GEPHE SUMMARY

Gephebase Gene
SLB1/2

GephelD
GP00001631

Entry Status
Published

Main curator
Prigent

PHENOTYPIC CHANGE

Trait Category
Physiology

Trait
Pathogen resistance (Root parasitic plant) (root parasitic plant)

Trait State in Taxon A
Rice cultivar Azucena exudes high strigolactone (SL) levels and induces high germination of the root parasitic plant Striga hermonthica. Azucena is a low-tillering variety as Sls inhibit shoot branching

Trait State in Taxon B
Rice cultivar Bala is a low strigolactone producer and stimulate less Striga germination. It is highly tillered

Ancestral State
Unknown

Taxonomic Status
Intraspecific

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; Oryzeae; Oryzinae; Oryza

Parent
Oryza () - (Rank: genus)

NCBI Taxonomy ID
4530

is Taxon A an Infraspecies?
Yes

Taxon A Description
Rice cultivar Azucena exudes high strigolactone (SL) levels and induces high germination of the root parasitic plant Striga hermonthica. Azucena is a low-tillering variety as Sls inhibit shoot branching

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; Oryzeae; Oryzinae; Oryza

Parent
Oryza () - (Rank: genus)

NCBI Taxonomy ID
4530

is Taxon B an Infraspecies?
Yes

Taxon B Description
Rice cultivar Bala is a low strigolactone producer and stimulate less Striga germination. It is highly tillered

GENOTYPIC CHANGE

Generic Gene Name
Os01g0700900

Synonyms
SLB1; Os01g0700900

String
-

Sequence Similarities
Belongs to the cytochrome P450 family.

GO - Molecular Function
GO:0020037 : heme binding
GO:0005506 : iron ion binding
GO:0004497 : monooxygenase activity

UniProtKB Oryza sativa subsp. japonica
M9R6D3

GenebankID or UniProtKB

GO:0016705 : oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen

GO - Biological Process

-

GO - Cellular Component

GO:0016021 : integral component of membrane

Presumptive Null

Yes

Molecular Type

Gene Loss

Aberration Type

Deletion

Deletion Size

10-100 kb

Molecular Details of the Mutation

deletion of 2 cytochrome P450 genes (Os010700900 & Os01g0701400)

Experimental Evidence

Linkage Mapping

Main Reference

Natural variation of rice strigolactone biosynthesis is associated with the deletion of two MAX1 orthologs. (2014)

Authors

Cardoso C; Zhang Y; Jamil M; Hepworth J; Charnikhova T; Dimkpa SO; Meharg C; Wright MH; Liu J; Meng X; Wang Y; Li J; McCouch SR; Leyser O; Price AH; Bouwmeester HJ; Ruyter-Spira C

Abstract

Rice (Oryza sativa) cultivar Azucena--belonging to the Japonica subspecies--exudes high strigolactone (SL) levels and induces high germination of the root parasitic plant Striga hermonthica. Consistent with the fact that SLs also inhibit shoot branching, Azucena is a low-tillering variety. In contrast, Bala, an Indica cultivar, is a low-SL producer, stimulates less Striga germination, and is highly tillered. Using a Bala Ã— Azucena F6 population, a major quantitative trait loci--qSLB1.1--for the exudation of SL, tillering, and induction of Striga germination was detected on chromosome 1. Sequence analysis of the corresponding locus revealed a rearrangement of a 51- to 59-kbp stretch between 28.9 and 29 Mbp in the Bala genome, resulting in the deletion of two cytochrome P450 genes--SLB1 and SLB2--with high homology to the Arabidopsis SL biosynthesis gene, MAX1. Both rice genes rescue the Arabidopsis max1-1 highly branched mutant phenotype and increase the production of the SL, ent-2′-epi-5-deoxystrigol, when overexpressed in Bala. Furthermore, analysis of this region in 367 cultivars of the publicly available Rice Diversity Panel population shows that the rearrangement at this locus is a recurrent natural trait associated with the Indica/Japonica divide in rice.

Additional References

RELATED GEPHE

Related Genes

15 (Pi-ta, Pi2 (Nbs4-Pi2), Pi36, Pi37, Pi5-1 + Pi5-2 cluster, Pi9 (= Nbs2-Pi9), Pib, Pid3, PigmR, Pikm1-TS + Pikm2-TS cluster, Pit, Piz-t, Xa1, Xa21, Xa26)

Related Haplotypes

No matches found.

COMMENTS

homologs of Arabidopsis strigolactone biosynthesis gene MAX1