ISHS
International Society for Horticultural Science

ETH
Eidgenössische Technische Hochschule Zürich
Swiss Federal Institute of Technology Zurich

13th International Fire Blight Workshop
2.-5. July 2013, Zürich, Switzerland
ETH Zürich Main Building, HG E7

Local Organizing Committee
Fabio Rezzonico (Agroscope Changins-Wädenswil, Wädenswil)
Cesare Gessler (ETH, Institute of Integrative Biology, Zürich)
Brion Duffy (Agroscope Changins-Wädenswil, Wädenswil)
Katja Gruber (Agroscope Changins-Wädenswil, Wädenswil)
Eduard Holliger (Agroscope Changins-Wädenswil, Wädenswil)
Markus Kellerhals (Agroscope Changins-Wädenswil, Wädenswil)
Cosima Pelludat (Agroscope Changins-Wädenswil, Wädenswil)

Agroscope

Schweizerische Eidgenossenschaft
Confédération suisse
Confederazione Svizzera
Confederaziun svizra

Eidgenössisches Departement für
Wirtschaft, Bildung und Forschung WBF
Agroscope

Expression of some *PR* genes of apples in responses to attack of *Erwinia amylovora*

Maryam Hassani[1], Alireza Salami[2], Leila Hamzaban[3], Hamid Abdollahi[4], Sara Sadeghnejad[1]

[1]Faculty of Agriculture and Natural Resources, Azad University (Science and Research Branch), Tehran, 14155, P.O.Box. 4933, Iran; [2]Faculty of Agriculture and Natural Resources, Horticulture Sciences Dept., Tehran University, Karaj, 31587. P.O.Box. 4111, Iran; [3]Faculty of Agriculture and Natural Resources, Azad University of Miyaneh, 53158-36511, Iran; [4]Horticulture Research Dept., Seed and Plant Improvement Inst., Karaj, 31585, P.O.Box. 4119, Iran.

Pathogenesis related genes play important role in defense strategies of plants against biotic stresses. In order to evaluate responses of apples to *Erwinia amylovora*, expression of some candidate *PR* genes from chitinase family including *PR3-Ch2*, *PR3-Ch4, PR3-Ch5* and *catalase-I* was studied in a 72 h time course of host/pathogen interaction. *In vitro* grown shootlets of MM-111 (resistant) and MM-106 (semi susceptible) were inoculated by strain Ea273 of pathogen and sampling for RNA extraction followed at 0, 18, 31, 48 and 72 h after inoculation. RNA extraction and purification successfully achieved by using lithium chloride method and use of DNase I. Specific primers for real time expression studies were designed following isolation, sequencing and deposition of candidate genes, respecting maximum 150 to 200 bp length for each EST and using *elongation factor1α* (*ef1α*) as reference gene in all reactions. The results firstly showed that 31 h after inoculation is a threshold point of variation in expression of candidate defense genes in apples. Interestingly, in MM-106, expression of *catalase-I* gene was significantly higher than more resistant apple, MM-111. This expression pattern is likely subsidiary of reactive oxygen generation of host cells. Expression of *PR* genes showed more complicated expression pattern and seems to be under co-control of more defensive pathways of hosts.

Role of calcium dependent protein kinases (CDPKs) in resistant and susceptible cultivars of *Malus* x domestica in response to the pathogen *Erwinia amylovora*

Chidananda Nagamangala Kanchiswamy[1], Tapan Kumar Mohanta[2], Andrea Capuzzo[3], Francesca Verrillo[3], Massimo E. Maffei[3], Mickael Malnoy[1]

[1]Research and Innovation Center Biology and Genomic of Fruit Plants, Fondazione Edmund Mach (FEM), Istituto Agrario San Michele (IASMA), Via Mach 1, 38010 San Michele all'Adige (TN), Italy; [3]Department of Life Sciences and Systems Biology, Innovation Centre, University of Turin, Via Quarello 15/A, 10135 Turin, Italy.

Plant calcium (Ca^{2+}) signals are involved in a wide array of intracellular signaling pathways after pathogen invasion. Ca^{2+}-binding sensory proteins such as Ca^{2+}-dependent protein kinases (CDPKs) have been predicted to mediate the signaling following Ca^{2+} influx after pathogen infection. However, until now this prediction remains elusive. We conducted a genome-wide analysis of *Malus* x *domestica* CDPKs and identified 30 CDPK genes. *Malus* CDPKs were found to be similar to their counterparts in *Arabidospis thaliana* in gene structure and subgroup classification. Furthermore, comparative quantitative real-time RT-PCR and intracellular cytosolic calcium analysis were conducted between a fire blight resistant and susceptible *M.* x *domestica* cultivar upon invasive pathogen (*Erwinia amylovora*) and/or mechanical damage. We found that there is striking difference between resistant and susceptible cultivars. Our genomic and bioinformatics analyses will provide important information about the *M. x domestica* CDPKs role in modulating the defense responses between the susceptible and resistant cultivars. It also sheds light for the further elucidation of early signaling and downstream signaling cascades for the pathogen and wound responses.