

GEPHE SUMMARY

<p>PRR37 pseudoresponse regulator protein 37 (#Gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00001632</p> <p>Prigent</p>	<p>GepheID</p> <p>Main curator</p>
--	---	----------------------------------	------------------------------------

PHENOTYPIC CHANGE

<p>Physiology (#Gephebase-summary-title)</p> <p>Flowering time (heading date) (https://www.gephebase.org/search-criteria?/and+Trait=Flowering time (heading date)#Gephebase-summary-title)</p> <p>Middle-late-flowering Tongil-type (japonica/indica hybrid) rice Milyang23 (116 days)</p> <p>Extremely early-flowering japonica rice H143 (74 days)</p> <p>Taxon A</p> <p>Domesticated (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>Oryza sativa (#Gephebase-summary-title)</p> <p>rice</p> <p>rice; red rice; <i>Oryza sativa</i> L.</p> <p>species</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>Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527)</p> <p>4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530)</p> <p>is Taxon A an Intraspecies?</p> <p>Yes</p> <p>Middle-late-flowering Tongil-type (japonica/indica hybrid) rice Milyang23 (116 days)</p>	<p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Rank</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p> <p>is Taxon B an Intraspecies?</p> <p>Taxon B Description</p>	<p>Taxon B</p> <p>Oryza sativa Japonica Group (#Gephebase-summary-title)</p> <p>Japanese rice</p> <p>Oryza sativa (japonica cultivar-group); Oryza sativa subsp. japonica; Japanese rice; Japonica rice; Oryza sativa (japonica cultivar-group); Oryza sativa japonica; Oryza sativa ssp. japonica</p> <p>no rank</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; Oryza sativa</p> <p>Oryza sativa (rice) - (Rank: species) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530)</p> <p>39947 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=39947)</p> <p>is Taxon B an Intraspecies?</p> <p>Yes</p> <p>Extremely early-flowering japonica rice H143 (74 days)</p>	<p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Rank</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p> <p>is Taxon B an Intraspecies?</p> <p>Taxon B Description</p>
--	---	--	---	--	---

GENOTYPIC CHANGE

<p>PRR37</p> <p>PRR37; OsPRR37; DTH7; HD2; Os07g0695100; LOC_Os07g49460; P0627E10.21</p> <p>39947.LOC_Os07g49460.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=39947.LOC_Os07g49460.1)</p> <p>Belongs to the ARR-like family.</p> <p>-</p> <p>GO:0009908 : flower development (https://www.ebi.ac.uk/QuickGO/term/GO:0009908)</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>UniProtKB Oryza sativa subsp. japonica Q0D3B6 (http://www.uniprot.org/uniprot/Q0D3B6)</p> <p>()</p> <p>GenebankID or UniProtKB</p>
---	---	---

GO:0000160 : phosphorelay signal transduction system
 (https://www.ebi.ac.uk/QuickGO/term/GO:0000160)
 GO:0009585 : red, far-red light phototransduction
 (https://www.ebi.ac.uk/QuickGO/term/GO:0009585)
 GO:0048579 : negative regulation of long-day photoperiodism, flowering
 (https://www.ebi.ac.uk/QuickGO/term/GO:0048579)
 GO:0048511 : rhythmic process (https://www.ebi.ac.uk/QuickGO/term/GO:0048511)
 GO - Cellular Component
 GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title)

Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)

Aberration Type

SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title)

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Nonfunctional allele PRR37-2a: L710P missense mutation in the CONSTANS-Co-like and TOC1 domain of the protein

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Natural variation in OsPRR37 regulates heading date and contributes to rice cultivation at a wide range of latitudes. (2013) (https://pubmed.ncbi.nlm.nih.gov/23713079)

Authors

Koo BH; Yoo SC; Park JW; Kwon CT; Lee BD; An G; Zhang Z; Li J; Li Z; Paek NC

Abstract

Heading date and photoperiod sensitivity are fundamental traits that determine rice adaptation to a wide range of geographic environments. By quantitative trait locus (QTL) mapping and candidate gene analysis using whole-genome re-sequencing, we found that *Oryza sativa* Pseudo-Response Regulator37 (OsPRR37; hereafter PRR37) is responsible for the Early heading7-2 (EH7-2)/Heading date2 (Hd2) QTL which was identified from a cross of late-heading rice 'Milyang23 (M23)' and early-heading rice 'H143'. H143 contains a missense mutation of an invariantly conserved amino acid in the CCT (CONSTANS, CO-like, and TOC1) domain of PRR37 protein. In the world rice collection, different types of nonfunctional PRR37 alleles were found in many European and Asian rice cultivars. Notably, the japonica varieties harboring nonfunctional alleles of both Ghd7/Hd4 and PRR37/Hd2 flower extremely early under natural long-day conditions, and are adapted to the northernmost regions of rice cultivation, up to 53° N latitude. Genetic analysis revealed that the effects of PRR37 and Ghd7 alleles on heading date are additive, and PRR37 down-regulates Hd3a expression to suppress flowering under long-day conditions. Our results demonstrate that natural variations in PRR37/Hd2 and Ghd7/Hd4 have contributed to the expansion of rice cultivation to temperate and cooler regions.

Additional References

RELATED GEPHE

Related Genes

9 (DTH2, EARLY FLOWERING 3/Hd17, Hd1, Hd6a, se5, Early flowering1 (EL1), HEADING DATE 1, Ehd1 (Response regulator), Ghd7) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^4530^/and+Trait=Flowering time/or+Taxon ID=^39947^/and+Trait=Flowering time/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

3 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^PRR37 pseudoresponse regulator protein 37^/and+Taxon ID=^4530^/or+Gene Gephebase=^PRR37 pseudoresponse regulator protein 37^/and+Taxon ID=^39947^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

@GxE

