

## GEPHE SUMMARY

**Gephebase Gene**  
HEADING DATE 1

**Entry Status**  
Published

**GepheID**  
GP00001674

**Main curator**  
Prigent

## PHENOTYPIC CHANGE

**Trait Category**  
Physiology

**Trait**  
Flowering time (latitudinal adaptation)

**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

### Taxon A

**Latin Name**  
*Oryza sativa*

**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)

**NCBI Taxonomy ID**  
4530

**is Taxon A an Intraspecies?**  
Yes

**Taxon A Description**  
Nipponbare (NB) japonica cultivar

### Taxon B

**Latin Name**  
*Oryza sativa Japonica Group*

**Common Name**  
Japanese rice

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

**NCBI Taxonomy ID**  
39947

**is Taxon B an Intraspecies?**  
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

**Sequence Similarities**  
Belongs to the CONSTANS family.

**GO - Molecular Function**  
GO:0003700 : DNA-binding transcription factor activity  
GO:0008270 : zinc ion binding  
GO:0003677 : DNA binding

**GO - Biological Process**  
GO:0030154 : cell differentiation  
GO:0045892 : negative regulation of transcription, DNA-templated  
GO:0009908 : flower development

**UniProtKB** *Oryza sativa* subsp. japonica  
Q9FDX8

**GenebankID or UniProtKB**  
AB300057.1

GO:0009909 : regulation of flower development  
GO:0048579 : negative regulation of long-day photoperiodism, flowering  
GO:0048571 : long-day photoperiodism  
GO:0048576 : positive regulation of short-day photoperiodism, flowering  
GO:0048572 : short-day photoperiodism

GO - Cellular Component  
GO:0005634 : nucleus

Presumptive Null  
Yes

Molecular Type  
Cis-regulatory

Aberration Type  
Insertion

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

Main Reference  
Transcriptional and Post-transcriptional Mechanisms Limit Heading Date 1 (Hd1) Function to Adapt Rice to High Latitudes. (2017)

Authors  
Goretti D; Martignago D; Landini M; Brambilla V; GÃmez-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)  
Related Haplotypes  
No matches found.

## COMMENTS

null mutation