

# Linkage map development using the cherry 6k whole genome genotyping array and the identification of a novel locus controlling flesh colour

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# Overview

1. STSM objectives
2. Cherry 6K SNP array
3. C417 mapping population
4. Linkage map construction
5. Flesh colour QTL



# STSM Objectives

1. To genotype the population with the 6K cherry SNP array
2. To construct a genetic linkage map for the C417 population
3. To identify QTL associated with fruit quality traits.



# Infinium 6k cherry array



Developed by the RosBREED consortium

- 16 sweet and 8 sour cherry accessions
- 5,969 SNPs
- Targets 76% sweet and 24% sour genomes
- Anchored to peach genome sequence
- Rapid genotyping and linkage map construction of experimental populations
  - Regina x Lapins (RxL) and Black Tartarian x Kordia (BTxK).





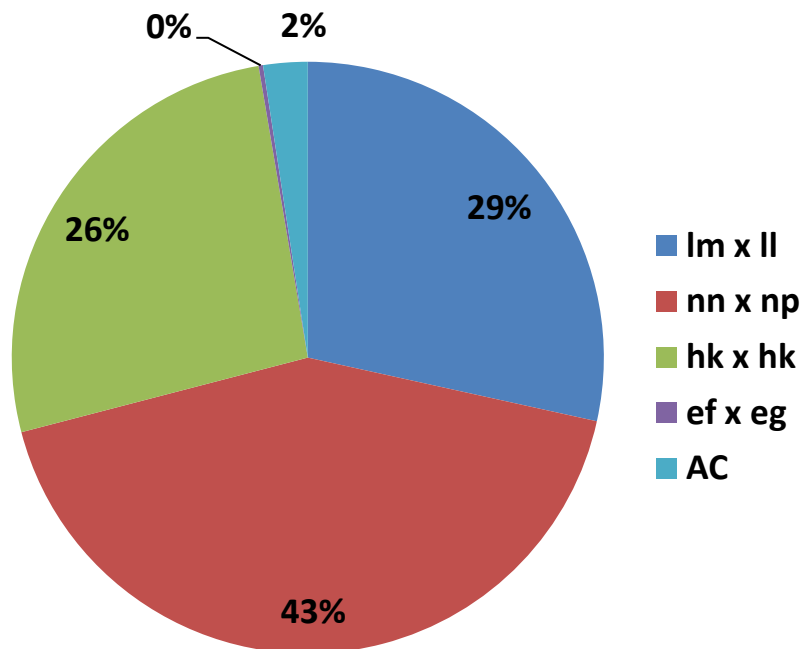
# C417 mapping population

- Colney x C210-7 (Lapins x Sweet September).
- 337 seedlings
  - 138 individuals genotyped
  - Evaluated in 2013 for fruit quality traits.



# SNP genotyping

Monomorphic	Failed	Polymorphic	Total
4659	211	826	5969
81.8%	3.7%	14.5%	



- Genome Studio Genotyping software
- 71% heterozygous in one parent (*lmxll* and *nnxnp*)
- 26.6 % heterozygous in both parents (*hkxhk* and *efxeg*)
- 2.4% ambiguous clustering (AC)

# Linkage Map Construction



- JoinMap 4.0
- Two rounds of mapping
- 748 markers mapped (94%)

Marker Class				
LG	<i>lmxll</i>	<i>nnxnp</i>	<i>hkxhk</i>	Total
1	43	79	16	138
2	20	44	24	88
3	24	37	18	79
4	35	53	19	107
5	14	29	42	85
6	41	26	29	96
7	31	26	12	69
8	22	45	19	86
<b>Total</b>	<b>230</b>	<b>339</b>	<b>179</b>	<b>748</b>

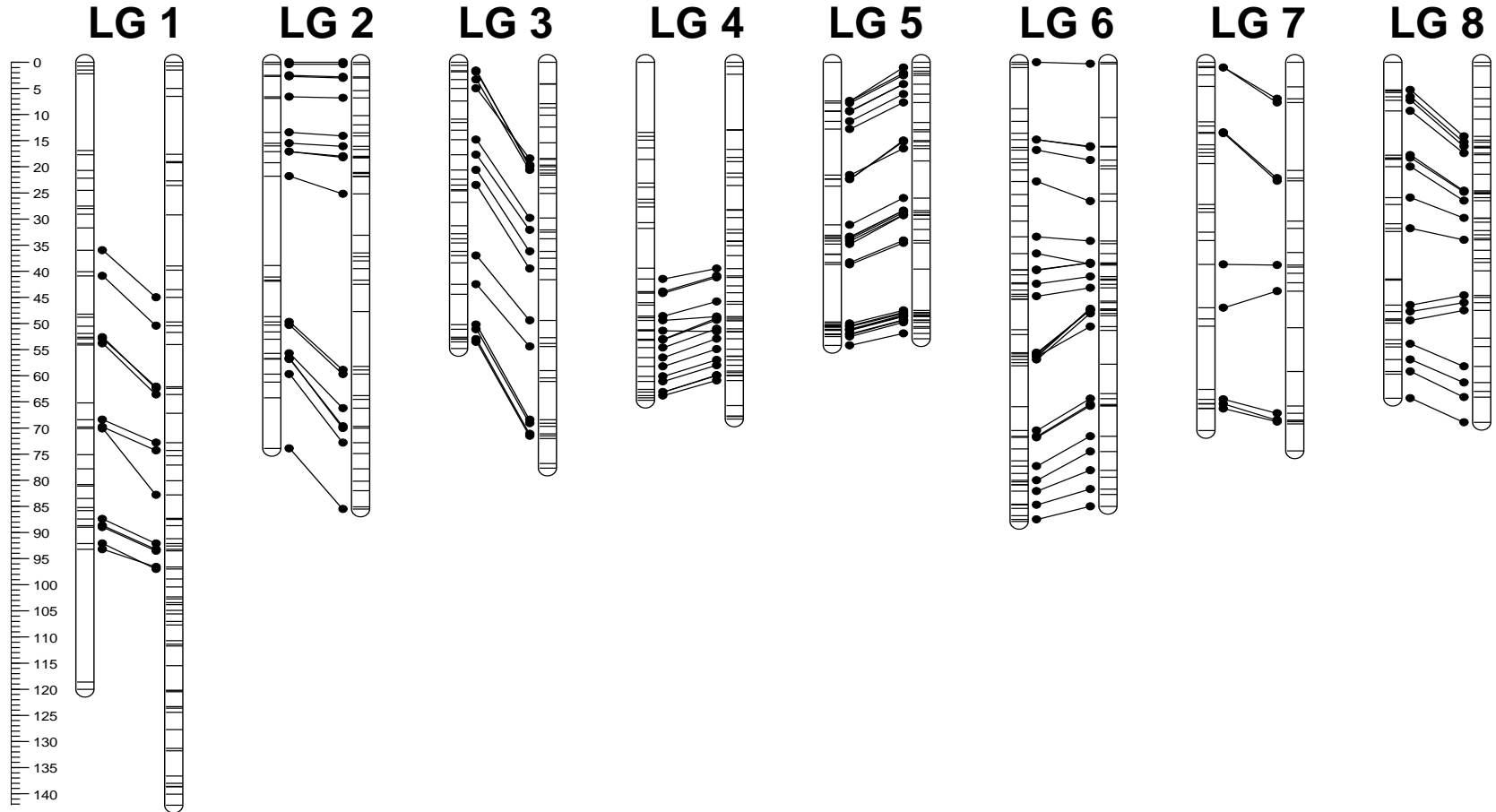
# Linkage Map Construction



	LG1	LG2	LG3	LG4	LG5	LG6	LG7	LG8	Total
<b>Number of mapped markers</b>									
Colney	59	44	42	54	56	70	43	41	409
C210-7	95	68	55	72	71	55	38	64	518
<b>Linkage Group Length (cM)</b>									
Colney	120	74	55	65	54	88	71	64	590
C210-7	142	86	78	68	53	85	74	69	655
<b>Average marker distance (cM)</b>									
Colney	2.0	1.7	1.3	1.2	1.0	1.3	1.6	1.6	1.5
C210-7	1.5	1.3	1.4	0.9	0.7	1.5	2.0	1.1	1.3



# Colney x C210-7 Linkage Map



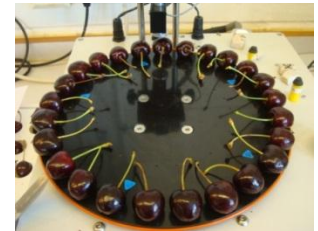
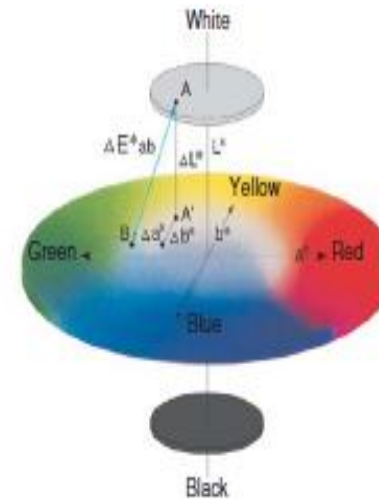
# Segregation Distortion

	Colney						C210-7					
	*	**	***	Total	%	Region (cM)	*	**	***	Total	%	Region (cM)
<b>LG 1</b>	4	-	26	30	50.8	36-119	4	1	65	70	73.7	23-131
<b>LG 3</b>	1	-	-	1	2.4	53	1	-	-	1	1.5	71
<b>LG 4</b>	2	-	-	2	3.7	61	9	-	-	9	12.5	55-58 68
<b>LG 5</b>	-	-	-	0	0.0	-	9	-	-	9	12.7	1-2 12-13
<b>LG 6</b>	15	3	1	19	27.1	14-40 42-45	11	2	6	19	34.5	0-10 20-39 41-46
<b>LG 7</b>	1	-	-	1	2.3	66	5	-	3	8	21.1	0-4 30-39

# Measuring Flesh Colour

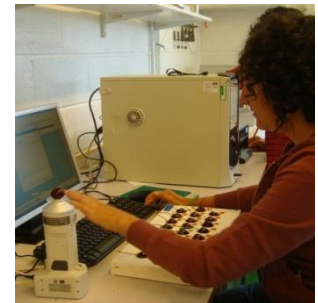
## Flesh Colour (n =25)

- Hand held colourimeter
- Colour co-ordinates
  - Lightness (L)
  - Red-Green (a)
  - Blue-Yellow (b)



## Calculate chroma (C) and hue angle ( $h^\circ$ )

- $C = \sqrt{(a^2) + (b^2)}$
- $h^\circ = \tan^{-1}(b/a)$



# QTL analysis: Flesh Colour

C417-070

C417-129

C417-062

C417-111

C417-100

C417-131

C417-120

C417-047



$h^{\circ} = 7.36$

$h^{\circ} = 8.81$

$h^{\circ} = 10.64$

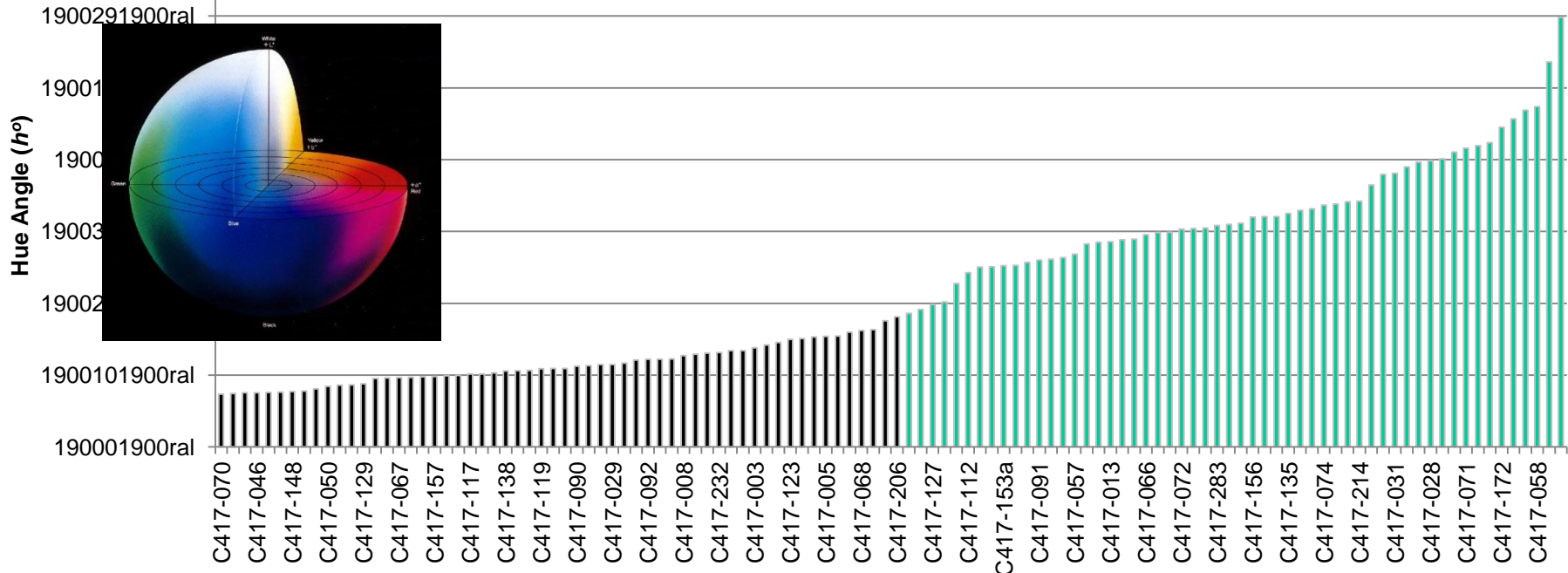
$h^{\circ} = 12.92$

$h^{\circ} = 25.02$

$h^{\circ} = 26.37$

$h^{\circ} = 31.12$

$h^{\circ} = 42.38$

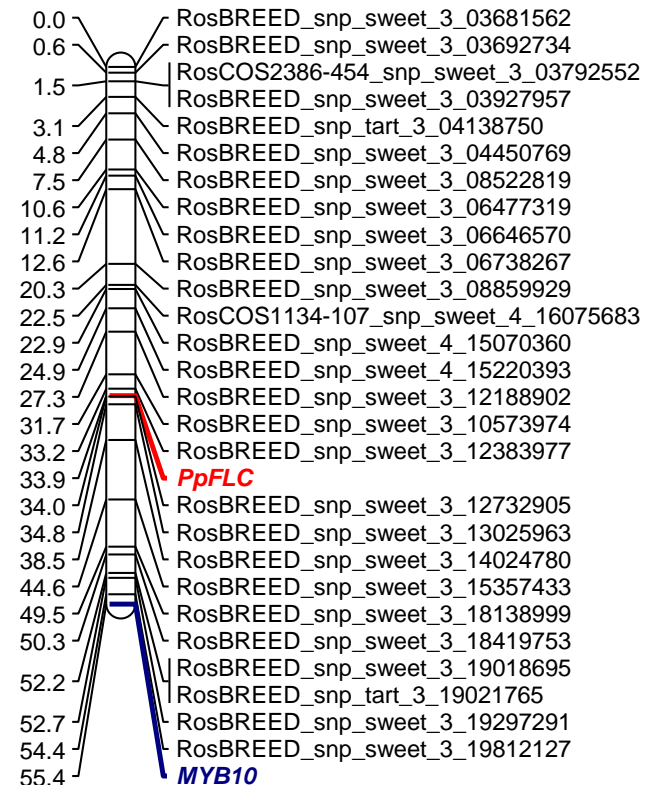


# QTL analysis: Flesh Colour

## Novel QTL identified on LG 3

- MapQTL 6.0
- Genome wide QTL ( $P > 0.001$ )
- Maps to a different region in LG 3 compared to *PvaMYB10*

### Prunus\_avium\_PG3



# Summary



- Quick and efficient tool for genotyping and linkage map construction
- High-throughout and relatively low cost
- Good marker saturation and genome coverage
- Anchorage to the peach genome for identification of candidate genes underlying traits



# Acknowledgements



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