

GEPHE SUMMARY

<p>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)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>GP00001620</p> <p>Prigent</p> <p>Entry Status</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

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

GENOTYPIC CHANGE

<p>F3'5'H1</p> <p>F3'5'Ha</p> <p>-</p> <p>Belongs to the cytochrome P450 family.</p> <p>GO:0020037 : heme binding (https://www.ebi.ac.uk/QuickGO/term/GO:0020037)</p> <p>GO:0005506 : iron ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005506)</p> <p>GO:0004497 : monooxygenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004497)</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p>	<p>A3KLR7 (http://www.uniprot.org/uniprot/A3KLR7)</p> <p>()</p>	<p>UniProtKB Camellia sinensis</p> <p>GenebankID or UniProtKB</p>
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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](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=))

Molecular Type

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

Aberration Type

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

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](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=))

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

Jin JQ; Ma JQ; Yao MZ; Ma CL; Chen L

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 diplotypes 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

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS