

GEPHE SUMMARY

ACS11 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^ACS11^#gephebase-summary-title)	Gephebase Gene	GP00001235	GepheID
	Entry Status	Courtier	Main curator
	Published		

PHENOTYPIC CHANGE

Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Morphology^#gephebase-summary-title)		Trait Category	
Plant architecture (petiole-to-leaf-length ratio) (https://www.gephebase.org/search-criteria?/and+Trait=~Plant architecture (petiole-to-leaf-length ratio)^#gephebase-summary-title)		Trait	
Arabidopsis thaliana		Trait State in Taxon A	
Arabidopsis thaliana- Swedish accessions		Trait State in Taxon B	
Data not curated		Ancestral State	
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Intraspecific^#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Arabidopsis thaliana^#gephebase-summary-title)		Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Arabidopsis thaliana^#gephebase-summary-title)	
thale cress		thale cress	
thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress		thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress	
species		species	
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis	
Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)		Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)	
3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)		3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)	
No		Yes	
		Taxon B Description	
		Arabidopsis thaliana- Swedish accessions	

GENOTYPIC CHANGE

ACS11		Generic Gene Name		UniProtKB Arabidopsis thaliana	
1-aminocyclopropane-1-carboxylate synthase 11; T17A2.2; T17A2_2; At4g08040		Synonyms		GenebankID or UniProtKB	
3702.AT4G08040.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT4G08040.1)		String		NM_116873.1 (https://www.ncbi.nlm.nih.gov/nucore/NM_116873.1)	
Belongs to the class-I pyridoxal-phosphate-dependent aminotransferase family.		Sequence Similarities			
GO:0016847 : 1-aminocyclopropane-1-carboxylate synthase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016847)		GO - Molecular Function			
GO:0030170 : pyridoxal phosphate binding					

(<https://www.ebi.ac.uk/QuickGO/term/GO:0030170>)

GO - Biological Process

GO:0009693 : ethylene biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009693>)

GO:0009835 : fruit ripening (<https://www.ebi.ac.uk/QuickGO/term/GO:0009835>)

GO - Cellular Component

-

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

several candidate amino acid changes

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Genome-Wide Association Mapping and Genomic Prediction Elucidate the Genetic Architecture of Morphological Traits in Arabidopsis. (2016) (<https://pubmed.ncbi.nlm.nih.gov/26869705>)

Authors

Kooke R; Kruijer W; Bours R; Becker F; Kuhn A; van de Geest H; Buntjer J; Doeswijk T; Guerra J; Bouwmeester H; Vreugdenhil D; Keurentjes JJ

Abstract

Quantitative traits in plants are controlled by a large number of genes and their interaction with the environment. To disentangle the genetic architecture of such traits, natural variation within species can be explored by studying genotype-phenotype relationships. Genome-wide association studies that link phenotypes to thousands of single nucleotide polymorphism markers are nowadays common practice for such analyses. In many cases, however, the identified individual loci cannot fully explain the heritability estimates, suggesting missing heritability. We analyzed 349 Arabidopsis accessions and found extensive variation and high heritabilities for different morphological traits. The number of significant genome-wide associations was, however, very low. The application of genomic prediction models that take into account the effects of all individual loci may greatly enhance the elucidation of the genetic architecture of quantitative traits in plants. Here, genomic prediction models revealed different genetic architectures for the morphological traits. Integrating genomic prediction and association mapping enabled the assignment of many plausible candidate genes explaining the observed variation. These genes were analyzed for functional and sequence diversity, and good indications that natural allelic variation in many of these genes contributes to phenotypic variation were obtained. For ACS11, an ethylene biosynthesis gene, haplotype differences explaining variation in the ratio of petiole and leaf length could be identified.

Â© 2016 American Society of Plant Biologists. All Rights Reserved.

Additional References

RELATED GEPHE

Related Genes

4 (AGAMOUS-Like6, ERECTA, ICARUS1, phytochrome D (PHYD)) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~3702~/and+Trait=Plant architecture/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@GxE

