GEPHE SUMMARY

Gephebase Gene

Lr67 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Lr67^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001535

Main curator

Prigent

PHENOTYPIC CHANGE

Trait Category

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

Pathogen resistance (rust ; mildew) (https://www.gephebase.org/search-criteria?/and+Trait=^Pathogen resistance (rust ; mildew)^#gephebase-summary-title)

Trait State in Taxon A

Wheat susceptible to pathogens

Trait State in Taxon B

Wheat resistant to multiple pathogens

Ancestral State

Taxon A

Taxonomic Status

Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)

Taxon A

Latin Name

Triticum aestivum (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Triticum aestivum^#gephebase-summary-title)

Common Name

bread wheat

Synonyms

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 aestivam; Triticum aestivum8

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum

Parent

Triticum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4564)

NCBI Taxonomy ID

4565 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4565)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Triticum aestivum (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Triticum aestivum^#gephebase-summary-title)

Common Name

bread wheat

Synonyms

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 aestivam; Triticum aestivum8

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum

Parent

Triticum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4564)

NCBI Taxonomy ID

4565 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4565)

is Taxon B an Infraspecies?

Yes

Taxon B Description

-

GENOTYPIC CHANGE

Generic Gene Name

-

Synonyms

-

String

-

Sequence Similarities

Belongs to the major facilitator superfamily. Sugar transporter (TC 2.A.1.1) family.

GO - Molecular Function

GO:0022857 : transmembrane transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0022857)

GO - Biological Process

-

GO - Cellular Component

UniProtKB Triticum aestivum

A0A0S1LH45 (http://www.uniprot.org/uniprot/A0A0S1LH45)

GenebankID or UniProtKB

()

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)

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)

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)

	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)

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