

GEPHE SUMMARY

	Gephebase Gene	GephelD
OsC1 (https://www.gephebase.org/search-criteria/?and+Gene Gephebase=^OsC1^#gephebase-summary-title)	GP00000806	
	Entry Status	Main curator
Published	Martin	

PHENOTYPIC CHANGE

	Trait Category	
Morphology (https://www.gephebase.org/search-criteria/?and+Trait Category=^Morphology^#gephebase-summary-title)	Trait	
Coloration (loss of apiculus color) (https://www.gephebase.org/search-criteria/?and+Trait=^Coloration+(loss+of+apiculus+color)^#gephebase-summary-title)	Trait State in Taxon A	
Oryza sativa	Trait State in Taxon B	
Oryza sativa - var. japonica	Ancestral State	
Taxon A	Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria/?and+Taxonomic Status=^Domesticated^#gephebase-summary-title)		

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)	
rice	Common Name	rice	Common Name
rice; red rice; Oryza sativa L.	Synonyms	rice; red rice; Oryza sativa L.	Synonyms
species	Rank	species	Rank
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza	
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 Infraspecies?	Yes	is Taxon B an Infraspecies?
		Oryza sativa - var. japonica	Taxon B Description

GENOTYPIC CHANGE

C	Generic Gene Name	UniProtKB Oryza sativa
-	Synonyms	GenebankID or UniProtKB
-	String	
-	Sequence Similarities	
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)	GO - Molecular Function	
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)	GO - Biological Process	
-	GO - Cellular Component	
Yes (https://www.gephebase.org/search-criteria/?and+Presumptive+Null=^Yes^#gephebase-summary-title)		Presumptive Null

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=%5BCoding%5D#gephebase-summary-title)	Molecular Type
Deletion (https://www.gephebase.org/search-criteria?/and+Aberration Type=%5BDeletion%5D#gephebase-summary-title)	Aberration Type
1-9 bp	Deletion Size
2bp deletion	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=%5BLinkage Mapping%5D#gephebase-summary-title)	Experimental Evidence
Allelic diversification at the C (OsC1) locus of wild and cultivated rice: nucleotide changes associated with phenotypes. (2004) (https://pubmed.ncbi.nlm.nih.gov/15514070)	Main Reference
Saitoh K; Onishi K; Mikami I; Thidar K; Sano Y	Authors
Divergent phenotypes are often detected in domesticated plants despite the existence of invariant phenotypes in their wild forms. One such example in rice is the occurrence of varying degrees of apiculus coloration due to anthocyanin pigmentation, which was previously reported to be caused by a series of alleles at the C locus. The present study reveals, on the basis of comparison of its maps, that the C gene appears to be the rice homolog (OsC1) of maize C1, which belongs to the group of R2R3-Myb factors. Two different types of deletions causing a frameshift were detected in the third exon, and both of the deleted nucleotides corresponded to the positions of putative base-contacting residues, suggesting that the Indica and Japonica types carry loss-of-function mutations with independent origins. In addition, replacement substitutions were frequently detected in OsC1 of strains carrying the previously defined C alleles. Molecular population analysis revealed that 17 haplotypes were found in 39 wild and cultivated rices, and the haplotypes of most cultivated forms could be classified into one of three distinct groups, with few shared haplotypes among taxa, including Indica and Japonica types. The genealogy of the OsC1 gene suggests that allelic diversification causing phenotypic change might have resulted from mutations in the coding region rather than from recombination between preexisting alleles. The McDonald and Kreitman test revealed that the changes in amino acids might be associated with selective forces acting on the lineage of group A whose haplotypes were carried by most Asian cultivated forms. The results regarding a significant implication for genetic diversity in landraces of rice are also discussed.	Abstract
Genome-wide association studies of 14 agronomic traits in rice landraces. (2010) (https://pubmed.ncbi.nlm.nih.gov/20972439)	Additional References
A map of rice genome variation reveals the origin of cultivated rice. (2012) (https://pubmed.ncbi.nlm.nih.gov/23034647)	

RELATED GEPHE

2 (Bh4, Rc) (https://www.gephebase.org/search-criteria?/or+Taxon ID=%5E4530%5D/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=%5BOsC1%5D/and+Taxon ID=%5E4530%5D/or+Gene Gephebase=%5BOsC1%5D/and+Taxon ID=%5E4530%5D#gephebase-summary-title)	Related Haplotypes

EXTERNAL LINKS

COMMENTS