GEPHE SUMMARY

Gephebase Gene

BADH2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^BADH2^#gephebase-summary-title)

GepheID

GP00000133

Entry Status

Published

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

Fragrance (https://www.gephebase.org/search-criteria?/and+Trait=^Fragrance^#gephebase-summary-title)

Trait State in Taxon A

Glycine max - non-fragrant Chiang Mai 60

Trait State in Taxon B

Glycine max- fragrant Kaori

Ancestral State

Data not curated

Taxonomic Status

Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)

Taxon A

Latin Name

Glycine max (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Glycine max^#gephebase-summary-title)

Common Name

soybean

Synonyms

soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye

Rank

species

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

Parent

Soja () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1462606)

NCBI Taxonomy ID

3847 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3847)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Glycine max - non-fragrant Chiang Mai 60

Taxon B

Latin Name

Glycine max (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Glycine max^#gephebase-summary-title)

Common Name

soybean

Synonyms

soybean; soybeans; Glycine max (L.) Merr.; Glycine max; cv. Wye

Rank

species

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

Parent

Soja () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1462606)

NCBI Taxonomy ID

3847 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3847)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Glycine max- fragrant Kaori

GENOTYPIC CHANGE

Generic Gene Name

BADH2

Synonyms

fgr; BADH2; OsBADH2; OsJ_27367; LOC_Os08g32870; Os08g0424500; OSJNBa0056L09.30; P0456B03.101

String

39947.LOC_Os08g32870.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=39947.LOC_Os08g32870.1)

Sequence Similarities

Belongs to the aldehyde dehydrogenase family.

GO - Molecular Function

GO:0008802 : betaine-aldehyde dehydrogenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008802)

GO - Biological Process

UniProtKB Oryza sativa subsp. japonica

Q84LK3 (http://www.uniprot.org/uniprot/Q84LK3)

GenebankID or UniProtKB

ADN03185 (https://www.ncbi.nlm.nih.gov/nuccore/ADN03185)

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

Juwattanasomran R; Somta P; Chankaew S; Shimizu T; Wongpornchai S; Kaga A; Srinives P

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 EGCRLGPIVS motif of GmBADH2, which is essential for functional activity of GmBADH2 protein, to EGCRLDPIVS 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