

GEPHE SUMMARY

	Gephebase Gene	GephelD
Barren inflorescence2 (BIF2) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Barren inflorescence2 (BIF2)^#gephebase-summary-title)	GP00000135	
	Entry Status	Main curator
Published	Martin	

PHENOTYPIC CHANGE

Trait #1	Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category="Morphology">#gephebase-summary-title)	Trait
Plant architecture (https://www.gephebase.org/search-criteria?/and+Trait=^Plant architecture^#gephebase-summary-title)	Trait State in Taxon A
Zea mays	Trait State in Taxon B
Zea mays	

Trait #2	Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category="Morphology">#gephebase-summary-title)	Trait
Inflorescence architecture (https://www.gephebase.org/search-criteria?/and+Trait=^Inflorescence+architecture #gephebase-summary-title)	Trait State in Taxon A
-	Trait State in Taxon B
-	

Ancestral State		
Taxonomic Status		
Data not curated		
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Domesticated">#gephebase-summary-title)		
Taxon A	Latin Name	Taxon B
Zea mays (#gephebase-summary-title)	Common Name	Latin Name
-	Synonyms	
Zea mays var. japonica; maize; Zea mays L.; Zea mays mays species	Rank	Common Name
-	Lineage	Synonyms
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllphyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonidae; Andropogoneae; Tripsacinae; Zea	Parent	Rank
Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4575)	NCBI Taxonomy ID	Lineage
4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4577)		Parent
	is Taxon A an Infraspecies?	NCBI Taxonomy ID
No		is Taxon B an Infraspecies?

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Zea mays
bif2	Synonyms	GenebankID or UniProtKB
GRMZM2G171822; 100125650; ZEAMMB73_Zm00001d031068	String	EF532402 (https://www.ncbi.nlm.nih.gov/nucore/EF532402)
-	Sequence Similarities	-
-	GO - Molecular Function	-
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)	GO - Biological Process	-
GO:0004674 : protein serine/threonine kinase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004674)	GO - Cellular Component	-
GO:0009908 : flower development (https://www.ebi.ac.uk/QuickGO/term/GO:0009908)	GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)	Presumptive Null
GO:0006468 : protein phosphorylation (https://www.ebi.ac.uk/QuickGO/term/GO:0006468)	GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)	Molecular Type
GO:0048364 : root development (https://www.ebi.ac.uk/QuickGO/term/GO:0048364)	GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)	Aberration Type
Unknown (https://www.gephbase.org/search-criteria?/and+Presumptive Null=%27Unknown%23gephbase-summary-title)	Unknown (https://www.gephbase.org/search-criteria?/and+Molecular Type=%27Unknown%23gephbase-summary-title)	Molecular Details of the Mutation
Unknown (https://www.gephbase.org/search-criteria?/and+Aberration Type=%27Unknown%23gephbase-summary-title)	unknown	Experimental Evidence
Linkage Mapping (https://www.gephbase.org/search-criteria?/and+Experimental Evidence=%27Linkage Mapping%23gephbase-summary-title)	Pressoir G; Brown PJ; Zhu W; Upadyayula N; Rocheford T; Buckler ES; Kresovich S	Main Reference
Natural variation in maize architecture is mediated by allelic differences at the PINOID co-ortholog barren inflorescence2. (2009) (https://pubmed.ncbi.nlm.nih.gov/19154226)	We characterized allelic variation at barren inflorescence2 (bif2), a maize co-ortholog of the <i>Arabidopsis</i> PINOID protein kinase (PID), and tested for trait associations with bif2 in both an association mapping population of 277 diverse maize inbreds and in the inter-mated B73 x Mo17 (IBM) linkage population. Results from the quantitative analyses were compared with previous reports of bif2 phenotypes in mutagenesis studies. All three approaches (association, linkage, and mutagenesis) detect a significant effect of bif2 on tassel architecture. Association mapping implicates bif2 in an unexpectedly wide range of traits including plant height, node number, leaf length, and flowering time. Linkage mapping finds a significant interaction effect for node number between bif2 and other loci, in keeping with previous reports that bif2;spi1 and Bif2;Bif1 double mutants produce fewer phytomers. The Mo17 allele is associated with a reduced tassel branch zone and shows lower expression than the B73 allele in hybrid B73-Mo17 F(1) inflorescences, consistent with the complete absence of tassel branches in the bif2 knockout mutant. Overall, these data suggest that allelic variation at bif2 affects maize architecture by modulating auxin transport during vegetative and inflorescence development.	Authors
The genetic architecture of maize flowering time. (2009) (https://pubmed.ncbi.nlm.nih.gov/19661422)	-	Abstract
-	-	Additional References

RELATED GEPHE

	Related Genes
2 (teosinte branched 1 (tb1), grassy tillers1) (https://www.gephbase.org/search-criteria?/or+Taxon ID=%274577%27/and+Trait=Plant architecture/or+Taxon ID=%274577%27/and+Trait=Inflorescence architecture/and+groupHaplotypes=true#gephbase-summary-title)	Related Haplotypes
No matches found.	-

EXTERNAL LINKS

COMMENTS