GEPHE SUMMARY

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

GepheID
GP00000496

Entry Status
Published

Main curator
Martin

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
Phaseolus vulgaris

Trait State in Taxon B
Phaseolus vulgaris - Mosaic virus resistant "Sprite"

Ancestral State
Taxon A

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

Taxon A

Latin Name
Phaseolus vulgaris (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Phaseolus vulgaris^#gephebase-summary-title)

Common Name
-

Synonyms
French bean; kidney bean; string bean; Phaseolus vulgaris L.

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae; 50 kb inversion clade; NPAAA clade; indigoferoid/millettioid clade; Phaseoleae; Phaseolus

Parent
Phaseolus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3883)

NCBI Taxonomy ID
3885 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3885)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Phaseolus vulgaris (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Phaseolus vulgaris^#gephebase-summary-title)

Common Name
-

Synonyms
French bean; kidney bean; string bean; Phaseolus vulgaris L.

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae; 50 kb inversion clade; NPAAA clade; indigoferoid/millettioid clade; Phaseoleae; Phaseolus

Parent
Phaseolus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3883)

NCBI Taxonomy ID
3885 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3885)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
-

Synonyms
-

String
-

Sequence Similarities
-

GO - Molecular Function
GO:0043531 : ADP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043531)

GO - Biological Process
-

GO - Cellular Component
-

UniProtKB Vigna aconitifolia
U5YMY7 (http://www.uniprot.org/uniprot/U5YMY7)

GenebankID or UniProtKB
()

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

unknown; maps to a cluster of R-proteins

Experimental Evidence

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

Main Reference

Genetic and molecular characterization of the I locus of Phaseolus vulgaris. (2006) (https://pubmed.ncbi.nlm.nih.gov/16322513)

Authors

Vallejos CE; Astua-Monge G; Jones V; Plyler TR; Sakiyama NS; Mackenzie SA

Abstract

The I locus of the common bean, Phaseolus vulgaris, controls the development of four different phenotypes in response to inoculation with Bean common mosaic virus, Bean common mosaic necrosis virus, several other related potyviruses, and one comovirus. We have generated a high-resolution linkage map around this locus and have aligned it with a physical map constructed with BAC clones. These clones were obtained from a library of the cultivar "Sprite," which carries the dominant allele at the I locus. We have identified a large cluster of TIR-NBS-LRR sequences associated within this locus, which extends over a distance >425 kb. Bean cultivars from the Andean or Mesoamerican gene pool that contain the dominant allele share the same haplotypes as revealed by gel blot hybridizations with a TIR probe. In contrast, beans with a recessive allele display simpler and variable haplotypes. A survey of wild accessions from Argentina to Mexico showed that this multigene family has expanded significantly during evolution and domestication. RNA gel blot analysis indicated that the TIR family of genes plays a role in the response to inoculations with BCMV or BCMNV.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS