

GEPHE SUMMARY

	Gephebase Gene		GepheID
Rp3 cluster (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~Rp3+cluster^#gephebase-summary-title)	GP00000999		Main curator
Published	Entry Status	Martin	

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology^#gephebase-summary-title)	Trait		
Pathogen resistance (https://www.gephebase.org/search-criteria?/and+Trait=~Pathogen+resistance^#gephebase-summary-title)	Trait State in Taxon A		
Zea mays - rust susceptible	Trait State in Taxon B		
Zea mays - rust resistant	Ancestral State		
Data not curated	Taxonomic Status		
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Domesticated^#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Zea mays (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Zea+mays^#gephebase-summary-title)	Zea mays (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Zea+mays^#gephebase-summary-title)		
-	Common Name	-	Common Name
	Synonyms		Synonyms
Zea mays var. japonica; maize; Zea mays L.; Zea mays mays	Rank	Zea mays var. japonica; maize; Zea mays L.; Zea mays mays	Rank
species	Lineage	species	Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea	Parent	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea	Parent
Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4575)	NCBI Taxonomy ID	Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4575)	NCBI Taxonomy ID
4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4577)	is Taxon A an Intraspecies?	4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4577)	is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Zea mays
rp3-1	Synonyms	Q6PW75 (http://www.uniprot.org/uniprot/Q6PW75)	GenebankID or UniProtKB
ZmBb24C02/130N21.1	String	AY574035 (https://www.ncbi.nlm.nih.gov/nuccore/AY574035)	
-			
	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
Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive+Null=~Unknown^#gephebase-summary-title)			
			Molecular Type
Unknown (https://www.gephebase.org/search-criteria?/and+Molecular+Type=~Unknown^#gephebase-summary-title)			

Unknown (https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Unknown~#gephebase-summary-title)	Aberration Type
unknown	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Linkage+Mapping~#gephebase-summary-title)	Experimental Evidence
Genetic and molecular characterization of the maize rp3 rust resistance locus. (2002) (https://pubmed.ncbi.nlm.nih.gov/12242248)	Main Reference
Webb CA; Richter TE; Collins NC; Nicolas M; Trick HN; Pryor T; Hulbert SH	Authors
In maize, the Rp3 gene confers resistance to common rust caused by Puccinia sorghi. Flanking marker analysis of rust-susceptible rp3 variants suggested that most of them arose via unequal crossing over, indicating that rp3 is a complex locus like rp1. The PIC13 probe identifies a nucleotide binding site-leucine-rich repeat (NBS-LRR) gene family that maps to the complex. Rp3 variants show losses of PIC13 family members relative to the resistant parents when probed with PIC13, indicating that the Rp3 gene is a member of this family. Gel blots and sequence analysis suggest that at least 9 family members are at the locus in most Rp3-carrying lines and that at least 5 of these are transcribed in the Rp3-A haplotype. The coding regions of 14 family members, isolated from three different Rp3-carrying haplotypes, had DNA sequence identities from 93 to 99%. Partial sequencing of clones of a BAC contig spanning the rp3 locus in the maize inbred line B73 identified five different PIC13 paralogues in a region of approximately 140 kb.	Abstract
	Additional References

RELATED GEPHE

5 (HM1 = HC toxin reductase (HCTR), HM1 = HC toxin reductase (HCTR) [possible pseudo-replicate from other Maize entry], HM2 = HC toxin reductase (HCTR), Lysine histidine transporter 1, Rp1-D) (https://www.gephebase.org/search-criteria?/or+Taxon+ID=~4577~/and+Trait=Pathogen+resistance/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

Cluster of paralogous genes