

GEPHE SUMMARY

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

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	
	Latin Name		Latin Name
Brassica napus (#gephebase-summary-title)		Brassica napus (#gephebase-summary-title)	
	Common Name		Common Name
rape		rape	
	Synonyms		Synonyms
rape; oilseed rape; rapeseeds; Brassica napus L., 1753		rape; oilseed rape; rapeseeds; Brassica napus L., 1753	
	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; Brassicaceae; Brassica		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Brassicaceae; Brassica	
	Parent		Parent
Brassica () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3705)		Brassica () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3705)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
3708 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3708)		3708 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3708)	
	is Taxon A an Infrasppecies?		is Taxon B an Infrasppecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Arabidopsis thaliana
CCR1		Q9S9N9 (http://www.uniprot.org/uniprot/Q9S9N9)	GenebankID or UniProtKB
	Synonyms		
ATCCR1; CINNAMOYL COA REDUCTASE; cinnamoyl coa reductase 1; IRREGULAR XYLEM 4; IRX4; T24D18.5; T24D18_5; At1g15950		()	
	String		
3702.AT1G15950.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT1G15950.1)			
	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 ([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

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

Molecular Details of the Mutation

Frameshift mutation in exon1

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))

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 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 kbp (0.75 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

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

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