

GEPHE SUMMARY

	Gephebase Gene		GepheID
FaO-methyl-transferase (FaOMT) (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^FaO-methyl-transferase (FaOMT)^#gephebase-summary-title)	GP00000303		
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=^Physiology^#gephebase-summary-title)		Trait	
		Fragrance (flavor) (https://www.gephebase.org/search-criteria?/and+Trait=^Fragrance (flavor)^#gephebase-summary-title)	
	Trait State in Taxon A		
Fragaria ananassa		Trait State in Taxon B	
Fragaria ananassa			
	Ancestral State		
Data not curated		Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=^Domesticated^#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Fragaria x ananassa (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Fragaria x ananassa^#gephebase-summary-title)		Fragaria x ananassa (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Fragaria x ananassa^#gephebase-summary-title)	
	Common Name		Common Name
strawberry		strawberry	
	Synonyms		Synonyms
Fragaria ananassa; Fragaria chiloensis x Fragaria virginiana; Fragaria virginiana x Fragaria chiloensis; strawberry; Fragaria x ananassa (Weston) Duchesne ex Rozier; Fragaria x ananassa		Fragaria ananassa; Fragaria chiloensis x Fragaria virginiana; Fragaria virginiana x Fragaria chiloensis; strawberry; Fragaria x ananassa (Weston) Duchesne ex Rozier; Fragaria x ananassa	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Rosales; Rosaceae; Rosoideae; Potentilleae; Fragariinae; Fragaria		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Rosales; Rosaceae; Rosoideae; Potentilleae; Fragariinae; Fragaria	
	Parent		Parent
Fragaria () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3746)		Fragaria () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3746)	
3747 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3747)	NCBI Taxonomy ID	3747 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3747)	NCBI Taxonomy ID
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Fragaria ananassa
omt1		Q9M602 (http://www.uniprot.org/uniprot/Q9M602)	
	Synonyms		GenebankID or UniProtKB
-		AF220491 (https://www.ncbi.nlm.nih.gov/nucore/AF220491)	
	String		
-			
	Sequence Similarities		
Belongs to the class I-like SAM-binding methyltransferase superfamily. Cation-independent O-methyltransferase family.			
	GO - Molecular Function		
GO:0046983 : protein dimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046983)			
GO:0008171 : O-methyltransferase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008171)			
	GO - Biological Process		
-			

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^No^#gephebase-summary-title))

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

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

Promoter variation – there are several single nucleotide polymorphisms (SNPs); insertion/deletions (indels); and rearrangements in the promoter

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

Genetic analysis of strawberry fruit aroma and identification of O-methyltransferase FaOMT as the locus controlling natural variation in mesifurane content. (2012) (<https://pubmed.ncbi.nlm.nih.gov/22474217>)

Zorrilla-Fontanesi Y; Rambla JL; Cabeza A; Medina JJ; SÁnchez-Sevilla JF; Valpuesta V; Botella MA; Granell A; Amaya I

Improvement of strawberry (*Fragaria* A— *anassa*) fruit flavor is an important goal in breeding programs. To investigate genetic factors controlling this complex trait, a strawberry mapping population derived from genotype '1392', selected for its superior flavor, and '232' was profiled for volatile compounds over 4 years by headspace solid phase microextraction coupled to gas chromatography and mass spectrometry. More than 300 volatile compounds were detected, of which 87 were identified by comparison of mass spectrum and retention time to those of pure standards. Parental line '1392' displayed higher volatile levels than '232', and these and many other compounds with similar levels in both parents segregated in the progeny. Cluster analysis grouped the volatiles into distinct chemically related families and revealed a complex metabolic network underlying volatile production in strawberry fruit. Quantitative trait loci (QTL) detection was carried out over 3 years based on a double pseudo-testcross strategy. Seventy QTLs covering 48 different volatiles were detected, with several of them being stable over time and mapped as major QTLs. Loci controlling ¹³-decalactone and mesifurane content were mapped as qualitative traits. Using a candidate gene approach we have assigned genes that are likely responsible for several of the QTLs. As a proof of concept we show that one homoeolog of the O-methyltransferase gene (FaOMT) is the locus responsible for the natural variation of mesifurane content. Sequence analysis identified 30 bp in the promoter of this FaOMT homoeolog containing putative binding sites for basic/helix-loop-helix, MYB, and BZIP transcription factors. This polymorphism fully cosegregates with both the presence of mesifurane and the high expression of FaOMT during ripening.

RELATED GEPHE

No matches found.

No matches found.

EXTERNAL LINKS

COMMENTS