

GEPHE SUMMARY

Hd1 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+^Hd1+^#gephebase-summary-title)	Gephebase Gene	GP00000441	GepheID
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category+^Physiology+^#gephebase-summary-title)	Trait Category		
Flowering time (https://www.gephebase.org/search-criteria?/and+Trait+^Flowering+time+^#gephebase-summary-title)	Trait		
Oryza sativa - var. japonica Nipponbare	Trait State in Taxon A		
Oryza sativa - var. indica Kasalath	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
Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+^Oryza+sativa+^#gephebase-summary-title)	Latin Name	Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+^Oryza+sativa+^#gephebase-summary-title)	Latin Name
rice	Common Name	rice	Common Name
rice; red rice; Oryza sativa L.	Synonyms	rice; red rice; Oryza sativa L.	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; Oryzinae; Oryza	Lineage	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; Oryzinae; Oryza	Lineage
Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527)	Parent	Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527)	Parent
4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530)	NCBI Taxonomy ID	4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530)	NCBI Taxonomy ID
Yes	is Taxon A an Intraspecies?	Yes	is Taxon B an Intraspecies?
Oryza sativa - var. japonica Nipponbare	Taxon A Description	Oryza sativa - var. indica Kasalath	Taxon B Description

GENOTYPIC CHANGE

HD1	Generic Gene Name	UniProtKB Oryza sativa subsp. japonica Q9FDX8 (http://www.uniprot.org/uniprot/Q9FDX8)
Hd1; SE1; OsHd1; Os06g0275000; LOC_Os06g16370; P0038C05.23; P0676F10.34	Synonyms	GenebankID or UniProtKB AFK31549 (https://www.ncbi.nlm.nih.gov/nucleotide/AFK31549)
39947.LOC_Os06g16370.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=39947.LOC_Os06g16370.1)	String	
Belongs to the CONSTANS family.	Sequence Similarities	
GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)	GO - Molecular Function	
GO:0008270 : zinc ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008270)		
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)		
	GO - Biological Process	

GO:0030154 : cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030154>)
GO:0045892 : negative regulation of transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045892>)
GO:0009908 : flower development (<https://www.ebi.ac.uk/QuickGO/term/GO:0009908>)
GO:0009909 : regulation of flower development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009909>)
GO:0048579 : negative regulation of long-day photoperiodism, flowering
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048579>)
GO:0048571 : long-day photoperiodism
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048571>)
GO:0048576 : positive regulation of short-day photoperiodism, flowering
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048576>)
GO:0048572 : short-day photoperiodism
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048572>)

GO - Cellular Component

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

Presumptive Null

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))

Molecular Type

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))

Aberration Type

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

Deletion Size

1-9 bp

Molecular Details of the Mutation

2bp deletion in the putative exon 2

Experimental Evidence

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))

Main Reference

Hd1, a major photoperiod sensitivity quantitative trait locus in rice, is closely related to the Arabidopsis flowering time gene CONSTANS. (2000) (<https://pubmed.ncbi.nlm.nih.gov/11148291>)

Authors

Yano M; Katayose Y; Ashikari M; Yamanouchi U; Monna L; Fuse T; Baba T; Yamamoto K; Umehara Y; Nagamura Y; Sasaki T

Abstract

A major quantitative trait locus (QTL) controlling response to photoperiod, Hd1, was identified by means of a map-based cloning strategy. High-resolution mapping using 1505 segregants enabled us to define a genomic region of approximately 12 kb as a candidate for Hd1. Further analysis revealed that the Hd1 QTL corresponds to a gene that is a homolog of CONSTANS in Arabidopsis. Sequencing analysis revealed a 43-bp deletion in the first exon of the photoperiod sensitivity 1 (se1) mutant HS66 and a 433-bp insertion in the intron in mutant HS110. Se1 is allelic to the Hd1 QTL, as determined by analysis of two se1 mutants, HS66 and HS110. Genetic complementation analysis proved the function of the candidate gene. The amount of Hd1 mRNA was not greatly affected by a change in length of the photoperiod. We suggest that Hd1 functions in the promotion of heading under short-day conditions and in inhibition under long-day conditions.

Additional References

Variations in Hd1 proteins, Hd3a promoters, and Ehd1 expression levels contribute to diversity of flowering time in cultivated rice. (2009) (<https://pubmed.ncbi.nlm.nih.gov/19246394>)

RELATED GEPHE

Related Genes

9 (DTH2, EARLY FLOWERING 3/Hd17, Hd6a, PRR37 pseudoresponse regulator protein 37, se5, Early flowering1 (EL1), HEADING DATE 1, Ehd1 (Response regulator), Ghd7)
([https://www.gephebase.org/search-criteria?/or+Taxon ID=~4530^/and+Trait=Flowering time/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=~4530^/and+Trait=Flowering+time/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

5 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~Hd1^/and+Taxon ID=~4530^/or+Gene Gephebase=~Hd1^/and+Taxon ID=~4530^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=~Hd1^/and+Taxon+ID=~4530^/or+Gene+Gephebase=~Hd1^/and+Taxon+ID=~4530^#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS