

GEPHE SUMMARY

	Gephebase Gene		GepheID
Pid3 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~Pid3^#gephebase-summary-title)		GP00000883	
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology^#gephebase-summary-title)		Trait	
Pathogen resistance (https://www.gephebase.org/search-criteria?/and+Trait=~Pathogenresistance^#gephebase-summary-title)			
	Trait State in Taxon A		
Oryza sativa - blast susceptible Nipponbare		Trait State in Taxon B	
Oryza sativa - blast resistant Gumei2			
	Ancestral State		
Taxon A		Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Domesticated^#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Oryzasativa^#gephebase-summary-title)		Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Oryzasativa^#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?	
Yes		Yes	
	Taxon A Description		Taxon B Description
Oryza sativa - blast susceptible Nipponbare		Oryza sativa - blast resistant Gumei2	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Oryza sativa subsp. japonica
Pid3		CoLMX9 (http://www.uniprot.org/uniprot/CoLMX9)	
	Synonyms		GenebankID or UniProtKB
Pi25		ACN79514 (https://www.ncbi.nlm.nih.gov/nuccore/ACN79514)	
-		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
Yes (https://www.gephebase.org/search-criteria?/and+Presumptive+Null=~Yes^#gephebase-summary-title)			

Coding (https://www.gephebase.org/search-criteria?/and+Molecular+Type=~Coding~#gephebase-summary-title)	Molecular Type
Deletion (https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Deletion~#gephebase-summary-title)	Aberration Type
1-9 bp	Deletion Size
1bp deletion resulting in truncated protein	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Linkage+Mapping~#gephebase-summary-title)	Experimental Evidence
A <i>Pid3</i> allele from rice cultivar Gumei2 confers resistance to <i>Magnaporthe oryzae</i> . (2011) (https://pubmed.ncbi.nlm.nih.gov/21621742)	Main Reference
Chen J; Shi Y; Liu W; Chai R; Fu Y; Zhuang J; Wu J	Authors
Rice blast, caused by <i>Magnaporthe oryzae</i> , is one of the most devastating diseases. Using map-based strategy and in silico approach we isolated a new rice (<i>Oryza sativa</i> L.) blast resistance allele of <i>Pid3</i> , designated <i>Pi25</i> , from a stable blast resistance cultivar Gumei2. Over-expression analysis and complementation test showed that <i>Pi25</i> conferred blast resistance to <i>M. oryzae</i> isolate js001-20. Sequence analysis showed that <i>Pi25</i> was an intronless gene of 2,772 nucleotides with single nucleotide substitution in comparison to <i>Pid3</i> at the nucleotide position 459 and predicatively encoded a typical coiled coil--nucleotide binding site--leucine rich repeat (CC--NBS--LRR) protein of 924 amino acid residuals with 100% identity to <i>Pid3</i> putative protein. The susceptible allele <i>pi25</i> in Nipponbare contained a nonsense mutation at the nucleotide position 2,209 resulting in a truncated protein with 736 amino acid residuals. In addition, 14 nucleotide substitutions resulting in 10 amino acid substitutions were identified between <i>Pi25</i> and <i>pi25</i> upstream the premature stop codon in the susceptible allele. Although the mechanism of <i>Pi25</i> / <i>Pid3</i> -mediated resistance needs to be further investigated, the isolation of the allele would facilitate the utilization of <i>Pi25</i> / <i>Pid3</i> in rice blast resistance breeding program via transgenic approach and marker assisted selection.	Abstract
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RELATED GEPHE

15 (<i>Pi</i> -ta, <i>Pi2</i> (Nbs4- <i>Pi2</i>), <i>Pi36</i> , <i>Pi37</i> , <i>Pi5</i> -1 + <i>Pi5</i> -2 cluster, <i>Pi9</i> (= Nbs2- <i>Pi9</i>), <i>Pib</i> , <i>PigmR</i> , <i>Pikm1</i> -TS + <i>Pikm2</i> -TS cluster, <i>Pit</i> , <i>Piz</i> -t, SLB1/2, <i>Xa1</i> , <i>Xa21</i> , <i>Xa26</i>) (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