

GEPHE SUMMARY

	Gephebase Gene	Gephebase ID
CINNAMOYL CO-A REDUCTASE 1 (#gephebase-summary-title)	GP00000186	Main curator
	Entry Status	
Published	Martin	

PHENOTYPIC CHANGE

	Trait Category		
Physiology (#gephebase-summary-title)	Trait		
Fiber content (#gephebase-summary-title)	Trait State in Taxon A		
Brassica napus	Trait State in Taxon B		
Brassica napus	Ancestral State		
Data not curated	Taxonomic Status		
Domesticated (#gephebase-summary-title)			
Taxon A		Taxon B	
Brassica napus (#gephebase-summary-title)	Latin Name	Brassica napus (#gephebase-summary-title)	Latin Name
rape	Common Name	rape	Common Name
rape; oilseed rape; rapeseeds; Brassica napus L., 1753	Synonyms	rape; oilseed rape; rapeseeds; Brassica napus L., 1753	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Brassiceae; Brassica	Lineage	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Brassiceae; Brassica	Lineage
Brassica () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3705)	Parent	Brassica () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3705)	Parent
3708 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3708)	NCBI Taxonomy ID	3708 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3708)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

CCR1	Generic Gene Name	UniProtKB Arabidopsis thaliana
	Synonyms	GenebankID or UniProtKB
ATCCR1; CINNAMOYL COA REDUCTASE; cinnamoyl coa reductase 1; IRREGULAR XYLEM 4; IRX4; T24D18.5; T24D18_5; At1g15950	Q9S9N9 (http://www.uniprot.org/uniprot/Q9S9N9)	
3702.AT1G15950.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT1G15950.1)	String	
	Sequence Similarities	
Belongs to the NAD(P)-dependent epimerase/dehydratase family. Dihydroflavonol-4-reductase subfamily.		
	GO - Molecular Function	
GO:0016491 : oxidoreductase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016491)		
GO:0016621 : cinnamoyl-CoA reductase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016621)		
GO:0050662 : coenzyme binding (https://www.ebi.ac.uk/QuickGO/term/GO:0050662)		

GO:0016616 : oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor (<https://www.ebi.ac.uk/QuickGO/term/GO:0016616>)

GO - Biological Process

GO:0007623 : circadian rhythm (<https://www.ebi.ac.uk/QuickGO/term/GO:0007623>)

GO:0009809 : lignin biosynthetic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0009809>)

GO:0009409 : response to cold (<https://www.ebi.ac.uk/QuickGO/term/GO:0009409>)

GO - Cellular Component

GO:0005829 : cytosol (<https://www.ebi.ac.uk/QuickGO/term/GO:0005829>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

Frameshift mutation in exon1

Experimental Evidence

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

Main Reference

A knockout mutation in the lignin biosynthesis gene CCR1 explains a major QTL for acid detergent lignin content in *Brassica napus* seeds. (2012) (<https://pubmed.ncbi.nlm.nih.gov/22350089/>)

Authors

Liu L; Stein A; Wittkop B; Sarvari P; Li J; Yan X; Dreyer F; Frauen M; Friedt W; Snowdon RJ

Abstract

Seed coat phenolic compounds represent important antinutritive fibre components that cause a considerable reduction in value of seed meals from oilseed rape (*Brassica napus*). The nutritionally most important fibre compound is acid detergent lignin (ADL), to which a significant contribution is made by phenylpropanoid-derived lignin precursors. In this study, we used bulked-segregant analysis in a population of recombinant inbred lines (RILs) from a cross of the Chinese oilseed rape lines GH06 (yellow seed, low ADL) and P174 (black seed, high ADL) to identify markers with tight linkage to a major quantitative trait locus (QTL) for seed ADL content. Fine mapping of the QTL was performed in a backcross population comprising 872 BC(1)F(2) plants from a cross of an F(7) RIL from the above-mentioned population, which was heterozygous for this major QTL and P174. A 3:1 phenotypic segregation for seed ADL content indicated that a single, dominant, major locus causes a substantial reduction in ADL. This locus was successively narrowed to 0.75 Å cM using *in silico* markers derived from a homologous *Brassica rapa* sequence contig spanning the QTL. Subsequently, we located a *B. rapa* orthologue of the key lignin biosynthesis gene CINNAMOYL CO-A REDUCTASE 1 (CCR1) only 600 Å kbp (0.75 Å cM) upstream of the nearest linked marker. Sequencing of PCR amplicons, covering the full-length coding sequences of Bna.CCR1 homologues, revealed a locus in P174 whose sequence corresponds to the *Brassica oleracea* wild-type allele from chromosome C8. In GH06, however, this allele is replaced by a homologue derived from chromosome A9 that contains a loss-of-function frameshift mutation in exon 1. Genetic and physical map data infer that this loss-of-function allele has replaced a functional Bna.CCR1 locus on chromosome C8 in GH06 by homoeologous non-reciprocal translocation.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

The nucleotidic nature of the frameshift is not mentionned in the article