# **CHARACTERIZATION OF DELETIONS CAUSING BERRY COLOR VARIATION IN GARNACHA AND TEMPRANILLO**

**Carolina Royo**, Maite Rodríguez-Lorenzo, Pablo Carbonell-Bejerano, Nuria Mauri, Félix Cibríain, Julián Suberviola, Ana Sagüés, Javier Ibáñez, José M. Martínez-Zapater

DE NAVARRA



#### Grape ripening and anthocyanin accumulation



## **Somatic Variation**



# Loss Of Heterozygosity around color locus on chr2

Chromosome 2																						
	Chr2_start							SNP4165				SNP6097			VvMybA2 VvMybA1 VvMybA1				Chi2 end			
		13,0	013 13,42	0 13,77	2 13,920	14,031	14,069	14,149	14,151	14,181	1	14,25	50	14,	,288 14,2	292 14,32	25 15,77	6 16,287	7 16,539	17,098	18,271	
Cv	Clone	Tissue 0	V SV 2 06	SV 09	SV 10	sv 12	SNP 4045	VVN TMI	VVN J TM2 p	wMybA2 promoter	pror	Vv:My& noter	41 exon 37		VN SN MI3 723	IP VV2 34 TM	8 SNP 5 4071	SNP 7054	VVI U20	SNP 6166	VMC 7G3	
Cultivar	Repository	v Tissue code	Mb Layer	9987 SNP 6097	12674 SC8 010	12970 SC8 026	14069 SNP 4045	14149 VVN TM1	14151 VVN TM2	14248 VvMyb Promote	8 A1 er†	14288 VVN TM3	14292 SNP 7234	14325 VVN TM5	14330 VVN TM6	14384 VVN TM4	15776 SNP 4071	16287 SNP 7054	16539 VVI U20	17098 SNP 6166	18270 VMC 7G3	Deletion range (Mb)
Grenache	CRA-VIT	L, S	L1 + L2	N.D.	ho	he	he	he	he	Gret/non-	Gret	he	he	he	he	ho	ho	he	he	ho	he	_
Garnacha	FEM	r, r L, S	L2 L1 + L2	N.D.	ho	he	he	he	he	Gret/non- Gret/non-	-Gret	he	he	he	he	ho	ho	he	he	ho	he	_
Tinto		F, R	L2	N.D.	ho	he	he	he	he	Gret/non-	Gret	he	he	he	he	ho	ho	he	he	ho	he	_
linta	IMIDRA	L, S E R	L1 + L2 L2	N.D. N.D.	ho	he	he	he	he	Gret/non- Gret/non-	-Gret -Gret	he	he	he	he	ho	ho	he	he	ho	he	_
Grenache	CRA-VIT	L, S	L1 + L2	N.D.	ho	he	he	he	he	Gret/non-	Gret	he	he	he	he	ho	ho	he	he	ho	he	_
Gris	EEM	F, R	L2	N.D.	ho	he	hd	hd	hd	Gret/-	Cast	hd	hd	hd	hd	ho	ho	he	he	ho	he	0.2-1.4
	PEM	E R	LI + L2 L2	N.D.	ho	he	hd	hd	hd	Gret/-	-Gret	he	he	he	he	ho	ho	he	he	ho	he	0.2-1.3
Garnacha	IMIDRA	L, S	L1 + L2	N.D.	ho	he	he	he	he	Gret/non-	-Gret	he	he	he	he	ho	ho	he	he	ho	he	_
Roia		F, R	L2	N.D.	ho	he	hd	hd	hd	Gret/-		he	he	he	he	ho	ho	he	he	ho	he	0.2-1.3
Noja	INRA	L, S	L1 + L2	N.D.	ho	he	he	he	he	Gret/non-	-Gret	he	he	he	he	ho	ho	he	he	ho	he	0.2.1.2
Grenache	CRA-VIT	г, к L. S	L1 + L2	N.D.	ho	he	he	he	he	Gret/-		hd	hd	hd	hd	ho	ho	he	he	ho	he	0.2-1.5
Blanc		F, R	L2	N.D.	ho	he	he	he	he	Gret/-		hd	hd	hd	hd	ho	ho	he	he	ho	he	0.08-0.2
Garnacha	IMIDRA	L, S	L1 + L2	N.D.	ho	he	he	hd	hd	Gret/-		hd	hd	hd	hd	ho	ho	he	he	ho	he	0.2-0.3
Diama	INID 4	F, R	L2	N.D.	ho	he	he	hd	hd	Gret/-		hd	hd	hd	hd	ho	ho	he	he	ho	he	0.2-0.3
Blanca	INKA	L, S F R	LI + L2 L2	N.D.	ho	he	he	he	he	Gret/-		na hd	hd	hd	nd hd	ho	ho	he	he	ho	he	0.08-0.2
Tempranillo	D IMIDRA	L, S	L1 + L2	N.D.	he	he	he	he	he	Gret/non-	Gret	he	ho	he	he	he	he	he	ho	ho	he	
Tinto		F, R	L2	N.D.	he	he	he	he	he	Gret/non-	Gret	he	ho	he	he	he	he	he	ho	ho	he	_
Tempranillo	D	L, S	L1 + L2	N.D.	he	he	he	he	he	Gret/non-	-Gret	he	ho	he	he	he	he	he	ho	ho	he	0.2.1.4
Tempranille	D	L. S	L1 + L2	N.D.	he	he	hd	hd	hd	Gret/-		hd	hd	hd	hd	he	he	he	ho	ho	he	0.3-1.4
Blanco		F, R	L2	N.D.	he	he	hd	hd	hd	Gret/-		hd	hd	hd	hd	he	he	he	ho	ho	he	0.3-1.4

(Adapted from Vezzulli et al 2012, Migliaro et al 2014)

#### Background

### Tempranillo Tinto and Blanco Whole Genome Sequence

Α

Structural rearrangement graph:

Deletion-type







## **Tempranillo Blanco Affected Traits**

#### **Rearranged chromosomes are gamete-lethal**

Fruit set



#### Complex genome rearrangements cause side-effects in yield production

#### **Plant Materials**

## **Tempranillo and Garnacha accessions**

Tempranillo Tinto



9



6



Tempranillo Gris



1

Garnacha Tinta

Garnacha Roja

Garnacha Blanca







60

5

2





#### SNP genotyping along chromosome 2

Chromosome 2 LOH genotyping: 48 SNP chip:

Heterozygous in Garnacha Tinta and Tempranillo Tinto

- Heterozygous in Garnacha Tinta
  - Heterozygous in Tempranillo Tinto



#### **SNP** selection from:

Lijavetzky et al., 2007, Carbonell-Bejerano et al., 2017, Laucou et al., 2018

**M**inor **A**llele **F**requency (MAF)  $\approx 0.5$ 

#### Loss Of Heterozygosity (LOH) delimits likely deleted fragments

### Loss Of Heterozygosity in Tempranillo Gris

Chromosome 2 LOH genotyping: 48 SNP chip:

- Heterozygous in Garnacha Tinta and Tempranillo Tinto
- Heterozygous in Garnacha Tinta
  - Heterozygous in Tempranillo Tinto



Results obtained in roots = L2



#### Loss Of Heterozygosity in Tempranillo Gris

Chromosome 2 LOH genotyping: 48 SNP chip:

- Heterozygous in Garnacha Tinta and Tempranillo Tinto
- Heterozygous in Garnacha Tinta
  - Heterozygous in Tempranillo Tinto



Tempranillo Blanco regeneration through somatic embryogenesis from Tempranillo Gris type 1

#### Loss Of Heterozygosity in Tempranillo and Garnacha

Chromosome 2 LOH genotyping: 48 SNP chip:

- Heterozygous in Garnacha Tinta and Tempranillo Tinto
- Heterozygous in Garnacha Tinta
- Heterozygous in Tempranillo Tinto



#### Loss Of Heterozygosity in Garnacha Blanca

Chromosome 2 LOH genotyping chip: 48 SNP

Heterozygous in Garnacha Tinta and Tempranillo Tinto

- Heterozygous in Garnacha Tinta
- Heterozygous in Tempranillo Tinto



Selection of two pairs of Garnacha for Whole Gemone Sequencing (WGS)

#### **Garnacha Whole Genome Sequence analysis in progress**

Loss Of Heterozygosity (LOH)

**Copy Number Variation (CNV):** 

Structural variation as deletions, insertions, and duplications.

# Plant Physiology

# Catastrophic unbalanced genome rearrangements cause somatic loss of berry color in grapevine

Pablo Carbonell-Bejerano, Carolina Royo, Rafael Torres-Pérez, Jérôme Grimplet, Lucie Fernandez, Jose M. Franco-Zorrilla, Diego Lijavetzky, Elisa Baroja, Juana Martínez, Enrique García-Escudero, Javier Ibáñez, José M. Martínez-Zapater

Published August 2017. DOI: https://doi.org/10.1104/pp.17.00715 [Altmetric]

#### Garnacha WGS: Heterozygosity on chromosome 2

Garnacha Blanca type 1

Garnacha Blanca type 2



## **Garnacha WGS: LOH and Copy Number Variation on chromosome 2**

Garnacha Blanca type 1

Garnacha Blanca type 2



#### Conclusions

- 1. The genotyping tool that we design proved useful to delimit deletions on chromosome 2.
- The loss of color is related to hemizygous deletions at the color locus in all the variants studied by whole-genome sequencing.
- In Tempranillo, multiple independent SV types were detected, including minimal deletion lines suited for the development of improved clones of Tempranillo Blanco.
- 4. In Garnacha Blanca, the results indicate the likely presence of recurrent SV fragile sites.



# **ACKNOWLEDGEMENTS**







Nafarroako Gobernua Landa Garapeneko, Ingurumeneko eta Toki Administrazioko Departamentua





Gobierno de Navarra

Departamento de Desarrollo Rural,

Medio Ambiente y Administración Local

Carolina Royo

Maite Rodríguez-Lorenzo

Pablo Carbonell-Bejerano

Nuria Mauri

Javier Ibáñez

José M. Martínez-Zapater

**Félix Cibríain** 

Julián Suberviola

Ana Sagüés

# **THANKS FOR YOUR ATENTION**

