

# GEPHE SUMMARY

	Gephebase Gene	GephelD
R/glyma09g36983 ( <a href="https://www.gephebase.org/search-criteria?/and+Gene">https://www.gephebase.org/search-criteria?/and+Gene</a> Gephebase= <sup>~</sup> R/glyma09g36983 <sup>#</sup> gephebase-summary-title)	GP00000946	
	Entry Status	Main curator
Published	Martin	

## PHENOTYPIC CHANGE

	Trait Category
Morphology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a> Category= <sup>~</sup> Morphology <sup>#</sup> gephebase-summary-title)	Trait
Coloration (seeds) ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=&lt;sup&gt;~&lt;/sup&gt;Coloration">https://www.gephebase.org/search-criteria?/and+Trait=<sup>~</sup>Coloration</a> (seeds) <sup>#</sup> gephebase-summary-title)	Trait State in Taxon A
Glycine max - black hilum	Trait State in Taxon B
Glycine max - brown hilum	Ancestral State
Data not curated	Taxonomic Status
Domesticated ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic">https://www.gephebase.org/search-criteria?/and+Taxonomic</a> Status= <sup>~</sup> Domesticated <sup>#</sup> gephebase-summary-title)	

Taxon A	Latin Name	Taxon B	Latin Name
Glycine max ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=&lt;sup&gt;~&lt;/sup&gt;Glycine+max&lt;sup&gt;#&lt;/sup&gt;gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=<sup>~</sup>Glycine+max<sup>#</sup>gephebase-summary-title</a> )	Common Name	Glycine max ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=&lt;sup&gt;~&lt;/sup&gt;Glycine+max&lt;sup&gt;#&lt;/sup&gt;gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=<sup>~</sup>Glycine+max<sup>#</sup>gephebase-summary-title</a> )	Common Name
soybean	Synonyms	soybean	Synonyms
soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye	Rank	soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye	Rank
species	Lineage	species	Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Euphyllophyta; Spermatophytina; Magnoliophytina; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae; 50 kb inversion clade; NPAAA clade; indigoferoid/millettoid clade; Phaseoleae; Glycine; Soja	Parent	cellular organisms; Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Euphyllophyta; Spermatophytina; Magnoliophytina; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae; 50 kb inversion clade; NPAAA clade; indigoferoid/millettoid clade; Phaseoleae; Glycine; Soja	Parent
Soja () - (Rank: subgenus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1462606">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1462606</a> )	NCBI Taxonomy ID	Soja () - (Rank: subgenus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1462606">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1462606</a> )	NCBI Taxonomy ID
3847 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3847">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3847</a> )		3847 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3847">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3847</a> )	
Yes	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
Glycine max - black hilum	Taxon A Description	Glycine max - brown hilum	Taxon B Description

## GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Glycine max
100780023		K7LFP2 ( <a href="http://www.uniprot.org/uniprot/K7LFP2">http://www.uniprot.org/uniprot/K7LFP2</a> )
GLYMA_09G235100	Synonyms	AB934281 ( <a href="https://www.ncbi.nlm.nih.gov/nuccore/AB934281">https://www.ncbi.nlm.nih.gov/nuccore/AB934281</a> )
3847.GLYMA09G36983.1 ( <a href="http://string-db.org/newstring_cgi/show_network_section.pl?identifier=3847.GLYMA09G36983.1">http://string-db.org/newstring_cgi/show_network_section.pl?identifier=3847.GLYMA09G36983.1</a> )	String	
	Sequence Similarities	
-		GO - Molecular Function
GO:0043565 : sequence-specific DNA binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0043565">https://www.ebi.ac.uk/QuickGO/term/GO:0043565</a> )		
GO:0044212 : transcription regulatory region DNA binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0044212">https://www.ebi.ac.uk/QuickGO/term/GO:0044212</a> )		

## GO - Biological Process

GO:0030154 : cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030154>)

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

SNP (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=%SNP%#gephebase-summary-title>)

SNP Coding Change

Nonsense

Molecular Details of the Mutation

C377- creating premature Stop

Experimental Evidence

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=%Linkage+Mapping%#gephebase-summary-title>)

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

## Main Reference

Loss-of-function mutations affecting a specific Glycine max R2R3 MYB transcription factor result in brown hilum and brown seed coats. (2011) (<https://pubmed.ncbi.nlm.nih.gov/22070454>)

Authors

Gillman JD; Tetlow A; Lee JD; Shannon JG; Bilyeu K

Abstract

Although modern soybean cultivars feature yellow seed coats, with the only color variation found at the hilum, the ancestral condition is black seed coats. Both seed coat and hilum coloration are due to the presence of phenylpropanoid pathway derivatives, principally anthocyanins. The genetics of soybean seed coat and hilum coloration were first investigated during the resurgence of genetics during the 1920s, following the rediscovery of Mendel's work. Despite the inclusion of this phenotypic marker into the extensive genetic maps developed for soybean over the last twenty years, the genetic basis behind the phenomenon of brown seed coats (the R locus) has remained undetermined until now.

In order to identify the gene responsible for the r gene effect (brown hilum or seed coat color), we utilized bulk segregant analysis and identified recombinant lines derived from a population segregating for two phenotypically distinct alleles of the R locus. Fine mapping was accelerated through use of a novel, bioinformatically determined set of Simple Sequence Repeat (SSR) markers which allowed us to delimit the genomic region containing the r gene to less than 200 kbp, despite the use of a mapping population of only 100 F<sub>6</sub> lines. Candidate gene analysis identified a loss of function mutation affecting a seed coat-specific expressed R2R3 MYB transcription factor gene (Glyma09g36990) as a strong candidate for the brown hilum phenotype. We observed a near perfect correlation between the mRNA expression levels of the functional R gene candidate and an UDP-glucose:flavonoid 3'-O-glucosyltransferase (UF3GT) gene, which is responsible for the final step in anthocyanin biosynthesis. In contrast, when a null allele of Glyma09g36990 is expressed no upregulation of the UF3GT gene was found.

We discovered an allelic series of four loss of function mutations affecting our R locus gene candidate. The presence of any one of these mutations was perfectly correlated with the brown seed coat/hilum phenotype in a broadly distributed survey of soybean cultivars, barring the presence of the epistatic dominant l allele or gray pubescence, both of which can mask the effect of the r allele, resulting in yellow or buff hilum. These findings strongly suggest that loss of function for one particular seed coat-expressed R2R3 MYB gene is responsible for the brown seed coat/hilum phenotype in soybean.

## Additional References

Methylation affects transposition and splicing of a large CACTA transposon from a MYB transcription factor regulating anthocyanin synthase genes in soybean seed coats. (2014) (<https://pubmed.ncbi.nlm.nih.gov/25369033>)

## RELATED GEPHE

## Related Genes

4 (Flavonoid 3'-hydroxylase (F3'H), flavonoid 3';5'-hydroxylase (F3'5'H), flavonoid 3'-hydroxylase (F3'H), PH4/GmMYB-G20-1) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=%3847%and+Trait=Coloration+and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

