GEPHE SUMMARY

Gephebase Gene
RPP8 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^RPP8^#gephebase-summary-title)

GepheID
GP00001010

Entry Status
Published

Main curator
Courtier

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

Trait State in Taxon B
Arabidopsis thaliana- Ler0

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

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- Ler0

GENOTYPIC CHANGE

Generic Gene Name
RPP8

Synonyms
DISEASE RESISTANCE PROTEIN RPP8; HRT; HYPERSENSITIVE RESPONSE TO TCV; MWF20.19; MWF20_19; RCY1; RECOGNITION OF PERONOSPORA PARASITICA 8; RESISTANT TO CMV(Y) 1; At5g43470

String
3702.AT5G43470.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT5G43470.1)

Sequence Similarities
Belongs to the disease resistance NB-LRR family. RPP8/HRT subfamily.

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)

UniProtKB Arabidopsis thaliana
Q8W4J9 (http://www.uniprot.org/uniprot/Q8W4J9)

GenebankID or UniProtKB
AD089710 (https://www.ncbi.nlm.nih.gov/nuccore/AD089710)

GO:0043531 : ADP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043531)

GO - Biological Process

GO:0006952 : defense response (https://www.ebi.ac.uk/QuickGO/term/GO:0006952)
GO:0009637 : response to blue light (https://www.ebi.ac.uk/QuickGO/term/GO:0009637)
GO:0071446 : cellular response to salicylic acid stimulus
(https://www.ebi.ac.uk/QuickGO/term/GO:0071446)
GO:0009416 : response to light stimulus
(https://www.ebi.ac.uk/QuickGO/term/GO:0009416)
GO:0009751 : response to salicylic acid
(https://www.ebi.ac.uk/QuickGO/term/GO:0009751)
GO:0051607 : defense response to virus
(https://www.ebi.ac.uk/QuickGO/term/GO:0051607)
GO:0009646 : response to absence of light
(https://www.ebi.ac.uk/QuickGO/term/GO:0009646)
GO:0009611 : response to wounding (https://www.ebi.ac.uk/QuickGO/term/GO:0009611)
GO:0002230 : positive regulation of defense response to virus by host
(https://www.ebi.ac.uk/QuickGO/term/GO:0002230)
GO:0009626 : plant-type hypersensitive response
(https://www.ebi.ac.uk/QuickGO/term/GO:0009626)
GO:0002239 : response to oomycetes
(https://www.ebi.ac.uk/QuickGO/term/GO:0002239)
GO:0051707 : response to other organism
(https://www.ebi.ac.uk/QuickGO/term/GO:0051707)

GO - Cellular Component

GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)

Aberration Type

Complex Change (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Complex Change^#gephebase-summary-title)

Molecular Details of the Mutation

Chimeric fusion of two paralogues followed by coding divergence

Experimental Evidence

Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)

Main Reference

Intragenic recombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPP8 locus of Arabidopsis. (1998) (https://pubmed.ncbi.nlm.nih.gov/9811794)

Authors

McDowell JM; Dhandaydham M; Long TA; Aarts MG; Goff S; Holub EB; Dangl JL

Abstract

Pathogen resistance (R) genes of the NBS-LRR class (for nucleotide binding site and leucine-rich repeat) are found in many plant species and confer resistance to a diverse spectrum of pathogens. Little is known about the mechanisms that drive NBS-LRR gene evolution in the host-pathogen arms race. We cloned the RPP8 gene (for resistance to Peronospora parasitica) and compared the structure of alleles at this locus in resistant Landsberg erecta (Ler-0) and susceptible Columbia (Col-0) accessions. RPP8-Ler encodes an NBS-LRR protein with a putative N-terminal leucine zipper and is more closely related to previously cloned R genes that confer resistance to bacterial pathogens than it is to other known RPP genes. The RPP8 haplotype in Ler-0 contains the functional RPP8-Ler gene and a nonfunctional homolog, RPH8A. In contrast, the rpp8 locus in Col-0 contains a single chimeric gene, which was likely derived from unequal crossing over between RPP8-Ler and RPH8A ancestors within a Ler-like haplotype. Sequence divergence among RPP8 family members has been accelerated by positive selection on the putative ligand binding region in the LRRs. These observations indicate that NBS-LRR molecular evolution is driven by the same mechanisms that promote rapid sequence diversification among other genes involved in non-self-recognition.

Additional References

Genome-wide survey of Arabidopsis natural variation in downy mildew resistance using combined association and linkage mapping. (2010) (https://pubmed.ncbi.nlm.nih.gov/20479233)

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, RPP1-WsC, RPP13, RPP2A-RPP2B, RPP4, RPP5, 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

@ChimericGene