

GEPHE SUMMARY

	Gephebase Gene	GephelD
SaM + SaF (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=%SaM + SaF%#gephebase-summary-title)	GP00001022	Main curator
Published	Entry Status	Martin

PHENOTYPIC CHANGE

	Trait Category	
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=%Physiology%#gephebase-summary-title)	Trait	
Hybrid incompatibility (F1 male sterility) (https://www.gephebase.org/search-criteria?/and+Trait=%Hybrid incompatibility (F1 male sterility)%#gephebase-summary-title)	Trait State in Taxon A	
Oryza sativa japonica	Trait State in Taxon B	
Oryza sativa indica	Ancestral State	
Data not curated	Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=%Domesticated%#gephebase-summary-title)		
Taxon A		Taxon B
Oryza sativa	Latin Name	Latin Name
(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=%Oryza sativa%#gephebase-summary-title)		
rice	Common Name	Common Name
rice; red rice; Oryza sativa L.	Synonyms	Synonyms
species	Rank	Rank
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza	Lineage	Lineage
Oryza () - (Rank: genus)	Parent	Parent
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527)	NCBI Taxonomy ID	NCBI Taxonomy ID
4530		
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530)		
Yes	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?
Oryza sativa japonica	Taxon A Description	Taxon B Description
	Oryza sativa indica	

GENOTYPIC CHANGE

SaF+	Generic Gene Name	UniProtKB Oryza sativa subsp. indica
-	Synonyms	B6RRX2 (http://www.uniprot.org/uniprot/B6RRX2)
-	String	GenebankID or UniProtKB
-	Sequence Similarities	ACA52286 (https://www.ncbi.nlm.nih.gov/nuccore/ACA52286)
-	GO - Molecular Function	
-	GO - Biological Process	
-	GO - Cellular Component	
-		Presumptive Null
Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=%Unknown%#gephebase-summary-title)		

Unknown (https://www.gephebase.org/search-criteria?/and+Molecular Type=%5EUnknown%23gephebase-summary-title)	Molecular Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=%5EUnknown%23gephebase-summary-title)	Aberration Type
Intron structure + aa changes on two adjacent coding genes	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=%5ELinkage Mapping%23gephebase-summary-title)	Experimental Evidence
Hybrid male sterility in rice controlled by interaction between divergent alleles of two adjacent genes. (2008) (https://pubmed.ncbi.nlm.nih.gov/19033192)	Main Reference
Long Y; Zhao L; Niu B; Su J; Wu H; Chen Y; Zhang Q; Guo J; Zhuang C; Mei M; Xia J; Wang L; Wu H; Liu YG	Authors
Sterility is common in hybrids between divergent populations, such as the indica and japonica subspecies of Asian cultivated rice (<i>Oryza sativa</i>). Although multiple loci for plant hybrid sterility have been identified, it remains unknown how alleles of the loci interact at the molecular level. Here we show that a locus for indica-japonica hybrid male sterility, <i>Sa</i> , comprises two adjacent genes, <i>SaM</i> and <i>SaF</i> , encoding a small ubiquitin-like modifier E3 ligase-like protein and an F-box protein, respectively. Most indica cultivars contain a haplotype <i>SaM(+)</i> <i>SaF(+)</i> , whereas all japonica cultivars have <i>SaM(-)</i> <i>SaF(-)</i> that diverged by nucleotide variations in wild rice. Male semi-sterility in this heterozygous complex locus is caused by abortion of pollen carrying <i>SaM(-)</i> . This allele-specific gamete elimination results from a selective interaction of <i>SaF(+)</i> with <i>SaM(-)</i> , a truncated protein, but not with <i>SaM(+)</i> because of the presence of an inhibitory domain, although <i>SaM(+)</i> is required for this male sterility. Lack of any one of the three alleles in recombinant plants does not produce male sterility. We propose a two-gene/three-component interaction model for this hybrid male sterility system. The findings have implications for overcoming male sterility in inter-subspecific hybrid rice breeding.	Abstract
Allele distributions at hybrid incompatibility loci facilitate the potential for gene flow between cultivated and weedy rice in the US. (2014) (https://pubmed.ncbi.nlm.nih.gov/24489758)	Additional References

RELATED GEPHE

2 (S5, S5 (ORF3-ORF4-ORF5 gene complex)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=%5E4530%23gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

The locus for indica-japonica hybrid male sterility, *Sa*; comprises two adjacent genes; *SaM* and *SaF*; encoding a small ubiquitin-like modifier E3 ligase-like protein and an F-box protein; respectively