

GEPHE SUMMARY

KCS18 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~KCS18~#gephebase-summary-title) Published	Gephebase Gene	GP00000512	GepheID
	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

		Trait Category	
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology~#gephebase-summary-title)		Trait	
Oil composition (https://www.gephebase.org/search-criteria?/and+Trait=~Oilcomposition~#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+TaxonomicStatus=~Intraspecific~#gephebase-summary-title)			
Taxon A		Taxon B	
Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Arabidopsis+thaliana~#gephebase-summary-title)		Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Arabidopsis+thaliana~#gephebase-summary-title)	
thale cress		thale cress	
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	
species		species	
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis	
Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701)		Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701)	
3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702)		3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702)	
Yes		Yes	
Arabidopsis thaliana- Bay-0		Arabidopsis thaliana- Shahdara	

GENOTYPIC CHANGE

FAE1		Generic Gene Name		UniProtKB Arabidopsis thaliana	
3-ketoacyl-CoA synthase 18; FAE1; FATTY ACID ELONGATION1; T4L20.100; T4L20_100; KCS18; At4g34520		Synonyms		GenebankID or UniProtKB	
3702.AT4G34520.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT4G34520.1)		String		CP002687 (https://www.ncbi.nlm.nih.gov/nucleotide/CP002687)	
Belongs to the chalcone/stilbene synthases family.		Sequence Similarities			
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		GO - Molecular Function			

(<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](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](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](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](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; L  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   2-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

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

