

GEPHE SUMMARY

	Gephebase Gene	GephelD
Pi-ta (#gephebase-summary-title)	GP00000876	Main curator
Published	Entry Status	Martin

PHENOTYPIC CHANGE

	Trait Category	
Physiology (#gephebase-summary-title)	Trait	
Pathogen resistance (#gephebase-summary-title)	Trait State in Taxon A	
Oryza spp. - wild-type	Trait State in Taxon B	
Oryza sativa- resistant	Ancestral State	
Data not curated	Taxonomic Status	
Domesticated (#gephebase-summary-title)		
Taxon A	Latin Name	Latin Name
Oryza sativa (#gephebase-summary-title)	Oryza sativa (#gephebase-summary-title)	Oryza sativa (#gephebase-summary-title)
rice	Common Name	Common Name
rice; red rice; Oryza sativa L.	Synonyms	Synonyms
species	Rank	Rank
	Lineage	Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza
	Parent	Parent
Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527)	Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527)	Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527)
4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530)	NCBI Taxonomy ID is Taxon A an Infraspecies?	NCBI Taxonomy ID is Taxon B an Infraspecies?
No		

GENOTYPIC CHANGE

	Generic Gene Name	
Pi-ta		UniProtKB Oryza sativa subsp. japonica
KPt.1	Synonyms	C9E6G5 (http://www.uniprot.org/uniprot/C9E6G5)
-	String	ACY25064 (https://www.ncbi.nlm.nih.gov/nuccore/ACY25064)
	Sequence Similarities	
Belongs to the disease resistance NB-LRR family.		
GO:0043531 : ADP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043531)	GO - Molecular Function	
GO:0045454 : cell redox homeostasis (https://www.ebi.ac.uk/QuickGO/term/GO:0045454)	GO - Biological Process	
GO:0005623 : cell (https://www.ebi.ac.uk/QuickGO/term/GO:0005623)	GO - Cellular Component	Presumptive Null
No (#gephebase-summary-title)		Molecular Type

Coding ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular%20Type=%Coding))

Aberration Type

SNP ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration%20Type=%SNP))

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Ala918Ser

Experimental Evidence

Linkage Mapping ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental%20Evidence=%Linkage%20Mapping))

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

Main Reference

tA single amino acid difference distinguishes resistant and susceptible alleles of the rice blast resistance gene Pi-ta. (2000) (<https://pubmed.ncbi.nlm.nih.gov/11090207>)

Authors

Bryan GT; Wu KS; Farrall L; Jia Y; Hershey HP; McAdams SA; Faulk KN; Donaldson GK; Tarchini R; Valent B

Abstract

The rice blast resistance (R) gene Pi-ta mediates gene-for-gene resistance against strains of the fungus Magnaporthe grisea that express avirulent alleles of AVR-Pita. Using a map-based cloning strategy, we cloned Pi-ta, which is linked to the centromere of chromosome 12. Pi-ta encodes a predicted 928-amino acid cytoplasmic receptor with a centrally localized nucleotide binding site. A single-copy gene, Pi-ta shows low constitutive expression in both resistant and susceptible rice. Susceptible rice varieties contain pi-ta(-) alleles encoding predicted proteins that share a single amino acid difference relative to the Pi-ta resistance protein: serine instead of alanine at position 918. Transient expression in rice cells of a Pi-ta(+) R gene together with AVR-Pita(+) induces a resistance response. No resistance response is induced in transient assays that use a naturally occurring pi-ta(-) allele differing only by the serine at position 918. Rice varieties reported to have the linked Pi-ta(2) gene contain Pi-ta plus at least one other R gene, potentially explaining the broadened resistance spectrum of Pi-ta(2) relative to Pi-ta. Molecular cloning of the AVR-Pita and Pi-ta genes will aid in deployment of R genes for effective genetic control of rice blast disease.

Additional References

Two evolutionary histories in the genome of rice: the roles of domestication genes. (2011) (<https://pubmed.ncbi.nlm.nih.gov/21695282>)

Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. (2011) (<https://pubmed.ncbi.nlm.nih.gov/22158310>)

RELATED GEPHE

Related Genes

15 (Pi2 (Nbs4-Pi2), Pi36, Pi37, Pi5-1 + Pi5-2 cluster, Pi9 (= Nbs2-Pi9), Pib, Pid3, PigmR, Pikm1-TS + Pikm2-TS cluster, Pit, Piz-t, SLB1/2, Xa1, Xa21, Xa26) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=%4530^/and+Trait=Pathogen resistance/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon%20ID=%4530^/and+Trait=Pathogen%20resistance/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS