene		GepheID
Resistance related Kinase 1 (RKS1) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+Resistance+related+Kinase+1+(RKS1)+#gephebase-summary-title)		GP00001599	
Published	Entry Status	Prigent	Main curator

PHENOTYPIC CHANGE

	Trait Category	
Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category+Physiology+#gephebase-summary-title)		
	Trait	
Pathogen resistance (plant bacteria) (https://www.gephebase.org/search-criteria?/and+Trait+Pathogen+resistance+(plant+bacteria)+#gephebase-summary-title)		
	Trait State in Taxon A	
Arabidopsis thaliana Kas-1 susceptible to Xanthomonas campestris		
	Trait State in Taxon B	
Arabidopsis thaliana Col-0 resistant to Xanthomonas campestris		
	Ancestral State	
Unknown		
	Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status+Domesticated+#gephebase-summary-title)		

Taxon A	Latin Name	Taxon B	Latin Name
Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Arabidopsis+thaliana+#gephebase-summary-title)		Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Arabidopsis+thaliana+#gephebase-summary-title)	
	Common Name		Common Name
thale cress		thale cress	
	Synonyms		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	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis	
	Parent		Parent
Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701)		Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702)		3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
Yes		Yes	
	Taxon A Description		Taxon B Description
Arabidopsis thaliana Kas-1 susceptible with short transcript (370bp) RKS1-S expressed in leaves		Arabidopsis thaliana Col-0 resistant with long transcript RKS1-L expressed in leaves	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Arabidopsis thaliana
F15B8.100		Q9SVY5 (http://www.uniprot.org/uniprot/Q9SVY5)	
	Synonyms		GenebankID or UniProtKB
Resistance related KinaSe 1; RKS1; At3g57710		()	
	String		
3702.AT3G57710.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT3G57710.1)			
	Sequence Similarities		
-			
	GO - Molecular Function		
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)			
GO:0004674 : protein serine/threonine kinase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004674)			

GO - Biological Process

GO:0007166 : cell surface receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007166>)

GO - Cellular Component

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)

Presumptive Null

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

Molecular Type

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

Aberration Type

SNP ([https://www.gephebase.org/search-criteria?/and+Aberration Type=~SNP^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration+Type=~SNP^#gephebase-summary-title))

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

a single-SNP difference in the coding region resulting in an amino acid change in the activation segment relative to the catalytic kinase loop. Other polymorphisms were found in the 5' and 3' regulatory regions. RKS1-L expression is 235.1 fold higher

Experimental Evidence

Linkage Mapping ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Linkage+Mapping^#gephebase-summary-title))

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

An atypical kinase under balancing selection confers broad-spectrum disease resistance in Arabidopsis. (2013) (<https://pubmed.ncbi.nlm.nih.gov/24068949>)

Authors

Huard-Chauveau C; Perchepped L; Debieu M; Rivas S; Kroj T; Kars I; Bergelson J; Roux F; Roby D

Abstract

The failure of gene-for-gene resistance traits to provide durable and broad-spectrum resistance in an agricultural context has led to the search for genes underlying quantitative resistance in plants. Such genes have been identified in only a few cases, all for fungal or nematode resistance, and encode diverse molecular functions. However, an understanding of the molecular mechanisms of quantitative resistance variation to other enemies and the associated evolutionary forces shaping this variation remain largely unknown. We report the identification, map-based cloning and functional validation of QRX3 (RKS1, Resistance related KinaSe 1), conferring broad-spectrum resistance to *Xanthomonas campestris* (Xc), a devastating worldwide bacterial vascular pathogen of crucifers. RKS1 encodes an atypical kinase that mediates a quantitative resistance mechanism in plants by restricting bacterial spread from the infection site. Nested Genome-Wide Association mapping revealed a major locus corresponding to an allelic series at RKS1 at the species level. An association between variation in resistance and RKS1 transcription was found using various transgenic lines as well as in natural accessions, suggesting that regulation of RKS1 expression is a major component of quantitative resistance to Xc. The co-existence of long lived RKS1 haplotypes in *A. thaliana* is shared with a variety of genes involved in pathogen recognition, suggesting common selective pressures. The identification of RKS1 constitutes a starting point for deciphering the mechanisms underlying broad spectrum quantitative disease resistance that is effective against a devastating and vascular crop pathogen. Because putative RKS1 orthologous have been found in other Brassica species, RKS1 provides an exciting opportunity for plant breeders to improve resistance to black rot in crops.

Additional References

RELATED GEPHE

Related Genes

20 (ACD6 = ACCELERATED CELL DEATH 6, ERECTA, RAC1, RLM1, RLM2 cluster, RLM3, RPM1, RPP1-WsA, RPP1-WsB, RPP1-WsC, RPP13, RPP2A-RPP2B, RPP4, RPP5, RPP8, RPS2, RPS4, RPS5, RRS1, WRR4) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=~3702^/and+Trait=Pathogen resistance/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=~3702^/and+Trait=Pathogen+resistance/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@BalancingSelection population study showed that resistance and susceptibility are associated with other mutations in the gene