

GEPHE SUMMARY

	Gephebase Gene		GepheID
Delta-1-pyrroline-5-carboxylate synthase A ( <a +delta-1-pyrroline-5-carboxylate+synthase+a`#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene Gephebase="Delta-1-pyrroline-5-carboxylate synthase A`#gephebase-summary-title</a> )		GP00001280	
	Entry Status	Courtier	Main curator
Published			

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</a> )		Trait	
Drought response (drought-induced proline accumulation) ( <a +drought+response+(drought-induced+proline+accumulation)`#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="Drought response (drought-induced proline accumulation)`#gephebase-summary-title</a> )			
	Trait State in Taxon A		
Arabidopsis thaliana- Ler0		Trait State in Taxon B	
Arabidopsis thaliana- Shahdara			
	Ancestral State		
Taxon A		Taxonomic Status	
Intraspecific ( <a +intraspecific`#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Intraspecific`#gephebase-summary-title</a> )			
Taxon A		Taxon B	
	Latin Name		Latin Name
Arabidopsis thaliana ( <a +arabidopsis+thaliana`#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Arabidopsis thaliana`#gephebase-summary-title</a> )		Arabidopsis thaliana ( <a +arabidopsis+thaliana`#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Arabidopsis thaliana`#gephebase-summary-title</a> )	
	Common Name		Common Name
thale cress		thale cress	
	Synonyms		Synonyms
thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress		thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis	
	Parent		Parent
Arabidopsis () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701</a> )		Arabidopsis () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701</a> )	
	NCBI Taxonomy ID		NCBI Taxonomy ID
3702 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702</a> )		3702 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702</a> )	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
Yes		Yes	
	Taxon A Description		Taxon B Description
Arabidopsis thaliana- Ler0		Arabidopsis thaliana- Shahdara	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Arabidopsis thaliana
P5CSA		P54887 ( <a href="http://www.uniprot.org/uniprot/P54887">http://www.uniprot.org/uniprot/P54887</a> )	
	Synonyms		GenebankID or UniProtKB
ATP5CS; delta1-pyrroline-5-carboxylate synthase 1; T5l7.10; T5l7_10; P5CS1; At2g39800		818566 ( <a href="https://www.ncbi.nlm.nih.gov/nuccore/818566">https://www.ncbi.nlm.nih.gov/nuccore/818566</a> )	
	String		
3702.AT2G39800.1 ( <a href="http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT2G39800.1">http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT2G39800.1</a> )			
	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 ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005524">https://www.ebi.ac.uk/QuickGO/term/GO:0005524</a> )			

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

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

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

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

1-9 bp

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

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

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>)

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

Presumptive Null

Molecular Type

Aberration Type

Insertion Size

Molecular Details of the Mutation

Experimental Evidence

Main Reference

Authors

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

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

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

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

-

G-to-T in intron 3 causing alternative splicing

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

Presumptive Null

Molecular Type

Aberration Type

SNP Coding Change

Molecular Details of the Mutation

Experimental Evidence

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

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

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Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

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