

GEPHE SUMMARY

	Gephebase Gene	GephelD
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)	GP00000481	
	Entry Status	Main curator
Published		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 - Pr - sensitive	Ancestral State	
Taxon A	Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)		
	Taxon A	Taxon B
	Latin Name	Latin Name
Zea mays (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Zea mays^#gephebase-summary-title)	Zea mays (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Zea mays^#gephebase-summary-title)	Zea mays (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Zea mays^#gephebase-summary-title)
-	Common Name	Common Name
Zea mays var. japonica; maize; Zea mays L.; Zea mays mays	Synonyms	Synonyms
species	Rank	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	Lineage
Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4575)	Parent	Parent
4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4577)	NCBI Taxonomy ID	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?
	Yes	Yes
	Zea mays - Pr - sensitive	Zea mays - Pr - sensitive

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Zea mays
hm1	O49163 (http://www.uniprot.org/uniprot/O49163)	
GRMZM5G881887	String	AF041043 (https://www.ncbi.nlm.nih.gov/nuccore/AF041043)
	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	

Yes (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)	Molecular Type
Insertion (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)	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 <i>Cochliobolus carbonum</i> 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+TaxonID=%4577%and+Trait=Pathogen+resistance/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

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