

## GEPHE SUMMARY

	Gephebase Gene		GepheID
Pi2 (Nbs4-Pi2) ( <a href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^Pi2+(Nbs4-Pi2)^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^Pi2+(Nbs4-Pi2)^#gephebase-summary-title</a> )		GP00000877	
	Entry Status	Courtier	Main curator
Published			

## PHENOTYPIC CHANGE

	Trait Category		
Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title</a> )			
	Trait		
Pathogen resistance ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=^Pathogen+resistance^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait=^Pathogen+resistance^#gephebase-summary-title</a> )			
	Trait State in Taxon A		
Oryza sativa - blast susceptible CO39			
	Trait State in Taxon B		
Oryza sativa - blast resistant C101A51			
	Ancestral State		
Data not curated			
	Taxonomic Status		
Domesticated ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Domesticated^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Domesticated^#gephebase-summary-title</a> )			
Taxon A		Taxon B	
	Latin Name		Latin Name
Oryza sativa ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryza+sativa^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryza+sativa^#gephebase-summary-title</a> )		Oryza sativa ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryza+sativa^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryza+sativa^#gephebase-summary-title</a> )	
	Common Name		Common Name
rice		rice	
	Synonyms		Synonyms
rice; red rice; Oryza sativa L.		rice; red rice; Oryza sativa L.	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; Oryzinae; Oryza		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; Oryzinae; Oryza	
	Parent		Parent
Oryza () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527</a> )		Oryza () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527</a> )	
	NCBI Taxonomy ID		NCBI Taxonomy ID
4530 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530</a> )		4530 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530</a> )	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
Yes		Yes	
	Taxon A Description		Taxon B Description
Oryza sativa - blast susceptible CO39		Oryza sativa - blast resistant C101A51	

## GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Oryza sativa subsp. japonica
Pi2		M1EC06 ( <a href="http://www.uniprot.org/uniprot/M1EC06">http://www.uniprot.org/uniprot/M1EC06</a> )	
	Synonyms		GenebankID or UniProtKB
-		0	
	String		
-			
	Sequence Similarities		
-			
	GO - Molecular Function		
GO:0046983 : protein dimerization activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0046983">https://www.ebi.ac.uk/QuickGO/term/GO:0046983</a> )			
GO:0003700 : DNA-binding transcription factor activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0003700">https://www.ebi.ac.uk/QuickGO/term/GO:0003700</a> )			
GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0000977">https://www.ebi.ac.uk/QuickGO/term/GO:0000977</a> )			
	GO - Biological Process		

GO:0045944 : positive regulation of transcription by RNA polymerase II  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)

GO - Cellular Component

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

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=))

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=))

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 Coding Change

Nonsynonymous

Molecular Details of the Mutation

eight amino acid changes - exact causing change(s) unknown

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=))

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

Main Reference

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>)

Authors

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

Abstract

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.

Additional References

## RELATED GEPHE

Related Genes

15 (Pi-ta, 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+ID=))

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

Cluster of paralogous genes