

## GEPHE SUMMARY

**Gephebase Gene**  
qSW5

**Entry Status**  
Published

**GepheID**  
GP00000944

**Main curator**  
Martin

## PHENOTYPIC CHANGE

**Trait Category**  
Morphology

**Trait**  
Grain size

**Trait State in Taxon A**  
Oryza sativa indica - Kasalath

**Trait State in Taxon B**  
Oryza sativa japonica- Nipponbare

**Ancestral State**  
Taxon A

**Taxonomic Status**  
Domesticated

### Taxon A

**Latin Name**  
*Oryza sativa*

**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; Oryzaceae; Oryzinae; Oryza

**Parent**  
Oryza () - (Rank: genus)

**NCBI Taxonomy ID**  
4530

**is Taxon A an Intraspecies?**  
Yes

**Taxon A Description**  
Oryza sativa indica - Kasalath

### Taxon B

**Latin Name**  
*Oryza sativa*

**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; Oryzaceae; Oryzinae; Oryza

**Parent**  
Oryza () - (Rank: genus)

**NCBI Taxonomy ID**  
4530

**is Taxon B an Intraspecies?**  
Yes

**Taxon B Description**  
Oryza sativa japonica- Nipponbare

## GENOTYPIC CHANGE

**Generic Gene Name**  
qSW5

**Synonyms**  
-

**String**  
-

**Sequence Similarities**  
-

**GO - Molecular Function**  
-

**GO - Biological Process**  
-

**GO - Cellular Component**  
-

**Presumptive Null**

**UniProtKB** Oryza sativa subsp. japonica  
F8SPD1

**GenebankID or UniProtKB**  
AEI87386

Yes

**Molecular Type**  
Coding

**Aberration Type**  
Deletion

**Deletion Size**  
1-10 kb

**Molecular Details of the Mutation**  
1212bp deletion

**Experimental Evidence**  
Linkage Mapping

**Main Reference**  
[Deletion in a gene associated with grain size increased yields during rice domestication. \(2008\)](#)

**Authors**  
Shomura A; Izawa T; Ebana K; Ebitani T; Kanegae H; Konishi S; Yano M

**Abstract**  
The domestication of crops involves a complex process of selection in plant evolution and is associated with changes in the DNA regulating agronomically important traits. Here we report the cloning of a newly identified QTL, qSW5 (QTL for seed width on chromosome 5), involved in the determination of grain width in rice. Through fine mapping, complementation testing and association analysis, we found that a deletion in qSW5 resulted in a significant increase in sink size owing to an increase in cell number in the outer glume of the rice flower; this trait might have been selected by ancient humans to increase yield of rice grains. In addition, we mapped two other defective functional nucleotide polymorphisms of rice domestication-related genes with genome-wide RFLP polymorphisms of various rice landraces. These analyses show that the qSW5 deletion had an important historical role in artificial selection, propagation of cultivation and natural crossings in rice domestication, and shed light on how the rice genome was domesticated.

**Additional References**  
[Genome-wide association studies of 14 agronomic traits in rice landraces. \(2010\)](#)

## RELATED GEPHE

**Related Genes**  
[9 \(GL3.1, GS3, GS5, GW2, OsPPKL1/qGL3, OsSPL13, GL7, Os07g0603400, OsSPL16\)](#)  
**Related Haplotypes**  
No matches found.

## COMMENTS