

GEPHE SUMMARY

<p>TFL1 / HvCEN (#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00001119</p> <p>Martin</p>	<p>GepheID</p> <p>Main curator</p>
--	---	---------------------------------	------------------------------------

PHENOTYPIC CHANGE

<p>Physiology (#gephebase-summary-title)</p> <p>Growth determination habit (#gephebase-summary-title)</p> <p>Hordeum vulgare - winter cultivar</p> <p>Hordeum vulgare - spring cultivar</p> <p>Data not curated</p> <p>Domesticated (#gephebase-summary-title)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Hordeum vulgare</p> <p>Hordeum vulgare</p> <p>Hordeum vulgare</p> <p>Hordeum vulgare</p> <p>Hordeum vulgare</p> <p>Hordeum vulgare</p>
--	---	---

Taxon A	Latin Name	Taxon B	Latin Name
Hordeum vulgare (#gephebase-summary-title)	Hordeum vulgare (#gephebase-summary-title)	Hordeum vulgare (#gephebase-summary-title)	Hordeum vulgare (#gephebase-summary-title)
-	Common Name	-	Common Name
barley; Hordeum vulgare L.; Horedum vulgare	Synonyms	barley; Hordeum vulgare L.; Horedum vulgare	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Triticeae; Triticeae; Hordeinae; Hordeum	Lineage	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Triticeae; Triticeae; Hordeinae; Hordeum	Lineage
Hordeum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4512)	Parent	Hordeum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4512)	Parent
4513 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4513)	NCBI Taxonomy ID	4513 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4513)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

<p>TFL1</p> <p>MED24.6; TERMINAL FLOWER 1; TFL-1; At5g03840; F8F6_50</p> <p>3702.AT5G03840.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=3702.AT5G03840.1)</p> <p>Belongs to the phosphatidylethanolamine-binding protein family.</p> <p>GO:0003712 : transcription coregulator activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003712)</p> <p>GO:0030154 : cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0030154)</p> <p>GO:0009908 : flower development (https://www.ebi.ac.uk/QuickGO/term/GO:0009908)</p> <p>GO:0009910 : negative regulation of flower development (https://www.ebi.ac.uk/QuickGO/term/GO:0009910)</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p> <p>GO - Biological Process</p>	<p>UniProtKB Arabidopsis thaliana</p> <p>P93003 (http://www.uniprot.org/uniprot/P93003)</p> <p>GenebankID or UniProtKB</p> <p>ABF85670 (https://www.ncbi.nlm.nih.gov/nuccore/ABF85670)</p>
--	---	--

GO:0009744 : response to sucrose (<https://www.ebi.ac.uk/QuickGO/term/GO:0009744>)
 GO:0090344 : negative regulation of cell aging
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0090344>)
 GO:0006623 : protein targeting to vacuole
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0006623>)

GO - Cellular Component

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
 GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)
 GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)
 GO:0031982 : vesicle (<https://www.ebi.ac.uk/QuickGO/term/GO:0031982>)
 GO:0005773 : vacuole (<https://www.ebi.ac.uk/QuickGO/term/GO:0005773>)

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null="No" #gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive Null=)) Presumptive Null
 Coding ([https://www.gephebase.org/search-criteria?/and+Molecular Type="Coding" #gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular Type=)) Molecular Type
 SNP ([https://www.gephebase.org/search-criteria?/and+Aberration Type="SNP" #gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration Type=)) Aberration Type
 Nonsynonymous SNP Coding Change
 P135A Molecular Details of the Mutation
 Linkage Mapping ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence="Linkage Mapping" #gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental Evidence=)) Experimental Evidence

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

Natural variation in a homolog of Antirrhinum CENTRORADIALIS contributed to spring growth habit and environmental adaptation in cultivated barley. (2012)
 (<https://pubmed.ncbi.nlm.nih.gov/23160098>) Main Reference

Comadran J; Kilian B; Russell J; Ramsay L; Stein N; Ganal M; Shaw P; Bayer M; Thomas W; Marshall D; Hedley P; Tondelli A; Pecchioni N; Francia E; Korzun V; Walther A; Waugh R Authors
 Abstract

As early farming spread from the Fertile Crescent in the Near East around 10,000 years before the present, domesticated crops encountered considerable ecological and environmental change. Spring-sown crops that flowered without the need for an extended period of cold to promote flowering and day length-insensitive crops able to exploit the longer, cooler days of higher latitudes emerged and became established. To investigate the genetic consequences of adaptation to these new environments, we identified signatures of divergent selection in the highly differentiated modern-day spring and winter barleys. In one genetically divergent region, we identify a natural variant of the barley homolog of Antirrhinum CENTRORADIALIS (HvCEN) as a contributor to successful environmental adaptation. The distribution of HvCEN alleles in a large collection of wild and landrace accessions indicates that this involved selection and enrichment of preexisting genetic variants rather than the acquisition of mutations after domestication.

Additional References

RELATED GEPHE

No matches found. Related Genes
 No matches found. Related Haplotypes

EXTERNAL LINKS

COMMENTS