GEPHE SUMMARY

Gephebase Gene

AGAMOUS-LIKE 50 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^AGAMOUS-LIKE 50^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001450

Main curator

Prigent

PHENOTYPIC CHANGE

Trait Category

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

Trait

Leaf number (at flowering time) (https://www.gephebase.org/search-criteria?/and+Trait=^Leaf number (at flowering time)^#gephebase-summary-title)

Trait State in Taxon A

Arabidopsis thaliana reference (TueWa1-2 & TueScha-9 & Yeg-1) with Leaf Number n=24.9

Trait State in Taxon B

Arabidopsis thaliana nonreference (ICE92 & ICE228 & ICE72) with increased Leaf Number n=35.1

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 reference (TueWa1-2 & TueScha-9 & Yeg-1) with Leaf Number n=24.9

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 nonreference (ICE92 & ICE228 & ICE72) with increased Leaf Number n=35.1

GENOTYPIC CHANGE

Generic Gene Name

AGAMOUS-like 50

Synonyms

AGAMOUS-like 50; F23H11.13; F23H11_13; AGL50; At1g59810

String

3702.AT1G59810.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT1G59810.1)

Sequence Similarities

-

GO - Molecular Function

GO:0046983 : protein dimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046983)

UniProtKB Arabidopsis thaliana

Q9XIE7 (http://www.uniprot.org/uniprot/Q9XIE7)

GenebankID or UniProtKB

()

GO:0003700 : DNA-binding transcription factor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0003700)
GO:0043565 : sequence-specific DNA binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0043565)
GO:0008134 : transcription factor binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0008134)
GO:0000982 : transcription factor activity, RNA polymerase II proximal promoter sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000982)
GO:0044212 : transcription regulatory region DNA binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0044212)
GO:0000987 : proximal promoter sequence-specific DNA binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0000987)

GO - Biological Process

GO:0007275 : multicellular organism development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007275)
GO:0045944 : positive regulation of transcription by RNA polymerase II
(https://www.ebi.ac.uk/QuickGO/term/GO:0045944)
GO:0009909 : regulation of flower development
(https://www.ebi.ac.uk/QuickGO/term/GO:0009909)
GO:0010048 : vernalization response
(https://www.ebi.ac.uk/QuickGO/term/GO:0010048)

GO - Cellular Component

GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)

Presumptive Null

Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title)

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

unknown

Experimental Evidence

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

Main Reference

Genetic architecture of nonadditive inheritance in Arabidopsis thaliana hybrids. (2016) (https://pubmed.ncbi.nlm.nih.gov/27803326)

Authors

Seymour DK; Chae E; Grimm DG; MartÃn Pizarro C; Habring-MÃ¼ller A; Vasseur F; Rakitsch B; Borgwardt KM; Koenig D; Weigel D

Abstract

The ubiquity of nonparental hybrid phenotypes, such as hybrid vigor and hybrid inferiority, has interested biologists for over a century and is of considerable agricultural importance. Although examples of both phenomena have been subject to intense investigation, no general model for the molecular basis of nonadditive genetic variance has emerged, and prediction of hybrid phenotypes from parental information continues to be a challenge. Here we explore the genetics of hybrid phenotype in 435 Arabidopsis thaliana individuals derived from intercrosses of 30 parents in a half diallel mating scheme. We find that nonadditive genetic effects are a major component of genetic variation in this population and that the genetic basis of hybrid phenotype can be mapped using genome-wide association (GWA) techniques. Significant loci together can explain as much as 20% of phenotypic variation in the surveyed population and include examples that have both classical dominant and overdominant effects. One candidate region inherited dominantly in the half diallel contains the gene for the MADS-box transcription factor AGAMOUS-LIKE 50 (AGL50), which we show directly to alter flowering time in the predicted manner. Our study not only illustrates the promise of GWA approaches to dissect the genetic architecture underpinning hybrid performance but also demonstrates the contribution of classical dominance to genetic variance.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS