

GEPHE SUMMARY

	Gephebase Gene	GepheID
Flavonoid 3'-5'-hydroxylase (F3'5'H) (https://www.gephebase.org/search-criteria/?and+Gene+Gephebase=^Flavonoid+3'-5'-hydroxylase+(F3'5'H)+#gephebase-summary-title)	GP00001620	
	Entry Status	Main curator
Published	Prigent	

PHENOTYPIC CHANGE

	Trait Category	
Physiology (https://www.gephebase.org/search-criteria/?and+Trait+Category=^Physiology+#gephebase-summary-title)	Trait	
Plant secondary metabolite (catechin) (https://www.gephebase.org/search-criteria/?and+Trait=^Plant+secondary+metabolite+(catechin)+#gephebase-summary-title)	Trait State in Taxon A	
Yingshuang tea cultivar (<i>C. sinensis</i> var. <i>sinensis</i>) with moderate catechin content and other tea accessions (ratio of di/tri-hydroxylated catechins)	Trait State in Taxon B	
Beiyue Danzhu tea cultivar (<i>C. sinensis</i> var. <i>pubilimba</i>) with higher catechin content and other tea accessions	Ancestral State	
Unknown	Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria/?and+Taxonomic+Status=^Intraspecific+#gephebase-summary-title)		
	Taxon A	Taxon B
	Latin Name	Latin Name
Camellia sinensis (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Camellia+sinensis+#gephebase-summary-title)	Camellia sinensis (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Camellia+sinensis+#gephebase-summary-title)	
	Common Name	Common Name
-	-	-
	Synonyms	Synonyms
Thea sinensis; black tea; Camellia sinensis L.; Camelia sinensis	Thea sinensis; black tea; Camellia sinensis L.; Camelia sinensis	
	Rank	Rank
species	species	species
	Lineage	Lineage
cellular organisms; Eukaryota; Viriplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphylophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; Ericales; Theaceae; Camellia	cellular organisms; Eukaryota; Viriplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphylophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; Ericales; Theaceae; Camellia	
	Parent	Parent
Camellia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4441)	Camellia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4441)	
	NCBI Taxonomy ID	NCBI Taxonomy ID
4442 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4442)	4442 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4442)	
	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?
Yes	Yes	Yes
	Taxon A Description	Taxon B Description
Yingshuang tea cultivar (<i>C. sinensis</i> var. <i>sinensis</i>) with moderate catechin content and other tea accessions	Beiyue Danzhu tea cultivar (<i>C. sinensis</i> var. <i>pubilimba</i>) with higher catechin content and other tea accessions	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Camellia sinensis
F3'5'H1	A3KLR7 (http://www.uniprot.org/uniprot/A3KLR7)	
	Synonyms	GenebankID or UniProtKB
F3'5'Ha	0	
	String	
-		
	Sequence Similarities	
Belongs to the cytochrome P450 family.		
	GO - Molecular Function	
GO:0020037 : heme binding (https://www.ebi.ac.uk/QuickGO/term/GO:0020037)		
GO:0005506 : iron ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005506)		
GO:0004497 : monooxygenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004497)		

GO:0016705 : oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen (<https://www.ebi.ac.uk/QuickGO/term/GO:0016705>)

GO - Biological Process

- GO - Cellular Component

GO:0016021 : integral component of membrane

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

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^No^#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

several candidate SNPs

Experimental Evidence

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

Main Reference

Functional natural allelic variants of flavonoid 3',5'-hydroxylase gene governing catechin traits in tea plant and its relatives. (2017) (<https://pubmed.ncbi.nlm.nih.gov/27896431>)

Authors

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Abstract

Functional allelic variants of the flavonoid 3',5'-hydroxylase (F3'5'H) gene provides new information of F3'5'H function of tea plant and its relatives. This insight may serve as the foundation upon which to advance molecular breeding in the tea plant. Catechins are the active components of tea that determine its quality and health attributes. This study established the first integrated genomic strategy for deciphering the genetic basis of catechin traits of tea plant. With the RNA-sequencing analysis of bulked segregants representing the tails of a F1 population segregated for total catechin content, we identified a flavonoid 3',5'-hydroxylase (F3'5'H) gene. F3'5'H had one copy in the genomic DNA of tea plant. Among 202 tea accessions, we identified 120 single nucleotide polymorphisms (SNPs) at F3'5'H locus. Seventeen significant marker-trait associations were identified by association mapping in multiple environments, which were involved in 10 SNP markers, and the traits including the ratio of di/tri-hydroxylated catechins and catechin contents. The associated individual and combination of SNPs explained 4.5-25.2 and 53.0-63.0% phenotypic variations, respectively. In the F1 population (validation population), the catechin trait variation percentages explained by F3'5'H diplotype were 6.9-74.3%. The genotype effects of ten functional SNPs in the F1 population were all consistent with the association population. Furthermore, the function of SNP-711/-655 within F3'5'H was validated by gene expression analysis. Altogether, our work indicated functional SNP allelic variants within F3'5'H governing the ratio of di/tri-hydroxylated catechins and catechin contents. The strong catechin-associated SNPs identified in this study can be used for future marker-assisted selection to improve tea quality.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS