GEPHE SUMMARY

Gephebase Gene

HvbHLH1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^HvbHLH1^#gephebase-summary-title)

GepheID

GP00000493

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

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

Trait State in Taxon A

Hordeum vulgare - Saffron

Trait State in Taxon B

Hordeum vulgare - Retriever

Ancestral State

Taxon A

Taxonomic Status

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

Taxon A

Latin Name

Hordeum vulgare (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Hordeum vulgare^#gephebase-summary-title)

Common Name

-

Synonyms

barley; Hordeum vulgare L.; Horedum vulgare

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Triticodae; Triticeae; Hordeinae; Hordeum

Parent

Hordeum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4512)

NCBI Taxonomy ID

4513 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4513)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Hordeum vulgare - Saffron

Taxon B

Latin Name

Hordeum vulgare (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Hordeum vulgare^#gephebase-summary-title)

Common Name

-

Synonyms

barley; Hordeum vulgare L.; Horedum vulgare

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Triticodae; Triticeae; Hordeinae; Hordeum

Parent

Hordeum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4512)

NCBI Taxonomy ID

4513 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4513)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Hordeum vulgare - Retriever

GENOTYPIC CHANGE

Generic Gene Name

bHLH1

Synonyms

-

String

-

Sequence Similarities

-

GO - Molecular Function

GO:0046983 : protein dimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046983)

GO - Biological Process

-

GO - Cellular Component

-

UniProtKB Hordeum vulgare subsp. vulgare

E5FCX3 (http://www.uniprot.org/uniprot/E5FCX3)

GenebankID or UniProtKB

ADR30773 (https://www.ncbi.nlm.nih.gov/nuccore/ADR30773)

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title)

Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)

Aberration Type

Deletion (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Deletion^#gephebase-summary-title)

Deletion Size

10-99 bp

Molecular Details of the Mutation

16bp deletion resulting in premature stop codon

Experimental Evidence

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

Main Reference

Genome-wide association mapping to candidate polymorphism resolution in the unsequenced barley genome. (2010) (https://pubmed.ncbi.nlm.nih.gov/21115826)

Authors

Cockram J; White J; Zuluaga DL; Smith D; Comadran J; Macaulay M; Luo Z; Kearsey MJ; Werner P; Harrap D; Tapsell C; Liu H; Hedley PE; Stein N; Schulte D; Steuernagel B; Marshall DF; Thomas WT; Ramsay L; Mackay I; Balding DJ; ; Waugh R; O'Sullivan DM

Abstract

Although commonplace in human disease genetics, genome-wide association (GWA) studies have only relatively recently been applied to plants. Using 32 phenotypes in the inbreeding crop barley, we report GWA mapping of 15 morphological traits across â^¼4500 cultivars genotyped with 1,536 SNPs. In contrast to the majority of human GWA studies, we observe high levels of linkage disequilibrium within and between chromosomes. Despite this, GWA analysis readily detected common alleles of high penetrance. To investigate the potential of combining GWA mapping with comparative analysis to resolve traits to candidate polymorphism level in unsequenced genomes, we fine-mapped a selected phenotype (anthocyanin pigmentation) within a 140-kb interval containing three genes. Of these, resequencing the putative anthocyanin pathway gene HvbHLH1 identified a deletion resulting in a premature stop codon upstream of the basic helix-loop-helix domain, which was diagnostic for lack of anthocyanin in our association and biparental mapping populations. The methodology described here is transferable to species with limited genomic resources, providing a paradigm for reducing the threshold of map-based cloning in unsequenced crops.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS