

GEPHE SUMMARY

<p>ATR13 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+^ATR13^#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00000128</p> <p>Martin</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

<p>Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category+^Physiology^#gephebase-summary-title)</p> <p>Pathogenicity (https://www.gephebase.org/search-criteria?/and+Trait+^Pathogenicity^#gephebase-summary-title)</p> <p>Hyaloperonospora parasitica - pathogenic</p> <p>Hyaloperonospora parasitica - non pathogenic</p> <p>Data not curated</p> <p>Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status+^Intraspecific^#gephebase-summary-title)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Taxon A</p> <p>Latin Name</p> <p>Hyaloperonospora parasitica (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+^Hyaloperonospora+parasitica^#gephebase-summary-title)</p> <p>-</p> <p>Common Name</p> <p>-</p> <p>Synonyms</p> <p>Peronospora parasitica; Hyaloperonospora parasitica (Persoon: Fries) Constantinescu species</p> <p>Rank</p> <p>cellular organisms; Eukaryota; Stramenopiles; Oomycetes; Peronosporales; Peronosporaceae; Hyaloperonospora; Hyaloperonospora parasitica species group</p> <p>Lineage</p> <p>Parent</p> <p>Hyaloperonospora parasitica species group () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=453155)</p> <p>NCBI Taxonomy ID</p> <p>123356 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=123356)</p> <p>is Taxon A an Intraspecies?</p> <p>No</p>	<p>Taxon B</p> <p>Latin Name</p> <p>Hyaloperonospora parasitica (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+^Hyaloperonospora+parasitica^#gephebase-summary-title)</p> <p>-</p> <p>Common Name</p> <p>-</p> <p>Synonyms</p> <p>Peronospora parasitica; Hyaloperonospora parasitica (Persoon: Fries) Constantinescu species</p> <p>Rank</p> <p>cellular organisms; Eukaryota; Stramenopiles; Oomycetes; Peronosporales; Peronosporaceae; Hyaloperonospora; Hyaloperonospora parasitica species group</p> <p>Lineage</p> <p>Parent</p> <p>Hyaloperonospora parasitica species group () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=453155)</p> <p>NCBI Taxonomy ID</p> <p>123356 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=123356)</p> <p>is Taxon B an Intraspecies?</p> <p>No</p>
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GENOTYPIC CHANGE

<p>Atr13</p> <p>-</p> <p>-</p> <p>-</p> <p>-</p> <p>-</p> <p>-</p> <p>-</p> <p>-</p> <p>No (https://www.gephebase.org/search-criteria?/and+Presumptive+Null+^No^#gephebase-summary-title)</p> <p>Coding (https://www.gephebase.org/search-criteria?/and+Molecular+Type+^Coding^#gephebase-summary-title)</p> <p>SNP (https://www.gephebase.org/search-criteria?/and+Aberration+Type+^SNP^#gephebase-summary-title)</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p> <p>GO - Biological Process</p> <p>GO - Cellular Component</p>	<p>UniProtKB Hyaloperonospora parasitica Q5G7K8 (http://www.uniprot.org/uniprot/Q5G7K8)</p> <p>GenebankID or UniProtKB AY785305 (https://www.ncbi.nlm.nih.gov/nuccore/AY785305)</p>	<p>Presumptive Null</p> <p>Molecular Type</p> <p>Aberration Type</p>
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Nonsynonymous

Molecular Details of the Mutation

Multiple coding changes - the avirulence allele ATR13^{Maks9} and the virulence allele ATR13^{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

Experimental Evidence

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

Allen RL; Bittner-Eddy PD; Grenville-Briggs LJ; Meitz JC; Rehmany AP; Rose LE; Beynon JL

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

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect