

GEPHE SUMMARY

BADH2 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^BADH2^#gephebase-summary-title)	Gephebase Gene	GP00000134	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		
Oryza sativa indica and japonica - non-fragrant	Trait State in Taxon A		
Oryza sativa indica and japonica - fragrant	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
Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryza+sativa^#gephebase-summary-title)	Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryza+sativa^#gephebase-summary-title)	Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryza+sativa^#gephebase-summary-title)	Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryza+sativa^#gephebase-summary-title)
rice	Common Name	rice	Common Name
rice; red rice; Oryza sativa L.	Synonyms	rice; red rice; Oryza sativa L.	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; Oryzinae; Oryza	Lineage	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; Oryzinae; Oryza	Lineage
Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527)	Parent	Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527)	Parent
4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530)	NCBI Taxonomy ID	4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

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) ALZ42021 (https://www.ncbi.nlm.nih.gov/nuccore/ALZ42021)
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:0071454 : cellular response to anoxia (https://www.ebi.ac.uk/QuickGO/term/GO:0071454)	GO - Biological Process	
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 ([#gpepbase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=~Yes))

Molecular Type

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

Aberration Type

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

Deletion Size

1-9 bp

Molecular Details of the Mutation

8bp deletion resulting in premature stop codon

Experimental Evidence

Linkage Mapping ([#gpepbase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Linkage+Mapping))

Main Reference

The gene for fragrance in rice. (2005) (<https://pubmed.ncbi.nlm.nih.gov/17129318>)

Authors

Bradbury LM; Fitzgerald TL; Henry RJ; Jin Q; Waters DL

Abstract

The flavour or fragrance of basmati and jasmine rice is associated with the presence of 2-acetyl-1-pyrroline. A recessive gene (*fgr*) on chromosome 8 of rice has been linked to this important trait. Here, we show that a gene with homology to the gene that encodes betaine aldehyde dehydrogenase (BAD) has significant polymorphisms in the coding region of fragrant genotypes relative to non-fragrant genotypes. The accumulation of 2-acetyl-1-pyrroline in fragrant rice genotypes may be explained by the presence of mutations resulting in a loss of function of the *fgr* gene product. The allele in fragrant genotypes has a mutation introducing a stop codon upstream of key amino acid sequences conserved in other BADs. The *fgr* gene corresponds to the gene encoding BAD2 in rice, while BAD1 is encoded by a gene on chromosome 4. BAD has been linked to stress tolerance in plants. However, the apparent loss of function of BAD2 does not seem to limit the growth of fragrant rice genotypes. Fragrance in domesticated rice has apparently originated from a common ancestor and may have evolved in a genetically isolated population, or may be the outcome of a separate domestication event. This is an example of effective human selection for a recessive trait during domestication.

Additional References

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

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#gpepbase-summary-title>)

EXTERNAL LINKS

COMMENTS