

GEPHE SUMMARY

Pit (https://www.gephebase.org/search-criteria/?and+Gene Gephebase=%22Pit%22#gephebase-summary-title)	Gephebase Gene	GP00002052	GephelD
	Entry Status	Courtier	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category	Trait	
Physiology (https://www.gephebase.org/search-criteria/?and+Trait Category=%22Physiology%22#gephebase-summary-title)			
Pathogen resistance (rice blast disease; fungal pathogen; Magnaporthe grisea) (https://www.gephebase.org/search-criteria/?and+Trait=%22Pathogen resistance (rice blast disease; fungal pathogen; Magnaporthe grisea)%22#gephebase-summary-title)			
sensitive	Trait State in Taxon A		
resistant	Trait State in Taxon B		
Taxon A	Ancestral State		
Domesticated (https://www.gephebase.org/search-criteria/?and+Taxonomic Status=%22Domesticated%22#gephebase-summary-title)	Taxonomic Status		
Oryza sativa (https://www.gephebase.org/search-criteria/?and+Taxon and Synonyms=%22Oryza sativa%22#gephebase-summary-title)	Taxon A	Latin Name	Taxon B
rice	Common Name	Oryza sativa (https://www.gephebase.org/search-criteria/?and+Taxon and Synonyms=%22Oryza sativa%22#gephebase-summary-title)	Latin Name
rice; red rice; Oryza sativa L.	Synonyms	rice	Common Name
species	Rank	rice; red rice; Oryza sativa L.	Synonyms
cellular organisms; Eukaryota; Viriplantae; Streptophytina; Embryophytina; Tracheophytina; Euphylophyta; Spermatophytina; Magnoliophytina; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza	Lineage	cellular organisms; Eukaryota; Viriplantae; Streptophytina; Embryophytina; Tracheophytina; Euphylophyta; Spermatophytina; Magnoliophytina; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza	Rank
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
4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530)	NCBI Taxonomy ID	4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
		K59	Taxon B Description

GENOTYPIC CHANGE

Pit	Generic Gene Name	UniProtKB Oryza sativa subsp. japonica B9A1G4 (http://www.uniprot.org/uniprot/B9A1G4)
-	Synonyms	GenebankID or UniProtKB AB379815.1 (https://www.ncbi.nlm.nih.gov/nuccore/AB379815.1)
-	String	
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	
		Presumptive Null

No ([#gepheebase-summary-title](https://www.gepheebase.org/search-criteria?/and+Presumptive Null=%No))

Molecular Type

Cis-regulatory ([#gepheebase-summary-title](https://www.gepheebase.org/search-criteria?/and+Molecular Type=%Cis-regulatory))

Aberration Type

Insertion ([#gepheebase-summary-title](https://www.gepheebase.org/search-criteria?/and+Aberration Type=%Insertion))

Insertion Size

1-10 kb

Molecular Details of the Mutation

insertion of a 5.5-kb LTR retrotransposon Renovator upstream of the gene (256 bp upstream of the predicted start codon for NBSt2K59; in the same orientation as the gene)

Experimental Evidence

Linkage Mapping ([#gepheebase-summary-title](https://www.gepheebase.org/search-criteria?/and+Experimental Evidence=%Linkage Mapping))

Main Reference

Refunctionalization of the ancient rice blast disease resistance gene Pit by the recruitment of a retrotransposon as a promoter. (2009) (<https://pubmed.ncbi.nlm.nih.gov/18808453>)

Authors

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Abstract

The plant genome contains a large number of disease resistance (R) genes that have evolved through diverse mechanisms. Here, we report that a long terminal repeat (LTR) retrotransposon contributed to the evolution of the rice blast resistance gene Pit. Pit confers race-specific resistance against the fungal pathogen Magnaporthe grisea, and is a member of the nucleotide-binding site leucine-rich repeat (NBS-LRR) family of R genes. Compared with the non-functional allele Pit(Npb), the functional allele Pit(K59) contains four amino acid substitutions, and has the LTR retrotransposon Renovator inserted upstream. Pathogenesis assays using chimeric constructs carrying the various regions of Pit(K59) and Pit(Npb) suggest that amino acid substitutions might have a potential effect in Pit resistance; more importantly, the upregulated promoter activity conferred by the Renovator sequence is essential for Pit function. Our data suggest that transposon-mediated transcriptional activation may play an important role in the refunctionalization of additional 'sleeping' R genes in the plant genome.

Additional References

RELATED GEPHE

Related Genes

15 (Pi-ta, Pi2 (Nb4-Pi2), Pi36, Pi37, Pi5-1 + Pi5-2 cluster, Pi9 (= Nb2-Pi9), Pib, Pid3, PigmR, Pikm1-TS + Pikm2-TS cluster, Piz-t, SLB1/2, Xa1, Xa21, Xa26) ([#gepheebase-summary-title](https://www.gepheebase.org/search-criteria?/or+Taxon ID=%4530^/and+Trait=Pathogen resistance/and+groupHaplotypes=true))

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@TE - activation of an R gene not only by an intragenic polymorphism but also by transcriptional alteration through a flanking retrotransposon - Pit belongs to the CCâ€¢NBSâ€¢LRR family