GEPHE SUMMARY

Gephebase Gene

CBF gene cluster (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^CBF gene cluster^#gephebase-summary-title)

GepheID

GP00000174

Entry Status

Published

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

Arabidopsis thaliana- Col0

Trait State in Taxon B

Arabidopsis thaliana- Can-0

Ancestral State

Data not curated

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- Col0

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- Can-0

GENOTYPIC CHANGE

Generic Gene Name

-

Synonyms

-

String

-

Sequence Similarities

-

GO - Molecular Function

GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)

GO - Biological Process

GO:0006351 : transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0006351)

UniProtKB Triticum monococcum

B1NSN2 (http://www.uniprot.org/uniprot/B1NSN2)

GenebankID or UniProtKB

AIU34717 (https://www.ncbi.nlm.nih.gov/nuccore/AIU34717)

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

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

Main Reference

Natural variation in the freezing tolerance of Arabidopsis thaliana: effects of RNAi-induced CBF depletion and QTL localisation vary among accessions. (2011) (https://pubmed.ncbi.nlm.nih.gov/21421342)

Authors

Gery C; Zuther E; Schulz E; Legoupi J; Chauveau A; McKhann H; Hincha DK; TÃ©oulÃ© E

Abstract

Plants from temperate regions are able to withstand freezing temperatures and to increase their freezing tolerance during exposure to low, but non-freezing, temperatures through a process known as cold acclimation. Key regulatory proteins in this process are the cold-induced CBF1, 2 and 3 transcription factors which control many cold regulated genes. Although much work has focused on this signal transduction pathway, the details of its regulation and of its quantitative contribution to cold acclimation are still unclear. Here, we have used the large natural variation present in the 48 accessions of the Versailles core collection of Arabidopsis thaliana to further elucidate the function of the CBF transcription factors. CBF gene expression studies showed that the freezing sensitive accessions had mostly low expression levels 2h after transfer of plants to 5Â°C, while the most tolerant accessions showed a wide range of CBF expression levels. To investigate the quantitative contribution of CBF expression to plant freezing tolerance and low temperature growth performance, RNAi lines targeting all three CBF genes were produced in eight different accessions. We observed striking differences between different accessions in the effects that reduced CBF expression had on freezing tolerance, while effects on growth were generally too small to draw firm conclusions. Analysis of CBF expression indicated a tight co-regulation between CBF1 and CBF3, while the relationship between the expression levels of CBF2 and CBF1 or CBF3 strongly depended on the genetic background of the RNAi lines. In agreement with the observed differences between the different accessions, QTL analyses with two different RIL populations indicated that QTL localisation varies strongly between populations. Collectively, these results show that both the regulation of the CBF genes and their relative contribution to freezing tolerance strongly depend on the accession studied. In addition, natural variation is suggested to be an interesting source of novel regulatory pathways and genes that may be useful in the future for improving plant freezing tolerance.

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Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Cluster of paralogous genes