

GEPHE SUMMARY

Gephebase Gene		GepheID
RPP1-WsC (<a +rpp1-wsc+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+RPP1-WsC+"#gephebase-summary-title)	GP00001004	
Entry Status		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	
Arabidopsis thaliana- Col0 - resistant		Trait State in Taxon B	
Arabidopsis thaliana- Ws0 - sensitive		Ancestral State	
Data not curated		Taxonomic Status	
Intraspecific (<a +intraspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Intraspecific+"#gephebase-summary-title)			
Taxon A		Taxon B	
Arabidopsis thaliana (<a +arabidopsis+thaliana+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Arabidopsis+thaliana+"#gephebase-summary-title)		Arabidopsis thaliana (<a +arabidopsis+thaliana+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Arabidopsis+thaliana+"#gephebase-summary-title)	
Common Name		Common Name	
thale cress		thale cress	
Synonyms		Synonyms	
thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress		thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress	
Rank		Rank	
species		species	
Lineage		Lineage	
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis	
Parent		Parent	
Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701)		Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701)	
NCBI Taxonomy ID		NCBI Taxonomy ID	
3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702)		3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
Yes		Yes	
Taxon A Description		Taxon B Description	
Arabidopsis thaliana- Col0 - resistant		Arabidopsis thaliana- Ws0 - sensitive	

GENOTYPIC CHANGE

Generic Gene Name		UniProtKB Arabidopsis thaliana
RPP1		F4J339 (http://www.uniprot.org/uniprot/F4J339)
Synonyms		GenebankID or UniProtKB
cog1; recognition of peronospora parasitica 1; At3g44480; F14L2_30		CP002686 (https://www.ncbi.nlm.nih.gov/nucleotide/CP002686)
String		
3702.AT3G44480.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT3G44480.1)		
Sequence Similarities		
-		
GO - Molecular Function		
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)		
GO:0043531 : ADP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043531)		
GO:0030275 : LRR domain binding (https://www.ebi.ac.uk/QuickGO/term/GO:0030275)		
GO - Biological Process		

GO:0006952 : defense response (<https://www.ebi.ac.uk/QuickGO/term/GO:0006952>)
GO:0007165 : signal transduction (<https://www.ebi.ac.uk/QuickGO/term/GO:0007165>)
GO:0009817 : defense response to fungus, incompatible interaction (<https://www.ebi.ac.uk/QuickGO/term/GO:0009817>)
GO:0002239 : response to oomycetes (<https://www.ebi.ac.uk/QuickGO/term/GO:0002239>)

GO - Cellular Component

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0000139 : Golgi membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0000139>)
GO:0005789 : endoplasmic reticulum membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005789>)

	Presumptive Null
Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Unknown~#gephebase-summary-title)	Molecular Type
Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Coding~#gephebase-summary-title)	Aberration Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Unknown~#gephebase-summary-title)	Molecular Details of the Mutation
unknown	Experimental Evidence
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title)	Main Reference

Three genes of the Arabidopsis RPP1 complex resistance locus recognize distinct Peronospora parasitica avirulence determinants. (1998) (https://pubmed.ncbi.nlm.nih.gov/9811793)	Authors
Botella MA; Parker JE; Frost LN; Bittner-Eddy PD; Beynon JL; Daniels MJ; Holub EB; Jones JD	Abstract

Plant resistance (R) genes have evolved specific recognition capabilities in defense against pathogens. The evolution of R gene function and maintenance of R gene diversity within a plant species are therefore of great interest. In the Arabidopsis accession Wassilewskija, the RPP1 region on chromosome 3 contains four genetically linked recognition specificities, conditioning resistance to different isolates of the biotrophic oomycete *Peronospora parasitica* (downy mildew). We show that three of four tightly linked genes in this region, designated RPP1-WsA, RPP1-WsB, and RPP1-WsC, encode functional products of the NBS-LRR (nucleotide binding site-leucine-rich repeat) R protein class. They possess a TIR (Toll, interleukin-1, resistance) domain that is characteristic of certain other NBS-LRR-type R proteins, but in addition, they have unique hydrophilic or hydrophobic N termini. Together, the three RPP1 genes account for the spectrum of resistance previously assigned to the RPP1 region and thus comprise a complex R locus. The distinct but partially overlapping resistance capabilities conferred by these genes are best explained by the hypothesis that each recognizes a different pathogen avirulence determinant. We present evidence suggesting that the RPP genes at this locus are subject to the same selective forces that have been demonstrated for structurally different LRR-type R genes.

Additional References

RELATED GEPHE

	Related Genes
20 (ACD6 = ACCELERATED CELL DEATH 6, ERECTA, RAC1, Resistance related Kinase 1 (RKS1), RLM1, RLM2 cluster, RLM3, RPM1, RPP1-WsA, RPP1-WsB, RPP13, RPP2A-RPP2B, RPP4, RPP5, RPP8, RPS2, RPS4, RPS5, RRS1, WRR4) (https://www.gephebase.org/search-criteria?/or+Taxon ID=~3702~/and+Trait=Pathogen resistance/and+groupHaplotypes=true#gephebase-summary-title)	Related Haplotypes
No matches found.	

EXTERNAL LINKS

COMMENTS

Cluster of paralogous genes