

# GEPHE SUMMARY

Pid3 ( <a href="https://www.gephebase.org/search-criteria?/and+Gene">https://www.gephebase.org/search-criteria?/and+Gene</a> Gephebase=^Pid3^#gephebase-summary-title)	Gephebase Gene	GP00000883	GephelD
	Entry Status	Martin	Main curator
Published			

## PHENOTYPIC CHANGE

Trait Category			
Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a> Category=^Physiology^#gephebase-summary-title)	Trait		
Pathogen resistance ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=^Pathogen">https://www.gephebase.org/search-criteria?/and+Trait=^Pathogen</a> resistance^#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 ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic">https://www.gephebase.org/search-criteria?/and+Taxonomic</a> Status=^Domesticated^#gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	Latin Name
Oryza sativa ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryza">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryza</a> sativa^#gephebase-summary-title)	Oryza sativa ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryza">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryza</a> sativa^#gephebase-summary-title)		
rice	Common Name		Common Name
rice; red rice; Oryza sativa L.	Synonyms	rice; red rice; Oryza sativa L.	Synonyms
species	Rank	species	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	
	Parent		Parent
Oryza () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527</a> )	Oryza () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527</a> )		
4530 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530</a> )	NCBI Taxonomy ID 4530 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530</a> )		NCBI Taxonomy ID 4530 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530</a> )
Yes	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
	Taxon A Description		Taxon B Description
Oryza sativa - blast susceptible Nipponbare		Oryza sativa - blast resistant Gumei2	

## GENOTYPIC CHANGE

Pid3	Generic Gene Name	UniProtKB Oryza sativa subsp. japonica CoLMX9 ( <a href="http://www.uniprot.org/uniprot/CoLMX9">http://www.uniprot.org/uniprot/CoLMX9</a> )
Pi25	Synonyms	GenebankID or UniProtKB ACN79514 ( <a href="https://www.ncbi.nlm.nih.gov/nuccore/ACN79514">https://www.ncbi.nlm.nih.gov/nuccore/ACN79514</a> )
-	String	
	Sequence Similarities	
Belongs to the disease resistance NB-LRR family.		
	GO - Molecular Function	
GO:0043531 : ADP binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0043531">https://www.ebi.ac.uk/QuickGO/term/GO:0043531</a> )		
	GO - Biological Process	
-		
	GO - Cellular Component	
-		
Yes ( <a href="https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^Yes^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^Yes^#gephebase-summary-title</a> )		Presumptive Null

Coding ( <a href="https://www.gephebase.org/search-criteria?/and+Molecular%20Type=%5BCoding%5D#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Molecular Type=%5BCoding%5D#gephebase-summary-title</a> )	Molecular Type
Deletion ( <a href="https://www.gephebase.org/search-criteria?/and+Aberration%20Type=%5BDeletion%5D#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Aberration Type=%5BDeletion%5D#gephebase-summary-title</a> )	Aberration Type
1-9 bp	Deletion Size
1bp deletion resulting in truncated protein	Molecular Details of the Mutation
Linkage Mapping ( <a href="https://www.gephebase.org/search-criteria?/and+Experimental%20Evidence=%5BLinkage%20Mapping%5D#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Experimental Evidence=%5BLinkage%20Mapping%5D#gephebase-summary-title</a> )	Experimental Evidence
A Pid3 allele from rice cultivar Gumei2 confers resistance to Magnaporthe oryzae. (2011) ( <a href="https://pubmed.ncbi.nlm.nih.gov/21621742">https://pubmed.ncbi.nlm.nih.gov/21621742</a> )	Main Reference
Chen J; Shi Y; Liu W; Chai R; Fu Y; Zhuang J; Wu J	Authors
Rice blast, caused by Magnaporthe oryzae, is one of the most devastating diseases. Using map-based strategy and in silico approach we isolated a new rice ( <i>Oryza sativa L.</i> ) blast resistance allele of Pid3, designated Pi25, from a stable blast resistance cultivar Gumei2. Over-expression analysis and complementation test showed that Pi25 conferred blast resistance to <i>M. oryzae</i> isolate js001-20. Sequence analysis showed that Pi25 was an intronless gene of 2,772 nucleotides with single nucleotide substitution in comparison to Pid3 at the nucleotide position 459 and predictively encoded a typical coiled coil--nucleotide binding site--leucine rich repeat (CC--NBS--LRR) protein of 924 amino acid residuals with 100% identity to Pid3 putative protein. The susceptible allele pi25 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 Pi25 and pi25 upstream the premature stop codon in the susceptible allele. Although the mechanism of Pi25/Pid3-mediated resistance needs to be further investigated, the isolation of the allele would facilitate the utilization of Pi25/Pid3 in rice blast resistance breeding program via transgenic approach and marker assisted selection.	Abstract
Copyright © 2011. Published by Elsevier Ltd.	Additional References

## RELATED GEPHE

15 (Pi-ta, Pi2 (Nbs4-Pi2), Pi36, Pi37, Pi5-1 + Pi5-2 cluster, Pi9 (= Nbs2-Pi9), Pib, PigmR, Pikm1-TS + Pikm2-TS cluster, Pit, Piz-t, SLB1/2, Xa1, Xa21, Xa26) ( <a href="https://www.gephebase.org/search-criteria?/or+Taxon%20ID=%5B4530%5D/and+Trait=Pathogen%20resistance/and+groupHaplotypes=true#gephebase-summary-title">https://www.gephebase.org/search-criteria?/or+Taxon ID=%5B4530%5D/and+Trait=Pathogen resistance/and+groupHaplotypes=true#gephebase-summary-title</a> )	Related Genes
No matches found.	Related Haplotypes

## EXTERNAL LINKS

## COMMENTS