

GEPHE SUMMARY

	Gephebase Gene		GepheID
Heading Date 1 (HD1) (https://www.gephebase.org/search-criteria?/and+Gene)		GP00001410	
Gephebase=^Heading Date 1 (HD1)^#gephebase-summary-title)			Main curator
	Entry Status	Prigent	
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+Trait)			
Category=^Physiology^#gephebase-summary-title)	Trait		
Flowering time (https://www.gephebase.org/search-criteria?/and+Trait=^Flowering)			
time^#gephebase-summary-title)	Trait State in Taxon A		
foxtail millet wild type	Trait State in Taxon B		
Domesticated foxtail millet with delayed flowering time	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
Setaria italica		Setaria italica	
(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Setaria		(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Setaria	
italica^#gephebase-summary-title)	Common Name	italica^#gephebase-summary-title)	Common Name
foxtail millet		foxtail millet	
	Synonyms		Synonyms
Chaetochloa italica; Panicum italicum; Setaria viridis subsp. italica; foxtail millet; Chaetochloa		Chaetochloa italica; Panicum italicum; Setaria viridis subsp. italica; foxtail millet; Chaetochloa	
italica (L.) Scribn.; Panicum italicum L.; Setaria italica (L.) P.Beauv.; Setaria viridis subsp.		italica (L.) Scribn.; Panicum italicum L.; Setaria italica (L.) P.Beauv.; Setaria viridis subsp.	
italica (L.) Briq.	Rank	italica (L.) Briq.	Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta;		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta;	
Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae;		Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae;	
Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae;		Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae;	
Panicodae; Paniceae; Cenchrinae; Setaria	Parent	Panicodae; Paniceae; Cenchrinae; Setaria	Parent
Setaria () - (Rank: genus)		Setaria () - (Rank: genus)	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4554)	NCBI Taxonomy ID	(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4554)	NCBI Taxonomy ID
4555		4555	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4555)	is Taxon A an Intraspecies?	(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4555)	is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Arabidopsis thaliana
CO		Q39057 (http://www.uniprot.org/uniprot/Q39057)	
	Synonyms		GenebankID or UniProtKB
B-box domain protein 1; BBX1; CONSTANS; F14F8.220; F14F8_220; FG; At5g15840		AB807720 (https://www.ncbi.nlm.nih.gov/nucleotide/AB807720)	
	String		
3702.AT5G15840.1			
(http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT5G15840.1			
)	Sequence Similarities		
Belongs to the CONSTANS family.			
	GO - Molecular Function		
GO:0003700 : DNA-binding transcription factor activity			
(https://www.ebi.ac.uk/QuickGO/term/GO:0003700)			
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: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:0010218 : response to far red light
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010218>)
GO:0010018 : far-red light signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010018>)

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

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

SNP Coding Change

-

Molecular Details of the Mutation

splicing variant at position 787 GT>AT resulting in a splicing shift to position 754 introducing a deletion of 33 bp in the transcript and 11 aa in the protein

Experimental Evidence

Association Mapping ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Association Mapping^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Association+Mapping^#gephebase-summary-title))

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Parallel Domestication of the Heading Date 1 Gene in Cereals. (2015) (<https://pubmed.ncbi.nlm.nih.gov/26116860>)

Authors

Liu H; Liu H; Zhou L; Zhang Z; Zhang X; Wang M; Li H; Lin Z

Abstract

Flowering time is one of the key determinants of crop adaptation to local environments during domestication. However, the genetic basis underlying flowering time is yet to be elucidated in most cereals. Although staple cereals, such as rice, maize, wheat, barley, and sorghum, have spread and adapted to a wide range of ecological environments during domestication, it is yet to be determined whether they have a common genetic basis for flowering time. In this study, we show, through map-based cloning, that flowering time in sorghum is controlled by a major quantitative trait locus (QTL) Heading Date 1 (HD1), located on chromosome 10. The causal gene encodes the CONSTANS gene family which contains a CCT domain. A 5-bp deletion of a minor allele present in the coding sequence leads to a gene frameshift that delays flowering in sorghum. In contrast, in foxtail millet, association mapping of HD1 showed a common causal site with a splicing variant from "GT" to "AT" that was highly correlated with flowering time. In addition, the rice HD1 gene is known to harbor several causal variants controlling flowering time. These data indicate that the major flowering time QTL HD1 was under parallel domestication in sorghum, foxtail millet, and rice. The pattern of common mixed minor, or even rare, causal alleles in HD1 across different species may be representative of the genetic basis of the domestication syndrome. Furthermore, large DNA sequence analysis of HD1 revealed multiple origins for domesticated sorghum and a single origin for domesticated foxtail millet.

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Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

@Splicing

