

GEPHE SUMMARY

BADH2 (<a +badh2+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">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 (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology+"#gephebase-summary-title)	Trait Category		
Fragrance (<a +fragrance+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">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 (<a +domesticated+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Domesticated+"#gephebase-summary-title)	Taxonomic Status		
	Taxon A		Taxon B
	Latin Name		Latin Name
Glycine max (<a +glycine+max+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Glycine+max+"#gephebase-summary-title)	Latin Name	Glycine max (<a +glycine+max+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Glycine+max+"#gephebase-summary-title)	Latin Name
soybean	Common Name	soybean	Common Name
soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye	Synonyms	soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye	Synonyms
species	Rank	species	Rank
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	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	Lineage
Soja () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1462606)	Parent	Soja () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1462606)	Parent
3847 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3847)	NCBI Taxonomy ID	3847 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3847)	NCBI Taxonomy ID
Yes	is Taxon A an Intraspecies?	Yes	is Taxon B an Intraspecies?
Glycine max - non-fragrant Chiang Mai 60	Taxon A Description	Glycine max- fragrant Kaori	Taxon B Description

GENOTYPIC CHANGE

BADH2	Generic Gene Name	UniProtKB Oryza sativa subsp. japonica Q84LK3 (http://www.uniprot.org/uniprot/Q84LK3)
fgr; BADH2; OsBADH2; OsJ_27367; LOC_Os08g32870; Os08g0424500; OSJNBa0056L09.30; P0456B03.101	Synonyms	GenebankID or UniProtKB 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](https://www.gephebase.org/search-criteria?/and+Presumptive Null=))

Molecular Type

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

Aberration Type

SNP ([https://www.gephebase.org/search-criteria?/and+Aberration Type="SNP"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration Type=))

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](https://www.gephebase.org/search-criteria?/and+Experimental Evidence=))

	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