

GEPHE SUMMARY

| | | |
|---|------------------------------|-------------------------|
| HM1 = HC toxin reductase (HCTR) [possible pseudo-replicate from other Maize entry] (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~HM1+HC+toxin+reductase+(HCTR)+[possible+pseudo-replicate+from+other+Maize+entry]^#gephebase-summary-title) | Gephebase Gene GP00000481 | GepheID Main curator |
| Published | Entry Status Martin | |

PHENOTYPIC CHANGE

| | | | |
|--|-----------------------------|--|-----------------------------|
| Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology^#gephebase-summary-title) | Trait Category | | |
| Pathogen resistance (https://www.gephebase.org/search-criteria?/and+Trait=~Pathogen+resistance^#gephebase-summary-title) | Trait | | |
| Zea mays - resistant | Trait State in Taxon A | | |
| Zea mays - Pr - sensitive | Trait State in Taxon B | | |
| Taxon A | Ancestral State | | |
| Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Domesticated^#gephebase-summary-title) | Taxonomic Status | | |
| | Taxon A | | Taxon B |
| Zea mays (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Zea+mays^#gephebase-summary-title) | Latin Name | Zea mays (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Zea+mays^#gephebase-summary-title) | Latin Name |
| - | Common Name | - | Common Name |
| Zea mays var. japonica; maize; Zea mays L.; Zea mays mays | Synonyms | Zea mays var. japonica; maize; Zea mays L.; Zea mays mays | Synonyms |
| species | Rank | species | Rank |
| cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea | 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 | Lineage |
| Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4575) | Parent | Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4575) | Parent |
| 4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4577) | NCBI Taxonomy ID | 4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4577) | NCBI Taxonomy ID |
| No | is Taxon A an Intraspecies? | Yes | is Taxon B an Intraspecies? |
| | | Zea mays - Pr - sensitive | Taxon B Description |

GENOTYPIC CHANGE

| | | | |
|---|-------------------------|--|-------------------------|
| hm1 | Generic Gene Name | O49163 (http://www.uniprot.org/uniprot/O49163) | UniProtKB Zea mays |
| GRMZM5G881887 | Synonyms | AF041043 (https://www.ncbi.nlm.nih.gov/nucore/AF041043) | GenebankID or UniProtKB |
| - | String | | |
| - | Sequence Similarities | | |
| GO:0050662 : coenzyme binding (https://www.ebi.ac.uk/QuickGO/term/GO:0050662) | GO - Molecular Function | | |
| GO:0003824 : catalytic activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003824) | GO - Biological Process | | |
| - | GO - Cellular Component | | |

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

Presumptive Null

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))

Molecular Type

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

Aberration Type

100-999 bp

Insertion Size

256-bp transposable element insertion in exon 4

Molecular Details of the Mutation

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))

Experimental Evidence

Reductase activity encoded by the HM1 disease resistance gene in maize. (1992) (<https://pubmed.ncbi.nlm.nih.gov/1359642>)

Main Reference

Johal GS; Briggs SP

Authors

The HM1 gene in maize controls both race-specific resistance to the fungus *Cochliobolus carbonum* race 1 and expression of the NADPH (reduced form of nicotinamide adenine dinucleotide phosphate)-dependent HC toxin reductase (HCTR), which inactivates HC toxin, a cyclic tetrapeptide produced by the fungus to permit infection. Several HM1 alleles were generated and cloned by transposon-induced mutagenesis. The sequence of wild-type HM1 shares homology with dihydroflavonol-4-reductase genes from maize, petunia, and snap-dragon. Sequence homology is greatest in the beta alpha beta-dinucleotide binding fold that is conserved among NADPH- and NADH (reduced form of nicotinamide adenine dinucleotide)-dependent reductases and dehydrogenases. This indicates that HM1 encodes HCTR.

Abstract

Plant-pathogen microevolution: molecular basis for the origin of a fungal disease in maize. (1998) (<https://pubmed.ncbi.nlm.nih.gov/9465077>)

Additional References

RELATED GEPHE

5 (HM1 = HC toxin reductase (HCTR), HM2 = HC toxin reductase (HCTR), 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](https://www.gephebase.org/search-criteria?/or+Taxon+ID=^4577^/and+Trait=Pathogen+resistance/and+groupHaplotypes=true#gephebase-summary-title))

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

@TE