

GEPHE SUMMARY

TT8 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^TT8^#gephebase-summary-title)	Gephebase Gene	GP00002077	GepheID
	Entry Status	Courtier	Main curator
	Published		

PHENOTYPIC CHANGE

		Trait Category	
Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=^Morphology^#gephebase-summary-title)		Trait	
Coloration (seed) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration(seed)^#gephebase-summary-title)		Trait State in Taxon A	
Brassica rapa - black seeds		Trait State in Taxon B	
Brassica rapa - yellow seeds		Ancestral State	
Taxon A		Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=^Domesticated^#gephebase-summary-title)			
Taxon A		Taxon B	
Brassica rapa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Brassica rapa^#gephebase-summary-title)		Brassica rapa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Brassica rapa^#gephebase-summary-title)	
Common Name		Common Name	
field mustard		field mustard	
Synonyms		Synonyms	
field mustard; Brassica rapa L.; Brassica rapa L., 1753		field mustard; Brassica rapa L.; Brassica rapa L., 1753	
Rank		Rank	
species		species	
Lineage		Lineage	
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliopsida; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Brassicaceae; Brassica		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliopsida; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; 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	
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)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
No		Yes	
		Taxon B Description	
		Brassica rapa subsp. trilocularis - Indian yellow sarson	

GENOTYPIC CHANGE

		Generic Gene Name		UniProtKB Arabidopsis thaliana
TT8		Q9FT81 (http://www.uniprot.org/uniprot/Q9FT81)		
Synonyms		GenebankID or UniProtKB		
AtTT8; BHLH42; F17A8.170; F17A8_170; TRANSPARENT TESTA 8; EN32; At4g09820		F2X677 (https://www.ncbi.nlm.nih.gov/nuccore/F2X677)		
String				
3702.AT4G09820.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT4G09820.1)		Sequence Similarities		
Belongs to the bHLH protein family.		GO - Molecular Function		
GO:0046983 : protein dimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046983)				
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 (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
Insertion (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Insertion~#gephebase-summary-title)		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 (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title)		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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