GEPHE SUMMARY

Gephebase Gene
TFL1/GmTFL1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^TFL1/GmTFL1^#gephebase-summary-title)

GepheID
GP00001123

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
Growth determination habit (https://www.gephebase.org/search-criteria?/and+Trait=^Growth determination habit^#gephebase-summary-title)

Trait State in Taxon A
Glycine max; Glycine soja

Trait State in Taxon B
Glycine max (determinate growth habit)

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
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?
No

GENOTYPIC CHANGE

Generic Gene Name
TFL1

Synonyms
MED24.6; TERMINAL FLOWER 1; TFL-1; At5g03840; F8F6_50

String
3702.AT5G03840.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT5G03840.1)

Sequence Similarities
Belongs to the phosphatidylethanolamine-binding protein family.

GO - Molecular Function
GO:0003712 : transcription coregulator activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003712)

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:0009910 : negative regulation of flower development

UniProtKB Arabidopsis thaliana
P93003 (http://www.uniprot.org/uniprot/P93003)

GenebankID or UniProtKB
ABS57463 (https://www.ncbi.nlm.nih.gov/nuccore/ABS57463)

(https://www.ebi.ac.uk/QuickGO/term/GO:0009910)
GO:0009744 : response to sucrose (https://www.ebi.ac.uk/QuickGO/term/GO:0009744)
GO:0090344 : negative regulation of cell aging
(https://www.ebi.ac.uk/QuickGO/term/GO:0090344)
GO:0006623 : protein targeting to vacuole
(https://www.ebi.ac.uk/QuickGO/term/GO:0006623)

GO - Cellular Component

GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
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:0031982 : vesicle (https://www.ebi.ac.uk/QuickGO/term/GO:0031982)
GO:0005773 : vacuole (https://www.ebi.ac.uk/QuickGO/term/GO:0005773)

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

R130K

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Artificial selection for determinate growth habit in soybean. (2010) (https://pubmed.ncbi.nlm.nih.gov/20421496)

Authors

Tian Z; Wang X; Lee R; Li Y; Specht JE; Nelson RL; McClean PE; Qiu L; Ma J

Abstract

Determinacy is an agronomically important trait associated with the domestication in soybean (Glycine max). Most soybean cultivars are classifiable into indeterminate and determinate growth habit, whereas Glycine soja, the wild progenitor of soybean, is indeterminate. Indeterminate (Dt1/Dt1) and determinate (dt1/dt1) genotypes, when mated, produce progeny that segregate in a monogenic pattern. Here, we show evidence that Dt1 is a homolog (designated as GmTfl1) of Arabidopsis terminal flower 1 (TFL1), a regulatory gene encoding a signaling protein of shoot meristems. The transition from indeterminate to determinate phenotypes in soybean is associated with independent human selections of four distinct single-nucleotide substitutions in the GmTfl1 gene, each of which led to a single amino acid change. Genetic diversity of a minicore collection of Chinese soybean landraces assessed by simple sequence repeat (SSR) markers and allelic variation at the GmTfl1 locus suggest that human selection for determinacy took place at early stages of landrace radiation. The GmTfl1 allele introduced into a determinate-type (tfl1/tfl1) Arabidopsis mutants fully restored the wild-type (TFL1/TFL1) phenotype, but the Gmtfl1 allele in tfl1/tfl1 mutants did not result in apparent phenotypic change. These observations indicate that GmTfl1 complements the functions of TFL1 in Arabidopsis. However, the GmTfl1 homeolog, despite its more recent divergence from GmTfl1 than from Arabidopsis TFL1, appears to be sub- or neo-functionalized, as revealed by the differential expression of the two genes at multiple plant developmental stages and by allelic analysis at both loci.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

3 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^TFL1/GmTFL1^/and+Taxon ID=^3847^/or+Gene Gephebase=^TFL1/GmTFL1^/and+Taxon ID=^3847^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS