

ANALYSIS OF THE ORIGIN OF PARTHENO-CARPY IN THE GRAPEVINE CULTIVAR CORINTO BIANCO

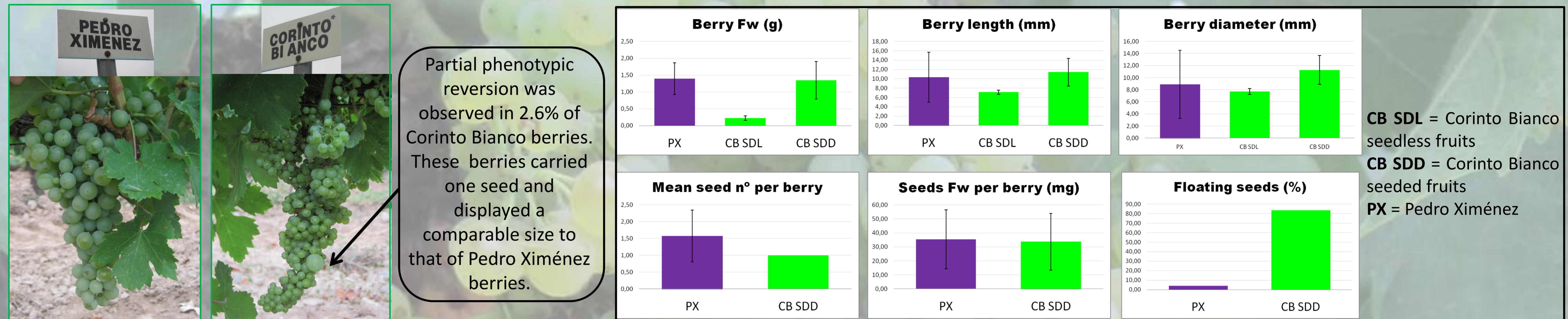
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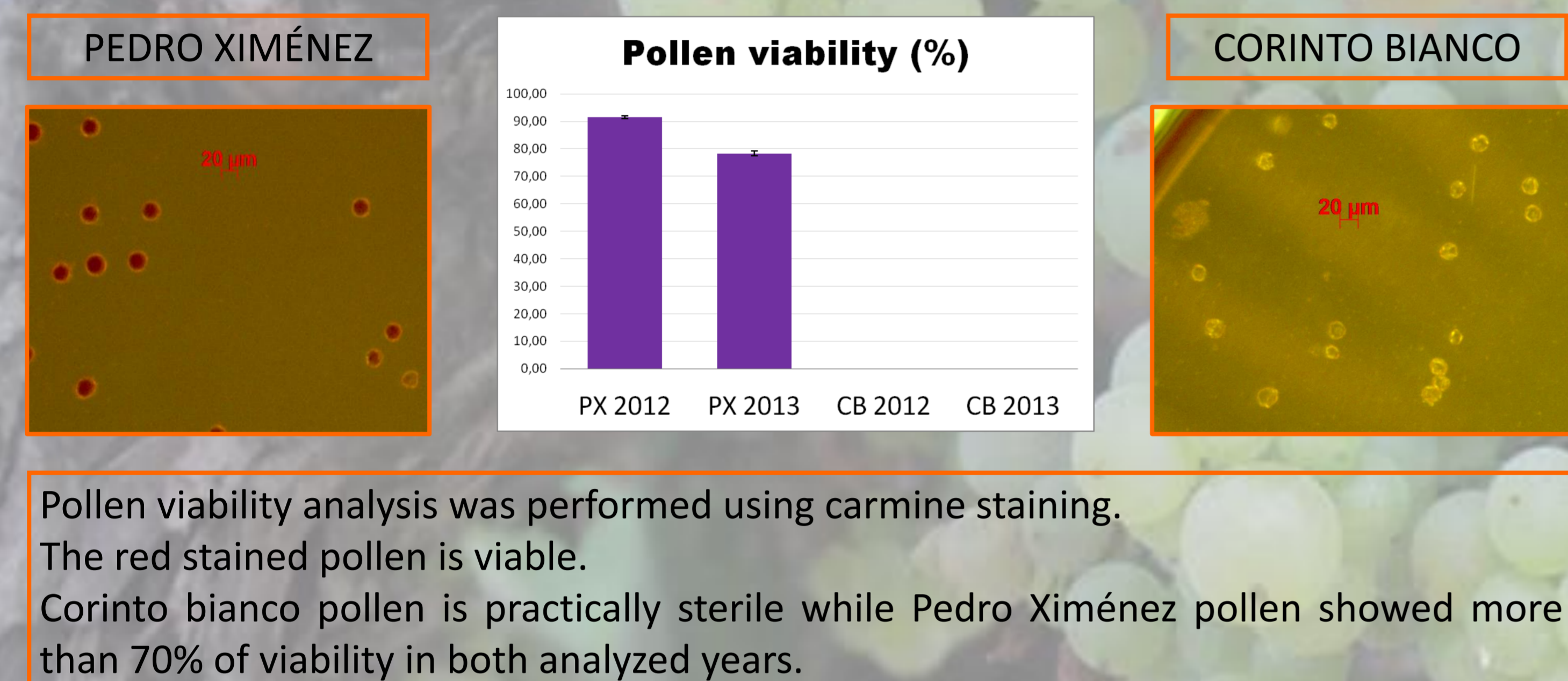
INTRODUCTION

Seedless fruits appear spontaneously in grapevine (*Vitis vinifera* L.) as a result of somatic variation. Stenospermocarpic and parthenocarpic seedlessness are known. The first type is widely used in table grapes production because seed development aborts after fertilization giving rise to seed traces and almost normal size berries. In contrast, small berries without seeds develop in the absence of fertilization in parthenocarpic cultivars that are appreciated for raisin production. The cultivar Corinto Bianco is a parthenocarpic somatic variant of the Spanish seeded cultivar Pedro Ximénez. Morphological and molecular comparison of flower development and gametogenesis between both genotypes were directed to understand the genetic and molecular basis of this parthenocarpic phenotype.

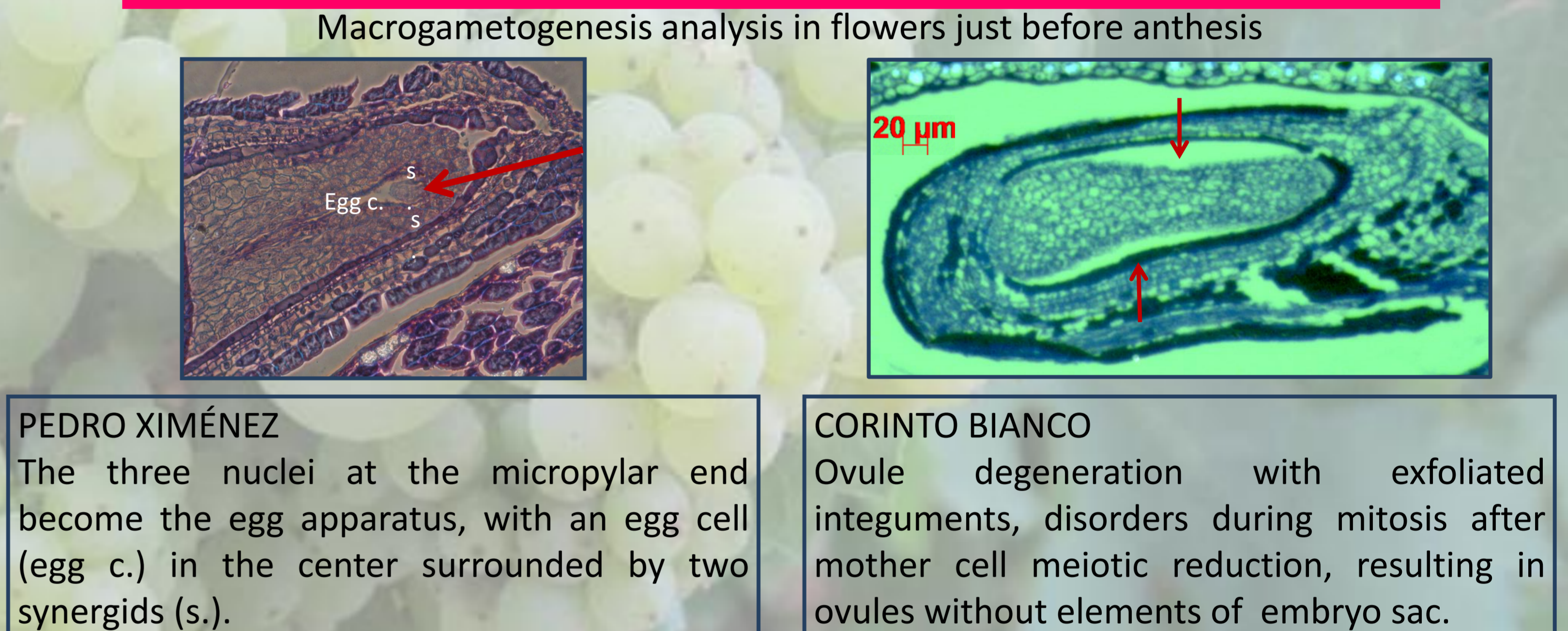
FRUIT AND SEED PHENOTYPE



MICROGAMETOGENESIS ANALYSIS



MACROGAMETOGENESIS ANALYSIS



TRANSCRIPTOME COMPARISON

Transcriptomic analyses of closed flowers were done comparing both genotypes at 50% bloom time using the NimbleGen Vitis HX12 microarray. Significant genes according to a 5% FDR in a 2-class SAM (Significance Analysis Microarrays). We identified 441 genes up-regulated and 949 down-regulated in the parthenocarpic somatic variant (≥ 2 -FC). Functional enrichment analysis indicated that transcripts related with sugar metabolism and transport, vesicular transport and seed storage proteins were more highly expressed in Pedro Ximénez. In contrast, secondary metabolism, responses to biotic stress and to oxidative stress, and salicylate and brassinosteroid signaling were over-represented within Corinto Bianco up-regulated transcripts. The responses activated in Corinto Bianco flowers could be related with the observed ovule degeneration at the same stage. Interestingly, genes related with cell cycle and gametogenesis were down-regulated in Corinto Bianco. The expression of these genes could be related with defects in macro- and micro-gametogenesis in Corinto Bianco.

Cb Downregulated regulatory genes FC>4

Unique ID	Annotation	log2 (Cb/PX)	FDR in SAM (%)
VIT_06s0009g02090	cyclin CYCB1_2	-4,75	0,0E+00
VIT_13s00064g00600	cyclin-related	-3,22	0,0E+00
VIT_08s0007g08350	cyclin-related	-2,72	0,0E+00
VIT_14s0108g01270	cyclin-dependent kinase CDC2C	-2,72	0,0E+00
VIT_13s0064g00590	cyclin-related	-2,71	0,0E+00
VIT_09s0070g00390	TMM (TOO MANY MOUTHS)	-2,48	0,0E+00
VIT_07s0031g01610	Programmed cell death 2 C-terminal domain-containing protein	-2,04	1,7E-01
VIT_01s0010g00340	Embryo sac development arrest 18	-2,51	0,0E+00
VIT_07s0197g00030	LBD36_3	-2,14	9,3E-02
VIT_10s0092g00030	bHLH family	-2,44	0,0E+00
VIT_18s0001g03010	bZIP transcription factor	-3,98	0,0E+00
VIT_03s0038g03700	zinc finger (C2H2 type) family	-3,33	0,0E+00
VIT_15s0021g02710	zinc finger (C2H2 type) family	-3,12	0,0E+00
VIT_17s0000g07750	ZINC FINGER PROTEIN 5	-3,11	0,0E+00
VIT_07s0003g02160	protein phosphatase 2C DBP	-2,29	0,0E+00
VIT_16s0039g01890	transcription factor jumonji (jmi)	-4,15	0,0E+00
VIT_00s1364g00020	EMB1674_3	-2,08	0,0E+00
VIT_18s0001g07610	EMB1674_1	-3,89	0,0E+00
VIT_00s0483g00050	EMB1674_4	-2,50	0,0E+00
VIT_15s0046g03370	LIM domain containing protein 3	-3,72	0,0E+00
VIT_02s0025g03980	LIM domain containing protein 5	-3,29	0,0E+00
VIT_03s0091g01010	LIM domain protein WLIM1	-3,06	0,0E+00
VIT_07s0031g01140	MADS-box AGAMOUS-LIKE 66	-4,42	0,0E+00
VIT_18s0007g08790	MADS-box AGAMOUS-LIKE 15	-3,70	0,0E+00
VIT_05s0021g02040	Myb DUO POLLEN 1	-2,06	9,5E-02
VIT_04s0023g00470	WRKY DNA-binding protein 2	-2,57	0,0E+00
VIT_12s0059g00700	MYB33/GAMYB	-4,08	0,0E+00
VIT_03s0038g01370	ABA-responsive protein HVA22H	-2,66	7,8E-02
VIT_07s0005g05400	ABI3_2	-2,53	0,0E+00
VIT_08s0007g02530	ABA-responsive protein HVA22J	-2,23	0,0E+00
VIT_06s0004g01800	ethylene-responsive TF PLETHORA 2	-3,28	0,0E+00

Cb Upregulated regulatory genes >2-FC

Unique ID	Annotation	log2 (Cb/PX)	FDR in SAM (%)
VIT_11s0052g00240	ACCELERATED CELL DEATH 11	2,02	2,1E-01
VIT_12s0059g02770	SHOOT GRAVITROPISM 7	1,55	5,5E-01
VIT_01s0011g02680	MYB3R1_5	1,01	3,1E-01
VIT_12s0134g00490	MYB14_1	1,05	1,4E+00
VIT_05s0049g01020	MYB14_3	1,12	2,1E+00
VIT_14s0006g00450	MYB20	1,23	3,9E+00
VIT_04s0008g00150	NAC036_1	1,08	2,4E+00
VIT_03s0038g03410	NAC036_2	1,45	8,9E-01
VIT_12s0028g00860	NAC042_5	1,90	3,7E+00
VIT_13s0067g02290	BTB/POZ domain-containing prot.	1,55	6,9E-01
VIT_13s0067g03140	WRKY70_1	1,27	2,7E+00
VIT_01s0010g03930	WRKY75_1	1,33	4,1E+00
VIT_07s0031g01710	WRKY51_3	2,13	0,0E+00
VIT_08s0058g01390	WRKY70_2	2,20	3,8E-01
VIT_17s0000g06200	MINI ZINC FINGER 1 MIF1	1,08	2,3E+00
VIT_04s0023g00320	auxin efflux carrier protein 8	1,51	3,8E-01
VIT_04s0008g05560	IAA29	1,98	9,1E-02
VIT_00s0425g00020	BAK1	1,01	1,4E-01
VIT_00s0258g00080	BAK1	1,02	1,0E+00
VIT_00s0258g00140	BAK1	1,11	3,0E+00
VIT_16s0039g01150	BAK1	1,20	3,9E-01
VIT_00s0258g00090	BAK1	1,25	4,9E-01
VIT_00s2588g00010	BAK1	1,42	5,5E-01



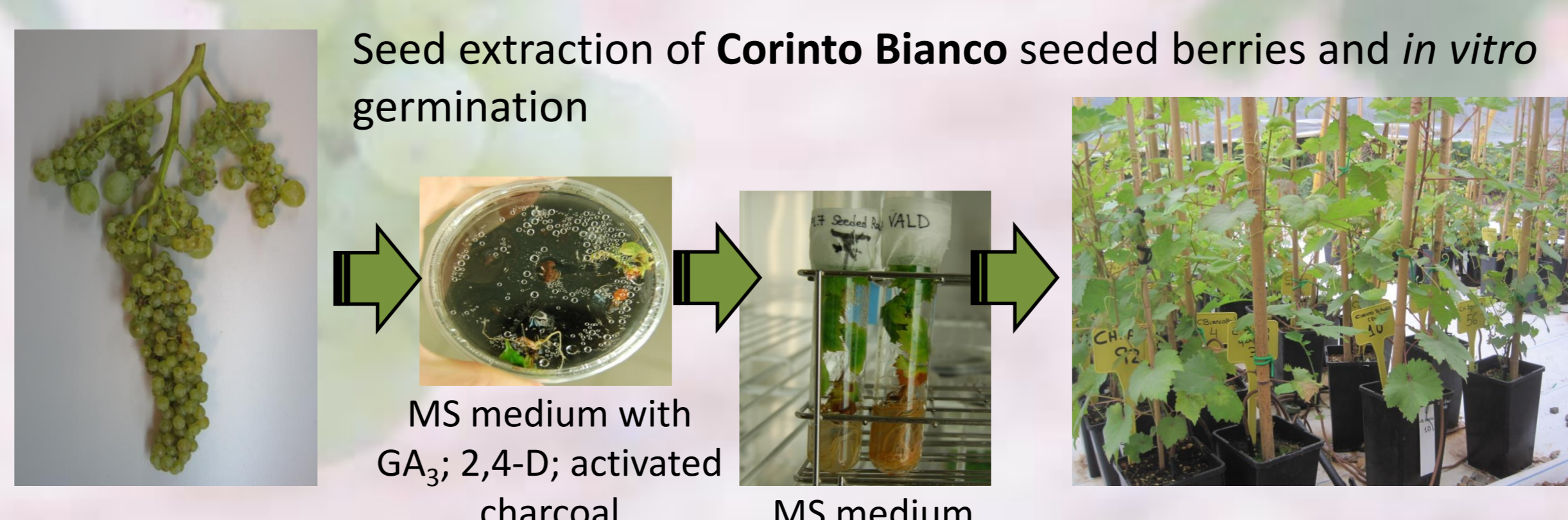
Functional enrichment analysis

Category	Level adj	Pvalue	Cb Down (%)	Genome (%)
Pectin modification	6	2,59E-04	1,68	0,38
Microtubule-driven movement	5	3,18E-03	1,36	0,35
SNARE interactions in vesicular transport	5	1,37E-03	1,05	0,18
Fructose and mannose metabolism	5	1,48E-04	1,57	0,31
Trehalose metabolism	5	3,49E-03	0,63	0,07
Starch and sucrose metabolism	5	3,28E-03	2,62	1,08
Storage proteins	4	7,24E-06	1,99	0,38
KIP1 SANTA	5	1,48E-02	0,31	0,01
Drought stress response	4	1,31E-02	0,79	0,13
G-protein signaling pathway	3	4,13E-03	1,23	0,72
Phosphatidylinositol Signaling	3	1,01E-03	1,57	0,4
Unconventional Protein Secretion System	4	1,14E-03	0,52	0,02
Proton transport	4	5,35E-04	1,68	0,41
Sugar transport	4	1,24E-03	1,36	0,31
Protein coat	4	4,71E-03	1,88	0,67

Category	Level adj	Pvalue	Cb Up (%)	Genome (%)
Xyloglucan modification	6	2,27E-02	43	5
AAA-type ATPase domain family	3	4,02E-03	64	7
NBS-LRR superfamily	3	1,69E-03	418	19
Amino sugar metabolism	5	3,73E-05	80	10
Ascorbate and aldarate metabolism	4	6,55E-04	66	13
Flavonoid metabolism	4	3,25E-02	306	8
Monoterpenoid biosynthesis	5	2,16E-02	181	10
Plant-pathogen interaction	4	1,12E-02	666	23
Oxidative stress response	4	4,90E-02	3,42	1,33
Brassinosteroid-mediated Signaling pathway	4	1,27E-02	57	6
Salicylic acid-mediated Signaling pathway	5	8,40E-03	7	3
Protein kinase	3	1,66E-41	1566	110

OFFSPRING

To analyze the inheritance of the parthenocarpic trait, we collected the seeds of **Corinto Bianco** seeded berries. Plants from those seeds were obtained using an *in vitro* germination protocol because these seeds did not germinate under regular conditions. In addition we generated a self-cross progeny of **Pedro Ximénez**. Genetic analysis of parthenocarpic will be performed in these progenies when they set fruits.



CONCLUSIONS

Preliminary results suggest the presence of defects in the meiotic mechanisms central to the process of gametogenesis in Corinto Bianco, providing clues for further characterization of the origin of parthenocarpic in this cultivar.