GEPHE SUMMARY

Gephebase Gene
EARLY FLOWERING 3(ELF3) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^EARLY FLOWERING 3(ELF3)^#gephebase-summary-title)

GepheID
GP00001683

Entry Status
Published

Main curator
Courtier

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
Glycine max

Trait State in Taxon B
LJ trait - LJ soybean varieties flower much later than temperate varieties under inductive short-day conditions and also show delayed maturity; leading to improvements in plant height; node number; lodging degree; grain yield; and other important agronomic characteristics in the field at low latitudes

Ancestral State
Taxon A

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

Taxon A

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

Common Name
soybean

Synonyms
soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae; 50 kb inversion clade; NPAAA clade; indigoferoid/millettioid clade; Phaseoleae; Glycine; Soja

Parent
Soja () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1462606)

NCBI Taxonomy ID
3847 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3847)

is Taxon A an Infraspecies?
No

Taxon B

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

Common Name
soybean

Synonyms
soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae; 50 kb inversion clade; NPAAA clade; indigoferoid/millettioid clade; Phaseoleae; Glycine; Soja

Parent
Soja () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1462606)

NCBI Taxonomy ID
3847 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3847)

is Taxon B an Infraspecies?
Yes

Taxon B Description
LJ soybean

GENOTYPIC CHANGE

Generic Gene Name
CYP75B1

Synonyms
CYP75B1; CYTOCHROME P450 75B1; D501; F13G24.190; F13G24_190; F3′H; FLAVONOID 3′-HYDROXYLASE; TRANSPARENT TESTA 7; TT7; At5g07990

String
3702.AT5G07990.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT5G07990.1)

Sequence Similarities
Belongs to the cytochrome P450 family.

GO - Molecular Function

UniProtKB Arabidopsis thaliana
Q9SD85 (http://www.uniprot.org/uniprot/Q9SD85)

GenebankID or UniProtKB
()

GO:0020037 : heme binding (https://www.ebi.ac.uk/QuickGO/term/GO:0020037)
GO:0005506 : iron ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005506)
GO:0016709 : oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen (https://www.ebi.ac.uk/QuickGO/term/GO:0016709)

GO - Biological Process

GO:0009733 : response to auxin (https://www.ebi.ac.uk/QuickGO/term/GO:0009733)
GO:0009813 : flavonoid biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0009813)

GO - Cellular Component

GO:0016021 : integral component of membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
GO:0016020 : membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016020)
GO:0005789 : endoplasmic reticulum membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005789)

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

10-99 bp

Molecular Details of the Mutation

recessive allele responsible for the LJ trait - 10-bp deletion predicted to cause a frameshift resulting in premature termination of translation after 195 amino acids in the 714-amino-acid protein

Experimental Evidence

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

Main Reference

Natural variation at the soybean J locus improves adaptation to the tropics and enhances yield. (2017) (https://pubmed.ncbi.nlm.nih.gov/28319089)

Authors

Lu S; Zhao X; Hu Y; Liu S; Nan H; Li X; Fang C; Cao D; Shi X; Kong L; Su T; Zhang F; Li S; Wang Z; Yuan X; Cober ER; Weller JL; Liu B; Hou X; Tian Z; Kong F

Abstract

Soybean is a major legume crop originating in temperate regions, and photoperiod responsiveness is a key factor in its latitudinal adaptation. Varieties from temperate regions introduced to lower latitudes mature early and have extremely low grain yields. Introduction of the long-juvenile (LJ) trait extends the vegetative phase and improves yield under short-day conditions, thereby enabling expansion of cultivation in tropical regions. Here we report the cloning and characterization of J, the major classical locus conferring the LJ trait, and identify J as the ortholog of Arabidopsis thaliana EARLY FLOWERING 3 (ELF3). J depends genetically on the legume-specific flowering repressor E1, and J protein physically associates with the E1 promoter to downregulate its transcription, relieving repression of two important FLOWERING LOCUS T (FT) genes and promoting flowering under short days. Our findings identify an important new component in flowering-time control in soybean and provide new insight into soybean adaptation to tropical regions.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS