

GEPHE SUMMARY

ore (<a +ore+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene Gephebase="+ore+"#gephebase-summary-title)	Gephebase Gene	GepheID	
		GP00001390	Main curator
	Entry Status	Prigent	
Published			

PHENOTYPIC CHANGE

		Trait Category	
Morphology, Physiology (<a +morphology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait Category=^Morphology^/and+Trait Category=^Physiology^#gephebase-summary-title)		Trait	
Taste (fruit) (<a +taste+(fruit)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait=^Taste (fruit)^#gephebase-summary-title)		Trait State in Taxon A	
wild cucumber		Trait State in Taxon B	
cultivated cucumber		Ancestral State	
Taxon A		Taxonomic Status	
Intraspecific (<a +intraspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)			
Taxon A		Taxon B	
Cucumis sativus (<a +cucumis+sativus+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Cucumis sativus^#gephebase-summary-title)		Cucumis sativus (<a +cucumis+sativus+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Cucumis sativus^#gephebase-summary-title)	
cucumber		cucumber	
cucumber; cucumbers; Cucumis sativus L.; Cucumis sativu		cucumber; cucumbers; Cucumis sativus L.; Cucumis sativu	
species		species	
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Cucurbitales; Cucurbitaceae; Benincaseae; Cucumis		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Cucurbitales; Cucurbitaceae; Benincaseae; Cucumis	
Cucumis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3655)		Cucumis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3655)	
3659 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3659)		3659 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3659)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
No		Yes	
		Taxon B Description	
		Cultivated cucumber	

GENOTYPIC CHANGE

		Generic Gene Name	
BCH1		E9JE14 (http://www.uniprot.org/uniprot/E9JE14)	
BCH1; ZmcrtrRB3; GRMZM2G164318; 732775; crtRB3; ZEAMMB73_Zm00001d002589		()	
4577.GRMZM2G164318_P01 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4577.GRMZM2G164318_P01)			
		Sequence Similarities	
Belongs to the sterol desaturase family.		UniProtKB Zea mays	
GO:0016491 : oxidoreductase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016491)		GenebankID or UniProtKB	
GO:0005506 : iron ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005506)			
GO:0008610 : lipid biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0008610)			

GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)

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

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

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

Nonsynonymous

p.Ala257Asp

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

Presumptive Null

Molecular Type

Aberration Type

SNP Coding Change

Molecular Details of the Mutation

Experimental Evidence

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

Main Reference

A genomic variation map provides insights into the genetic basis of cucumber domestication and diversity. (2013) (<https://pubmed.ncbi.nlm.nih.gov/24141363>)

Authors

Qi J; Liu X; Shen D; Miao H; Xie B; Li X; Zeng P; Wang S; Shang Y; Gu X; Du Y; Li Y; Lin T; Yuan J; Yang X; Chen J; Chen H; Xiong X; Huang K; Fei Z; Mao L; Tian L; Ståhl T; Renner SS; Kamoun S; Lucas WJ; Zhang Z; Huang S

Abstract

Most fruits in our daily diet are the products of domestication and breeding. Here we report a map of genome variation for a major fruit that encompasses ~3.6 million variants, generated by deep resequencing of 115 cucumber lines sampled from 3,342 accessions worldwide. Comparative analysis suggests that fruit crops underwent narrower bottlenecks during domestication than grain crops. We identified 112 putative domestication sweeps; 1 of these regions contains a gene involved in the loss of bitterness in fruits, an essential domestication trait of cucumber. We also investigated the genomic basis of divergence among the cultivated populations and discovered a natural genetic variant in a β -carotene hydroxylase gene that could be used to breed cucumbers with enhanced nutritional value. The genomic history of cucumber evolution uncovered here provides the basis for future genomics-enabled breeding.

Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

the paper also treats of fruit length - leaf size and fruit bitterness but only at the level of QTL and large candidate regions