GEPHE SUMMARY

Gephebase Gene

Flowering locus T (LpFT3) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Flowering locus T (LpFT3)^#gephebase-summary-title)

GepheID

GP00000347

Entry Status

Published

Main curator

Martin

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

Lolium perenne

Trait State in Taxon B

Lolium perenne

Ancestral State

Data not curated

Taxonomic Status

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

Taxon A

Latin Name

Lolium perenne (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Lolium perenne^#gephebase-summary-title)

Common Name

-

Synonyms

Festuca perennis; Festuca perennis (L.) Columbus & J.P.Sm., 2010; Lolium vulgare; perennial ryegrass; Lolium perenne L., 1753; Lolium vulgare Host, 1801

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Poodae; Poeae; Poeae Chloroplast Group 2 (Poeae type); Loliinae; Lolium

Parent

Lolium () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4520)

NCBI Taxonomy ID

4522 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4522)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Lolium perenne (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Lolium perenne^#gephebase-summary-title)

Common Name

-

Synonyms

Festuca perennis; Festuca perennis (L.) Columbus & J.P.Sm., 2010; Lolium vulgare; perennial ryegrass; Lolium perenne L., 1753; Lolium vulgare Host, 1801

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Poodae; Poeae; Poeae Chloroplast Group 2 (Poeae type); Loliinae; Lolium

Parent

Lolium () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4520)

NCBI Taxonomy ID

4522 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4522)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

FT

Synonyms

F5I14.3; F5I14_3; FLOWERING LOCUS T; REDUCED STEM BRANCHING 8; RSB8; At1g65480

String

3702.AT1G65480.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT1G65480.1)

Sequence Similarities

Belongs to the phosphatidylethanolamine-binding protein family.

GO - Molecular Function

GO:0008429 : phosphatidylethanolamine binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008429)

GO - Biological Process

GO:0030154 : cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0030154)
GO:0009911 : positive regulation of flower development

UniProtKB Arabidopsis thaliana

Q9SXZ2 (http://www.uniprot.org/uniprot/Q9SXZ2)

GenebankID or UniProtKB

CBN73222 (https://www.ncbi.nlm.nih.gov/nuccore/CBN73222)

(https://www.ebi.ac.uk/QuickGO/term/GO:0009911)
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:0048573 : photoperiodism, flowering
(https://www.ebi.ac.uk/QuickGO/term/GO:0048573)
GO:0010119 : regulation of stomatal movement
(https://www.ebi.ac.uk/QuickGO/term/GO:0010119)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)
GO:0005783 : endoplasmic reticulum
(https://www.ebi.ac.uk/QuickGO/term/GO:0005783)

Presumptive Null

Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title)

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

unknown

Experimental Evidence

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

Main Reference

Allelic variation in the perennial ryegrass FLOWERING LOCUS T gene is associated with changes in flowering time across a range of populations. (2011)
(https://pubmed.ncbi.nlm.nih.gov/21115808)

Authors

SkÃ¸t L; Sanderson R; Thomas A; SkÃ¸t K; Thorogood D; Latypova G; Asp T; Armstead I

Abstract

The Arabidopsis (Arabidopsis thaliana) FLOWERING LOCUS T (FT) gene and its orthologs in other plant species (e.g. rice [Oryza sativa] OsFTL2/Hd3a) have an established role in the photoperiodic induction of flowering response. The genomic and phenotypic variations associated with the perennial ryegrass (Lolium perenne) ortholog of FT, designated LpFT3, was assessed in a diverse collection of nine European germplasm populations, which together constituted an association panel of 864 plants. Sequencing and genotyping of a series of amplicons derived from the nine populations, containing the complete exon and intron sequences as well as 5′ and 3′ noncoding sequences of LpFT3, identified a total of seven haplotypes. Genotyping assays designed to detect the genomic variation showed that three haplotypes were present in approximately equal proportions and represented 84% of the total, with a fourth representing a further 11%. Of the three major haplotypes, two were predicted to code for identical protein products and the third contained two amino acid substitutions. Association analysis using either a mixed model with a relationship matrix to correct for population structure and relatedness or structured association with further correction using genomic control indicated significant associations between LpFT3 and variation in flowering time. These associations were corroborated in a validation population segregating for the same major alleles. The most "diagnostic" region of genomic variation was situated 5′ of the coding sequence. Analysis of this region identified that the interhaplotype variation was closely associated with sequence motifs that were apparently conserved in the 5′ region of orthologs of LpFT3 from other plant species. These may represent cis-regulatory elements involved in influencing the expression of this gene.

Additional References

RELATED GEPHE

Related Genes

1 (VRN1) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^4522^/and+Trait=Flowering time/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS