

GEPHE SUMMARY

	Gephebase Gene	GephelD
RLM2 cluster (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^RLM2 cluster^#gephebase-summary-title)	GP00000992	Main curator
Published	Entry Status	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- Ler-0 (sensitive)	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
Arabidopsis thaliana	Latin Name	Latin Name
(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Arabidopsis thaliana^#gephebase-summary-title)		
thale cress	Common Name	Common Name
thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress	Synonyms	Synonyms
species	Rank	Rank
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelinae; Arabidopsis	Lineage	Lineage
Arabidopsis () - (Rank: genus)	Parent	Parent
(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)		
Yes	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?
Arabidopsis thaliana- Col0 - resistant	Taxon A Description	Taxon B Description

GENOTYPIC CHANGE

RLM1B	Generic Gene Name	UniProtKB Arabidopsis thaliana
T12P18.10; T12P18_10; At1g63880	Synonyms	GenebankID or UniProtKB
3702.AT1G63880.1	String	CP002684 (https://www.ncbi.nlm.nih.gov/nuccore/CP002684)
(http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT1G63880.1)	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 - Biological Process	
GO:0007165 : signal transduction (https://www.ebi.ac.uk/QuickGO/term/GO:0007165)		

GO:0050832 : defense response to fungus

(<https://www.ebi.ac.uk/QuickGO/term/GO:0050832>)

GO - Cellular Component

-	Presumptive Null
Yes (https://www.gephebase.org/search-criteria/?and+Presumptive+Null=%Yes%#gephebase-summary-title)	Molecular Type
Gene Loss (https://www.gephebase.org/search-criteria/?and+Molecular+Type=%Gene+Loss%#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
the locus contains two paralogues; one of which is deleted and the other pseudogenized in Ler-0	Experimental Evidence
Linkage Mapping (https://www.gephebase.org/search-criteria/?and+Experimental+Evidence=%Linkage+Mapping%#gephebase-summary-title)	Main Reference
Transgressive segregation reveals two <i>Arabidopsis</i> TIR-NB-LRR resistance genes effective against <i>Leptosphaeria maculans</i> , causal agent of blackleg disease. (2006) (https://pubmed.ncbi.nlm.nih.gov/16623885)	Authors
Staal J; Kaliff M; Bohman S; Dixielius C	Abstract
In a cross between the two resistant accessions Col-0 and Ler-0, a 15:1 segregation was found in F2, suggesting the presence of unlinked resistance loci to <i>Leptosphaeria maculans</i> . One hundred Col-4 x Ler-0, and 50 Ler-2 x Cvi-1 recombinant inbred lines, and seven susceptible Ler-0 x Ws-0 F2 progenies were examined to identify the two loci. Resistance in Col-4, Ws-0 and Cvi-1 (RLM1) was mapped to the marker m305 on chromosome 1. Col-4 x Ler-0 and Ler-2 x Cvi-1 mapping populations located RLM2(Ler) on the same arm of chromosome 4. A tight physical location of RLM2 was established through near-isogenic lines. This region was found to correspond to an ancient duplication event between the RLM1 and RLM2 loci. Two independent T-DNA mutants in a TIR-NB-LRR R gene (At1g64070) displayed susceptibility, and <i>L. maculans</i> susceptible mutant phenotypes were confirmed to be allelic for rlm1 in F1 after crosses with susceptible rlm1(Ler)rlm2(Col) plants. Complementation of rlm1(Ler)rlm2(Col) with the genomic Col-0 sequence of At1g64070 conferred resistance. In addition, two T-DNA mutants in a neighbouring homologous TIR-NB-LRR gene (At1g63880) displayed moderate susceptibility to <i>L. maculans</i> . Sequence analysis revealed that At1g64070 was truncated by a premature stop codon, and that At1g63880 was absent in Ler-0. RNA interference confirmed that Ler-0 resistance is dependent on genes structurally related to RLM1. Camalexin was identified as a quantitative co-dominant resistance factor of Col-0 origin, but independent of RLM1. RLM1/RLM2 resistance was, however, found to require RAR1 and partially HSP90.1.	Additional References

RELATED GEPHE

20 (ACD6 = ACCELERATED CELL DEATH 6, ERECTA, RAC1, Resistance related Kinase 1 (RKS1), RLM1, RLM3, RPM1, RPP1-WsA, 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 Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS