

GEPHE SUMMARY

sugary 1 (su1) = isoamylase-type starch-debranching enzymes (<a +su1+"isoamylase-type+starch-debranching+enzymes"+gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+su1+"isoamylase-type+starch-debranching+enzymes"+Gephebase-summary-title)	Gephebase Gene	GP00001082	GepheID
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

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 Category		
Fruit sugar content (<a +fruit+sugar+content"+gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Fruit+sugar+content"+Gephebase-summary-title)	Trait		
Zea mays - allele Su1	Trait State in Taxon A		
Zea mays - allele su1-Ref	Trait State in Taxon B		
Data not curated	Ancestral State		
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)	Taxonomic Status		
	Taxon A		Taxon B
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)	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)	Latin Name
-	Common Name	-	Common Name
Zea mays var. japonica; maize; Zea mays L.; Zea mays mays	Synonyms	Zea mays var. japonica; maize; Zea mays L.; Zea mays mays	Synonyms
species	Rank	species	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	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	Lineage
Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4575)	Parent	Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4575)	Parent
4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4577)	NCBI Taxonomy ID	4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4577)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

sugary1	Generic Gene Name	O22637 (http://www.uniprot.org/uniprot/O22637)	UniProtKB Zea mays
su1; sugary1; isoamylase; GRMZM2G138060	Synonyms	CM000780 (https://www.ncbi.nlm.nih.gov/nuccore/CM000780)	GenebankID or UniProtKB
4577.GRMZM2G138060_P01 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4577.GRMZM2G138060_P01)	String		
-	Sequence Similarities		
GO:0004553 : hydrolase activity, hydrolyzing O-glycosyl compounds (https://www.ebi.ac.uk/QuickGO/term/GO:0004553)	GO - Molecular Function		
GO:0005975 : carbohydrate metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0005975)	GO - Biological Process		
	GO - Cellular Component		

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

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

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

Nonsynonymous SNP Coding Change

F163L and/or W578R; W738R is more likely to be the mutation responsible as it affect a residue conserved in plants and bacteria Molecular Details of the Mutation

Candidate Gene (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title>) Experimental Evidence

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Trp	Arg	738

Molecular structure of three mutations at the maize sugary1 locus and their allele-specific phenotypic effects. (2001) (<https://pubmed.ncbi.nlm.nih.gov/11244120>) Main Reference

Dinges JR; Colleoni C; Myers AM; James MG Authors

Starch production in all plants examined is altered by mutations of isoamylase-type starch-debranching enzymes (DBE), although how these proteins affect glucan polymer assembly is not understood. Various allelic mutations in the maize (*Zea mays*) gene sugary1 (*su1*), which codes for an isoamylase-type DBE, condition distinct kernel phenotypes. This study characterized the recessive mutations *su1-Ref*, *su1-R4582::Mu1*, and *su1-st*, regarding their molecular basis, chemical phenotypes, and effects on starch metabolizing enzymes. The *su1-Ref* allele results in two specific amino acid substitutions without affecting the *Su1* mRNA level. The *su1-R4582::Mu1* mutation is a null allele that abolishes transcript accumulation. The *su1-st* mutation results from insertion of a novel transposon-like sequence, designated *Toad*, which causes alternative pre-mRNA splicing. Three *su1-st* mutant transcripts are produced, one that is nonfunctional and two that code for modified *SU1* polypeptides. The *su1-st* mutation is dominant to the null allele *su1-R4582::Mu1*, but recessive to *su1-Ref*, suggestive of complex effects involving quaternary structure of the *SU1* enzyme. All three *su1*- alleles severely reduce or eliminate isoamylase-type DBE activity, although *su1-st* kernels accumulate less phytyglycogen and Suc than *su1-Ref* or *su1-R4582::Mu1* mutants. The chain length distribution of residual amylopectin is significantly altered by *su1-Ref* and *su1-R4582::Mu1*, whereas *su1-st* has modest effects. These results, together with *su1* allele-specific effects on other starch- metabolizing enzymes detected in zymograms, suggest that total DBE catalytic activity is the not the sole determinant of *Su1* function and that specific interactions between *SU1* and other components of the starch biosynthetic system are required.

Characterization of the maize gene sugary1, a determinant of starch composition in kernels. (1995) (<https://pubmed.ncbi.nlm.nih.gov/7773016>) Additional References

RELATED GEPHE

No matches found. Related Genes

No matches found. Related Haplotypes

EXTERNAL LINKS

COMMENTS