

GEPHE SUMMARY

	Gephebase Gene	GepheID
brittle endosperm2 (Bt2) = endosperm ADP-glucose pyrophosphorylase small subunit (#gephebase-summary-title)	GP00000158	
	Martin	Main curator
	Entry Status	
Published		

PHENOTYPIC CHANGE

	Trait Category	
Physiology (#gephebase-summary-title)	Trait	
Sweet and brittle seed (#gephebase-summary-title)	Trait State in Taxon A	
Zea mays - allele Bt2	Trait State in Taxon B	
Zea mays - allele bt2	Ancestral State	
Data not curated	Taxonomic Status	
Domesticated (#gephebase-summary-title)		
	Taxon A	Taxon B
	Latin Name	Latin Name
Zea mays (#gephebase-summary-title)	Zea mays (#gephebase-summary-title)	
	Common Name	Common Name
-	-	
	Synonyms	Synonyms
Zea mays var. japonica; maize; Zea mays L.; Zea mays mays	Zea mays var. japonica; maize; Zea mays L.; Zea mays mays	
	Rank	Rank
species	species	
	Lineage	Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea	
	Parent	Parent
Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4575)	Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4575)	
	NCBI Taxonomy ID	NCBI Taxonomy ID
4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4577)	4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4577)	
	is Taxon A an Intraspecies?	is Taxon B an Intraspecies?
No	No	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Zea mays
bt2	Q84J79 (http://www.uniprot.org/uniprot/Q84J79)	
	Synonyms	GenebankID or UniProtKB
-	CM000780 (https://www.ncbi.nlm.nih.gov/nuccore/CM000780)	
	String	
-		
	Sequence Similarities	
Belongs to the bacterial/plant glucose-1-phosphate adenylyltransferase family.		
	GO - Molecular Function	
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)		
GO:0008878 : glucose-1-phosphate adenylyltransferase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008878)		
	GO - Biological Process	
GO:0019252 : starch biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0019252)		
GO:0005978 : glycogen biosynthetic process		

(<https://www.ebi.ac.uk/QuickGO/term/GO:0005978>)

GO - Cellular Component

GO:0009507 : chloroplast (<https://www.ebi.ac.uk/QuickGO/term/GO:0009507>)

Presumptive Null

Unknown (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Unknown~#gephebase-summary-title>)

Molecular Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Molecular Type=~Unknown~#gephebase-summary-title>)

Aberration Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Aberration Type=~Unknown~#gephebase-summary-title>)

Molecular Details of the Mutation

Not identified

Experimental Evidence

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title>)

Main Reference

Molecular Characterization of the Brittle-2 Gene Effect on Maize Endosperm ADPglucose Pyrophosphorylase Subunits. (1990) (<https://pubmed.ncbi.nlm.nih.gov/16667400>)

Authors

Preiss J; Danner S; Summers PS; Morell M; Barton CR; Yang L; Nieder M

Abstract

Activity of the enzyme ADPglucose pyrophosphorylase is known to be reduced in maize (*Zea mays* L.) endosperm mutants at two independent loci, Shrunk-2 (Sh(2)) and Brittle-2 (Bt(2)). Spinach leaf ADPglucose pyrophosphorylase has previously been shown to comprise two subunits of 51 and 54 kilodaltons. Anti-bodies raised to each of the two subunits of spinach leaf ADPglucose pyrophosphorylase were found to cross-react to different bands on Western blots prepared from polyacrylamide gel electrophoresis separated wild-type maize endosperm proteins. The anti-spinach leaf 51 kilodalton subunit antibody cross-reacted with a 55 kilodalton maize endosperm protein and the anti-spinach leaf 54 kilodalton subunit antibody cross-reacted with a 60 kilodalton maize endosperm protein. These immunological reactions were observed in maize endosperm extracts and with a highly purified preparation of maize endosperm ADPglucose pyrophosphorylase. Mutant bt(2) endosperm lacked the 55 kilodalton subunit while mutant sh(2) endosperm lacked the 60 kilodalton subunit on Western blots. These results suggest that the maize endosperm ADPglucose pyrophosphorylase is made up of two immunologically dissimilar subunits and that the bt(2) and sh(2) mutations cause reduction in ADPglucose pyrophosphorylase activity through the lack of one of these two subunits. An ADPglucose pyrophosphorylase cDNA clone antigenically selected from a rice seed cDNA expression library was found to hybridize strongly with a cDNA corresponding to a maize endosperm transcript which is absent in a W64A bt(2) mutant. Thus, the bt(2) mutant causes the absence not only of the small subunit but of the corresponding transcript. Bt(2) is implicated as the structural gene for the small (54 kilodalton) subunit of maize endosperm ADPglucose pyrophosphorylase.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS