

GEPHE SUMMARY

	Gephebase Gene		GepheID
HvbHLH1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~HvbHLH1~#gephebase-summary-title)		GP00000493	
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~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+TaxonomicStatus=~Domesticated~#gephebase-summary-title)			
		Taxon B	
	Latin Name		Latin Name
Hordeum vulgare (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Hordeumvulgare~#gephebase-summary-title)		Hordeum vulgare (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Hordeumvulgare~#gephebase-summary-title)	
-	Common Name	-	Common Name
	Synonyms		Synonyms
barley; Hordeum vulgare L.; Horedum vulgare		barley; Hordeum vulgare L.; Horedum vulgare	
	Rank		Rank
species		species	
	Lineage		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		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		Parent
Hordeum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4512)		Hordeum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4512)	
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 Intraspecies?		is Taxon B an Intraspecies?
Yes		Yes	
	Taxon A Description		Taxon B Description
Hordeum vulgare - Saffron		Hordeum vulgare - Retriever	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Hordeum vulgare subsp. vulgare
bHLH1		E5FCX3 (http://www.uniprot.org/uniprot/E5FCX3)
	Synonyms	GenebankID or UniProtKB
-		ADR30773 (https://www.ncbi.nlm.nih.gov/nuccore/ADR30773)
	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	
-		
		Presumptive Null

Yes (#www.gephebase.org/search-criteria?/and+Presumptive Null=~Yes`#gephebase-summary-title)	Molecular Type
Coding (#www.gephebase.org/search-criteria?/and+Molecular Type=~Coding`#gephebase-summary-title)	Aberration Type
Deletion (#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 (#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 1/4500 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

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

EXTERNAL LINKS

COMMENTS