

GEPHE SUMMARY

<p>Lr67 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=Lr67#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00001535</p> <p>Prigent</p>	<p>GepheID</p> <p>Main curator</p>
--	---	----------------------------------	------------------------------------

PHENOTYPIC CHANGE

<p>Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=Physiology#gephebase-summary-title)</p> <p>Pathogen resistance (rust ; mildew) (https://www.gephebase.org/search-criteria?/and+Trait=Pathogen+resistance+(rust+;+mildew)#gephebase-summary-title)</p> <p>Wheat susceptible to pathogens</p> <p>Wheat resistant to multiple pathogens</p> <p>Taxon A</p> <p>Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=Domesticated#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>Triticum aestivum (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=Triticum+aestivum#gephebase-summary-title)</p> <p>Common Name</p> <p>bread wheat</p> <p>Synonyms</p> <p>Triticum aestivum subsp. aestivum; Triticum vulgare; bread wheat; Canadian hard winter wheat; common wheat; wheat; Triticum aestivum L.; Triticum vulgare L.; Triticum vulgare Vill., nom. illeg.; Tricum aestivum; Triticum aestivum; Triticum aestivum8</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Triticoideae; Triticeae; Triticinae; Triticum</p> <p>Parent</p> <p>Triticum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4564)</p> <p>NCBI Taxonomy ID</p> <p>4565 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4565)</p> <p>is Taxon A an Intraspecies?</p> <p>No</p>	<p>Taxon B</p> <p>Latin Name</p> <p>Triticum aestivum (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=Triticum+aestivum#gephebase-summary-title)</p> <p>Common Name</p> <p>bread wheat</p> <p>Synonyms</p> <p>Triticum aestivum subsp. aestivum; Triticum vulgare; bread wheat; Canadian hard winter wheat; common wheat; wheat; Triticum aestivum L.; Triticum vulgare L.; Triticum vulgare Vill., nom. illeg.; Tricum aestivum; Triticum aestivum; Triticum aestivum8</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Triticoideae; Triticeae; Triticinae; Triticum</p> <p>Parent</p> <p>Triticum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4564)</p> <p>NCBI Taxonomy ID</p> <p>4565 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4565)</p> <p>is Taxon B an Intraspecies?</p> <p>Yes</p> <p>Taxon B Description</p> <p>-</p>
--	---	--	---

GENOTYPIC CHANGE

<p>-</p> <p>-</p> <p>-</p> <p>Belongs to the major facilitator superfamily. Sugar transporter (TC 2.A.1.1) family.</p> <p>GO:0022857 : transmembrane transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0022857)</p> <p>-</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 Triticum aestivum A0A0S1LH45 (http://www.uniprot.org/uniprot/A0A0S1LH45)</p> <p>GenebankID or UniProtKB</p> <p>0</p>
--	--	---

GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)

Presumptive Null

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No^#gephebase-summary-title](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](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](https://www.gephebase.org/search-criteria?/and+Aberration+Type=~SNP^#gephebase-summary-title))

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Gly144Arg (exon 2) leads to a protein incapable of glucose import; LR67res exerts a dominant-negative effect through heterodimerization with these functional transporters to reduce glucose uptake.; alterations in hexose transport in infected leaves may explain its ability to reduce the growth of multiple biotrophic pathogen species

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=~Linkage+Mapping^#gephebase-summary-title))

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

Main Reference

A recently evolved hexose transporter variant confers resistance to multiple pathogens in wheat. (2015) (<https://pubmed.ncbi.nlm.nih.gov/26551671>)

Authors

Moore JW; Herrera-Foessel S; Lan C; Schnippenkoetter W; Ayliffe M; Huerta-Espino J; Lillemo M; Viccars L; Milne R; Periyannan S; Kong X; Spielmeyer W; Talbot M; Bariana H; Patrick JW; Dodds P; Singh R; Lagudah E

Abstract

As there are numerous pathogen species that cause disease and limit yields of crops, such as wheat (*Triticum aestivum*), single genes that provide resistance to multiple pathogens are valuable in crop improvement. The mechanistic basis of multi-pathogen resistance is largely unknown. Here we use comparative genomics, mutagenesis and transformation to isolate the wheat Lr67 gene, which confers partial resistance to all three wheat rust pathogen species and powdery mildew. The Lr67 resistance gene encodes a predicted hexose transporter (LR67res) that differs from the susceptible form of the same protein (LR67sus) by two amino acids that are conserved in orthologous hexose transporters. Sugar uptake assays show that LR67sus, and related proteins encoded by homeoalleles, function as high-affinity glucose transporters. LR67res exerts a dominant-negative effect through heterodimerization with these functional transporters to reduce glucose uptake. Alterations in hexose transport in infected leaves may explain its ability to reduce the growth of multiple biotrophic pathogen species.

Additional References

RELATED GEPHE

Related Genes

4 (Lr21, Pm3, Pore-forming toxin-like (PFT), Mla (=Sr33/AetRGA1e)) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=~4565^/and+Trait=Pathogen resistance/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=~4565^/and+Trait=Pathogen+resistance/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Resistant allele of LR67 causes reduced hexose transport through a dominant-negative interference mechanism by forming inactive heteromultimeric protein complexes. The LR67res inhibition of hexose retrieval may mimic the ubiquitous plant response to pathogen invasion of elevated cell wall invertase activity which alters the extracellular apoplastic hexose/sucrose ratio and elicits a hexose-mediated defense response. Val387Leu (exon 3) is observed in the same haplotype but experimental replacement shows it is not responsible for the phenotype