

## GEPHE SUMMARY

**Gephebase Gene**  
Flowering locus T (FT1)

**Entry Status**  
Published

**GepheID**  
GP00000346

**Main curator**  
Martin

## PHENOTYPIC CHANGE

**Trait Category**  
Physiology

**Trait**  
Flowering time

**Trait State in Taxon A**  
Helianthus annuus

**Trait State in Taxon B**  
Helianthus annuus

**Ancestral State**  
Taxon A

**Taxonomic Status**  
Domesticated

	Taxon A
<b>Latin Name</b>	<i>Helianthus annuus</i>
<b>Common Name</b>	common sunflower
<b>Synonyms</b>	common sunflower; Helianthus annuus L.; Helianthus annua; Helianthus annus; Helianthus annuus8
<b>Rank</b>	species
<b>Lineage</b>	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae alliance; Heliantheae; Helianthus
<b>Parent</b>	Helianthus () - (Rank: genus)
<b>NCBI Taxonomy ID</b>	4232
<b>is Taxon A an Intraspecies?</b>	No

	Taxon B
<b>Latin Name</b>	<i>Helianthus annuus</i>
<b>Common Name</b>	common sunflower
<b>Synonyms</b>	common sunflower; Helianthus annuus L.; Helianthus annua; Helianthus annus; Helianthus annuus8
<b>Rank</b>	species
<b>Lineage</b>	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae alliance; Heliantheae; Helianthus
<b>Parent</b>	Helianthus () - (Rank: genus)
<b>NCBI Taxonomy ID</b>	4232
<b>is Taxon B an Intraspecies?</b>	No

## GENOTYPIC CHANGE

**Generic Gene Name**  
FT

**Synonyms**  
F5l14.3; F5l14\_3; FLOWERING LOCUS T; REDUCED STEM BRANCHING 8; RSB8; At1g65480

**String**  
3702.AT1G65480.1

**Sequence Similarities**  
Belongs to the phosphatidylethanolamine-binding protein family.

**GO - Molecular Function**  
GO:0008429 : phosphatidylethanolamine binding

**GO - Biological Process**  
GO:0030154 : cell differentiation  
GO:0009911 : positive regulation of flower development  
GO:0009908 : flower development  
GO:0009909 : regulation of flower development  
GO:0048573 : photoperiodism, flowering  
GO:0010119 : regulation of stomatal movement

**UniProtKB Arabidopsis thaliana**  
Q9SXZ2

**GenebankID or UniProtKB**  
AEN70128

GO - Cellular Component  
GO:0005737 : cytoplasm  
GO:0005634 : nucleus  
GO:0005783 : endoplasmic reticulum

**Presumptive Null**

Yes

**Molecular Type**

Coding

**Aberration Type**

Deletion

**Deletion Size**

1-9 bp

**Molecular Details of the Mutation**

1bp deletion; frameshift

**Experimental Evidence**

Linkage Mapping

**Main Reference**

The role of recently derived FT paralogs in sunflower domestication. (2010)

**Authors**

Blackman BK; Strasburg JL; Raduski AR; Michaels SD; Rieseberg LH

**Abstract**

Gene duplication provides an important source of genetic raw material for phenotypic diversification, but few studies have detailed the mechanisms through which duplications produce evolutionary novelty within species. Here, we investigate how a set of recently duplicated homologs of the floral inducer FLOWERING LOCUS T (FT) has contributed to sunflower domestication. We find that changes in expression of these duplicates are associated with differences in flowering behavior between wild and domesticated sunflower. In addition, we present genetic and functional evidence demonstrating that a frameshift mutation in one paralog, *Helianthus annuus* FT 1 (HaFT1), underlies a major QTL for flowering time and experienced a selective sweep during early domestication. Notably, this dominant-negative allele delays flowering through interference with action of another paralog, HaFT4. Together, these data reveal that changes affecting the expression, sequence, and gene interactions of HaFT paralogs have played key roles during sunflower domestication. Our findings also illustrate the important role that evolving interactions between new gene family members may play in fostering phenotypic change.

**Additional References**

**RELATED GEPHE**

**Related Genes**

No matches found.

**Related Haplotypes**

No matches found.

**COMMENTS**