

Gephebase Gene		GepheID
AtGA20ox1 (=GA5=Sd1) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="^AtGA20ox1 (=GA5=Sd1)^#gephebase-summary-title")	GP00000115	Main curator
Published	Entry Status	Martin

Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Morphology^#gephebase-summary-title)		Trait Category
Plant size (dwarfism) (https://www.gephebase.org/search-criteria?/and+Trait=~Plant size (dwarfism)^#gephebase-summary-title)		Trait
Arabidopsis thaliana - Col		Trait State in Taxon A
Arabidopsis thaliana - dwarf accession (see manuscript)		Trait State in Taxon B
Taxon A		Ancestral State
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Domesticated^#gephebase-summary-title)		Taxonomic Status
Taxon A		Taxon B
	Latin Name	Latin Name
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)
	Common Name	Common Name
thale cress		thale cress
	Synonyms	Synonyms
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
	Rank	Rank
species		species
	Lineage	Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis
	Parent	Parent
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)
	NCBI Taxonomy ID	NCBI Taxonomy ID
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)
	is Taxon A an Intraspecies?	is Taxon B an Intraspecies?
Yes		Yes
	Taxon A Description	Taxon B Description
Arabidopsis thaliana - Col		Arabidopsis thaliana - dwarf accession (see manuscript)

GA20OX1	Generic Gene Name	Q39110 (http://www.uniprot.org/uniprot/Q39110)	UniProtKB Arabidopsis thaliana
	Synonyms		GenebankID or UniProtKB
ARABIDOPSIS THALIANA GIBBERELLIN 20-OXIDASE 1; AT2301; ATGA20OX1; GA REQUIRING 5; GA5; GIBBERELLIN 20-OXIDASE; T30C3.90; T30C3_90; 20ox1; At2301; At4g25420		U20872 (https://www.ncbi.nlm.nih.gov/nuccore/U20872)	
	String		
3702.AT4G25420.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 3702.AT4G25420.1)			
	Sequence Similarities		
Belongs to the iron/ascorbate-dependent oxidoreductase family. GA20OX subfamily.			
	GO - Molecular Function		
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)			
GO:0051213 : dioxygenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0051213)			

GO:0045544 : gibberellin 20-oxidase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045544>)

GO - Biological Process

GO:0009908 : flower development (<https://www.ebi.ac.uk/QuickGO/term/GO:0009908>)
GO:0009740 : gibberellic acid mediated signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009740>)
GO:0009686 : gibberellin biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009686>)
GO:0048366 : leaf development (<https://www.ebi.ac.uk/QuickGO/term/GO:0048366>)
GO:0009739 : response to gibberellin
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009739>)
GO:0048575 : short-day photoperiodism, flowering
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048575>)
GO:0009826 : unidimensional cell growth
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009826>)

GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)

Presumptive Null

Yes (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Yes~#gephebase-summary-title>)

Molecular Type

Coding (<https://www.gephebase.org/search-criteria?/and+Molecular Type=~Coding~#gephebase-summary-title>)

Aberration Type

Insertion (<https://www.gephebase.org/search-criteria?/and+Aberration Type=~Insertion~#gephebase-summary-title>)

Insertion Size

1-9 bp

Molecular Details of the Mutation

+1bp at +1270

Experimental Evidence

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

Main Reference

Arabidopsis semidwarfs evolved from independent mutations in GA20ox1, ortholog to green revolution dwarf alleles in rice and barley. (2013) (<https://pubmed.ncbi.nlm.nih.gov/24023067>)

Authors

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Abstract

Understanding the genetic bases of natural variation for developmental and stress-related traits is a major goal of current plant biology. Variation in plant hormone levels and signaling might underlie such phenotypic variation occurring even within the same species. Here we report the genetic and molecular basis of semidwarf individuals found in natural Arabidopsis thaliana populations. Allelism tests demonstrate that independent loss-of-function mutations at GA locus 5 (GA5), which encodes gibberellin 20-oxidase 1 (GA20ox1) involved in the last steps of gibberellin biosynthesis, are found in different populations from southern, western, and northern Europe; central Asia; and Japan. Sequencing of GA5 identified 21 different loss-of-function alleles causing semidwarfness without any obvious general tradeoff affecting plant performance traits. GA5 shows signatures of purifying selection, whereas GA5 loss-of-function alleles can also exhibit patterns of positive selection in specific populations as shown by Fay and Wu’s H statistics. These results suggest that antagonistic pleiotropy might underlie the occurrence of GA5 loss-of-function mutations in nature. Furthermore, because GA5 is the ortholog of rice SD1 and barley Sdw1/Denso green revolution genes, this study illustrates the occurrence of conserved adaptive evolution between wild A.thaliana and domesticated plants.

Additional References

RELATED GEPHE

Related Genes

2 (ACD6 = ACCELERATED CELL DEATH 6, phytochrome D (PHYD)) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~3702~/and+Trait=Plant size/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

19 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~AtGA20ox1 \(=GA5=Sd1\)~/and+Taxon ID=~3702~/or+Gene Gephebase=~AtGA20ox1 \(=GA5=Sd1\)~/and+Taxon ID=~3702~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~AtGA20ox1 (=GA5=Sd1)~/and+Taxon ID=~3702~/or+Gene Gephebase=~AtGA20ox1 (=GA5=Sd1)~/and+Taxon ID=~3702~#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS