

GEPHE SUMMARY

Pi36 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^Pi36^#gephebase-summary-title)	Gephebase Gene	GP00000878	GepheID
	Entry Status	Martin	Main curator
	Published		

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=^Physiology^#gephebase-summary-title)		Trait Category	
Pathogen resistance (https://www.gephebase.org/search-criteria?/and+Trait=^Pathogenresistance^#gephebase-summary-title)		Trait	
Oryza sativa - blast susceptible Nipponbare		Trait State in Taxon A	
Oryza sativa - blast resistant Kasalath		Trait State in Taxon B	
Data not curated		Ancestral State	
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=^Domesticated^#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Oryza sativa (https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=^Oryzasativa^#gephebase-summary-title)		Oryza sativa (https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=^Oryzasativa^#gephebase-summary-title)	
rice		rice	
rice; red rice; Oryza sativa L.		rice; red rice; Oryza sativa L.	
species		species	
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	
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)		4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
Yes		Yes	
Oryza sativa - blast susceptible Nipponbare		Oryza sativa - blast resistant Kasalath	

GENOTYPIC CHANGE

Pi36	Generic Gene Name	UniProtKB Oryza sativa subsp. japonica	
	Synonyms	D5J6W0 (http://www.uniprot.org/uniprot/D5J6W0)	
	String	GenebankID or UniProtKB ADF29629 (https://www.ncbi.nlm.nih.gov/nuccore/ADF29629)	
Belongs to the disease resistance NB-LRR family.		Sequence Similarities	
GO:0043531 : ADP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043531)		GO - Molecular Function	
		GO - Biological Process	
		GO - Cellular Component	
No (https://www.gephebase.org/search-criteria?/and+PresumptiveNull=^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

Asp590Ser

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 in silico map-based cloning of Pi36, a rice coiled-coil nucleotide-binding site leucine-rich repeat gene that confers race-specific resistance to the blast fungus. (2007)
(<https://pubmed.ncbi.nlm.nih.gov/17507669>)

Liu X; Lin F; Wang L; Pan Q

Main Reference

Authors

The indica rice variety Kasalath carries Pi36, a gene that determines resistance to Chinese isolates of rice blast and that has been located to a 17-kb interval on chromosome 8. The genomic sequence of the reference japonica variety Nipponbare was used for an in silico prediction of the resistance (R) gene content of the interval and hence for the identification of candidate gene(s) for Pi36. Three such sequences, which all had both a nucleotide-binding site and a leucine-rich repeat motif, were present. The three candidate genes were amplified from the genomic DNA of a number of varieties by long-range PCR, and the resulting amplicons were inserted into pCAMBIA1300 and/or pYLAC27 vectors to determine sequence polymorphisms correlated to the resistance phenotype and to perform transgenic complementation tests. Constructs containing each candidate gene were transformed into the blast-susceptible variety Q1063, which allowed the identification of Pi36-3 as the functional gene, with the other two candidates being probable pseudogenes. The Pi36-encoded protein is composed of 1056 amino acids, with a single substitution event (Asp to Ser) at residue 590 associated with the resistant phenotype. Pi36 is a single-copy gene in rice and is more closely related to the barley powdery mildew resistance genes Mla1 and Mla6 than to the rice blast R genes Pita, Pib, Pi9, and Piz-t. An RT-PCR analysis showed that Pi36 is constitutively expressed in Kasalath.

Additional References

RELATED GEPHE

15 (Pi-ta, Pi2 (Nbs4-Pi2), 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>)

No matches found.

Related Genes

Related Haplotypes

EXTERNAL LINKS

COMMENTS