GEPHE SUMMARY

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

GepheID
GP00001450

Entry Status
Published

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