

GEPHE SUMMARY

TT8 (#gephebase-summary-title)	Gephebase Gene	GP00002077	GepheID
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Trait Category			
Morphology (#gephebase-summary-title)	Trait		
Coloration (seed) (<a ?and+taxonomic+status='^Domesticated"' href="https://www.gephebase.org/search-criteria/?and+Trait=^Coloration+(seed)^#gephebase-summary-title)</td><td>Trait State in Taxon A</td><td></td><td></td></tr> <tr> <td>Brassica rapa - black seeds</td><td>Trait State in Taxon B</td><td></td><td></td></tr> <tr> <td>Brassica rapa - yellow seeds</td><td>Ancestral State</td><td></td><td></td></tr> <tr> <td>Taxon A</td><td>Taxonomic Status</td><td></td><td></td></tr> <tr> <td>Domesticated (#gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	Latin Name
Brassica rapa (#gephebase-summary-title)	Common Name	Brassica rapa (#gephebase-summary-title)	Common Name
field mustard	Synonyms	field mustard	Synonyms
field mustard; Brassica rapa L.; Brassica rapa L., 1753	Rank	field mustard; Brassica rapa L.; Brassica rapa L., 1753	Rank
species	Lineage	species	Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliopsida; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Brassiceae; Brassica	Parent	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliopsida; 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	Brassica () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3705)	NCBI Taxonomy ID
3711 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3711)		3711 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3711)	
No	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
			Taxon B Description
			Brassica rapa subsp. trilocularis - Indian yellow sarson

GENOTYPIC CHANGE

TT8	Generic Gene Name	UniProtKB Arabidopsis thaliana
AtTT8; BHLH42; F17A8.170; F17A8_170; TRANSPARENT TESTA 8; EN32; At4g09820	Synonyms	GenebankID or UniProtKB
3702.AT4G09820.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=3702.AT4G09820.1)	String	F2X677 (https://www.ncbi.nlm.nih.gov/nuccore/F2X677)
Belongs to the bHLH protein family.	Sequence Similarities	
GO:0046983 : protein dimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046983)	GO - Molecular Function	
GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)		
GO:0000976 : transcription regulatory region sequence-specific DNA binding		

(<https://www.ebi.ac.uk/QuickGO/term/GO:0000976>)

GO - Biological Process

GO:0009867 : jasmonic acid mediated signaling pathway

(<https://www.ebi.ac.uk/QuickGO/term/GO:0009867>)

GO:0009813 : flavonoid biosynthetic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0009813>)

GO:0031542 : positive regulation of anthocyanin biosynthetic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0031542>)

GO:0010026 : trichome differentiation

(<https://www.ebi.ac.uk/QuickGO/term/GO:0010026>)

GO:0048316 : seed development (<https://www.ebi.ac.uk/QuickGO/term/GO:0048316>)

GO:0009962 : regulation of flavonoid biosynthetic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0009962>)

GO:2000029 : regulation of proanthocyanidin biosynthetic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:2000029>)

GO:0010214 : seed coat development

(<https://www.ebi.ac.uk/QuickGO/term/GO:0010214>)

GO - Cellular Component

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Insertion Size

1-10 kb

Molecular Details of the Mutation

insertion of a Helitron transposon of 4320 bp in intron 2 starting with 5' TC and ending with 3'CTAG containing a 17 bp palindromic region forming a hairpin - prevents transcription

Experimental Evidence

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

Main Reference

A large insertion in bHLH transcription factor BrTT8 resulting in yellow seed coat in *Brassica rapa*. (2012) (<https://pubmed.ncbi.nlm.nih.gov/22984469>)

Authors

Li X; Chen L; Hong M; Zhang Y; Zu F; Wen J; Yi B; Ma C; Shen J; Tu J; Fu T

Abstract

Yellow seed is a desirable quality trait of the *Brassica* oilseed species. Previously, several seed coat color genes have been mapped in the *Brassica* species, but the molecular mechanism is still unknown. In the present investigation, map-based cloning method was used to identify a seed coat color gene, located on A9 in *B. rapa*. Blast analysis with the *Arabidopsis* genome showed that there were 22 *Arabidopsis* genes in this region including at4g09820 to at4g10620. Functional complementation test exhibited a phenotype reversion in the *Arabidopsis thaliana* tt8-1 mutant and yellow-seeded plant. These results suggested that the candidate gene was a homolog of TRANSPARENT TESTA8 (TT8) locus. BrTT8 regulated the accumulation of proanthocyanidins (PAs) in the seed coat. Sequence analysis of two alleles revealed a large insertion of a new class of transposable elements, Helitron in yellow sarson. In addition, no mRNA expression of BrTT8 was detected in the yellow-seeded line. It indicated that the natural transposon might have caused the loss in function of BrTT8. BrTT8 encodes a basic/helix-loop-helix (bHLH) protein that shares a high degree of similarity with other bHLH proteins in the *Brassica*. Further expression analysis also revealed that BrTT8 was involved in controlling the late biosynthetic genes (LBGs) of the flavonoid pathway. Our present findings provided with further studies could assist in understanding the molecular mechanism involved in seed coat color formation in *Brassica* species, which is an important oil yielding quality trait.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

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