

GEPHE SUMMARY

BADH2 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^BADH2^#gephebase-summary-title)	Gephebase Gene	GP00000133	GepheID
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title)	Trait Category
Fragrance (https://www.gephebase.org/search-criteria?/and+Trait=^Fragrance^#gephebase-summary-title)	Trait
Glycine max - non-fragrant Chiang Mai 60	Trait State in Taxon A
Glycine max- fragrant Kaori	Trait State in Taxon B
Data not curated	Ancestral State
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Domesticated^#gephebase-summary-title)	Taxonomic Status

Taxon A	Latin Name	Taxon B	Latin Name
Glycine max (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Glycine+max^#gephebase-summary-title)			
soybean	soybean	soybean	soybean
soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye	soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye	soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye	soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye
species	species	species	species
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	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
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)	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)
3847 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3847)			
is Taxon A an Intraspecies?	is Taxon A an Intraspecies?	is Taxon B an Intraspecies?	is Taxon B an Intraspecies?
Yes	Yes	Yes	Yes
Glycine max - non-fragrant Chiang Mai 60	Glycine max - non-fragrant Chiang Mai 60	Glycine max- fragrant Kaori	Glycine max- fragrant Kaori

GENOTYPIC CHANGE

BADH2	Generic Gene Name	UniProtKB Oryza sativa subsp. japonica
fgr; BADH2; OsBADH2; OsJ_27367; LOC_Os08g32870; Os08g0424500; OSJNBa0056L09.30; P0456B03.101	Synonyms	Q84LK3 (http://www.uniprot.org/uniprot/Q84LK3) ADN03185 (https://www.ncbi.nlm.nih.gov/nuccore/ADN03185)
39947.LOC_Os08g32870.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=39947.LOC_Os08g32870.1)	String	
Belongs to the aldehyde dehydrogenase family.	Sequence Similarities	
GO:0008802 : betaine-aldehyde dehydrogenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008802)	GO - Molecular Function	
	GO - Biological Process	

GO:0071454 : cellular response to anoxia
 (https://www.ebi.ac.uk/QuickGO/term/GO:0071454)
 GO:0019285 : glycine betaine biosynthetic process from choline
 (https://www.ebi.ac.uk/QuickGO/term/GO:0019285)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
 GO:0005777 : peroxisome (https://www.ebi.ac.uk/QuickGO/term/GO:0005777)

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null="No"#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

Nonsynonymous

Molecular Details of the Mutation

1 amino-acid substitution in conserved enzymatic domain

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

A SNP in GmBADH2 gene associates with fragrance in vegetable soybean variety "Kaori" and SNAP marker development for the fragrance. (2011)
 (https://pubmed.ncbi.nlm.nih.gov/21046066)

Authors

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Abstract

Fragrance in soybean is due to the presence of 2-acetyl-1-pyrroline (2AP). BADH2 gene coding for betaine aldehyde dehydrogenase has been identified as the candidate gene responsible for fragrance in rice (*Oryza sativa* L.). In this study, using the RIL population derived from fragrant soybean cultivar "Kaori" and non-fragrant soybean cultivar "Chiang Mai 60" (CM60), STS markers designed from BADH2 homolog were found associating with 2AP production. Genetic mapping demonstrated that QTL position of fragrance and 2AP production coincides with the position of GmBADH2 (Glycine max betaine aldehyde dehydrogenase 2). Sequence comparison of GmBADH2 between Kaori and non-fragrant soybeans revealed non-synonymous single-nucleotide polymorphism (SNP) in exon 10. Nucleotide substitution of G to A in the exon results in an amino acid change of glycine (GGC; G) to aspartic acid (GAC; D) in Kaori. The amino acid substitution changes the conserved EGCRDPIVS motif of GmBADH2, which is essential for functional activity of GmBADH2 protein, to EGCRDPIVS motif, suggesting that the SNP in GmBADH2 is responsible for the fragrance in Kaori. Five single nucleotide-amplified polymorphism (SNAP) markers which are PCR-based allele specific SNP markers were developed for fragrance based on the SNP in GmBADH2. Two markers specific to A allele produced a band in only Kaori, while three markers specific to G alleles produced a band in only CM60. The simple PCR-based allele specific SNAP markers developed in the present study are useful in marker-assisted breeding of fragrant soybean.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS