GEPHE SUMMARY

Gephebase Gene

FUMARASE 2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^FUMARASE 2^#gephebase-summary-title)

GepheID

GP00001286

Entry Status

Published

Main curator

Arnoult

PHENOTYPIC CHANGE

Trait #1

Trait Category

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

Trait

Plant metabolism (fumarate/malate ratio) (https://www.gephebase.org/search-criteria?/and+Trait=^Plant metabolism (fumarate/malate ratio)^#gephebase-summary-title)

Trait State in Taxon A

Arabidopsis thaliana- Col-0

Trait State in Taxon B

Arabidopsis thaliana- C24

Trait #2

Trait Category

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

Trait

Plant growth (bio-mass production) (https://www.gephebase.org/search-criteria?/and+Trait=^Plant growth (bio-mass production)^#gephebase-summary-title)

Trait State in Taxon A

-

Trait State in Taxon B

-

Ancestral State

Unknown

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

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- C24

GENOTYPIC CHANGE

Generic Gene Name

FUM2

Synonyms

FUMARASE 2; K3K7.11; K3K7_11; At5g50950

String

3702.AT5G50950.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT5G50950.1)

Sequence Similarities

Belongs to the class-II fumarase/aspartase family. Fumarase subfamily.

GO - Molecular Function

GO:0004333 : fumarate hydratase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004333)

GO - Biological Process

GO:0009651 : response to salt stress (https://www.ebi.ac.uk/QuickGO/term/GO:0009651)
GO:0009631 : cold acclimation (https://www.ebi.ac.uk/QuickGO/term/GO:0009631)
GO:0006099 : tricarboxylic acid cycle (https://www.ebi.ac.uk/QuickGO/term/GO:0006099)
GO:0006106 : fumarate metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0006106)
GO:0006108 : malate metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0006108)
GO:0042128 : nitrate assimilation (https://www.ebi.ac.uk/QuickGO/term/GO:0042128)
GO:0010109 : regulation of photosynthesis (https://www.ebi.ac.uk/QuickGO/term/GO:0010109)

GO - Cellular Component

GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)
GO:0005739 : mitochondrion (https://www.ebi.ac.uk/QuickGO/term/GO:0005739)
GO:0009507 : chloroplast (https://www.ebi.ac.uk/QuickGO/term/GO:0009507)
GO:0045239 : tricarboxylic acid cycle enzyme complex (https://www.ebi.ac.uk/QuickGO/term/GO:0045239)

UniProtKB Arabidopsis thaliana

Q9FI53 (http://www.uniprot.org/uniprot/Q9FI53)

GenebankID or UniProtKB

835168 (https://www.ncbi.nlm.nih.gov/nuccore/835168)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Indel Size

1-10 kb

Molecular Details of the Mutation

2068 bp in promotor region @position -395. AND 3833bp in promotor region @position -1107

Experimental Evidence

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

Main Reference

A naturally occurring promoter polymorphism of the Arabidopsis FUM2 gene causes expression variation, and is associated with metabolic and growth traits. (2016) (https://pubmed.ncbi.nlm.nih.gov/27520391)

Authors

Riewe D; Jeon HJ; Lisec J; Heuermann MC; Schmeichel J; Seyfarth M; Meyer RC; Willmitzer L; Altmann T

Abstract

Fumarate and malate are known intermediates of the TCA cycle, a mitochondrial metabolic pathway generating NADH for respiration. Arabidopsis thaliana and other Brassicaceae contain an additional cytosolic fumarase (FUM2) that functions in carbon assimilation and nitrogen use. Here, we report the identification of a hitherto unknown FUM2 promoter insertion/deletion (InDel) polymorphism found between the Col-0Â and C24 accessions, which also divides a large number of Arabidopsis accessions carrying either the Col-0 or the C24 allele. The polymorphism consists of two stretches of 2.1 and 3.8Â kb, which are both absent from the promotor region of Col-0 FUM2. By analysing mutants as well as mapping and natural populations with contrasting FUM2 alleles, the promotor insertion was linked to reduced FUM2 mRNA expression, reduced fumarase activity and reduced fumarate/malate ratio in leaves. In a large population of 174 natural accessions, the polymorphism was also found to be associated with the fumarate/malate ratio, malate and fumarate levels, and with dry weight at 15Â days after sowing (DAS). The association with biomass production was confirmed in an even larger (251) accession population for dry weight at 22Â DAS. The dominant Col-0 allele that results in increased fumarate/malate ratios and enhanced biomass production is predominantly found in central/eastern European accessions, whereas the C24 type allele is prevalent on the Iberian Peninsula, west of the Rhine and in the British Isles. Our findings support the role of FUM2 in diurnal carbon storage, and point to a growth advantage of accessions carrying the FUM2 Col-0 allele.

Additional References

Identification of metabolic and biomass QTL in Arabidopsis thaliana in a parallel analysis of RIL and IL populations. (2008) (https://pubmed.ncbi.nlm.nih.gov/18047556)

RELATED GEPHE

Related Genes

5 (EARLY FLOWERING 3(ELF3) [possible pseudo-replicate], Enhanced shoot growth under mannitol stress 2 (EGM2), IIL1, TZP, ICARUS1) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^3702^/and+Trait=Plant metabolism/or+Taxon ID=^3702^/and+Trait=Plant growth/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

FUM2 identified by QTL 18047556; 21536339. Indel identified by PCR in this paper. in FUM2 mRNA levels ~169 higher in Col-0 than in C24