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.

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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