

GEPHE SUMMARY

Gephebase Gene		GepheID
FAD2 (BnaA.FAD2.a) (<a +fad2+(bnaa.fad2.a)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+FAD2+(BnaA.FAD2.a)+"#gephebase-summary-title)		
Entry Status		Main curator
Published		Martin

PHENOTYPIC CHANGE

Trait #1	Trait Category
Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology+"#gephebase-summary-title)	
Oil composition (<a +oil+composition+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Oil+composition+"#gephebase-summary-title)	
Trait State in Taxon A	
Brassica napus	
Trait State in Taxon B	
Brassica napus -SW Hickory	

Trait #2	Trait Category
Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology+"#gephebase-summary-title)	
Oil yield (<a +oil+yield+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Oil+yield+"#gephebase-summary-title)	
Trait State in Taxon A	
-	
Trait State in Taxon B	
-	

Ancestral State	
Taxon A	
Taxonomic Status	
Domesticated (<a +domesticated+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Domesticated+"#gephebase-summary-title)	

Taxon A	Taxon B
Latin Name	
Brassica napus (<a +brassica+napus+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">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 Intraspecies?	
No	

Taxon B	Taxon B
Latin Name	
Brassica napus (<a +brassica+napus+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">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 Intraspecies?	
Yes	
Taxon B Description	
Brassica napus -SW Hickory	

GENOTYPIC CHANGE

FAD2	Generic Gene Name	P46313 (http://www.uniprot.org/uniprot/P46313)	UniProtKB Arabidopsis thaliana
AtFAD2; DELTA-12 DESATURASE; fatty acid desaturase 2; At3g12120; T21B14.6; T21B14_107; T23B7.6	Synonyms	ABQ81921 (https://www.ncbi.nlm.nih.gov/nuccore/ABQ81921)	GenebankID or UniProtKB
3702.AT3G12120.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT3G12120.1)	String		
Belongs to the fatty acid desaturase type 1 family.	Sequence Similarities		
GO:0102985 : Delta12-fatty-acid desaturase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0102985) GO:0045485 : omega-6 fatty acid desaturase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0045485)	GO - Molecular Function		
GO:0006636 : unsaturated fatty acid biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0006636)	GO - Biological Process		
GO:0016021 : integral component of membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016021) GO:0005789 : endoplasmic reticulum membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005789) GO:0031090 : organelle membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0031090)	GO - Cellular Component		
Yes (https://www.gephebase.org/search-criteria?/and+Presumptive+Null=~Yes~#gephebase-summary-title)	Presumptive Null		
Coding (https://www.gephebase.org/search-criteria?/and+Molecular+Type=~Coding~#gephebase-summary-title)	Molecular Type		
Insertion (https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Insertion~#gephebase-summary-title)	Aberration Type		
1-9 bp	Insertion Size		
4bp insertion resulting in frameshift and premature stop codon	Molecular Details of the Mutation		
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Linkage+Mapping~#gephebase-summary-title)	Experimental Evidence		
Identification of FAD2 and FAD3 genes in Brassica napus genome and development of allele-specific markers for high oleic and low linolenic acid contents. (2012) (https://pubmed.ncbi.nlm.nih.gov/22534790)	Main Reference		
Yang Q; Fan C; Guo Z; Qin J; Wu J; Li Q; Fu T; Zhou Y	Authors		
Modification of oleic acid (C18:1) and linolenic acid (C18:3) contents in seeds is one of the major goals for quality breeding after removal of erucic acid in oilseed rape (Brassica napus). The fatty acid desaturase genes FAD2 and FAD3 have been shown as the major genes for the control of C18:1 and C18:3 contents. However, the genome structure and locus distributions of the two gene families in amphidiploid B. napus are still not completely understood to date. In the present study, all copies of FAD2 and FAD3 genes in the A- and C-genome of B. napus and its two diploid progenitor species, Brassica rapa and Brassica oleracea, were identified through bioinformatic analysis and extensive molecular cloning. Two FAD2 genes exist in B. rapa and B. oleracea, and four copies of FAD2 genes exist in B. napus. Three and six copies of FAD3 genes were identified in diploid species and amphidiploid species, respectively. The genetic control of high C18:1 and low C18:3 contents in a double haploid population was investigated through mapping of the quantitative trait loci (QTL) for the traits and the molecular cloning of the underlying genes. One major QTL of BnaA.FAD2.a located on A5 chromosome was responsible for the high C18:1 content. A deleted mutation in the BnaA.FAD2.a locus was uncovered, which represented a previously unidentified allele for the high oleic variation in B. napus species. Two major QTLs on A4 and C4 chromosomes were found to be responsible for the low C18:3 content in the DH population as well as in SW Hickory. Furthermore, several single base pair changes in BnaA.FAD3.b and BnaC.FAD3.b were identified to cause the phenotype of low C18:3 content. Based on the results of genetic mapping and identified sequences, allele-specific markers were developed for FAD2 and FAD3 genes. Particularly, single-nucleotide amplified polymorphisms markers for FAD3 alleles were demonstrated to be a reliable type of SNP markers for unambiguous identification of genotypes with different content of C18:3 in amphidiploid B. napus.	Abstract		
	Additional References		

RELATED GEPHE

No matches found.	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

