

	Gephebase Gene	GepheID
RPM1 (<a +rpm1+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+RPM1+"#gephebase-summary-title)	GP00001001	
	Entry Status	Main curator
Published		

Trait Category		Trait	
Physiology (#https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology #gephebase-summary-title)			
Pathogen resistance (#https://www.gephebase.org/search-criteria?/and+Trait=~Pathogen+resistance #gephebase-summary-title)			
	Trait State in Taxon A		
Brassica napus			
	Trait State in Taxon B		
Brassica napus			
	Ancestral State		
Data not curated			
	Taxonomic Status		
Intraspecific (#https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Intraspecific #gephebase-summary-title)			
Taxon A		Taxon B	
	Latin Name		Latin Name
Brassica napus (#https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Brassica+napus #gephebase-summary-title)		Brassica napus (#https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Brassica+napus #gephebase-summary-title)	
	Common Name		Common Name
rape		rape	
	Synonyms		Synonyms
rape; oilseed rape; rapeseeds; Brassica napus L., 1753		rape; oilseed rape; rapeseeds; Brassica napus L., 1753	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Brassiceae; Brassica		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Brassiceae; Brassica	
	Parent		Parent
Brassica () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3705)		Brassica () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3705)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
3708 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3708)		3708 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3708)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

	Generic Gene Name		UniProtKB Arabidopsis thaliana
RPM1		Q39214 (http://www.uniprot.org/uniprot/Q39214)	
	Synonyms		GenebankID or UniProtKB
DISEASE RESISTANCE PROTEIN RPM1; RESISTANCE TO P. SYRINGAE PV MACULICOLA 1; RESISTANCE TO PSEUDOMONAS SYRINGAE 3; RPS3; At3g07040; F17A9.20		AAC99466 (https://www.ncbi.nlm.nih.gov/nuccore/AAC99466)	
	String		
3702.AT3G07040.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT3G07040.1)			
	Sequence Similarities		
Belongs to the disease resistance NB-LRR family.			
	GO - Molecular Function		
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)			
GO:0000166 : nucleotide binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000166)			
GO:0043531 : ADP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043531)			
	GO - Biological Process		
GO:0009626 : plant-type hypersensitive response			

(https://www.ebi.ac.uk/QuickGO/term/GO:0009626)	GO - Cellular Component	
GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)		
GO:0012505 : endomembrane system		
(https://www.ebi.ac.uk/QuickGO/term/GO:0012505)		
GO:0019897 : extrinsic component of plasma membrane		
(https://www.ebi.ac.uk/QuickGO/term/GO:0019897)		
		Presumptive Null
Yes (#gephebase-summary-title)		
		Molecular Type
Gene Loss (#gephebase-summary-title)		
		Aberration Type
Complex Change (#gephebase-summary-title)		
		Molecular Details of the Mutation
deletion		
		Experimental Evidence
Linkage Mapping (#gephebase-summary-title)		
		Main Reference
Independent deletions of a pathogen-resistance gene in Brassica and Arabidopsis. (1998) (https://pubmed.ncbi.nlm.nih.gov/9861058)		
		Authors
Grant MR; McDowell JM; Sharpe AG; de Torres Zabala M; Lydiate DJ; Dangl JL		
		Abstract

Plant disease resistance (R) genes confer race-specific resistance to pathogens and are genetically defined on the basis of intra-specific functional polymorphism. Little is known about the evolutionary mechanisms that generate this polymorphism. Most R loci examined to date contain alternate alleles and/or linked homologs even in disease-susceptible plant genotypes. In contrast, the resistance to *Pseudomonas syringae* pathovar *maculicola* (RPM1) bacterial resistance gene is completely absent (rpm1-null) in 5/5 *Arabidopsis thaliana* accessions that lack RPM1 function. The rpm1-null locus contains a 98-bp segment of unknown origin in place of the RPM1 gene. We undertook comparative mapping of RPM1 and flanking genes in *Brassica napus* to determine the ancestral state of the RPM1 locus. We cloned two *B. napus* RPM1 homologs encoding hypothetical proteins with approximately 81% amino acid identity to *Arabidopsis* RPM1. Collinearity of genes flanking RPM1 is conserved between *B. napus* and *Arabidopsis*. Surprisingly, we found four additional *B. napus* loci in which the flanking marker synteny is maintained but RPM1 is absent. These *B. napus* rpm1-null loci have no detectable nucleotide similarity to the *Arabidopsis* rpm1-null allele. We conclude that RPM1 evolved before the divergence of the Brassicaceae and has been deleted independently in the *Brassica* and *Arabidopsis* lineages. These results suggest that functional polymorphism at R gene loci can arise from gene deletions.

Additional References

RELATED GEPHE

	Related Genes
No matches found.	
	Related Haplotypes
No matches found.	

EXTERNAL LINKS

COMMENTS