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East-West Collaboration for Grapevine Diversity Exploration and
Mobilization of Adaptive Traits for Breeding

FULL PROGRAM & ABSTRACT BOOK

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ADVANCES IN GENOTYPING FOR GRAPE RESEARCH, MANAGEMENT AND INTERNATIONAL NETWORKING

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Molecular markers have recently become widespread tools for a wide range of uses in grape research and management. Technology developments and reduced costs encouraged their use for management of genetic resources, varieties and clones, rationalization of repositories and nurseries, and routine marked-assisted identification and selection, in addition to more traditional uses for research such as candidate genes mapping via QTL detection and association genetics. Two former European projects and the present COST FA1003 initiative have recently succeeded to merge cultivar fingerprints, based on Simple Sequence Repeats (SSR), from a large number of single labs and countries into a large European database. Together with the availability of variety's passport data and morphological descriptions, this achievement represents a significant progress both for identifying single varieties and to understand genetic diversity of the grapevine gene pool. The information about grape parentages and genetic structure allows today the research community to derive properly designed collections of samples, or core-collections, adapted to address specific research questions.

However, DNA technology has recently evolved very fast: the “next-generation sequencing” methodology is capable today to provide an almost unlimited amount of sequence and genotype information on a genome-wide basis. The grape community has not escaped this trend; at the contrary, owing to the short and simple grape genome ($2n=39$, $1C=480$ Mbp) and the availability of its sequence (clone PN40024, 12X), single labs or small grape consortia have quite pioneered many applications of this new technology. So far, DNA-SNP chips and genotyping-by-sequencing (GBS) regroup the most successful stories to date. Among the GBS technologies, re-sequencing reduced-complexity libraries such as restriction-site associated DNA or designed DNA capture probes sequencing are probably the most promising methods for future applications of interest for the Grape European COST Network.

For the purpose of devising future common targets and methodologies for grape research at the European level, in the present paper we will first present a synopsis of recent results based on genotyping in grapes, obtained from partners of the COST FA1003 project, followed by some remarkable examples conducted by independent external teams; secondly, we will draw a panorama of next-generation technologies available for future experiments. Finally we will try to envision which combination of technologies, could be useful for answering questions relevant for the grape European research community.