

GEPHE SUMMARY

	Gephebase Gene		GepheID
Pit (<a +pit+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+Pit+"#gephebase-summary-title)	GP00002052		
	Entry Status	Courtier	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology+"#gephebase-summary-title)		Trait	
Pathogen resistance (rice blast disease; fungal pathogen; Magnaporthe grisea) (<a +pathogen+resistance+(rice+blast+disease;+fungal+pathogen;+magnaporthe+grisea)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Pathogen+resistance+(rice+blast+disease;+fungal+pathogen;+Magnaporthe+grisea)+"#gephebase-summary-title)		Trait State in Taxon A	
sensitive		Trait State in Taxon B	
resistant		Ancestral State	
Taxon A		Taxonomic Status	
Domesticated (<a +domesticated+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Domesticated+"#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Oryza sativa (<a +oryza+sativa+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Oryza+sativa+"#gephebase-summary-title)		Oryza sativa (<a +oryza+sativa+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Oryza+sativa+"#gephebase-summary-title)	
	Common Name		Common Name
rice		rice	
	Synonyms		Synonyms
rice; red rice; Oryza sativa L.		rice; red rice; Oryza sativa L.	
	Rank		Rank
species		species	
	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)		Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527)	
	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)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		Yes	
			Taxon B Description
		K59	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Oryza sativa subsp. japonica
Pit		B9A1G4 (http://www.uniprot.org/uniprot/B9A1G4)	
	Synonyms		GenebankID or UniProtKB
-		AB379815.1 (https://www.ncbi.nlm.nih.gov/nuccore/AB379815.1)	
	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)	Molecular Type
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Cis-regulatory^#gephebase-summary-title)	Aberration Type
Insertion (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Insertion^#gephebase-summary-title)	Insertion Size
1-10 kb	Molecular Details of the Mutation
insertion of a 5.5-kb LTR retrotransposon Renovator upstream of the gene (256â€bp upstream of the predicted start codon for NBSt2K59; in the same orientation as the gene)	Experimental Evidence
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping^#gephebase-summary-title)	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
Hayashi K; Yoshida H	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

15 (Pi-ta, Pi2 (Nbs4-Pi2), Pi36, Pi37, Pi5-1 + Pi5-2 cluster, Pi9 (= Nbs2-Pi9), Pib, Pid3, PigmR, Pikm1-TS + Pikm2-TS cluster, 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

@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
