

GEPHE SUMMARY

Gephebase Gene	GepheID
FUMARASE 2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase= [^] FUMARASE 2 [#] gephebase-summary-title)	GP00001286
Entry Status	Main curator
Published	Arnoult

PHENOTYPIC CHANGE

Trait #1	Trait Category
Plant metabolism (fumarate/malate ratio) (https://www.gephbase.org/search-criteria/?and+Trait Category=^Physiology^#gephbase-summary-title)	Trait
Arabidopsis thaliana- Col-0	Trait State in Taxon A
Arabidopsis thaliana- C24	Trait State in Taxon B

Trait #2	Trait Category
Physiology (https://www.gephbase.org/search-criteria/?and+Trait+Category=%5EPhysiology%23gephbase-summary-title)	Trait
Plant growth (bio-mass production) (https://www.gephbase.org/search-criteria/?and+Trait=%5EPlant+growth+(bio-mass+production)%23gephbase-summary-title)	Trait State in Taxon A
-	Trait State in Taxon B
-	Trait State in Taxon B

Ancestral State		Taxonomic Status	
Taxon A	Latin Name	Taxon B	Latin Name
Unknown			
Intraspecific (https://www.gephbase.org/search-criteria/?and+Taxonomic Status=^Intraspecific^#gephbase-summary-title)			
Common Name		Common Name	
Arabidopsis thaliana (https://www.gephbase.org/search-criteria/?and+Taxon and Synonyms=^Arabidopsis thaliana^#gephbase-summary-title)	thale cress	Arabidopsis thaliana (https://www.gephbase.org/search-criteria/?and+Taxon and Synonyms=^Arabidopsis thaliana^#gephbase-summary-title)	thale cress
Synonyms		Synonyms	
thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbopsis thaliana; thale kress		thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbopsis thaliana; thale kress	
Rank		Rank	
species	Lineage	species	Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicots; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelinae; Arabidopsis		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicots; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelinae; Arabidopsis	
Parent		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)	Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)	NCBI Taxonomy ID 3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)
is Taxon A Infraspecies?		is Taxon B Infraspecies?	
Yes	Taxon A Description Arabidopsis thaliana- Col-0	Yes	Taxon B Description Arabidopsis thaliana- C24

GENOTYPIC CHANGE

FUM2	Generic Gene Name Synonyms String	UniProtKB Arabidopsis thaliana GenebankID or UniProtKB 835168 (https://www.ncbi.nlm.nih.gov/nuccore/835168)
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:0004333 : fumarate hydratase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004333)	GO - Molecular Function	
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 - Biological Process	
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)	GO - Cellular Component	Presumptive Null
No (https://www.gephebase.org/search-criteria/?and+Presumptive Null=%27No%27#gephebase-summary-title)		Molecular Type
Cis-regulatory (https://www.gephebase.org/search-criteria/?and+Molecular Type=%27Cis-regulatory%27#gephebase-summary-title)		Aberration Type
Indel (https://www.gephebase.org/search-criteria/?and+Aberration Type=%27Indel%27#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=%27Linkage Mapping%27#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
Rieve 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-0A 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 3.8 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 15 days after sowing (DAS). The association with biomass production was confirmed in an even larger (251) accession population for dry weight at 22 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.		

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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

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=%273702%27+and+Trait=Plant metabolism+or+Taxon ID=%273702%27+and+Trait=Plant growth+and+groupHaplotypes=true#gephebase-summary-title)	Related Genes 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