

GEPHE SUMMARY

Piz-t (#gephebase-summary-title)	Gephebase Gene	GepheID
	GP00000895	
	Entry Status	Main curator
Published	Courtier	

PHENOTYPIC CHANGE

Physiology (#gephebase-summary-title)		Trait Category		
Pathogen resistance (#gephebase-summary-title)		Trait		
Oryza sativa - blast susceptible CO39		Trait State in Taxon A		
Oryza sativa - blast resistant Toride-1		Trait State in Taxon B		
Data not curated		Ancestral State		
Domesticated (#gephebase-summary-title)		Taxonomic Status		
Taxon A		Taxon B		
Oryza sativa (#gephebase-summary-title)		Oryza sativa (#gephebase-summary-title)		Latin Name
rice		rice		Common Name
rice; red rice; Oryza sativa L.		rice; red rice; Oryza sativa L.		Synonyms
species		species		Rank
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		Lineage
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)		Parent
4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530)		4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530)		NCBI Taxonomy ID
Yes		Yes		is Taxon A an Intraspecies?
Oryza sativa - blast susceptible CO39		Oryza sativa - blast resistant Toride-1		Taxon A Description
				Taxon B Description

GENOTYPIC CHANGE

Piz-t	Generic Gene Name	UniProtKB Oryza sativa subsp. japonica
	Synonyms	Q0H213 (http://www.uniprot.org/uniprot/Q0H213)
	String	GenebankID or UniProtKB
-		ABC73398 (https://www.ncbi.nlm.nih.gov/nuccore/ABC73398)
-	Sequence Similarities	
Belongs to the disease resistance NB-LRR family.	GO - Molecular Function	
	GO - Biological Process	
-		
-	GO - Cellular Component	
-		
No (#gephebase-summary-title)		Presumptive Null

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

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

Nonsynonymous

Coding variation in the LRR domain

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

Molecular Type

Aberration Type

SNP Coding Change

Molecular Details of the Mutation

Experimental Evidence

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

The eight amino-acid differences within three leucine-rich repeats between Pi2 and Piz-t resistance proteins determine the resistance specificity to Magnaporthe grisea. (2006)
(<https://pubmed.ncbi.nlm.nih.gov/17073304>)

Zhou B; Qu S; Liu G; Dolan M; Sakai H; Lu G; Bellizzi M; Wang GL

Main Reference

Authors

The rice blast resistance (R) genes Pi2 and Piz-t confer broad-spectrum resistance against different sets of Magnaporthe grisea isolates. We first identified the Pi2 gene using a map-based cloning strategy. The Pi2 gene is a member of a gene cluster comprising nine gene members (named Nbs1-Pi2 to Nbs9-Pi2) and encodes a protein with a nucleotide-binding site and leucine-rich repeat (LRR) domain. Fine genetic mapping, molecular characterization of the Pi2 susceptible mutants, and complementation tests indicated that Nbs4-Pi2 is the Pi2 gene. The Piz-t gene, a Pi2 allele in the rice cultivar Toride 1, was isolated based on the Pi2 sequence information. Complementation tests confirmed that the family member Nbs4-Piz-t is Piz-t. Sequence comparison revealed that only eight amino-acid changes, which are confined within three consecutive LRR, differentiate Piz-t from Pi2. Of the eight variants, only one locates within the xxLxLxx motif. A reciprocal exchange of the single amino acid between Pi2 and Piz-t did not convert the resistance specificity to each other but, rather, abolished the function of both resistance proteins. These results indicate that the single amino acid in the xxLxLxx motif may be critical for maintaining the recognition surface of Pi2 and Piz-t to their respective avirulence proteins.

Abstract

Additional References

RELATED GEPHE

15 (Pi-ta, Pi2 (Nbs4-Pi2), Pi36, Pi37, Pi5-1 + Pi5-2 cluster, Pi9 (= Nbs2-Pi9), Pib, Pid3, PigmR, Pikm1-TS + Pikm2-TS cluster, Pit, 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>)

No matches found.

Related Genes

Related Haplotypes

EXTERNAL LINKS

COMMENTS