



Future IPM 3.0 towards a sustainable agriculture

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Future IPM 3.0

BOOK OF ABSTRACTS



The FEM grapevine breeding program for pathogen resistances: towards a sustainable viticulture

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Highlights

- Since 2011, the FEM grapevine breeding activity follows two main motives: the introgression of novel resistance to the pathogens of primary importance into vinifera background; the pyramiding of characterised resistance-associated (R) loci into unique superior genotypes, donors of durable resistances

Introduction

Downy mildew (DM) and powdery mildew (PM) are the two most important plagues affecting viticulture. Both reduce fruit quality and yield, either by direct infection of berries or as negative results derived from leaf infections. Their control is based on the massive use of fungicides, leading to problems such as environmental pollution and pathogen resistance development. The use of grapevine varieties showing durable resistance to DM and PM is a promising strategy.

Within the FEM grapevine breeding program, 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 of wines, while in the last decade the need for new varieties (mid-) resistant to pathogens has emerged. Lately, the FEM germplasm collection has increased its number of acquisitions in order to employ unknown and to valorise known genotypes as parents into the disease resistance (pre-) breeding program.

Material and methods

Genetic material. A total of 264 grapevine accessions acquired from (non-)European breeding programs, an Italian private breeding platform and wild-collected in north-eastern America during 2011 were studied. Most were phenotyped for DM and PM resistance, while all were genetically characterised at 190 microsatellite markers well-scattered across the grapevine genome.

Genotyping. Firstly, nine 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 selected and analysed with Cervus v.3.0.7 software (Kalinowski et al., 2007). Finally, 12 R-loci, as well as the flower sex and the monoterpen content loci, were screened in the entire sample set (VIVC, 2016).

Phenotyping. Within the overall genetic material, 100 accessions present at FEM were evaluated for their degree of resistance against DM and PM, through *in vitro* leaf disc bioassay and *in vivo*



pathogen inoculation on potted plants respectively. DM symptom annotation was performed based on three parameters: Severity (percentage of the disc area showing symptoms of sporulation), Incidence (number of discs with sporulation/total number of discs), according to OEPP/EPPO (OEPP/EPPO, 2001), and the OIV 452-1 descriptor (OIV, 2009). PM symptoms were evaluated based on the foliar OIV 455 descriptor.

Results and discussion

The overall genetic material resulted divisible into five classes: I. known and related (38 %); II. unknown and related (21 %); III. known and unrelated (10 %); IV. unknown and unrelated (23 %); and V. redundant (8 %). Within these classes, the most important resulted to be II and IV. The unknown and related genetic materials holds a great potential for the breeding activities of FEM and other institutes, since they provide indications about already known or unidentified R-loci that can be traced in their future progeny. The unknown and unrelated genotypes, obtained from abandoned breeding programs or derived from wild-collections, play a relevant role as exclusive genetic resources; in fact, once characterised through the identification of novel Quantitative Trait Loci (QTLs) associated to features of interests, they will provide molecular information for the ongoing Marker-Assisted Breeding, first in the introgression and thus in the pyramiding sub-programs. The 100 accessions analysed at phenotypic level are representative of all classes, except for V. (redundant). The *in vitro* evaluation demonstrated a wide phenotypic variability in terms of DM resistance. In particular, 41 accessions resulted highly resistant and will be employed as a direct source of resistance in breeding sub-programs with the objective of releasing novel sustainable grapevine cultivars presenting also good fruit/wine quality. Regarding PM, only 18 out of the 100 *in vivo* tested accessions resulted resistant. This demonstrates that PM is rarer than DM resistance and highlights the importance of discovering new genetic sources.

In conclusion, novel and exclusive genetic resources were identified, providing peculiar and preparatory information to ongoing and forthcoming Marker-Assisted (pre-) breeding programs. This specific genetic material - *in vitro* healthy maintained and propagated - contributed to enrich the FEM breeder Golden Book, a dynamic collection of parental genotypes suitable for crossing combinations with different purposes. In the next coming few years, FEM is going to launch eight new varieties which are mid-resistant to DM and PM.

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References

- Kalinowski et al. 2007. Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment. *Molecular Ecology* 16:1099-1106.
- OEPP/EPPO 2001. Guidelines for the efficacy evaluation of fungicides. *OEPP/EPPO Bulletin*, 31:313-317.
- OIV 2009. Descriptor list for grape varieties and *Vitis* species, 2nd ed. Office International de la Vigne et du Vin, Paris, <http://www.oiv.org>.
- VIVC. *Vitis* International Variety Catalogue. <http://www.vivc.de/index.php>: 16th December 2016 update.