

Natural Variation in Fruit Color among *Fragaria* Species Explained by Independent Mutations in a Single Transcriptional Factor: *MYB10*

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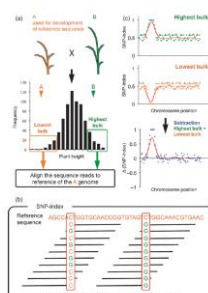
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Identification of the white mutation in acc. ESP138.596

Mapping by NGS

Rapid mapping of mutations and quantitative trait loci by whole genome resequencing of DNA from two bulked populations (QTL-seq)



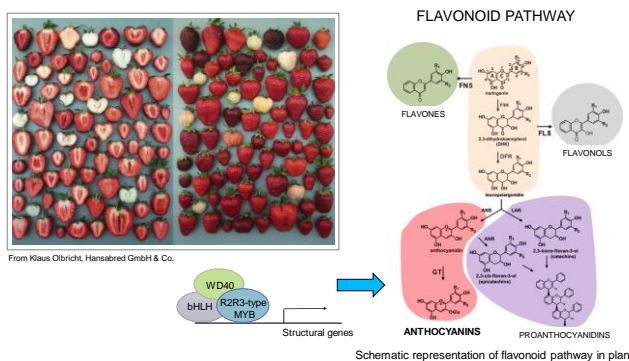
APPROACH:

- 50X Illumina HiSeq Re-sequencing of two pools:
 - Red fruits: 34 F2 lines
 - White fruits: 32 F2 lines
- Mapping to the H4 reference genome.
- SNP calling and estimation of allele frequencies in each pool.
- Representation of Δ SNP index across the genome.

Takagi, H. et al. (2013) QTL-seq: rapid mapping of QTL in rice by whole genome resequencing of DNA from two bulked populations. *Plant J*, 74, 174-183.



IFAPA Anthocyanins are the main pigments in Strawberry fruit



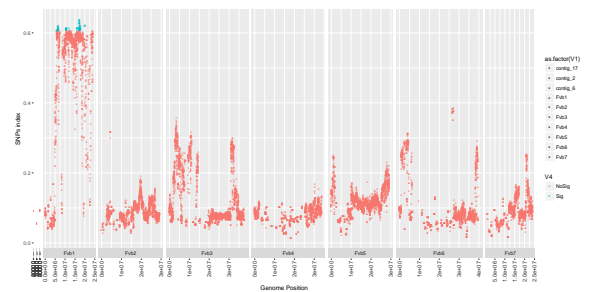
From Klaus Olbricht, Hansabred GmbH & Co.

Schematic representation of flavonoid pathway in plants (From Mouradov and Spangenberg (2014) *Front Plant Sci.* 5:620)



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SIGNIFICANT SNPs WERE ONLY PRESENT IN CHROMOSOME 1




Detection of a large 278_279ins in *FvMYB10*




IFAPA Identification of the white mutation in acc. ESP138.596

F. vesca MAPPING POPULATION

P1
Reine des Vallées



P2
ESP138.596



X
↓
F1
↓
F2 (n=145)

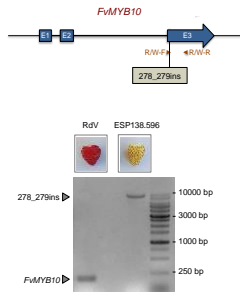
	Obs.	Exp.	Chi2
Red	103	103.5	0.922
White	35	34.5	

Red vs. white fruit color in *F. vesca* is controlled by a single gene (Brown and Wareing, 1965)

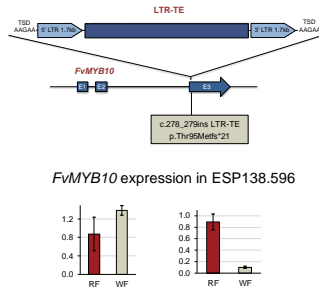


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278_279ins CONFIRMATION



GYPSY-like RETROTRANSPOSON INSERTION IN *FvMYB10*

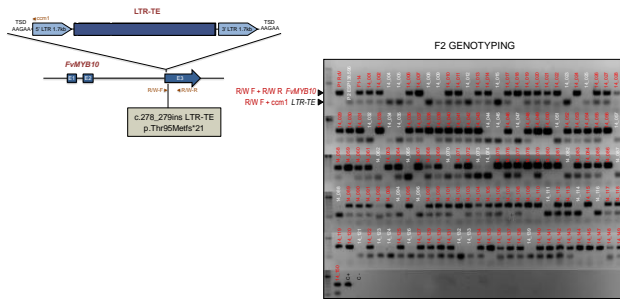




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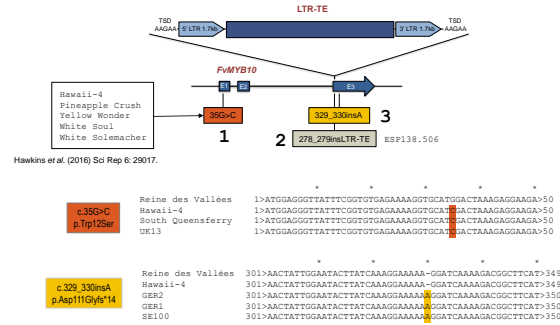
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THE GYPSY-like RETROTRANSPOSON INSERTION IN *FvMYB10* COSEGREGATES WITH THE WHITE PHENOTYPE IN THE ENTIRE F₂ POPULATION



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Characterization of other white *F. vesca* accessions



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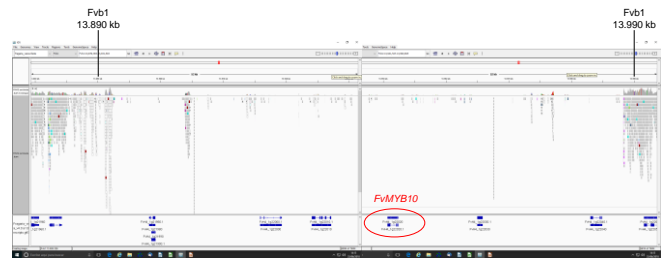
WHITE MUTATION COMPLEMENTATION IN ESP138.596



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Characterization of other white *F. vesca* accessions

FIN12 HAS A LARGE DELETION IN CHROMOSOME 1

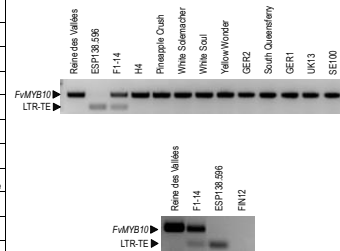


Collaboration with Tuomas Toivainen and Timo Hytönen, University of Helsinki, Finland, and David Posé, IHSM-UMA-CSIC, Spain.

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Characterization of other white *F. vesca* accessions

Number	Accession/cultivar	Origin
1	ESP138.596 <i>F. vesca</i> f. alba	Europe
2	Hawaii-4 <i>F. vesca</i> f. alba	Maryland, United States
3	Pineapple Crush <i>F. vesca</i> f. semperflorens	?
4	White Solemacher <i>F. vesca</i> f. alba	Germany, Europe
5	White Soul <i>F. vesca</i> f. alba	?
6	Yellow Wonder <i>F. vesca</i> f. semperflorens	United States
7	GER2 <i>F. vesca</i> f. alba	Mortzburg woods, near Dresden, Germany, Europe
8	South Queensferry <i>F. vesca</i> f. alba	South Queensferry, near Edinburgh, Scotland, Europe
9	GER1 <i>F. vesca</i> f. alba	Gatersleben, Germany, Europe
10	UK13 <i>F. vesca</i> f. alba	United Kingdom, Europe
11	SE100 <i>F. vesca</i> f. alba	Sweden, Europe
12	FIN12 <i>F. vesca</i> f. alba	Finland, Europe

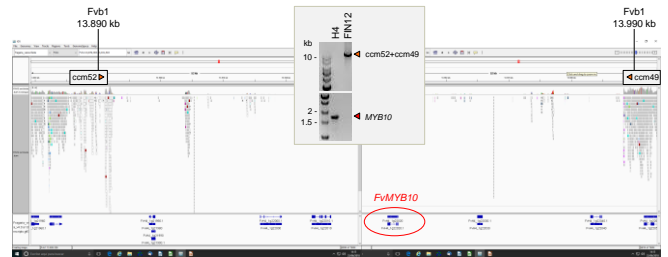


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WHITE MUTATION COMPLEMENTATION

35S:FvMYB10 RdV 35S:FvMYB10 ESP138.596

35S:FvMYB10 RdV 35S:FvMYB10 596

GER1 GER2 SE100

FvMYB10

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IFAPA Mapping fruit color variation in octoploid spp.

A mayor QTL for internal fruit color has been detected in LG I-3 in two years

Trait	QTL	KW*	Group	Position	Locus	Thrs.	LOD	mu_A	mu_H	mu_B	R² (%)
Fruit Flesh Color	qFleshColor-I-3	****	LG-3	54.22	180931-19-G-LG1	5.8	17.3	4.50178	3.64064	1.29332	54.7
Fruit Core Color	qCoreColor-I-3	****	LG-3	54.43	1791879-32-S-A-LG7	4.9	12.06	2.52174	2.20622	1.09501	42.8

LG I-3

WHITE MUTATION COMPLEMENTATION in *F. chiloensis*

F. chiloensis ESP138.0156

F. chiloensis ESP138.0160

F. chiloensis ESP138.0157

e. 4763T p. Glu150*

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IFAPA *Fragaria* genus

Diploid 2n=2x=14

- F. bucharica*
- F. daltoniana*
- F. x bifera*
- F. mandchurica*
- F. nilgimensis*
- F. hayatai*
- F. nipponica*
- F. rubicola*
- F. pentaphylla*
- F. chiloensis*
- F. virginiana*
- F. vesca*
- F. iinumae*

Tetraploid 2n=4x=28

- F. corymbosa*
- F. gracilis*
- F. moupinensis*
- F. orientalis*
- F. tibetica*

Hexaploid 2n=6x=42

- F. moschata*

Octoploid 2n=8x=56

- F. chiloensis*
- F. virginiana*
- F. x ananassa*

Decaploid 2n=10x=70

- F. x cuneifolia*
- F. x brughurstii*
- F. iturupensis*

***F. vesca* (wild or woodland strawberry) 2n=2x=14**

LG 1 LG 2 LG 3 LG 4 LG 5 LG 6 LG 7

***F. x ananassa* (cultivated strawberry) 2n=8x=56**

HG 1 HG 2 HG 3 HG 4 HG 5 HG 6 HG 7

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IFAPA CONCLUSIONS AND HYPOTHESIS

- Three independent mutations in *FvMYB10* has been identified in addition to the previously described G/C. We have not found any white fruit accessions with a WT *MYB10*.
- A mayor QTL that spans *FaMYB10* controls internal flesh color in the octoploid strawberry and transient expression of *FvMYB10* restores anthocyanin accumulation in white fruited *F. chiloensis*.
- Altogether, these results indicate that natural variation in white/red fruit color has been achieved by independent mutations in a single R2R3-MYB, *MYB10*, suggesting convergent evolution for anthocyanin biosynthesis in strawberry fruit.

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IFAPA Mapping fruit color variation in octoploid spp.

F2 POPULATION

F. x ananassa 'Senga Sengana' X *F. chiloensis* ssp. Lucida USA2 WITH 105 PROGENY LINES

MAP OF THE F1 HYBRID USING 2991 SNPs

Collaboration with Dr. K. Olbricht, Hansabred, Germany

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