GEPHE SUMMARY

Gephebase Gene
AtGA20ox1 (=GA5=Sd1) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^AtGA20ox1 (=GA5=Sd1)^#gephebase-summary-title)

GepheID
GP00000123

Entry Status
Published

Main curator
Martin

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
Arabidopsis thaliana - Col

Trait State in Taxon B
Arabidopsis thaliana - dwarf accession (see manuscript)

Ancestral State
Data not curated

Taxonomic Status
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#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 - Col

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 - dwarf accession (see manuscript)

GENOTYPIC CHANGE

Generic Gene Name
GA20OX1

Synonyms
ARABIDOPSIS THALIANA GIBBERELLIN 20-OXIDASE 1; AT2301; ATGA20OX1; GA REQUIRING 5; GA5; GIBBERELLIN 20-OXIDASE; T30C3.90; T30C3_90; 20ox1; At2301; At4g25420

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)

UniProtKB Arabidopsis thaliana
Q39110 (http://www.uniprot.org/uniprot/Q39110)

GenebankID or UniProtKB
U20872 (https://www.ncbi.nlm.nih.gov/nuccore/U20872)

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

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

-

Molecular Details of the Mutation

Splice Site mutation G742A

Experimental Evidence

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

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

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

Barboza L; Effgen S; Alonso-Blanco C; Kooke R; Keurentjes JJ; Koornneef M; AlcÃizar R

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)

EXTERNAL LINKS

COMMENTS

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