

## GEPHE SUMMARY

**Gephebase Gene**  
BRANCHED1a (BRC1a)

**Entry Status**  
Published

**GepheID**  
GP00000156

**Main curator**  
Martin

## PHENOTYPIC CHANGE

### Trait #1

**Trait Category**  
Morphology

**Trait**  
Plant architecture

**Trait State in Taxon A**  
Plant and Flower architecture of Capsicum and Petunia

**Trait State in Taxon B**  
Plant and Flower architecture of Solanum spp.

### Trait #2

**Trait Category**  
Morphology

**Trait**  
Inflorescence architecture

**Trait State in Taxon A**  
Plant and Flower architecture of Capsicum and Petunia

**Trait State in Taxon B**  
Plant and Flower architecture of Solanum spp.

### Ancestral State

Taxon A

### Taxonomic Status

Intergeneric or Higher

### Taxon A

**Latin Name**  
*Capsicum annuum*

**Common Name**  
-

**Synonyms**  
Capsicum annuum L.; Capsicum annum; Capsicum capsicum

**Rank**  
species

**Lineage**  
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Solanoideae; Capsiceae; Capsicum

**Parent**  
Capsicum (peppers) - (Rank: genus)

**NCBI Taxonomy ID**  
4072

**is Taxon A an Intraspecies?**  
No

### Taxon B

**Latin Name**  
*Solanum*

**Common Name**  
-

**Synonyms**  
Cyphomandra Mart. ex Sendtn.; Solanum L.

**Rank**  
genus

**Lineage**  
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Solanoideae; Solanaeae

**Parent**  
Solanaceae () - (Rank: tribe)

**NCBI Taxonomy ID**  
4107

**is Taxon B an Intraspecies?**  
No

## GENOTYPIC CHANGE

**Generic Gene Name**  
BRC1A

**Synonyms**

**UniProtKB** Solanum tuberosum  
F6KB94

**GenebankID or UniProtKB**

TCP18; 102578271

String

-

Sequence Similarities

-

GO - Molecular Function

GO:0003677 : DNA binding

GO - Biological Process

GO:0006355 : regulation of transcription, DNA-templated

GO:0006351 : transcription, DNA-templated

GO - Cellular Component

GO:0005634 : nucleus

Presumptive Null

No

Molecular Type

Coding

Aberration Type

SNP

SNP Coding Change

-

Molecular Details of the Mutation

Evolution of an alternative splice site (G>A) that unlocks a short isoform

Experimental Evidence

Candidate Gene

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

Main Reference

A Recently Evolved Alternative Splice Site in the BRANCHED1a Gene Controls Potato Plant Architecture. (2015)

Authors

Nicolas M; Rodrguez-Buey ML; Franco-Zorrilla JM; Cubas P

Abstract

Amplification and diversification of transcriptional regulators that control development is a driving force of morphological evolution. A major source of protein diversity is alternative splicing, which leads to the generation of different isoforms from a single gene. The mechanisms and timing of intron evolution nonetheless remain unclear, and the functions of alternative splicing-generated protein isoforms are rarely studied. In *Solanum tuberosum*, the BRANCHED1a (BRC1a) gene encodes a TCP transcription factor that controls lateral shoot outgrowth. Here, we report the recent evolution in *Solanum* of an alternative splice site in BRC1a that leads to the generation of two BRC1a protein isoforms with distinct C-terminal regions, BRC1a(Long) and BRC1a(Short), encoded by unspliced and spliced mRNA, respectively. The BRC1a(Long) C-terminal region has a strong activation domain, whereas that of BRC1a(S) lacks an activation domain and is predicted to form an amphipathic helix, the H domain, which prevents protein nuclear targeting. BRC1a(Short) is thus mainly cytoplasmic, while BRC1a(Long) is mainly nuclear. BRC1a(Long) functions as a transcriptional activator, whereas BRC1a(Short) appears to have no transcriptional activity. Moreover, BRC1a(Short) can heterodimerize with BRC1a(Long) and act as a dominant-negative factor; it increases BRC1a(Long) concentration in cytoplasm and reduces its transcriptional activity. This alternative splicing mechanism is regulated by hormones and external stimuli that control branching. The evolution of a new alternative splicing site and a novel protein domain in *Solanum* BRC1a led to a multi-level mechanism of post-transcriptional and post-translational BRC1a regulation that effectively modulates its branch suppressing activity in response to environmental and endogenous cues.

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Additional References

## RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

@Splicing @GxE

