

GEPHE SUMMARY

	Gephebase Gene	GepheID
HM2 = HC toxin reductase (HCTR) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^HM2+HC+toxin+reductase+(HCTR)^#gephebase-summary-title)	GP00000483	Main curator
	Martin	
Published	Entry Status	

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		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)	
	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)	
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
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		Yes	
			Taxon B Description
		Zea mays - B73 - sensitive	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Zea mays subsp. parviglumis
hm2		B8QWA3 (http://www.uniprot.org/uniprot/B8QWA3)
	Synonyms	GenebankID or UniProtKB
-		AAC04337 (https://www.ncbi.nlm.nih.gov/nuccore/AAC04337)
	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	
-		

Yes (#gephebase-summary-title)	Presumptive Null
Coding (#gephebase-summary-title)	Molecular Type
Insertion (#gephebase-summary-title)	Aberration Type
1-9 bp	Insertion Size
8-bp insertion in exon 1 that disrupt the reading frame and introduces a stop codon shortly after the beginning of the gene	Molecular Details of the Mutation
Candidate Gene (#gephebase-summary-title)	Experimental Evidence
Distinct mechanisms govern the dosage-dependent and developmentally regulated resistance conferred by the maize Hm2 gene. (2008) (https://pubmed.ncbi.nlm.nih.gov/18052885)	Main Reference
Chintamanani S; Multani DS; Ruess H; Johal GS	Authors
The maize Hm2 gene provides protection against the leaf spot and ear mold disease caused by <i>Cochliobolus carbonum</i> 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.	Abstract
	Additional References

RELATED GEPHE

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 Genes
1 (#gephebase-summary-title)	Related Haplotypes

EXTERNAL LINKS

COMMENTS