

GEPHE SUMMARY

<p>O_sC1 (<a href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^O<sub>s</sub>C1^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^O_sC1^#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00000806</p> <p>Martin</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

<p>Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Morphology^#gephebase-summary-title)</p> <p>Coloration (loss of apiculus color) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration+loss+of+apiculus+color^#gephebase-summary-title)</p> <p>Oryza sativa</p> <p>Oryza sativa - var. japonica</p> <p>Taxon A</p> <p>Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Domesticated^#gephebase-summary-title)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Taxon A</p> <p>Latin Name</p> <p>Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryza+sativa^#gephebase-summary-title)</p> <p>Common Name</p> <p>rice</p> <p>Synonyms</p> <p>rice; red rice; Oryza sativa L.</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; Oryzinae; Oryza</p> <p>Parent</p> <p>Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527)</p> <p>NCBI Taxonomy ID</p> <p>4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530)</p> <p>is Taxon A an Intraspecies?</p> <p>No</p>	<p>Taxon B</p> <p>Latin Name</p> <p>Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryza+sativa^#gephebase-summary-title)</p> <p>Common Name</p> <p>rice</p> <p>Synonyms</p> <p>rice; red rice; Oryza sativa L.</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; Oryzinae; Oryza</p> <p>Parent</p> <p>Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527)</p> <p>NCBI Taxonomy ID</p> <p>4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530)</p> <p>is Taxon B an Intraspecies?</p> <p>Yes</p> <p>Taxon B Description</p> <p>Oryza sativa - var. japonica</p>
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GENOTYPIC CHANGE

<p>C</p> <p>-</p> <p>-</p> <p>-</p> <p>GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)</p> <p>GO - Biological Process</p> <p>-</p> <p>GO - Cellular Component</p> <p>GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)</p> <p>Yes (https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^Yes^#gephebase-summary-title)</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p> <p>GO - Biological Process</p> <p>GO - Cellular Component</p>	<p>UniProtKB Oryza sativa</p> <p>Q76B79 (http://www.uniprot.org/uniprot/Q76B79)</p> <p>GenebankID or UniProtKB</p> <p>KJ934819 (https://www.ncbi.nlm.nih.gov/nucleotide/KJ934819)</p> <p>Presumptive Null</p>
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Coding ([https://www.gephebase.org/search-criteria?/and+Molecular+Type="+Coding+"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type=))

Molecular Type

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

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

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="+4530+"/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=))

Related Genes

1 ([https://www.gephebase.org/search-criteria?/or+Gene+Gephebase="+OsC1+"/and+Taxon+ID="+4530"/or+Gene+Gephebase="+OsC1"/and+Taxon+ID="+4530"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=))

Related Haplotypes

EXTERNAL LINKS

COMMENTS