GEPHE SUMMARY

Gephebase Gene

Delta-1-pyrroline-5-carboxylate synthase A (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Delta-1-pyrroline-5-carboxylate synthase A^#gephebase-summary-title)

GepheID

GP00001280

Entry Status

Published

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

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

Trait

Drought response (drought-induced proline accumulation) (https://www.gephebase.org/search-criteria?/and+Trait=^Drought response (drought-induced proline accumulation)^#gephebase-summary-title)

Trait State in Taxon A

Arabidopsis thaliana- Ler0

Trait State in Taxon B

Arabidopsis thaliana- Shahdara

Ancestral State

Taxon A

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

thale cress

Synonyms

thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis

Parent

Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)

NCBI Taxonomy ID

3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Arabidopsis thaliana- Ler0

Taxon B

Latin Name

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

Common Name

thale cress

Synonyms

thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis

Parent

Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)

NCBI Taxonomy ID

3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Arabidopsis thaliana- Shahdara

GENOTYPIC CHANGE

Generic Gene Name

P5CSA

Synonyms

ATP5CS; delta1-pyrroline-5-carboxylate synthase 1; T5I7.10; T5I7_10; P5CS1; At2g39800

String

3702.AT2G39800.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT2G39800.1)

Sequence Similarities

In the N-terminal section; belongs to the glutamate 5-kinase family.;In the C-terminal section; belongs to the gamma-glutamyl phosphate reductase family.

GO - Molecular Function

GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)

UniProtKB Arabidopsis thaliana

P54887 (http://www.uniprot.org/uniprot/P54887)

GenebankID or UniProtKB

818566 (https://www.ncbi.nlm.nih.gov/nuccore/818566)

GO:0017084 : delta1-pyrroline-5-carboxylate synthetase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0017084)
GO:0004349 : glutamate 5-kinase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0004349)
GO:0004350 : glutamate-5-semialdehyde dehydrogenase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0004350)

GO - Biological Process

GO:0009651 : response to salt stress (https://www.ebi.ac.uk/QuickGO/term/GO:0009651)
GO:0048364 : root development (https://www.ebi.ac.uk/QuickGO/term/GO:0048364)
GO:0009414 : response to water deprivation
(https://www.ebi.ac.uk/QuickGO/term/GO:0009414)
GO:0042538 : hyperosmotic salinity response
(https://www.ebi.ac.uk/QuickGO/term/GO:0042538)
GO:0006979 : response to oxidative stress
(https://www.ebi.ac.uk/QuickGO/term/GO:0006979)
GO:0055129 : L-proline biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0055129)
GO:0009555 : pollen development (https://www.ebi.ac.uk/QuickGO/term/GO:0009555)
GO:0006561 : proline biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006561)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0016020 : membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016020)
GO:0009507 : chloroplast (https://www.ebi.ac.uk/QuickGO/term/GO:0009507)

Mutation #1

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title)

Molecular Type

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

Aberration Type

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

Insertion Size

1-9 bp

Molecular Details of the Mutation

insertion of three or four TA repeats in intron 2 - together with the G>T mutation it causes frequent exon 3 skipping

Experimental Evidence

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

Main Reference

Intron-mediated alternative splicing of Arabidopsis P5CS1 and its association with natural variation in proline and climate adaptation. (2012)
(https://pubmed.ncbi.nlm.nih.gov/22615385)

Authors

Kesari R; Lasky JR; Villamor JG; Des Marais DL; Chen YJ; Liu TW; Lin W; Juenger TE; Verslues PE

Abstract

Drought-induced proline accumulation is widely observed in plants but its regulation and adaptive value are not as well understood. Proline accumulation of the Arabidopsis accession Shakdara (Sha) was threefold less than that of Landsberg erecta (Ler) and quantitative trait loci mapping identified a reduced function allele of the proline synthesis enzyme Î"(1)-pyrroline-5-carboxylate synthetase1 (P5CS1) as a basis for the lower proline of Sha. Sha P5CS1 had additional TA repeats in intron 2 and a G-to-T transversion in intron 3 that were sufficient to promote alternative splicing and production of a nonfunctional transcript lacking exon 3 (exon 3-skip P5CS1). In Sha, and additional accessions with the same intron polymorphisms, the nonfunctional exon 3-skip P5CS1 splice variant constituted as much as half of the total P5CS1 transcript. In a larger panel of Arabidopsis accessions, low water potential-induced proline accumulation varied by 10-fold and variable production of exon 3-skip P5CS1 among accessions was an important, but not the sole, factor underlying variation in proline accumulation. Population genetic analyses suggest that P5CS1 may have evolved under positive selection, and more extensive correlation of exon 3-skip P5CS1 production than proline abundance with climate conditions of natural accessions also suggest a role of P5CS1 in local adaptation to the environment. These data identify a unique source of alternative splicing in plants, demonstrate a role of exon 3-skip P5CS1 in natural variation of proline metabolism, and suggest an association of P5CS1 and its alternative splicing with environmental adaptation.

Additional References

Mutation #2

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

-

Molecular Details of the Mutation

G-to-T in intron 3 causing alternative splicing

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

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Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Splicing neither the small intron 2 TA-insertion nor the intron 3 polymorphism by itself are sufficient to cause frequent exon 3-skip transcript formation. The high exon 3-skip P5CS1 accessions (with exception of Pt-0) all have both the intron 3 G-to-T transition and insertion of three or four TA repeats in intron 2. Arabidopsis thaliana- Shahdara allele is a reduced functional allele