



5in International Rosaceae Genomics Conference 2010





PROGRAMME & ABSTRACT BOOK

WELCOME TO STELLENBOSCH SOUTH AFRICA

14 - 17 NOVEMBER 2010

www.rgc5.co.za reesj@arc.agric.za reventer@netactive.co.za

P33. SCREENING FOR LOW MAL D 1 CONTENT, HIGH CONTENT OF POLYPHENOLS AND RESISTANCE AGAINST APPLE SCAB

Helena Persson Hovmalm ¹, Kimmo Rumpunen ² and Hilde Nybom ²

SLU (Swedish University of Agricultural Sciences), Department of Plant Breeding and Biotechnology, PO Box 101, SE-230 53 Alnarp, Sweden, helena.persson@ltj.slu.se

SLU, Department of Plant Breeding and Biotechnology, Balsgård, Fjälkestadsvägen 459, SE-291

94 Kristianstad Sweden

In Sweden, apple breeding is carried out at SLU-Balsgård. One of the goals is to develop new apple cultivars that combine important traits like low content of the allergenic protein Mal d 1, high levels of polyphenols with antioxidant capacity, and durable resistance to apple scab. Such cultivars would be truly healthy for growers, consumers and environment. A substantial part of the population in the northern and central European countries is allergic to birch pollen. Many birch pollen-allergic patients become sensitised also to fresh apples, resulting in IgE-mediated symptoms like itching and swelling of lips, tongue and throat after ingestion, i.e. oral allergy syndrome (OAS). Several allergens have been identified in apple fruits, with the protein Mal d 1 being most well-known. There are differences in the allergenic potency of different apple cultivars. In addition, environmental factors, like different types of cultivation and storage, may affect Mal d 1 content. Polyphenols are secondary metabolites, which are widely found in apples. They have numerous important roles in the human diet and their beneficial effects have been attributed partly to their significant antioxidant capacity. The phenolic composition varies greatly between different cultivars, and between peel and pulp of the same cultivar. Apple scab, caused by the fungus Venturia inaequalis, is the most detrimental disease in commercial apple orchards. Several applications with fungicides per year are usually required in orchards with scab susceptible cultivars. Both dominantly inherited resistance and polygenically controlled so-called field resistance is available in the Malus germplasm. In this project, we screened cultivars, selections and progeny groups for content of Mal d 1 and polyphenols, using ELISA and HPLC-MS, respectively. Some of the individuals were also screened for resistance against apple scab using molecular markers. We found large differences in total content of Mal d 1 and polyphenols within as well as between progeny groups. In general, the levels of both Mal d 1 and polyphenols were lower in the pulp than in the peel. We also found quite pronounced variation between years. Some selections showed low Mal d 1 content and high polyphenolic content and may be marketed as new healthy cultivars. Some seedlings combined all three characters, since they had a low level of Mal d 1 and a relatively high level of polyphenols, and showed the marker for Vf-resistance.

P34. DIFFERENTIAL GENE EXPRESSION OF TWO APPLE CULTIVARS WITH CONTRASTING CHILLING REQUIREMENT

Diogo Denardi Porto¹, Vitor da Silveira Falavigna¹, Vanessa Buffon¹, Giancarlo Pasquali², Paulo Ricardo Dias de Oliveira¹, Henrique Pessoa dos Santos¹ and <u>Luís Fernando Revers¹</u> PO Box 130, Rua Livramento, 515, Bento Gonçalves, RS, Brazil, Iuis@cnpuv.embrapa.br ²PO Box 15005, Av Bento Gonçalves, 9500, Porto Alegre, RS, Brazil

Temperate fruit crops are of great economic importance worldwide, and its production depends on developmental processes, mainly the shift from juvenile to reproductive phase, dormancy transitions and flowering. Apple tree development is subjected to regulation by environmental inputs, specially chilling temperatures, which are needed to dormancy establishment and release. In this work, we aimed to investigate the differential gene expression between Gala and its derived bud sport Castel Gala, which are apple cultivars displaying medium and low chilling requirement, respectively. Bud samples were collected in 2007 at the beginning (May) and end (August) of the dormancy period. Total mRNA was isolated by LiCl precipitation, and suppressive subtractive

hybridization assays were performed using the PCR-select kit (Clontech Laboratories, Inc.) according to manufacturer instructions. Differentially expressed cDNA tags were sequenced by the Sanger method (ABI3100 Genetic Analyzer, Applied Biosystems). Sequences were manually processed and assembled with CodonCode software. BLAST searches and GO classification assignments and statistics were performed using the Blast2GO suite. 'Gala' buds showed increased number of transcripts related to stress and cold response (metallothioneins, dehydrins, etc.) at both dates. August 'Gala' samples contained several transcription factors associated to dormancy in the literature, like Kelch repeat-proteins, GRAS family and dormancy-associated MADS box genes. 'Castel Gala' samples were generally enriched in sequences related to cytoskeleton and photosynthesis. Our findings will be useful information to help unveil the molecular mechanisms of bud dormancy establishment and release in apple.

P35. IDENTIFICATION OF THE METABOLIC PATHWAY FOR NONADIENOL, AN INTERESTING VOLATILE COMPOUND IN FRAGARIA CHILOENSIS

Loreto Prat^{1,2}, Jonathan Maldonado¹, Eduardo Agosin³, Pablo Valenzuela⁴ and Herman Silva¹

¹Plant Functional Genomics and Bioinformatics Lab and Millennium Nucleus in Plant Cell Biotechnology (PCB), Universidad San Sebastián, Santiago, Chile, herman.silva@gmail.com

²Ph. D. Program in Biotechnology, Universidad Andres Bello, Santiago, Chile

³Centro del Aroma, PUC, Santiago, Chile

⁴Fundación Ciencia para la Vida, Santiago, Chile

Several volatiles compounds were identified in *Fragaria chiloensis* including a series of C9-aldehydes and alcohols. The green and fresh flavour of white strawberries detected by GC-MS and GC-O was attributed to E-2-Z-6-nonadien-1-ol. The identification of these compound, combined with enzymatic evidence, suggest that nonadienol are biosynthesized via unsaturated aldehydes from linolenic acid. A search for genes involved in the biosynthesis of nonadienol was carried out in a population of ESTs from *F. chiloensis* (MIFAB) and other Rosaceae databases. We were able to identified putative sequences of LOX and HPL, key enzymes in this pathway. In addition LOX and HPL activities were followed along strawberry development and ripening, from green fruits to white ripe fruits. Expression of these genes was studied by qPCR at different tissues and development stages of *F. chiloensis* fruits. The expression profiles along fruit receptacle development and ripening showed that *FcLOX2* and *FcHPL* reaches their maximal level of expression in the stage S3 and decrease in the full ripening stage (S4). This research was supported by PBCT R-11, ICM P06-065-F and UNAB DI-51-06/R.

P36. CHEMICAL AND GENETIC ANALYSIS TO TRY TO UNDERSTAND CRACKING SUSCEPTIBILITY IN DIFFERENT VARIETIES OF CHERRY

Juan Carlos Rios^{1,2}, Erika Lang³ and Herman Silva¹

¹Plant Functional Genomics and Bioinformatics Lab and Millennium Nucleus in Plant Cell Biotechnology (PCB), Universidad San Sebastián, Santiago, Chile, herman.silva@gmail.com ²Ph.D. Program in Biotechnology, Universidad Andres Bello, Santiago, Chile ³Center of Major Equipment, University of Chile, Santiago, Chile

Chile is the main exporter of sweet cherries (*Prunus avium*) from the south hemisphere; unfortunately these fruits suffer a series of superficial problems such as the cracking. This problem is one of major reason of losses in the worldwide production. The damage is produced when the cherry-tree became in contact with water rain for long periods of time. Analyses of the cuticular wax of cherries and tomatoes showed that their components and ratios are very similar and that

Mariette O13	Pacheco P13
Marti O42	Pagliarani P45, P47
Martinatti P17	Paris P45, P47
Martinez O8	Parravicini O17
Martínez-Gómez P38, P40	Pascal P9
Mattheis O55	Pasquali P34
Mbandi P28	Patocchi O17, O30
Mc Ferson O37	Pauly O22
	Peace O4, O19, O20, O24, O32, O37, O53
McCracken O24	P37 889 oldu9
McGhie O2, O11	Peart O38 SS SS SS SS SS Peart O38
Meisel O15, O50, P4	Peeters P11 810 0 gu/2
Mellidou O11	Peil O30 SNO 3 SNO 3
Meulenbroek P48	Pemberton P19
Micali P29, P49	Perazzolli O3
Micheletti O10, O33	Persson Hovmalm P33
Mochida P14	Pessoa dos Santos P34
Mocho P28	Petit O14
Mockaitis O39	Pina O39
Mockler O4	Pindo O11, O25
Moing O14	Pirona P13, P45
Molina-Bravo O34, P30	Policriti O49
Möller-Steinbach P47	Pons O42 849 019 840 ministrate
Monfort O6	Porto P34
Monfort P52	Pozzi P13
Monforte P39	Prat P35
Moretto O3, O31	Prieto O13
Morgante O4, O28, O46, O49	Quarta O49, P29, P49
Moya P31	Quero-Garcia O16, O40
Mueller O32	Quilot O16, O30
Nagayama P1	Ramina P50
Ndimba P20	Ranatunga O21
Nicolodi P46	Randoux O26
Nilo O35, P32	Rasori P50
Niu P19 880 manayaV	Rassam O11
Njuguna O36	Razavi O41
Noordijk P43, P48	Rees O4, O45, P5, P12, P20, P28
Norelli O4	Reighard O24, O54, P56
Nybom P16, P33, P42, P54, P55	Reignier O40
Okie O54, P56	Remay 026
Olmstead O32	Renaud 014
Olukolu O54	Revers P34
Oraguzie O15, O19, O20, O24, O32, O37	Richards O51, O52, P53
Orellana O22, O35, P32	Righetti O3