

GEPHE SUMMARY

Pi9 (= Nbs2-Pi9) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=%Pi9(=Nbs2-Pi9)^#gephebase-summary-title)	Gephebase Gene	GP00000881	GepheID
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=%Physiology^#gephebase-summary-title)	Trait
Pathogen resistance (https://www.gephebase.org/search-criteria?/and+Trait=%Pathogen+resistance^#gephebase-summary-title)	Trait State in Taxon A
Oryza sativa - blast susceptible CO39	Trait State in Taxon B
Oryza sativa - blast resistant indica	Ancestral State
Data not curated	Taxonomic Status

Domesticated (<https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=%Domesticated^#gephebase-summary-title>)

Taxon A	Latin Name	Taxon B	Latin Name
Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=%Oryza+sativa^#gephebase-summary-title)		Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=%Oryza+sativa^#gephebase-summary-title)	
rice	Common Name	rice	Common Name
rice; red rice; Oryza sativa L.	Synonyms	rice; red rice; Oryza sativa L.	Synonyms
species	Rank	species	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)	NCBI Taxonomy ID	Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527)	NCBI Taxonomy ID
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)	
Yes	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
Oryza sativa - blast susceptible CO39	Taxon A Description	Oryza sativa - blast resistant indica	Taxon B Description

GENOTYPIC CHANGE

Pi9	Generic Gene Name	UniProtKB Oryza sativa subsp. indica
Pi9	Synonyms	GenebankID or UniProtKB
-	String	
	Sequence Similarities	
Belongs to the disease resistance NB-LRR family.		
	GO - Molecular Function	
GO:0043531 : ADP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043531)		
	GO - Biological Process	
-	GO - Cellular Component	
		Presumptive Null
No (https://www.gephebase.org/search-criteria?/and+Presumptive+Null=%No^#gephebase-summary-title)		

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=%27Coding%27#gephebase-summary-title)	Molecular Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=%27Unknown%27#gephebase-summary-title)	Aberration Type
Coding variation; necessary for resistance in complementation assay	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=%27Linkage Mapping%27#gephebase-summary-title)	Experimental Evidence
The broad-spectrum blast resistance gene Pi9 encodes a nucleotide-binding site-leucine-rich repeat protein and is a member of a multigene family in rice. (2006) (https://pubmed.ncbi.nlm.nih.gov/16387888)	Main Reference
Qu S; Liu G; Zhou B; Bellizzi M; Zeng L; Dai L; Han B; Wang GL	Authors
Abstract	
The broad-spectrum rice blast resistance gene Pi9 was cloned using a map-based cloning strategy. Sequencing of a 76-kb bacterial artificial chromosome (BAC) contig spanning the Pi9 locus led to identification of six tandemly arranged resistance-like genes with a nucleotide-binding site (NBS) and leucine-rich repeats (LRRs) (NbS1-Pi9-NbS6-Pi9). Analysis of selected Pi9 deletion mutants and transformation of a 45-kb fragment from the BAC contig into the susceptible rice cultivar TP309 narrowed down Pi9 to the candidate genes NbS2-Pi9 and NbS3-Pi9. Disease evaluation of the transgenic lines carrying the individual candidate genes confirmed that NbS2-Pi9 is the Pi9 gene. Sequence comparison analysis revealed that the six paralogs at the Pi9 locus belong to four classes and gene duplication might be one of the major evolutionary forces contributing to the formation of the NBS-LRR gene cluster. Semiquantitative reverse transcriptase (RT)-PCR analysis showed that Pi9 was constitutively expressed in the Pi9-resistant plants and was not induced by blast infection. The cloned Pi9 gene provides a starting point to elucidate the molecular basis of the broad-spectrum disease resistance and the evolutionary mechanisms of blast resistance gene clusters in rice.	
Additional References	

RELATED GEPHE

15 (Pi-ta, Pi2 (NbS4-Pi2), Pi36, Pi37, Pi5-1 + Pi5-2 cluster, 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=%274530%27/and+Trait=Pathogen resistance/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS