GEPHE SUMMARY

Gephebase Gene

Enhanced shoot growth under mannitol stress 2 (EGM2) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Enhanced shoot growth under mannitol stress 2 (EGM2)^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001630

Main curator

Prigent

PHENOTYPIC CHANGE

Trait Category

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

Trait

Plant growth (shoot growth under stress) (https://www.gephebase.org/search-criteria?/and+Trait=^Plant growth (shoot growth under stress)^#gephebase-summary-title)

Trait State in Taxon A

Arabidopsis thaliana Col-0 accession sensitive to mannitol

Trait State in Taxon B

Arabidopsis thaliana Cvi-0 accession and 10 others of various origins with specific tolerance to mannitol

Ancestral State

Taxon A

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

thale cress

Synonyms

thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis

Parent

Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)

NCBI Taxonomy ID

3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Arabidopsis thaliana Col-0 accession

Taxon B

Latin Name

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

Common Name

thale cress

Synonyms

thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis

Parent

Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)

NCBI Taxonomy ID

3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Arabidopsis thaliana Cvi-0 accession and 10 others of various origins with specific tolerance to mannitol

GENOTYPIC CHANGE

Generic Gene Name

At1g11300

Synonyms

EGM1; enhanced shoot growth under mannitol stress 1; T28P6.6; T28P6_6; At1g11300

String

-

Sequence Similarities

Belongs to the protein kinase superfamily. Ser/Thr protein kinase family.

GO - Molecular Function

GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)
GO:0030246 : carbohydrate binding (https://www.ebi.ac.uk/QuickGO/term/GO:0030246)
GO:0005516 : calmodulin binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005516)

UniProtKB Arabidopsis thaliana

Q9SXB4 (http://www.uniprot.org/uniprot/Q9SXB4)

GenebankID or UniProtKB

()

GO:0004674 : protein serine/threonine kinase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004674)

GO - Biological Process

GO:0006468 : protein phosphorylation (https://www.ebi.ac.uk/QuickGO/term/GO:0006468)

GO:0048544 : recognition of pollen (https://www.ebi.ac.uk/QuickGO/term/GO:0048544)

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

2 non-synonymous mutations Ser149Gly and Cys345Gly responsible for hypo-functionality

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	Ser	Gly	149

Main Reference

A pair of receptor-like kinases is responsible for natural variation in shoot growth response to mannitol treatment in Arabidopsis thaliana. (2014) (https://pubmed.ncbi.nlm.nih.gov/24479634)

Authors

Trontin C; Kiani S; Corwin JA; HÃ©maty K; Yansouni J; Kliebenstein DJ; Loudet O

Abstract

Growth is a complex trait that adapts to the prevailing conditions by integrating many internal and external signals. Understanding the molecular origin of this variation remains a challenging issue. In this study, natural variation of shoot growth under mannitol-induced stress was analyzed by standard quantitative trait locus mapping methods in a recombinant inbred line population derived from a cross between the Col-0 and Cvi-0 Arabidopsis thaliana accessions. Cloning of a major QTL specific to mannitol-induced stress condition led to identification of EGM1 and EGM2, a pair of tandem-duplicated genes encoding receptor-like kinases that are potentially involved in signaling of mannitol-associated stress responses. Using various genetic approaches, we identified two non-synonymous mutations in the EGM2[Cvi] allele that are shared by at least ten accessions from various origins and are probably responsible for a specific tolerance to mannitol. We have shown that the enhanced shoot growth phenotype contributed by the Cvi allele is not linked to generic osmotic properties but instead to a specific chemical property of mannitol itself. This result raises the question of the function of such a gene in A.Â thaliana, a species that does not synthesize mannitol. Our findings suggest that the receptor-like kinases encoded by EGM genes may be activated by mannitol produced by pathogens such as fungi, and may contribute to plant defense responses whenever mannitol is present.

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

2 non-synonymous mutations Ser149Gly and Cys345Gly responsible for hypo-functionality

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	Cys	Gly	345

Main Reference

A pair of receptor-like kinases is responsible for natural variation in shoot growth response to mannitol treatment in Arabidopsis thaliana. (2014) (https://pubmed.ncbi.nlm.nih.gov/24479634)

Authors

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Additional References

RELATED GEPHE

Related Genes

5 (EARLY FLOWERING 3(ELF3) [possible pseudo-replicate], IIL1, TZP, FUMARASE 2, ICARUS1) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^3702^/and+Trait=Plant growth/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS