GEPHE SUMMARY

Gephebase Gene

sugary 1 (su1) = isoamylase-type starch-debranching enzymes (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^sugary 1 (su1) = isoamylase-type starch-debranching enzymes^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001082

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

Fruit sugar content (https://www.gephebase.org/search-criteria?/and+Trait=^Fruit sugar content^#gephebase-summary-title)

Trait State in Taxon A

Zea mays - allele Su1

Trait State in Taxon B

Zea mays - allele su1-Ref

Ancestral State

Data not curated

Taxonomic Status

Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)

Taxon A

Latin Name

Zea mays (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Zea mays^#gephebase-summary-title)

Common Name

-

Synonyms

Zea mays var. japonica; maize; Zea mays L.; Zea mays mays

Rank

species

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

Parent

Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4575)

NCBI Taxonomy ID

4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4577)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Zea mays (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Zea mays^#gephebase-summary-title)

Common Name

-

Synonyms

Zea mays var. japonica; maize; Zea mays L.; Zea mays mays

Rank

species

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

Parent

Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4575)

NCBI Taxonomy ID

4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4577)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

sugary1

Synonyms

su1; sugary1; isoamylase; GRMZM2G138060

String

4577.GRMZM2G138060_P01 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4577.GRMZM2G138060_P01)

Sequence Similarities

-

GO - Molecular Function

GO:0004553 : hydrolase activity, hydrolyzing O-glycosyl compounds (https://www.ebi.ac.uk/QuickGO/term/GO:0004553)

GO - Biological Process

GO:0005975 : carbohydrate metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0005975)

GO - Cellular Component

UniProtKB Zea mays

O22637 (http://www.uniprot.org/uniprot/O22637)

GenebankID or UniProtKB

CM000780 (https://www.ncbi.nlm.nih.gov/nuccore/CM000780)

-

Presumptive Null

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

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

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

Experimental Evidence

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

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

Main Reference

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

Authors

Dinges JR; Colleoni C; Myers AM; James MG

Abstract

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 phytoglycogen 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.

Additional References

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

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS