

GEPHE SUMMARY

Pi37 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^Pi37^#gephebase-summary-title)	Gephebase Gene	GP00000879	GepheID
	Entry Status	Courtier	Main curator
	Published		

PHENOTYPIC CHANGE

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

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

GENOTYPIC CHANGE

Pi37	Generic Gene Name	UniProtKB Oryza sativa subsp. japonica
	Synonyms	Q06AJ9 (http://www.uniprot.org/uniprot/Q06AJ9)
	String	GenebankID or UniProtKB
-	AB194578 (https://www.ncbi.nlm.nih.gov/nuccore/AB194578)	
	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	
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>)

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

V239A and I247M are the only amino acid substitutions found in all tested resistant strains- the effect of each individual amino acid change has not been tested

Experimental Evidence

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

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

Main Reference

The blast resistance gene Pi37 encodes a nucleotide binding site leucine-rich repeat protein and is a member of a resistance gene cluster on rice chromosome 1. (2007)
(<https://pubmed.ncbi.nlm.nih.gov/17947408>)

Authors

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Abstract

The resistance (R) gene Pi37, present in the rice cultivar St. No. 1, was isolated by an in silico map-based cloning procedure. The equivalent genetic region in Nipponbare contains four nucleotide binding site-leucine-rich repeat (NBS-LRR) type loci. These four candidates for Pi37 (Pi37-1, -2, -3, and -4) were amplified separately from St. No. 1 via long-range PCR, and cloned into a binary vector. Each construct was individually transformed into the highly blast susceptible cultivar Q1063. The subsequent complementation analysis revealed Pi37-3 to be the functional gene, while -1, -2, and -4 are probably pseudogenes. Pi37 encodes a 1290 peptide NBS-LRR product, and the presence of substitutions at two sites in the NBS region (V239A and I247M) is associated with the resistance phenotype. Semiquantitative expression analysis showed that in St. No. 1, Pi37 was constitutively expressed and only slightly induced by blast infection. Transient expression experiments indicated that the Pi37 product is restricted to the cytoplasm. Pi37-3 is thought to have evolved recently from -2, which in turn was derived from an ancestral -1 sequence. Pi37-4 is likely the most recently evolved member of the cluster and probably represents a duplication of -3. The four Pi37 paralogs are more closely related to maize rp1 than to any of the currently isolated rice blast R genes Pita, Pib, Pi9, Pi2, Piz-t, and Pi36.

Additional References

RELATED GEPHE

Related Genes

15 (Pi-ta, Pi2 (Nbs4-Pi2), Pi36, 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>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS