

## GEPHE SUMMARY

	Gephebase Gene	GephelD
zf2 ( <a href="https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^zf2">#gephebase-summary-title)</a>	GP00001226	Main curator
	Entry Status	Martin
Published		

## PHENOTYPIC CHANGE

	Trait Category		
Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology">#gephebase-summary-title)</a>		Trait	
Flowering time ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=^Flowering time">#gephebase-summary-title)</a>		Trait State in Taxon A	
Zea mays		Trait State in Taxon B	
Zea mays -Ky21		Ancestral State	
Taxon A		Taxonomic Status	
Domesticated ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated">#gephebase-summary-title)</a>			
Taxon A	Latin Name	Taxon B	Latin Name
Zea mays ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Zea mays">#gephebase-summary-title)</a>		Zea mays ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Zea mays">#gephebase-summary-title)</a>	
-	Common Name	-	Common Name
Zea mays var. japonica; maize; Zea mays L.; Zea mays mays species	Synonyms	Zea mays var. japonica; maize; Zea mays L.; Zea mays mays species	Synonyms
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea	Rank	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea	Rank
Zea () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4575">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4575</a> )	Lineage	Zea () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4575">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4575</a> )	Lineage
4577 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4577">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4577</a> )	Parent	4577 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4577">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4577</a> )	Parent
No	NCBI Taxonomy ID	is Taxon A an Infraspecies?	NCBI Taxonomy ID
		Yes	is Taxon B an Infraspecies?
		Zea mays -Ky21	Taxon B Description

## GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Zea mays
zf2		Q5Q1L6 ( <a href="http://www.uniprot.org/uniprot/Q5Q1L6">http://www.uniprot.org/uniprot/Q5Q1L6</a> )
-	Synonyms	GenebankID or UniProtKB
-	String	AY789022 ( <a href="https://www.ncbi.nlm.nih.gov/nuccore/AY789022">https://www.ncbi.nlm.nih.gov/nuccore/AY789022</a> )
-	Sequence Similarities	
	GO - Molecular Function	
GO:0003677 : DNA binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0003677">https://www.ebi.ac.uk/QuickGO/term/GO:0003677</a> )	GO - Biological Process	
GO:0006355 : regulation of transcription, DNA-templated ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0006355">https://www.ebi.ac.uk/QuickGO/term/GO:0006355</a> )	GO - Cellular Component	
-		Presumptive Null

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

Molecular Type

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

Aberration Type

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

Deletion Size

10-99 bp

Molecular Details of the Mutation

16a.a. deletion

Experimental Evidence

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

Main Reference

The genetic architecture of maize flowering time. (2009) (<https://pubmed.ncbi.nlm.nih.gov/19661422>)

Authors

Buckler ES; Holland JB; Bradbury PJ; Acharya CB; Brown PJ; Browne C; Ersoz E; Flint-Garcia S; Garcia A; Glaubitz JC; Goodman MM; Harjes C; Guill K; Kroon DE; Larsson S; Lepak NK; Li H; Mitchell SE; Pressoir G; Peiffer JA; Rosas MO; Rochefford TR; Romay MC; Romero S; Salvo S; Sanchez Villeda H; da Silva HS; Sun Q; Tian F; Upadyayula N; Ware D; Yates H; Yu J; Zhang Z; Kresovich S; McMullen MD

Abstract

Flowering time is a complex trait that controls adaptation of plants to their local environment in the outcrossing species *Zea mays* (maize). We dissected variation for flowering time with a set of 5000 recombinant inbred lines (maize Nested Association Mapping population, NAM). Nearly a million plants were assayed in eight environments but showed no evidence for any single large-effect quantitative trait loci (QTLs). Instead, we identified evidence for numerous small-effect QTLs shared among families; however, allelic effects differ across founder lines. We identified no individual QTLs at which allelic effects are determined by geographic origin or large effects for epistasis or environmental interactions. Thus, a simple additive model accurately predicts flowering time for maize, in contrast to the genetic architecture observed in the selfing plant species rice and *Arabidopsis*.

Additional References

## RELATED GEPHE

Related Genes

2 (Rap2.7 (vgt1), ZmCCT) ([#gephebase-summary-title\)](https://www.gephebase.org/search-criteria?/or+Taxon ID=^4577/and+Trait=Flowering time/and+groupHaplotypes=true)

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS