

## GEPHE SUMMARY

### Gephebase Gene

BADH2

### Entry Status

Published

### GepheID

GP00001775

### Main curator

Courtier

## PHENOTYPIC CHANGE

### Trait Category

Physiology

### Trait

Fragrance

### Trait State in Taxon A

Oryza sativa - non-fragrant

### Trait State in Taxon B

Oryza sativa - fragrant - variety from India

### Ancestral State

Taxon A

### Taxonomic Status

Domesticated

### Taxon A

#### Latin Name

*Oryza sativa*

#### Common Name

rice

#### Synonyms

rice; red rice; Oryza sativa L.

#### Rank

species

#### Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; Oryzinae; Oryza

#### Parent

Oryza () - (Rank: genus)

#### NCBI Taxonomy ID

4530

#### is Taxon A an Intraspecies?

No

### Taxon B

#### Latin Name

*Oryza sativa*

#### Common Name

rice

#### Synonyms

rice; red rice; Oryza sativa L.

#### Rank

species

#### Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; Oryzinae; Oryza

#### Parent

Oryza () - (Rank: genus)

#### NCBI Taxonomy ID

4530

#### is Taxon B an Intraspecies?

Yes

#### Taxon B Description

Vishunparag

## GENOTYPIC CHANGE

### Generic Gene Name

BADH2

### Synonyms

fgr; BADH2; OsBADH2; OsJ\_27367; LOC\_Os08g32870; Os08g0424500; OSJNBa0056L09.30; P0456B03.101

### String

39947.LOC\_Os08g32870.1

### Sequence Similarities

Belongs to the aldehyde dehydrogenase family.

### GO - Molecular Function

GO:0008802 : betaine-aldehyde dehydrogenase activity

### GO - Biological Process

GO:0071454 : cellular response to anoxia

GO:0019285 : glycine betaine biosynthetic process from choline

### GO - Cellular Component

GO:0005737 : cytoplasm

### UniProtKB Oryza sativa subsp. japonica

Q84LK3

### GenebankID or UniProtKB

ALZ42021

GO:0005777 : peroxisome

**Presumptive Null**

Yes

**Molecular Type**

Coding

**Aberration Type**

SNP

**SNP Coding Change**

Unknown

**Molecular Details of the Mutation**

G>T substitution in exon 10 - need to check the sequence to check if this mutation is nonsense or nonsynonymous

**Experimental Evidence**

[Candidate Gene](#)

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

**Main Reference**

[The origin and evolution of fragrance in rice \(\*Oryza sativa\* L.\). \(2009\)](#)

**Authors**

Kovach MJ; Calingacion MN; Fitzgerald MA; McCouch SR

**Abstract**

Fragrance in the grain is one of the most highly valued grain quality traits in rice, yet the origin and evolution of the betaine aldehyde dehydrogenase gene (BADH2) underlying this trait remains unclear. In this study, we identify eight putatively nonfunctional alleles of the BADH2 gene and show that these alleles have distinct geographic and genetic origins. Despite multiple origins of the fragrance trait, a single allele, badh2.1, is the predominant allele in virtually all fragrant rice varieties today, including the widely recognized Basmati and Jasmine types. Haplotype analysis allowed us to establish a single origin of the badh2.1 allele within the Japonica varietal group and demonstrate the introgression of this allele from Japonica to Indica. Basmati-like accessions were nearly identical to the ancestral Japonica haplotype across a 5.3-Mb region flanking BADH2 regardless of their fragrance phenotype, demonstrating a close evolutionary relationship between Basmati varieties and the Japonica gene pool. These results clarify the relationships among fragrant rice varieties and challenge the traditional assumption that the fragrance trait arose in the Indica varietal group.

**Additional References**

**RELATED GEPHE**

**Related Genes**

No matches found.

**Related Haplotypes**

9

**EXTERNAL LINKS**

**COMMENTS**

@Parallelism