

GEPHE SUMMARY

Gephebase Gene

VRS1 = SIX-ROWED SPIKE 1

Entry Status

Published

GepheID

GP00001191

Main curator

Martin

PHENOTYPIC CHANGE

Trait #1

Trait Category

Morphology

Trait

Plant architecture

Trait State in Taxon A

Hordeum vulgare

Trait State in Taxon B

Hordeum vulgare

Trait #2

Trait Category

Morphology

Trait

Inflorescence architecture

Trait State in Taxon A

-

Trait State in Taxon B

-

Ancestral State

Data not curated

Taxonomic Status

Domesticated

Taxon A

Latin Name

Hordeum vulgare

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; Triticoideae; Triticeae; Hordeinae; Hordeum

Parent

Hordeum () - (Rank: genus)

NCBI Taxonomy ID

4513

is Taxon A an Intraspecies?

No

Taxon B

Latin Name

Hordeum vulgare

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; Triticoideae; Triticeae; Hordeinae; Hordeum

Parent

Hordeum () - (Rank: genus)

NCBI Taxonomy ID

4513

is Taxon B an Intraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

Vrs1

Synonyms

UniProtKB Hordeum vulgare subsp. vulgare

A1IHK8

GenebankID or UniProtKB

Hox1

String

-

Sequence Similarities

-

GO - Molecular Function

GO:0043565 : sequence-specific DNA binding

GO - Biological Process

GO:0006355 : regulation of transcription, DNA-templated

GO - Cellular Component

GO:0005634 : nucleus

Presumptive Null

No

Molecular Type

Coding

Aberration Type

SNP

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Phe75Leu

Experimental Evidence

Linkage Mapping

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

Main Reference

Six-rowed barley originated from a mutation in a homeodomain-leucine zipper I-class homeobox gene. (2007)

Authors

Komatsuda T; Pourkheirandish M; He C; Azhaguvel P; Kanamori H; Perovic D; Stein N; Graner A; Wicker T; Tagiri A; Lundqvist U; Fujimura T; Matsuoka M; Matsumoto T; Yano M

Abstract

Increased seed production has been a common goal during the domestication of cereal crops, and early cultivators of barley (*Hordeum vulgare* ssp. *vulgare*) selected a phenotype with a six-rowed spike that stably produced three times the usual grain number. This improved yield established barley as a founder crop for the Near Eastern Neolithic civilization. The barley spike has one central and two lateral spikelets at each rachis node. The wild-type progenitor (*H. vulgare* ssp. *spontaneum*) has a two-rowed phenotype, with additional, strictly rudimentary, lateral rows; this natural adaptation is advantageous for seed dispersal after shattering. Until recently, the origin of the six-rowed phenotype remained unknown. In the present study, we isolated *vrs1* (six-rowed spike 1), the gene responsible for the six-rowed spike in barley, by means of positional cloning. The wild-type *Vrs1* allele (for two-rowed barley) encodes a transcription factor that includes a homeodomain with a closely linked leucine zipper motif. Expression of *Vrs1* was strictly localized in the lateral-spikelet primordia of immature spikes, suggesting that the *VRS1* protein suppresses development of the lateral rows. Loss of function of *Vrs1* resulted in complete conversion of the rudimentary lateral spikelets in two-rowed barley into fully developed fertile spikelets in the six-rowed phenotype. Phylogenetic analysis demonstrated that the six-rowed phenotype originated repeatedly, at different times and in different regions, through independent mutations of *Vrs1*.

Additional References

INTERMEDIUM-C, a modifier of lateral spikelet fertility in barley, is an ortholog of the maize domestication gene *TEOSINTE BRANCHED 1*. (2011)

RELATED GEPHE

Related Genes

1 (teosinte branched 1 (tb1) = IntC)

Related Haplotypes

2

EXTERNAL LINKS

COMMENTS

