

GEPHE SUMMARY

Gephebase Gene		GepheID
R/glyma09g36983 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~R/glyma09g36983~#gephebase-summary-title)		GP00000946
Entry Status		Main curator
Published		

PHENOTYPIC CHANGE

Trait Category			
Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Morphology~#gephebase-summary-title)		Trait	
Coloration (seeds) (https://www.gephebase.org/search-criteria?/and+Trait=~Coloration+seeds~#gephebase-summary-title)		Trait State in Taxon A	
Glycine max - black hila		Trait State in Taxon B	
Glycine max - brown hila		Ancestral State	
Data not curated		Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Domesticated~#gephebase-summary-title)			
Taxon A		Taxon B	
Glycine max (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Glycine+max~#gephebase-summary-title)		Glycine max (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Glycine+max~#gephebase-summary-title)	
Common Name		Common Name	
soybean		soybean	
Synonyms		Synonyms	
soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye		soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye	
Rank		Rank	
species		species	
Lineage		Lineage	
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae; 50 kb inversion clade; NPAAA clade; indigoferoid/millettioid clade; Phaseoleae; Glycine; Soja		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae; 50 kb inversion clade; NPAAA clade; indigoferoid/millettioid clade; Phaseoleae; Glycine; Soja	
Parent		Parent	
Soja () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1462606)		Soja () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1462606)	
NCBI Taxonomy ID		NCBI Taxonomy ID	
3847 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3847)		3847 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3847)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
Yes		Yes	
Taxon A Description		Taxon B Description	
Glycine max - black hila		Glycine max - brown hila	

GENOTYPIC CHANGE

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

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 hila, the ancestral condition is black seed coats. Both seed coat and hila 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 F6 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 I allele or gray pubescence, both of which can mask the effect of the r allele, resulting in yellow or buff hila. 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

