

## ANALYSIS OF MOLECULAR DIVERSITY AT CANDIDATE GENES FOR AROMA DETERMINATION IN GRAPE GERMPLASM

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Many traits of agricultural interest are defined by a multiplicity of genes with a different and partial contribution on phenotypic variation. Testing the role of candidate genes (CGs) in the expression of a trait could be carried out either by a conventional co-segregation analysis in structured segregating populations or by looking for allelic variation at the gene-trait associations in germplasm collections. In this work CGs were selected a priori based on their hypothetical biological function. The public EST database TIGR was then searched for berry gene sequences with Gene Ontology (GO) annotation related to berry quality and ripening. SNP markers were developed on these sequences and segregation analysis was carried out in a F1 mapping population of *V. vinifera* which had previously been genotyped with AFLP and SSR markers. QTL analysis in three years showed significant associations between three SNP markers (corresponding to 3 different genes) and ln-transformed contents of nerol, geraniol and linalool which are the main determinants of Muscat flavour. In order to confirm these associations in different genetic backgrounds we started to exploit the natural genetic variation of a grape collection with an approach of association genetics. Individual grapevines, for which phenotypic characterization was available, were sampled from Vassal collection (INRA, Montpellier). A first candidate gene, DOXP-synthase, was preliminary sequenced on 25 varieties representing Muscat aromatic and non aromatic cultivars. SNPs and INDELs were detected and used to reconstruct haplotypes. Preliminary association tests, which do not consider population structure, showed statistically significant correlations between some SNPs and Muscat flavour. A few number of haplotypes also emerged to be present only in Muscat aromatic varieties. Sequence analysis is being extended to a larger collection of 150 samples including Muscat varieties, highly diverse accessions, and non-aromatic grapevines genetically related to Muscat varieties. On the basis of SSR marker data, population structure and kinship will be then investigated in order to avoid false positive associations. Thus, structured association tests that include population structure and kinship estimation will enable to search for statistically significant association between CG haplotypes and Muscat flavour. This approach will be applied to each selected candidate gene and may lead to the identification of the alleles responsible for the variation of the trait under investigation.