

GEPHE SUMMARY

	Gephebase Gene		GepheID
HM1 = HC toxin reductase (HCTR) (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^HM1 = HC toxin reductase (HCTR)^#gephebase-summary-title)	GP00000480		
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=^Physiology^#gephebase-summary-title)		Trait	
Pathogen resistance (https://www.gephebase.org/search-criteria?/and+Trait=^Pathogenresistance^#gephebase-summary-title)			
	Trait State in Taxon A		
Zea mays - resistant		Trait State in Taxon B	
Zea mays - M021A - sensitive			
	Ancestral State		
Data not curated		Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=^Domesticated^#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Zea mays (https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=^Zeamays^#gephebase-summary-title)		Zea mays (https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=^Zeamays^#gephebase-summary-title)	
	Common Name		Common Name
-		-	
	Synonyms		Synonyms
Zea mays var. japonica; maize; Zea mays L.; Zea mays mays		Zea mays var. japonica; maize; Zea mays L.; Zea mays mays	
	Rank		Rank
species		species	
	Lineage		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		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		Parent
Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4575)		Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4575)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4577)		4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4577)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		Yes	
			Taxon B Description
		Zea mays - M021A - sensitive	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Zea mays
hm1		O49163 (http://www.uniprot.org/uniprot/O49163)	
	Synonyms		GenebankID or UniProtKB
GRMZM5G881887		AF041043 (https://www.ncbi.nlm.nih.gov/nucleotide/AF041043)	
	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		
-			
			Presumptive Null

Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title)	Molecular Type
Unknown (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Unknown^#gephebase-summary-title)	Aberration Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title)	Molecular Details of the Mutation
Not identified	Experimental Evidence
Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)	Main Reference
Plant-pathogen microevolution: molecular basis for the origin of a fungal disease in maize. (1998) (https://pubmed.ncbi.nlm.nih.gov/9465077)	Authors
Multani DS; Meeley RB; Paterson AH; Gray J; Briggs SP; Johal GS	Abstract
A new and severe disease of maize caused by a previously unknown fungal pathogen, <i>Cochliobolus carbonum</i> race 1, was first described in 1938. The molecular events that led to the sudden appearance of this disease are described in this paper. Resistance to <i>C. carbonum</i> race 1 was found to be widespread in maize and is conferred by a pair of unlinked duplicate genes, Hm1 and Hm2. Here, we demonstrate that resistance is the wild-type condition in maize. Two events, a transposon insertion in Hm1 and a deletion in Hm2, led to the loss of resistance, resulting in the origin of a new disease. None of the other plant species tested is susceptible to <i>C. carbonum</i> race 1, and they all possess candidate genes with high homology to Hm1 and Hm2. In sorghum and rice, these homologs map to two chromosomal regions that are syntenic with the maize Hm1 and Hm2 loci, indicating that they are related to the maize genes by vertical descent. These results suggest that the Hm-encoded resistance is of ancient origin and probably is conserved in all grasses.	
	Additional References

RELATED GEPHE

	Related Genes
5 (HM1 = HC toxin reductase (HCTR) [possible pseudo-replicate from other Maize entry], 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)	Related Haplotypes
No matches found.	

EXTERNAL LINKS

COMMENTS