

GEPHE SUMMARY

<p>NRT1.1B (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=NRT1.1B#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00001375</p> <p>Prigent</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

<p>Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=Physiology#gephebase-summary-title)</p> <p>Nitrogen use (metabolism) (https://www.gephebase.org/search-criteria?/and+Trait=Nitrogen+use+(metabolism)#gephebase-summary-title)</p> <p>Rice ; O. s. japonica ; Nipponbare ; low nitrate absorption</p> <p>Rice- O. s. indica ; IR24 ; high nitrate absorption</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>Yes</p> <p>Taxon A Description</p> <p>Rice ; O. s. japonica ; Nipponbare ; low nitrate absorption</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>Rice- O. s. indica ; IR24 ; high nitrate absorption</p>
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GENOTYPIC CHANGE

<p>NPF6.3</p> <p>ARABIDOPSIS THALIANA NITRATE TRANSPORTER 1; AtNPF6.3; ATNRT1; ATNRT1.1; B-1; CHL1; CHL1-1; CHLORATE/NITRATE TRANSPORTER; CHLORINA 1; F12F1.1; F12F1_1; NITRATE TRANSPORTER 1; nitrate transporter 1.1; NITRATE/CHLORATE TRANSPORTER; NPF6.3; NRT1; NRT1/ PTR family 6.3; NRT1.1; At1g12110; T28K15_13</p> <p>String</p> <p>3702.AT1G12110.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT1G12110.1)</p> <p>Sequence Similarities</p> <p>Belongs to the PTR2/POT transporter (TC 2.A.17) family.</p> <p>GO - Molecular Function</p> <p>GO:0015293 : symporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0015293)</p> <p>GO:0015112 : nitrate transmembrane transporter activity</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p>	<p>UniProtKB Arabidopsis thaliana</p> <p>Q05085 (http://www.uniprot.org/uniprot/Q05085)</p> <p>GenebankID or UniProtKB</p> <p>0</p>
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(<https://www.ebi.ac.uk/QuickGO/term/GO:0015112>)

GO - Biological Process

GO:0009734 : auxin-activated signaling pathway

(<https://www.ebi.ac.uk/QuickGO/term/GO:0009734>)

GO:0009414 : response to water deprivation

(<https://www.ebi.ac.uk/QuickGO/term/GO:0009414>)

GO:0006857 : oligopeptide transport

(<https://www.ebi.ac.uk/QuickGO/term/GO:0006857>)

GO:0042128 : nitrate assimilation (<https://www.ebi.ac.uk/QuickGO/term/GO:0042128>)

GO:0015706 : nitrate transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0015706>)

GO:0009635 : response to herbicide (<https://www.ebi.ac.uk/QuickGO/term/GO:0009635>)

GO:0010167 : response to nitrate (<https://www.ebi.ac.uk/QuickGO/term/GO:0010167>)

GO - Cellular Component

GO:0016021 : integral component of membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)

Presumptive Null

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null+No^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null+No^#gephebase-summary-title))

Molecular Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

c.980C>T p.Met327Thr

Experimental Evidence

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+Linkage+Mapping^#gephebase-summary-title))

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

Main Reference

Variation in NRT1.1B contributes to nitrate-use divergence between rice subspecies. (2015) (<https://pubmed.ncbi.nlm.nih.gov/26053497>)

Authors

Hu B; Wang W; Ou S; Tang J; Li H; Che R; Zhang Z; Chai X; Wang H; Wang Y; Liang C; Liu L; Piao Z; Deng Q; Deng K; Xu C; Liang Y; Zhang L; Li L; Chu C

Abstract

Asian cultivated rice (*Oryza sativa* L.) consists of two main subspecies, indica and japonica. Indica has higher nitrate-absorption activity than japonica, but the molecular mechanisms underlying that activity remain elusive. Here we show that variation in a nitrate-transporter gene, NRT1.1B (*OsNPF6.5*), may contribute to this divergence in nitrate use. Phylogenetic analysis revealed that NRT1.1B diverges between indica and japonica. NRT1.1B-indica variation was associated with enhanced nitrate uptake and root-to-shoot transport and upregulated expression of nitrate-responsive genes. The selection signature of NRT1.1B-indica suggests that nitrate-use divergence occurred during rice domestication. Notably, field tests with near-isogenic and transgenic lines confirmed that the japonica variety carrying the NRT1.1B-indica allele had significantly improved grain yield and nitrogen-use efficiency (NUE) compared to the variety without that allele. Our results show that variation in NRT1.1B largely explains nitrate-use divergence between indica and japonica and that NRT1.1B-indica can potentially improve the NUE of japonica.

Additional References

RELATED GEPHE

Related Genes

1 (DEP1 (DENSE AND ERECT PANICLES 1)) ([https://www.gephebase.org/search-criteria?/or+Taxon ID+4530^/and+Trait=Nitrogen use/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID+4530^/and+Trait+Nitrogen+use/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Wild ancestors are *O. rufipogon*-I and *O. rufipogon*-III in which the SNP was polymorphic; the variant of indica has probably been selected during domestication

