

GEPHE SUMMARY

	Gephebase Gene	GephelD
ATR13 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^ATR13^#gephebase-summary-title)	GP00000128	
	Entry Status	Main curator
Published	Martin	

PHENOTYPIC CHANGE

	Trait Category	
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)	Trait	
Pathogenicity (https://www.gephebase.org/search-criteria?/and+Trait=^Pathogenicity^#gephebase-summary-title)	Trait State in Taxon A	
Hyaloperonospora parasitica - pathogenic	Trait State in Taxon B	
Hyaloperonospora parasitica - non pathogenic	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
Hyaloperonospora parasitica (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Hyaloperonospora+parasitica^#gephebase-summary-title)	Hyaloperonospora parasitica (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Hyaloperonospora+parasitica^#gephebase-summary-title)	
	Common Name	Common Name
-	Synonyms	Synonyms
Peronospora parasitica; Hyaloperonospora parasitica (Persoon: Fries) Constantinescu	Peronospora parasitica; Hyaloperonospora parasitica (Persoon: Fries) Constantinescu	
species	Rank	Rank
	Lineage	Lineage
cellular organisms; Eukaryota; Stramenopiles; Oomycetes; Peronosporales; Peronosporaceae; Hyaloperonospora; Hyaloperonospora parasitica species group		
	Parent	Parent
Hyaloperonospora parasitica species group () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=453155)	Hyaloperonospora parasitica species group () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=453155)	
123356 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=123356)	NCBI Taxonomy ID	NCBI Taxonomy ID
	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?
No	No	

GENOTYPIC CHANGE

Atr13	Generic Gene Name	UniProtKB Hyaloperonospora parasitica Q5G7K8 (http://www.uniprot.org/uniprot/Q5G7K8)
-	Synonyms	GenebankID or UniProtKB AY785305 (https://www.ncbi.nlm.nih.gov/nucleotide/AY785305)
-	String	
-	Sequence Similarities	
-	GO - Molecular Function	
-	GO - Biological Process	
-	GO - Cellular Component	
-		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
SNP (https://www.gephebase.org/search-criteria?/and+Aberration+Type=^SNP^#gephebase-summary-title)		

Nonsynonymous

Multiple coding changes - the avirulence allele ATR13Maks9 and the virulence allele ATR13<ins>Emoy2 only encode differences in the C-terminal domain (in 11 amino acids) - domain swaps show that one or more of the amino acids in Region A are required for recognition and one or more in Region B are required to elicit a full recognition phenotype. - exact causing mutations unknown

Molecular Details of the Mutation

Linkage Mapping ([https://www.gephebase.org/search-criteria/?and+Experimental Evidence=%20Linkage Mapping%23gephebase-summary-title](https://www.gephebase.org/search-criteria/?and+Experimental%20Evidence=%20Linkage%20Mapping%23gephebase-summary-title))

Experimental Evidence

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Host-parasite coevolutionary conflict between *Arabidopsis* and downy mildew. (2004) (<https://pubmed.ncbi.nlm.nih.gov/15591208>)

Authors

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Abstract

Plants are constantly exposed to attack by an array of diverse pathogens but lack a somatically adaptive immune system. In spite of this, natural plant populations do not often suffer destructive disease epidemics. Elucidating how allelic diversity within plant genes that function to detect pathogens (resistance genes) counteracts changing structures of pathogen genes required for host invasion (pathogenicity effectors) is critical to our understanding of the dynamics of natural plant populations. The RPP13 resistance gene is the most polymorphic gene analyzed to date in the model plant *Arabidopsis thaliana*. Here we report the cloning of the avirulence gene, ATR13, that triggers RPP13-mediated resistance, and we show that it too exhibits extreme levels of amino acid polymorphism. Evidence of diversifying selection visible in both components suggests that the host and pathogen may be locked in a coevolutionary conflict at these loci, where attempts to evade host resistance by the pathogen are matched by the development of new detection capabilities by the host.

Additional References

Natural variation reveals key amino acids in a downy mildew effector that alters recognition specificity by an *Arabidopsis* resistance gene. (2008) (<https://pubmed.ncbi.nlm.nih.gov/18705864>)

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect