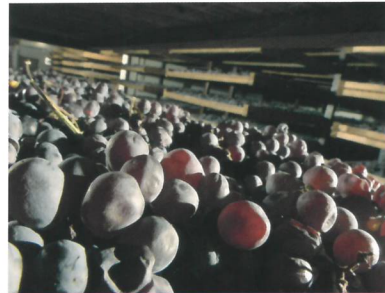




UNIVERSITÀ
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X INTERNATIONAL SYMPOSIUM ON GRAPEVINE PHYSIOLOGY AND BIOTECHNOLOGY



BOOK OF ABSTRACTS

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The grape NAC transcription factor gene was found to respond to powdery mildew (PM) colonization in a susceptible grapevine *Vitis vinifera* cv. Cabernet Sauvignon. *In planta* analysis demonstrated that the NAC transcription factor gene's promoter responded to PM in a salicylic acid (SA)-independent manner, that is, neither the SA, nor the SA-mediated signalling was required for control the NAC expression. To analyse the induction of this gene we amplified longer and longer fragments of the promoter region and fused them individually to the *gusA* reporter gene. Each of the *promoter::reporter* fusions were transferred into *Arabidopsis thaliana* Wassilewskija wild type plants which were infected with the PM, *Oidium neolycopersici*. Fourteen days after inoculation we found that the NAC induction of infected plants was significantly higher compared to the mock-infected ones. This significant difference ($p < 0.05$) was observed in transgenic lines containing a 3896 bp-, 2935 bp-, 2456 bp-, or a 1178-bp length promoter and not in 257-bp promoter fragment or in the no-promoter control. Using the promoter sequence analysis databases we identified AP/ERF, bHLH, bZIP, C2H2, HD-ZIP, WRKY, ZF-HD transcription factor binding sites and MADS boxes in the sequence of NAC promoter. We found light-, fungal elicitor-responsive and ethylene-, methyl jasmonic acid-sensitive elements also. The basal NAC expression was regulated in developing new shoots, trichomes, axillary buds, stipules, hydathodes, in the vascular area of the style, in septum, and in abscission zone of gynoecium. The PM-induced NAC expression was detected only at the infected area of the leaf, and not in neighboring cells. The literature demonstrate that cytokinins are maximized in these zones of plants at different developmental stages or in response to PM, and this suggests that NAC gene may play a role in cytokinin signaling.

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P195

Downy mildew resistance QTL identification in multiple inter-specific populations of grapevine: a Pedigree-Based Analysis (PBA) approach

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Downy mildew (*Plasmopara viticola*, DM) resistance is a desirable trait for any new grapevine (*Vitis* spp.) cultivar grown in temperate-humid climate, as it directly impacts on grape yield and wine quality. Therefore, determining the genetic control of this trait in relevant breeding germplasm is a high priority. The objectives of this study were (i) to determine the number and positions of Quantitative Trait Loci (QTL) for DM resistance utilizing data from multiple families and their pedigreed ancestors simultaneously, and (ii) to estimate DM resistance QTL genotype probabilities and genomic breeding values for the plant materials.

The grapevine material used was an up-to-five-generation pedigree consisting of 16 founders, 10 relatives, 17 parents and 548 progeny individuals from 12 full-sib families, which were phenotyped in replicates for DM resistance and genotyped with a mid-throughput approach. In particular, as regarding phenotyping the genetic material was screened based on 11 optimized parameters, taking into account different aspect of the disease. As concerning genotyping, 190 microsatellite markers well-scattered across the grapevine genome were analyzed based on multiplex assays.

These data were analysed by adopting a Pedigree-Based Analysis (PBA) using the FlexQTLTM software. Among the identified QTL, some were previously discovered while other QTL were novel. The predicted QTL genotypes show that the identified QTL were segregating in a subset of the families. The progeny varied for breeding value, with some progeny having higher breeding values than their parents. These



results pinpoint the strength of the PBA approach as QTL may be missed when focussing on single full sib families. Furthermore, the simultaneous search for multiple QTL also yields estimated genomic breeding values that can be used for selecting progeny with favourable resistance.

P196

Unravelling the knot of disease resistant hybrid kinship

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Within the FEM grapevine breeding program, re-established in the middle '80s, the selection process has been based on the major need for innovation raised by grapevine growers. During the past years, this request has been addressed to increase the complexity and the originality of wines, while in the last decade the need for new varieties resistant/tolerant to abiotic and biotic stresses has emerged. In order to reach this goal, the germplasm collection has grown, increasing its number of acquisitions.

In this work, 264 accessions acquired from European and non-European breeding programs or wild accessions collected in northeastern America were studied. Most were phenotyped for downy and powdery mildew resistance, while all were genetically characterized at 190 microsatellite markers well-scattered across the grapevine genome.

Firstly, 9 reference markers were used for the true-to-type identification through international and private databases, where feasible. Secondly, in order to validate the available pedigree information and to infer new relationships, the 50 most informative microsatellite markers were chosen and analyzed with specialized software.

Finally, the overall genetic material was divided into five classes: known and related (38%); unknown and related (21%); known and unrelated (10%); unknown and unrelated (23%); and redundant (8%). The unknown (related and unrelated) accessions hold great potential as exclusive genetic resources, mainly donors of disease resistance traits, and will provide preparatory information to prospective Marker-Assisted Breeding programs.

P197

Light Emitting Dioxide inhibited gray mold and induced stilbene compound accumulations and defense-related gene expressions in *Vitis flexuosa*

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Light Emitting Dioxide inhibited gray mold and induced stilbene compound accumulations and defense-related gene expressions in *Vitis flexuosa*.

Light plays a key role throughout the entire lifecycle of plants and light quality has been considered important factor in management of plant disease associated with plant-pathogen interactions. In the present work, the accumulation of stilbenic compounds and defense related gene expression by light-