

GEPHE SUMMARY

	Gene	Gephebase Gene	GephelD
cly1 (#gephebase-summary-title)		GP00001314	Main curator
	Entry Status	Arnoult	
Published			

PHENOTYPIC CHANGE

	Trait Category
Morphology (#gephebase-summary-title)	Trait
Pollen shedding (Cleistogamy; Iodicule size) (#gephebase-summary-title)	Trait State in Taxon A
Hordeum vulgare - Barley AZ (noncleistogamous)	Trait State in Taxon B
Hordeum vulgare - Barley KNG (cleistogamous) and 7 other lines	Ancestral State
Taxon A	Taxonomic Status
Domesticated (#gephebase-summary-title)	

Taxon A	Latin Name	Taxon B	Latin Name
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; Viridiplanteae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphylophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Triticodae; Triticeae; Hordeinae; Hordeum	Lineage	cellular organisms; Eukaryota; Viridiplanteae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphylophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Triticodae; 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
is Taxon A an Infraspecies?		is Taxon B an Infraspecies?	
Yes	Taxon A Description	Yes	Taxon B Description
Hordeum vulgare - Barley AZ (noncleistogamous)		Hordeum vulgare - Barley KNG (cleistogamous) and 7 other lines	

GENOTYPIC CHANGE

AP2	Generic Gene Name	UniProtKB Arabidopsis thaliana
	Synonyms	GenebankID or UniProtKB
FLO2; AP22.49; AP22_49; APETALA 2; AtAP2; FL1; FLORAL HOMEOTIC PROTEIN APETALA 2; FLORAL MUTANT 2; FLOWER 1; At4g36920; C7A10.440		KF261342.1 (https://www.ncbi.nlm.nih.gov/nuccore/KF261342.1)
3702.AT4G36920.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT4G36920.1)	String	
Belongs to the AP2/ERF transcription factor family. AP2 subfamily.	Sequence Similarities	
GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)	GO - Molecular Function	
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)		

GO - Biological Process

GO:0030154 : cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030154>)
 GO:0048481 : plant ovule development
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0048481>)
 GO:0009908 : flower development (<https://www.ebi.ac.uk/QuickGO/term/GO:0009908>)
 GO:0010073 : meristem maintenance
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0010073>)
 GO:0048316 : seed development (<https://www.ebi.ac.uk/QuickGO/term/GO:0048316>)
 GO:0010093 : specification of floral organ identity
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0010093>)

GO - Cellular Component

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=%No%#gephebase-summary-title>)

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

A>G @position 3084; in a miRNA targeting site.

Experimental Evidence

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

Main Reference

Cleistogamous flowering in barley arises from the suppression of microRNA-guided HvAP2 mRNA cleavage. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20018663>)

Authors

Nair SK; Wang N; Turuspekov Y; Pourkheirandish M; Sinsuwongwat S; Chen G; Sameri M; Tagiri A; Honda I; Watanabe Y; Kanamori H; Wicker T; Stein N; Nagamura Y; Matsumoto T; Komatsuda T

Abstract

The cleistogamous flower sheds its pollen before opening, forcing plants with this habit to be almost entirely autogamous. Cleistogamy also provides a means of escape from cereal head blight infection and minimizes pollen-mediated gene flow. The lodicule in cleistogamous barley is atrophied. We have isolated cleistogamy 1 (Cly1) by positional cloning and show that it encodes a transcription factor containing two AP2 domains and a putative microRNA miR172 targeting site, which is an ortholog of *Arabidopsis thaliana* AP2. The expression of Cly1 was concentrated within the lodicule primordia. We established a perfect association between a synonymous nucleotide substitution at the miR172 targeting site and cleistogamy. Cleavage of mRNA directed by miR172 was detectable only in a noncleistogamous background. We conclude that the miR172-derived down-regulation of Cly1 promotes the development of the lodicules, thereby ensuring noncleistogamy, although the single nucleotide change at the miR172 targeting site results in the failure of the lodicules to develop properly, producing the cleistogamous phenotype.

Additional References

Identification and mapping of cleistogamy genes in barley. (2004) (<https://pubmed.ncbi.nlm.nih.gov/15138690>)

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

2 (<https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=%cly1%/and+Taxon+ID=%4513%/or+Gene+Gephebase=%cly1%/and+Taxon+ID=%4513%#gephebase-summary-title>)

EXTERNAL LINKS

COMMENTS