GEPHE SUMMARY

Gephebase Gene
RPP1-WsA (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^RPP1-WsA^#gephebase-summary-title)

GepheID
GP00001002

Entry Status
Published

Main curator
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
Arabidopsis thaliana- Col0 - resistant

Trait State in Taxon B
Arabidopsis thaliana- Ws0 - sensitive

Ancestral State
Data not curated

Taxonomic Status
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)

Taxon A

Latin Name
Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Arabidopsis thaliana^#gephebase-summary-title)

Common Name
thale cress

Synonyms
thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis

Parent
Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)

NCBI Taxonomy ID
3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)

is Taxon A an Infraspecies?
Yes

Taxon A Description
Arabidopsis thaliana- Col0 - resistant

Taxon B

Latin Name
Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Arabidopsis thaliana^#gephebase-summary-title)

Common Name
thale cress

Synonyms
thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis

Parent
Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)

NCBI Taxonomy ID
3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)

is Taxon B an Infraspecies?
Yes

Taxon B Description
Arabidopsis thaliana- Ws0 - sensitive

GENOTYPIC CHANGE

Generic Gene Name
RPP1

Synonyms
cog1; recognition of peronospora parasitica 1; At3g44480; F14L2_30

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

UniProtKB Arabidopsis thaliana
F4J339 (http://www.uniprot.org/uniprot/F4J339)

GenebankID or UniProtKB
CP002686 (https://www.ncbi.nlm.nih.gov/nuccore/CP002686)

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-WsB, RPP1-WsC, 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