GEPHE SUMMARY

Gephebase Gene

Nramp aluminum transporter1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Nramp aluminum transporter1^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00000740

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

Metal tolerance (https://www.gephebase.org/search-criteria?/and+Trait=^Metal tolerance^#gephebase-summary-title)

Trait State in Taxon A

Oryza sativa indica

Trait State in Taxon B

Oryza sativa - japonica

Ancestral State

Data not curated

Taxonomic Status

Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)

Taxon A

Latin Name

Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Oryza sativa^#gephebase-summary-title)

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) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527)

NCBI Taxonomy ID

4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Oryza sativa indica

Taxon B

Latin Name

Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Oryza sativa^#gephebase-summary-title)

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) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527)

NCBI Taxonomy ID

4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Oryza sativa - japonica

GENOTYPIC CHANGE

Generic Gene Name

NRAT1

Synonyms

Nrat1; OsJ_05257; OJ1007_D04.24; Os02g0131800; LOC_Os02g03900

String

39947.LOC_Os02g03900.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 39947.LOC_Os02g03900.1)

Sequence Similarities

Belongs to the NRAMP (TC 2.A.55) family.

GO - Molecular Function

GO:0015086 : cadmium ion transmembrane transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0015086)
GO:0015083 : aluminum ion transmembrane transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0015083)
GO:0005384 : manganese ion transmembrane transporter activity

UniProtKB Oryza sativa subsp. japonica

Q6ZG85 (http://www.uniprot.org/uniprot/Q6ZG85)

GenebankID or UniProtKB

()

(https://www.ebi.ac.uk/QuickGO/term/GO:0005384)

GO - Biological Process

GO:0015690 : aluminum cation transport
(https://www.ebi.ac.uk/QuickGO/term/GO:0015690)
GO:0034755 : iron ion transmembrane transport
(https://www.ebi.ac.uk/QuickGO/term/GO:0034755)
GO:0010044 : response to aluminum ion
(https://www.ebi.ac.uk/QuickGO/term/GO:0010044)

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)

Mutation #1

Presumptive Null

No (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)

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

3a.a. substitutions found in all tolerant lines - amino acid change with predicted effect = polymorphism #16 C>T causing Val500Ala and at least one of the other two amino acid changes as Val500Ala alone is found in non-tolerant plants

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	Val	Ala	500

Main Reference

Genetic architecture of aluminum tolerance in rice (Oryza sativa) determined through genome-wide association analysis and QTL mapping. (2011)
(https://pubmed.ncbi.nlm.nih.gov/21829395)

Authors

Famoso AN; Zhao K; Clark RT; Tung CW; Wright MH; Bustamante C; Kochian LV; McCouch SR

Abstract

Aluminum (Al) toxicity is a primary limitation to crop productivity on acid soils, and rice has been demonstrated to be significantly more Al tolerant than other cereal crops. However, the mechanisms of rice Al tolerance are largely unknown, and no genes underlying natural variation have been reported. We screened 383 diverse rice accessions, conducted a genome-wide association (GWA) study, and conducted QTL mapping in two bi-parental populations using three estimates of Al tolerance based on root growth. Subpopulation structure explained 57% of the phenotypic variation, and the mean Al tolerance in Japonica was twice that of Indica. Forty-eight regions associated with Al tolerance were identified by GWA analysis, most of which were subpopulation-specific. Four of these regions co-localized with a priori candidate genes, and two highly significant regions co-localized with previously identified QTLs. Three regions corresponding to induced Al-sensitive rice mutants (ART1, STAR2, Nrat1) were identified through bi-parental QTL mapping or GWA to be involved in natural variation for Al tolerance. Haplotype analysis around the Nrat1 gene identified susceptible and tolerant haplotypes explaining 40% of the Al tolerance variation within the aus subpopulation, and sequence analysis of Nrat1 identified a trio of non-synonymous mutations predictive of Al sensitivity in our diversity panel. GWA analysis discovered more phenotype-genotype associations and provided higher resolution, but QTL mapping identified critical rare and/or subpopulation-specific alleles not detected by GWA analysis. Mapping using Indica/Japonica populations identified QTLs associated with transgressive variation where alleles from a susceptible aus or indica parent enhanced Al tolerance in a tolerant Japonica background. This work supports the hypothesis that selectively introgressing alleles across subpopulations is an efficient approach for trait enhancement in plant breeding programs and demonstrates the fundamental importance of subpopulation in interpreting and manipulating the genetics of complex traits in rice.

Additional References

Mutation #2

Presumptive Null

No (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)

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

3a.a. substitutions found in all tolerant lines - amino acidchange with predicted effect = polymorphism nucl. C16T causing Val500Ala and at least one of the other two amino acid changes as Val500Ala alone is found in non-tolerant plants

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

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Additional References

RELATED GEPHE

Related Genes

1 (heavy metal atpase3 (HMA3)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^4530^/and+Trait=Metal tolerance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect