GEPHE SUMMARY

Gephebase Gene
CINNAMOYL CO-A REDUCTASE 1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^CINNAMOYL CO-A REDUCTASE 1^#gephebase-summary-title)

GepheID
GP00000186

Entry Status
Published

Main curator
Martin

PHENOTYPIC CHANGE

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

Trait
Fiber content (https://www.gephebase.org/search-criteria?/and+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 (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)

Taxon A

Latin Name
Brassica napus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Brassica napus^#gephebase-summary-title)

Common Name
rape

Synonyms
rape; oilseed rape; rapeseeds; Brassica napus L., 1753

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Brassiceae; Brassica

Parent
Brassica () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3705)

NCBI Taxonomy ID
3708 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3708)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Brassica napus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Brassica napus^#gephebase-summary-title)

Common Name
rape

Synonyms
rape; oilseed rape; rapeseeds; Brassica napus L., 1753

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Brassiceae; Brassica

Parent
Brassica () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3705)

NCBI Taxonomy ID
3708 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3708)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
CCR1

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)

UniProtKB Arabidopsis thaliana
Q9S9N9 (http://www.uniprot.org/uniprot/Q9S9N9)

GenebankID or UniProtKB
()

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)

Molecular Type

Coding (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)

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)

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 0.75Â 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 600Â kbp (0.75Â 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