GEPHE SUMMARY

Gephebase Gene

KCS18 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^KCS18^#gephebase-summary-title)

Entry Status

Published

GephelD

GP00000512

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

Arabidopsis thaliana- Bay-0

Trait State in Taxon B

Arabidopsis thaliana- Shahdara

Ancestral State

Data not curated

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- Bay-0

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

FAE1

Synonyms

3-ketoacyl-CoA synthase 18; FAE1; FATTY ACID ELONGATION1; T4L20.100; T4L20_100; KCS18; At4g34520

String

3702.AT4G34520.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT4G34520.1)

Sequence Similarities

Belongs to the chalcone/stilbene synthases family.

GO - Molecular Function

GO:0102336 : 3-oxo-arachidoyl-CoA synthase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0102336)
GO:0102337 : 3-oxo-cerotoyl-CoA synthase activity

UniProtKB Arabidopsis thaliana

Q38860 (http://www.uniprot.org/uniprot/Q38860)

GenebankID or UniProtKB

CP002687 (https://www.ncbi.nlm.nih.gov/nuccore/CP002687)

(https://www.ebi.ac.uk/QuickGO/term/GO:0102337)
GO:0102338 : 3-oxo-lignoceronyl-CoA synthase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0102338)
GO:0009922 : fatty acid elongase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0009922)
GO:0102756 : very-long-chain 3-ketoacyl-CoA synthase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0102756)

GO - Biological Process

GO:0006633 : fatty acid biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006633)

GO - Cellular Component

GO:0016021 : integral component of membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
GO:0005783 : endoplasmic reticulum
(https://www.ebi.ac.uk/QuickGO/term/GO:0005783)
GO:0031090 : organelle membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0031090)

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

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

L407V

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

Natural variation in seed very long chain fatty acid content is controlled by a new isoform of KCS18 in Arabidopsis thaliana. (2012) (https://pubmed.ncbi.nlm.nih.gov/23145136)

Authors

Jasinski S; LÃ©cureuil A; Miquel M; Loudet O; Raffaele S; Froissard M; Guerche P

Abstract

Oil from oleaginous seeds is mainly composed of triacylglycerols. Very long chain fatty acids (VLCFAs) are major constituents of triacylglycerols in many seed oils and represent valuable feedstock for industrial purposes. To identify genetic factors governing natural variability in VLCFA biosynthesis, a quantitative trait loci (QTL) analysis using a recombinant inbred line population derived from a cross between accessions Bay-0 and Shahdara was performed in Arabidopsis thaliana. Two fatty acid chain length ratio (CLR) QTL were identified, with one major locus, CLR.2, accounting for 77% of the observed phenotypic variation. A fine mapping and candidate gene approach showed that a key enzyme of the fatty acid elongation pathway, the Î²-ketoacyl-CoA synthase 18 (KCS18), was responsible for the CLR.2 QTL detected between Bay-0 and Shahdara. Association genetics and heterologous expression in yeast cells identified a single point mutation associated with an alteration of KCS18 activity, uncovering the molecular bases for the modulation of VLCFA content in these two natural populations of Arabidopsis. Identification of this kcs18 mutant with altered activity opens new perspectives for the modulation of oil composition in crop plants.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS