GEPHE SUMMARY

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

GepheID
GP00001674

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 (latitudinal adaptation) (https://www.gephebase.org/search-criteria?/and+Trait=^Flowering time (latitudinal adaptation)^#gephebase-summary-title)

Trait State in Taxon A
Nipponbare (NB) japonica cultivar

Trait State in Taxon B
Erythroceros Hokkaido (EH) temperate japonica variety from Poland

Ancestral State
Taxon A

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

Taxon A

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

Common Name
rice

Synonyms
rice; red rice; Oryza sativa L.

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza

Parent
Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527)

NCBI Taxonomy ID
4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530)

is Taxon A an Infraspecies?
Yes

Taxon A Description
Nipponbare (NB) japonica cultivar

Taxon B

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

Common Name
Japanese rice

Synonyms
Oryza sativa (japonica cultivar-group); Oryza sativa subsp. japonica; Japanese rice; Japonica rice; Oryza sativa (japonica culticar-group); Oryza sativa japonica; Oryza sativa ssp. japonica

Rank
no rank

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza; Oryza sativa

Parent
Oryza sativa (rice) - (Rank: species) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530)

NCBI Taxonomy ID
39947 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 39947)

is Taxon B an Infraspecies?
Yes

Taxon B Description
Erythroceros Hokkaido (EH) temperate japonica variety from Poland

GENOTYPIC CHANGE

Generic Gene Name
HD1

Synonyms
Hd1; SE1; OsHd1; Os06g0275000; LOC_Os06g16370; P0038C05.23; P0676F10.34

String
39947.LOC_Os06g16370.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=39947.LOC_Os06g16370.1)

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)

UniProtKB Oryza sativa subsp. japonica
Q9FDX8 (http://www.uniprot.org/uniprot/Q9FDX8)

GenebankID or UniProtKB
AB300057.1 (https://www.ncbi.nlm.nih.gov/nuccore/AB300057.1)

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)

Molecular Type

Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title)

Aberration Type

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

Insertion Size

10-100 kb

Molecular Details of the Mutation

Hd1(EH) allele with a 4.4 kb mobile element inserted at position -166pb that suppressed gene transcription

Experimental Evidence

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

Main Reference

Transcriptional and Post-transcriptional Mechanisms Limit Heading Date 1 (Hd1) Function to Adapt Rice to High Latitudes. (2017) (https://pubmed.ncbi.nlm.nih.gov/28068345)

Authors

Goretti D; Martignago D; Landini M; Brambilla V; GÃ³mez-Ariza J; Gnesutta N; Galbiati F; Collani S; Takagi H; Terauchi R; Mantovani R; Fornara F

Abstract

Rice flowering is controlled by changes in the photoperiod that promote the transition to the reproductive phase as days become shorter. Natural genetic variation for flowering time has been largely documented and has been instrumental to define the genetics of the photoperiodic pathway, as well as providing valuable material for artificial selection of varieties better adapted to local environments. We mined genetic variation in a collection of rice varieties highly adapted to European regions and isolated distinct variants of the long day repressor HEADING DATE 1 (Hd1) that perturb its expression or protein function. Specific variants allowed us to define novel features of the photoperiodic flowering pathway. We demonstrate that a histone fold domain scaffold formed by GRAIN YIELD, PLANT HEIGHT AND HEADING DATE 8 (Ghd8) and several NF-YC subunits can accommodate distinct proteins, including Hd1 and PSEUDO RESPONSE REGULATOR 37 (PRR37), and that the resulting OsNF-Y complex containing Hd1 can bind a specific sequence in the promoter of HEADING DATE 3A (Hd3a). Artificial selection has locally favored an Hd1 variant unable to assemble in such heterotrimeric complex. The causal polymorphism was defined as a single conserved lysine in the CCT domain of the Hd1 protein. Our results indicate how genetic variation can be stratified and explored at multiple levels, and how its description can contribute to the molecular understanding of basic developmental processes.

Additional References

RELATED GEPHE

Related Genes

9 (DTH2, EARLY FLOWERING 3/Hd17, Hd1, Hd6a, PRR37 pseudoresponse regulator protein 37, se5, Early flowering1 (EL1), Ehd1 (Response regulator), Ghd7) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^4530^/and+Trait=Flowering time/or+Taxon ID=^39947^/and+Trait=Flowering time/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

null mutation