

LeSPL-CNR (<a +lespl-cnr^#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene Gephebase="+LeSPL-CNR^#gephebase-summary-title)	Gephebase Gene	GepheID
	GP00000539	Main curator
Published	Entry Status	Martin

	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title)	
	Trait
Fruit ripening (https://www.gephebase.org/search-criteria?/and+Trait=^Fruit ripening^#gephebase-summary-title)	
	Trait State in Taxon A
<i>Solanum cheesmaniae</i>	
	Trait State in Taxon B
<i>Solanum lycopersicum</i> Cnr/Cnr	
	Ancestral State
Taxon A	
	Taxonomic Status
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Domesticated^#gephebase-summary-title)	

GENOTYPIC CHANGE

101256245	Generic Gene Name	UniProtKB Solanum lycopersicum
CNR-SPL; LeSPL-CNR	Synonyms	GenebankID or UniProtKB
4081.Solyc02g077920.2.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=4081.Solyc02g077920.2.1)	String	DQ672601 (https://www.ncbi.nlm.nih.gov/nuccore/DQ672601)
-	Sequence Similarities	
GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700) GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872) GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)	GO - Molecular Function	

GO:0006351 : transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006351>)
GO:0009908 : flower development (<https://www.ebi.ac.uk/QuickGO/term/GO:0009908>)
GO - Cellular Component
GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title>)

Molecular Type

Cis-regulatory (<https://www.gephebase.org/search-criteria?/and+Molecular Type=~Cis-regulatory~#gephebase-summary-title>)

Aberration Type

Epigenetic Change (<https://www.gephebase.org/search-criteria?/and+Aberration Type=~Epigenetic Change~#gephebase-summary-title>)

Molecular Details of the Mutation

Stable methylation in a 286bp region of the promoter

Experimental Evidence

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

Main Reference

A naturally occurring epigenetic mutation in a gene encoding an SBP-box transcription factor inhibits tomato fruit ripening. (2006) (<https://pubmed.ncbi.nlm.nih.gov/16832354>)

Authors

Manning K; TÃ¶r M; Poole M; Hong Y; Thompson AJ; King GJ; Giovannoni JJ; Seymour GB

Abstract

A major component in the regulatory network controlling fruit ripening is likely to be the gene at the tomato Colorless non-ripening (Cnr) locus. The Cnr mutation results in colorless fruits with a substantial loss of cell-to-cell adhesion. The nature of the mutation and the identity of the Cnr gene were previously unknown. Using positional cloning and virus-induced gene silencing, here we demonstrate that an SBP-box (SQUAMOSA promoter binding protein-like) gene resides at the Cnr locus. Furthermore, the Cnr phenotype results from a spontaneous epigenetic change in the SBP-box promoter. The discovery that Cnr is an epimutation was unexpected, as very few spontaneous epimutations have been described in plants. This study demonstrates that an SBP-box gene is critical for normal ripening and highlights the likely importance of epialleles in plant development and the generation of natural variation.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS