

GEPHE SUMMARY

	Gephebase Gene	GepheID
shrunk-en-2 (Sh2) = endosperm ADP-glucose pyrophosphorylase large subunit (<a +shrunk-en-2+(sh2)+endosperm+adp-glucose+pyrophosphorylase+large+subunit"+#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene Gephebase="shrunk-en-2 (Sh2) = endosperm ADP-glucose pyrophosphorylase large subunit"#gephebase-summary-title)	GP00001050	
	Martin	Main curator
Published	Entry Status	

PHENOTYPIC CHANGE

	Trait Category		
Physiology (<a +physiology"+#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait Category="Physiology"#gephebase-summary-title)		Trait	
Feather (<a +feather"+#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="Feather"#gephebase-summary-title)			
	Trait State in Taxon A		
Zea mays - allele Sh2		Trait State in Taxon B	
Zea mays - allele sh2-m1			
	Ancestral State		
Taxon A		Taxonomic Status	
Domesticated (<a +domesticated"+#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Domesticated"#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Zea mays (<a +zea+mays"+#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Zea mays"#gephebase-summary-title)		Zea mays (<a +zea+mays"+#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="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
SH2		P55241 (http://www.uniprot.org/uniprot/P55241)	
	Synonyms		GenebankID or UniProtKB
shrunk-en-2; GRMZM2G429899		M81603 (https://www.ncbi.nlm.nih.gov/nuccore/M81603)	
	String		
4577.GRMZM2G429899_P01 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4577.GRMZM2G429899_P01)			
	Sequence Similarities		
Belongs to the bacterial/plant glucose-1-phosphate adenyltransferase family.			
	GO - Molecular Function		
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)			
GO:0008878 : glucose-1-phosphate adenyltransferase 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:0009501 : amyloplast (<https://www.ebi.ac.uk/QuickGO/term/GO:0009501>)
GO:0009507 : chloroplast (<https://www.ebi.ac.uk/QuickGO/term/GO:0009507>)

	Presumptive Null
No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title)	
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Cis-regulatory~#gephebase-summary-title)	Molecular Type
Insertion (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Insertion~#gephebase-summary-title)	Aberration Type
1-10 kb	Insertion Size
insertion of the transposable element Dissociation	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title)	Experimental Evidence
Molecular Characterization of the Brittle-2 Gene Effect on Maize Endosperm ADPglucose Pyrophosphorylase Subunits. (1990) (https://pubmed.ncbi.nlm.nih.gov/16667400)	Main Reference
Preiss J; Danner S; Summers PS; Morell M; Barton CR; Yang L; Nieder M	Authors
Activity of the enzyme ADPglucose pyrophosphorylase is known to be reduced in maize (<i>Zea mays</i> L.) endosperm mutants at two independent loci, Shrunken-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.	Abstract
Identification and molecular characterization of shrunken-2 cDNA clones of maize. (1990) (https://pubmed.ncbi.nlm.nih.gov/1967077)	Additional References

RELATED GEPHE

No matches found.	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

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