



UNIVERSITÀ DEGLI STUDI
DI MILANO

Cost action FA1003 - GRAPENET
East-West Collaboration for Grapevine Diversity Exploration and
Mobilization of Adaptive Traits for Breeding

FULL PROGRAM & ABSTRACT BOOK

Final Conference

PROGRESS IN *VITIS VINIFERA* **DIVERSITY EVALUATION AND USE**

7-8 October 2014

Final Management committee

9 October 2014

INIAV - Instituto Nacional de Investigação Agrária e Veterinária
Av. da República, Quinta do Marquês, Oeiras (Lisbon - Portugal)

Edited by Gabriella De Lorenzis, Laura Rustioni and Osvaldo Failla

AN OVERVIEW OF GENETIC DIVERSITY WITHIN THE GRAPE GERMPLASM FROM SOUTHEAST EUROPE AND THE CAUCASUS SURVEYED UNDER THE COST ACTION GRAPENET

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INTRODUCTION – Grapevine (*Vitis vinifera* L.) is one of the most important fruit crops cultivated in the world. South-Eastern Europe and the Caucasus are widely considered to be a centre of grape diversity and domestication. From these regions, the cultivated forms of *V. vinifera* are thought to have moved westwards, and wine and vine have spread as an important part of the diet. Today, however, the genetic diversity of grape in Western Europe is reduced due to changes in viticulture, the invasion of pests and globalization of wine markets. On the other hand, grape genetic resources in the area of its domestication contain an unexplored richness.

AIMS AND SCOPES – Our objective was to investigate one of the main outcomes of the COST Action GRAPENET, i.e. a large set of unique genetic profiles derived from multiple accessions of *V. vinifera*, contributed from East European grape collections. We focused on the genetic diversity and subdivision of these accessions, and a comparison with the patterns of diversity observed in grape varieties from West European countries (e.g., Portugal, Spain, France, Germany, and Italy).

MATERIALS AND METHODS – For this study, 1427 accessions of *V. vinifera* were gathered from the germplasm collections located in 14 countries: Albania, Armenia, Azerbaijan, Bulgaria, Croatia, Hungary, Georgia, Greece, Lithuania, Moldova, Romania, Slovakia, Slovenia and Ukraine. Plants were genotyped with nine standard microsatellite markers, applied previously within the GrapeGen06 project. Next, 924 unique accessions were tested for population clustering to infer the best level of genetic subdivision. Here, we employed a Bayesian method implemented in the STRUCTURE program. To develop a set of accessions with reduced allele redundancy, and thus with enhanced richness of potentially useful alleles in the entire sample, the M (maximization) strategy was applied.

RESULTS AND DISCUSSIONS – There was high microsatellite variability present in the GRAPENET collection. The average expected heterozygosity in the entire sample was 0.87, with the greatest values observed for the set of grape cultivars gathered from the Caucasus region. The preliminary study of combined data obtained in this COST Action and in the GrapeGen06 project, showed a clear subdivision between East European and West European cultivars. Further analysis of the grape accessions collected for this survey suggested a high level of admixture and distinguished four ancestral clusters in the total sample. Representatives of all these clusters were present in the subsample from the Caucasus region (Georgia, Armenia and Azerbaijan). Accessions from these countries were also the largest part of the core collection (45 out of 63) selected from the entire GRAPENET collection.

CONCLUSIONS AND POSSIBLE APPLICATIONS – The aim of this study was to characterize, using molecular markers, a sample of unique, putatively most interesting and poorly known varieties, provided mainly by the research partners in the east European countries. The core collection developed in this survey may support one of the key following objectives of the GRAPENET project, namely the design of association mapping studies and mobilization of adaptive traits for breeding.