GEPHE SUMMARY

Gephebase Gene
Heading Date 1 (HD1) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Heading Date 1 (HD1)^#gephebase-summary-title)

GepheID
GP00001408

Entry Status
Published

Main curator
Prigent

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
early flowering Domesticated sorghum line TX623

Trait State in Taxon B
Late flowering wild sorghum & Domesticated sorghum from Ethiopia Yemen Germany & China

Ancestral State
Taxon A

Taxonomic Status
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)

Taxon A

Latin Name
Sorghum bicolor (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Sorghum bicolor^#gephebase-summary-title)

Common Name
sorghum

Synonyms
Andropogon sorghum; Sorghum bicolor subsp. bicolor; Sorghum nervosum; Sorghum saccharatum; Sorghum vulgare; sorghum; broomcorn; milo; Andropogon sorghum (L.) Brot.; Sorghum bicolor (L.) Moench; Sorghum nervosum Besser ex Schult.; Sorghum saccharatum (L.) Moench; Sorghum vulgare Pers.; Sorghum bicolor milo; Sorghum_bicolor

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliopsida; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Sorghinae; Sorghum

Parent
Sorghum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4557)

NCBI Taxonomy ID
4558 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4558)

is Taxon A an Infraspecies?
Yes

Taxon A Description
early flowering Domesticated sorghum line TX623

Taxon B

Latin Name
Sorghum virgatum (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Sorghum virgatum^#gephebase-summary-title)

Common Name
-

Synonyms
Sorghum bicolor var. virgatum; Sorghum bicolor var. virgatum (Hack.) de Wet & Huckabay, nom. inval.; Sorghum virgatum (Hack.) Stapf

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Sorghinae; Sorghum

Parent
Sorghum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4557)

NCBI Taxonomy ID
1428165 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1428165)

is Taxon B an Infraspecies?
Yes

Taxon B Description
Late flowering wild sorghum & Domesticated sorghum from Ethiopia Yemen Germany & China

GENOTYPIC CHANGE

Generic Gene Name
CO

Synonyms
B-box domain protein 1; BBX1; CONSTANS; F14F8.220; F14F8_220; FG; At5g15840

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

UniProtKB Arabidopsis thaliana
Q39057 (http://www.uniprot.org/uniprot/Q39057)

GenebankID or UniProtKB
()

(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)

Molecular Type

Coding (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)

Deletion Size

1-9 bp

Molecular Details of the Mutation

5bp deletion in the coding sequence leading to gene frameshift

Experimental Evidence

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

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

Related Genes

1 (PRR37 pseudoresponse regulator protein 37) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^4558^/and+Trait=Flowering time/or+Taxon ID=^1428165^/and+Trait=Flowering time/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

it is unclear in which allele is the mutation and paper is confusing wether wild type is early or late flowering