GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00001777

Main curator

Courtier

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

Oryza sativa - non-fragrant

Trait State in Taxon B

Oryza sativa - fragrant - variety from Taiwan and Japan

Ancestral State

Taxon A

Taxonomic Status

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

Taxon A

Latin Name

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

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; Oryzeae; Oryzinae; Oryza

Parent

Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527)

NCBI Taxonomy ID

4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

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; Oryzeae; Oryzinae; Oryza

Parent

Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527)

NCBI Taxonomy ID

4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Tainung 72; Shiratama

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

GO:0071454 : cellular response to anoxia

UniProtKB Oryza sativa subsp. japonica

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

GenebankID or UniProtKB

ALZ42021 (https://www.ncbi.nlm.nih.gov/nuccore/ALZ42021)

(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

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

Unknown

Molecular Details of the Mutation

C>T substitution in exon 13 - need to check the sequence to check if this mutation is nonsense or nonsynonymous

Experimental Evidence

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

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

Main Reference

The origin and evolution of fragrance in rice (Oryza sativa L.). (2009) (https://pubmed.ncbi.nlm.nih.gov/19706531)

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 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^BADH2^/and+Taxon ID=^4530^/or+Gene Gephebase=^BADH2^/and+Taxon ID=^4530^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

@Parallelism