Gephebase Gene GephelD CBF gene cluster (https://www.gephebase.org/search-criteria?/and+Gene GP00000174 Gephebase=^CBF gene cluster^#gephebase-summary-title) Main curator Entry Status Martin **Published** 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/searchcriteria?/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 Taxon B Latin Name Latin Name Arabidopsis thaliana Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Arabidopsis (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Arabidopsis thaliana^#gephebase-summary-title) thaliana^#gephebase-summary-title) Common Name Common Name thale cress thale cress Synonyms thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress species Lineage Lineage cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae;eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae;Camelineae; Arabidopsis Camelineae; Arabidopsis Parent Parent Arabidopsis () - (Rank: genus) Arabidopsis () - (Rank: genus) $(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701\,)$ $(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701\,)$ NCBI Taxonomy ID NCBI Taxonomy ID 3702 3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702) is Taxon A an Infraspecies? is Taxon B an Infraspecies? Yes Taxon A Description Taxon B Description Arabidopsis thaliana- Col0 Arabidopsis thaliana- Can-0 Generic Gene Name UniProtKB Triticum monococcum B1NSN2 (http://www.uniprot.org/uniprot/B1NSN2) GenebankID or UniProtKB Synonyms AlU34717 (https://www.ncbi.nlm.nih.gov/nuccore/AlU34717)

GENOTYPIC CHANGE

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)

GO - Cellular Component	
$GO:0005634: nucleus \ (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)$	_
Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title)	Presumptive Nul
Onkilowii (https://www.gephebase.org/search-chteira:/aird+i resumptive raun- Onkilowii #gephebase-summary-title/	Molecular Type
$Unknown \ (https://www.gephebase.org/search-criteria?/and+Molecular\ Type=^Unknown^\#gephebase-summary-title)$	
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title)	Aberration Type
Onknown (https://www.gephebase.org/search Chteria./and-7-bernation Type- Onknown #gephebase summary title)	Molecular Details of the Mutation
unknown	
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-	Experimental Evidence -title)
Zimage Mapping (https://mmigepriesuserigjsearen entenarjana Experimental Zinaenee Zimage Mapping // gepriesuse sammaly	Main Reference
Natural variation in the freezing tolerance of Arabidopsis thaliana: effects of RNAi-induced CBF depletion and QTL localisation vary an	nong accessions. (2011)
(https://pubmed.ncbi.nlm.nih.gov/21421342)	Author
Gery C; Zuther E; Schulz E; Legoupi J; Chauveau A; McKhann H; Hincha DK; TÃ⊚oulÃ⊚ E	
Plants from temperate regions are able to withstand freezing temperatures and to increase their freezing tolerance during exposure to low known as cold acclimation. Key regulatory proteins in this process are the cold-induced CBF1, 2 and 3 transcription factors which control focused on this signal transduction pathway, the details of its regulation and of its quantitative contribution to cold acclimation are still under the foliation of the Versailles core collection of Arabidopsis thaliana to further elucidate the function of the CBF transcription freezing sensitive accessions had mostly low expression levels 2h after transfer of plants to 5°C, while the most tolerant accessions investigate the quantitative contribution of CBF expression to plant freezing tolerance and low temperature growth performance, RNAi eight different accessions. We observed striking differences between different accessions in the effects that reduced CBF expression had generally too small to draw firm conclusions. Analysis of CBF expression indicated a tight co-regulation between CBF1 and CBF3, while and CBF1 or CBF3 strongly depended on the genetic background of the RNAi lines. In agreement with the observed differences between different RIL populations indicated that QTL localisation varies strongly between populations. Collectively, these results show that both contribution to freezing tolerance strongly depend on the accession studied. In addition, natural variation is suggested to be an interesting the useful in the future for improving plant freezing tolerance. Copyright © 2010 Elsevier Ireland Ltd. All rights reserved.	many cold regulated genes. Although much work has nclear. Here, we have used the large natural variation ption factors. CBF gene expression studies showed that showed a wide range of CBF expression levels. To lines targeting all three CBF genes were produced in d on freezing tolerance, while effects on growth were the relationship between the expression levels of CBF2 en the different accessions, QTL analyses with two the regulation of the CBF genes and their relative
RELATED GEPHE	
No matches found.	Related Genes
	Related Haplotypes
No matches found.	

EXTERNAL LINKS

COMMENTS

Cluster of paralogous genes