

GEPHE SUMMARY

	Gephebase Gene		GepheID
TFL1/GmTFL1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~TFL1/GmTFL1~#gephebase-summary-title)		GP00001122	
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~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+TaxonomicStatus=~Domesticated~#gephebase-summary-title)			
Taxon A		Taxon B	
	Latin Name		Latin Name
Glycine max (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Glycine+max~#gephebase-summary-title)		Glycine max (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Glycine+max~#gephebase-summary-title)	
	Common Name		Common Name
soybean		soybean	
	Synonyms		Synonyms
soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye		soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye	
	Rank		Rank
species		species	
	Lineage		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		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		Parent
Soja () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1462606)		Soja () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1462606)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
3847 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3847)		3847 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3847)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Arabidopsis thaliana
TFL1		P93003 (http://www.uniprot.org/uniprot/P93003)	
	Synonyms		GenebankID or UniProtKB
MED24.6; TERMINAL FLOWER 1; TFL-1; At5g03840; F8F6_50		ABS57463 (https://www.ncbi.nlm.nih.gov/nuccore/ABS57463)	
	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			

(<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

P113L

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

