GEPHE SUMMARY

Gephebase Gene

HM2 = HC toxin reductase (HCTR) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^HM2 = HC toxin reductase (HCTR)^#gephebase-summary-title)

GepheID

GP00000483

Entry Status

Published

Main curator

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

Zea mays - resistant

Trait State in Taxon B

Zea mays - B73 - sensitive

Ancestral State

Taxon A

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

-

Synonyms

Zea mays var. japonica; maize; Zea mays L.; Zea mays mays

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea

Parent

Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4575)

NCBI Taxonomy ID

4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4577)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

-

Synonyms

Zea mays var. japonica; maize; Zea mays L.; Zea mays mays

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea

Parent

Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4575)

NCBI Taxonomy ID

4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4577)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Zea mays - B73 - sensitive

GENOTYPIC CHANGE

Generic Gene Name

hm2

Synonyms

-

String

-

Sequence Similarities

-

GO - Molecular Function

GO:0050662 : coenzyme binding (https://www.ebi.ac.uk/QuickGO/term/GO:0050662)
GO:0003824 : catalytic activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003824)

GO - Biological Process

-

GO - Cellular Component

-

UniProtKB Zea mays subsp. parviglumis

B8QWA3 (http://www.uniprot.org/uniprot/B8QWA3)

GenebankID or UniProtKB

AAC04337 (https://www.ncbi.nlm.nih.gov/nuccore/AAC04337)

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title)

Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)

Aberration Type

Insertion (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Insertion^#gephebase-summary-title)

Insertion Size

1-9 bp

Molecular Details of the Mutation

8-bp insertion in exon 1 that disrupt the reading frame and introduces a stop codon shortly after the beginning of the gene

Experimental Evidence

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

Main Reference

Distinct mechanisms govern the dosage-dependent and developmentally regulated resistance conferred by the maize Hm2 gene. (2008) (https://pubmed.ncbi.nlm.nih.gov/18052885)

Authors

Chintamanani S; Multani DS; Ruess H; Johal GS

Abstract

The maize Hm2 gene provides protection against the leaf spot and ear mold disease caused by Cochliobolus carbonum race 1 (CCR1). In this regard, it is similar to Hm1, the better-known disease resistance gene of the maize-CCR1 pathosystem. However, in contrast to Hm1, which provides completely dominant resistance at all stages of plant development, Hm2-conferred resistance is only partially dominant and becomes fully effective only at maturity. To investigate why Hm2 behaves in this manner, we cloned it on the basis of its homology to Hm1. As expected, Hm2 is a duplicate of Hm1, although the protein it encodes is grossly truncated compared with HM1. The efficacy of Hm2 in conferring resistance improves gradually over time, changing from having little or no impact in seedling tissues to providing complete immunity at anthesis. The developmentally specified phenotype of Hm2 is not dictated transcriptionally, because the expression level of the gene, whether occurring constitutively or undergoing substantial and transient induction in response to infection, does not change with plant age. In contrast, however, the Hm2 transcript is much more abundant in plants homozygous for this gene compared with plants that contain only one copy of the gene, suggesting a transcriptional basis for the dosage-dependent nature of Hm2. Thus, different mechanisms seem to underlie the developmentally programmed versus the partially dominant resistance phenotype of Hm2.

Additional References

RELATED GEPHE

Related Genes

5 (HM1 = HC toxin reductase (HCTR), HM1 = HC toxin reductase (HCTR) [possible pseudo-replicate from other Maize entry], Lysine histidine transporter 1, Rp1-D, Rp3 cluster) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^4577^/and+Trait=Pathogen resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^HM2 = HC toxin reductase (HCTR)^/and+Taxon ID=^4577^/or+Gene Gephebase=^HM2 = HC toxin reductase (HCTR)^/and+Taxon ID=^4577^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS