

GEPHE SUMMARY

	Gephebase Gene		GepheID
Rp1-D (<a +rp1-d+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+Rp1-D+"#gephebase-summary-title)		GP00000998	
	Entry Status	Martin	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 (<a +pathogen+resistance+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">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 (<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
Zea mays (<a +zea+mays+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Zea+mays+"#gephebase-summary-title)		Zea mays (<a +zea+mays+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">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		Zea mays var. japonica; maize; Zea mays L.; Zea mays mays	
	Rank		Rank
species		species	
	Lineage		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		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		Parent
Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4575)		Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4575)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4577)		4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4577)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Zea mays
Rp1-D		Q9SWU0 (http://www.uniprot.org/uniprot/Q9SWU0)	
	Synonyms		GenebankID or UniProtKB
-		AF107293 (https://www.ncbi.nlm.nih.gov/nuccore/AF107293)	
	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 (<a +no+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Presumptive+Null=">https://www.gephebase.org/search-criteria?/and+Presumptive+Null="+No+"#gephebase-summary-title)			
			Molecular Type
Gene Amplification (<a +gene+amplification+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Molecular+Type=">https://www.gephebase.org/search-criteria?/and+Molecular+Type="+Gene+Amplification+"#gephebase-summary-title)			

Complex Change (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Complex Change~#gephebase-summary-title)	Aberration Type
Unequal crossing over between paralogues resulting in chimeric gene	Molecular Details of the Mutation
Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Candidate Gene~#gephebase-summary-title)	Experimental Evidence
Molecular characterization of the maize Rp1-D rust resistance haplotype and its mutants. (1999) (https://pubmed.ncbi.nlm.nih.gov/10402435)	Main Reference
Collins N; Drake J; Ayliffe M; Sun Q; Ellis J; Hulbert S; Pryor T	Authors
The Rp1-D gene for resistance to maize common rust (<i>Puccinia sorghi</i>) is a member of a complex locus (haplotype) composed of Rp1-D and approximately eight other gene homologs. The identity of Rp1-D was demonstrated by using two independent gene-tagging approaches with the transposons Mutator and Dissociation. PIC20, a disease resistance (R) gene analog probe previously mapped to the rp1 locus, detected insertion of Dissociation in an Rp1-D mutation and excision in three revertants. Independent libraries probed with the PIC20 or Mutator probes resulted in isolation of the same gene sequence. Rp1-D belongs to the nucleotide binding site, leucine-rich repeat class of R genes. However, unlike the rust resistance genes M and L6 from flax, the maize Rp1-D gene does not encode an N-terminal domain with similarity to the signal transduction domains of the <i>Drosophila</i> Toll protein and mammalian interleukin-1 receptor. Although the abundance of transcripts of genes from the rp1 complex changed with leaf age, there was no evidence of any change due to inoculation with avirulent or virulent rust biotypes. A set of 27 Rp1-D mutants displayed at least nine different deletions of Rp1-D gene family members that were consistent with unequal crossing-over events. One mutation (Rp1-D*-24) resulted in deletion of all but one gene family member. Other unique deletions were observed in the disease lesion mimic Rp1-D*-21 and the partially susceptible mutant Rp1-D*-5. Different rp1 specificities have distinct DNA fingerprints (haplotypes). Analysis of recombinants between rp1 specificities indicated that recombination had occurred within the rp1 gene complex. Similar analyses indicated that the rust R genes at the rp5 locus, 2 centimorgans distal to rp1, are not closely related to Rp1-D.	Abstract
Recombination between paralogues at the Rp1 rust resistance locus in maize. (2001) (https://pubmed.ncbi.nlm.nih.gov/11333250) Contrasting evolutionary patterns of the Rp1 resistance gene family in different species of Poaceae. (2011) (https://pubmed.ncbi.nlm.nih.gov/20713469)	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, Rp3 cluster) (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