

GEPHE SUMMARY

Pi5-1 + Pi5-2 cluster (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^Pi5-1 + Pi5-2 cluster^#gephebase-summary-title)	Gephebase Gene	GP00000880	GepheID
	Entry Status	Courtier	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 IR50		Trait State in Taxon A	
Oryza sativa - blast resistant RIL260		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)	
Yes		Yes	
Oryza sativa - blast susceptible IR50		Oryza sativa - blast resistant RIL260	

GENOTYPIC CHANGE

Pi5-1	Generic Gene Name	UniProtKB Oryza sativa subsp. japonica
-	Synonyms	C3SBK3 (http://www.uniprot.org/uniprot/C3SBK3)
-	String	GenebankID or UniProtKB ACJ54697 (https://www.ncbi.nlm.nih.gov/nuccore/ACJ54697)
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)	Molecular Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Unknown~#gephebase-summary-title)	Aberration Type
In genetic transformation experiments of a susceptible rice cultivar neither the Pi5-1 nor the Pi5-2 gene was found to confer resistance to <i>M. oryzae</i> . In contrast transgenic rice plants expressing both of these genes (generated by crossing transgenic lines carrying each gene individually) conferred Pi5-mediated resistance to <i>M. oryzae</i>	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Linkage+Mapping~#gephebase-summary-title)	Experimental Evidence
Rice Pi5-mediated resistance to Magnaporthe oryzae requires the presence of two coiled-coil-nucleotide-binding-leucine-rich repeat genes. (2009) (https://pubmed.ncbi.nlm.nih.gov/19153255)	Main Reference
Lee SK; Song MY; Seo YS; Kim HK; Ko S; Cao PJ; Suh JP; Yi G; Roh JH; Lee S; An G; Hahn TR; Wang GL; Ronald P; Jeon JS	Authors
Rice blast, caused by the fungus Magnaporthe oryzae, is one of the most devastating diseases of rice. To understand the molecular basis of Pi5-mediated resistance to <i>M. oryzae</i> , we cloned the resistance (R) gene at this locus using a map-based cloning strategy. Genetic and phenotypic analyses of 2014 F2 progeny from a mapping population derived from a cross between IR50, a susceptible rice cultivar, and the RIL260 line carrying Pi5 enabled us to narrow down the Pi5 locus to a 130-kb interval. Sequence analysis of this genomic region identified two candidate genes, Pi5-1 and Pi5-2, which encode proteins carrying three motifs characteristic of R genes: an N-terminal coiled-coil (CC) motif, a nucleotide-binding (NB) domain, and a leucine-rich repeat (LRR) motif. In genetic transformation experiments of a susceptible rice cultivar, neither the Pi5-1 nor the Pi5-2 gene was found to confer resistance to <i>M. oryzae</i> . In contrast, transgenic rice plants expressing both of these genes, generated by crossing transgenic lines carrying each gene individually, conferred Pi5-mediated resistance to <i>M. oryzae</i> . Gene expression analysis revealed that Pi5-1 transcripts accumulate after pathogen challenge, whereas the Pi5-2 gene is constitutively expressed. These results indicate that the presence of these two genes is required for rice Pi5-mediated resistance to <i>M. oryzae</i> .	Abstract
	Additional References

RELATED GEPHE

15 (Pi-ta, Pi2 (Nbs4-Pi2), Pi36, Pi37, 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 Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

Cluster of paralogous genes