

## TOWARDS AN ALTERNATIVE HIGH-RESOLUTION NON-MEIOTIC LINKAGE MAP OF GRAPE (*VITIS VINIFERA* L.)

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Classic linkage genetic maps are based on meiotic recombination and segregation. Resolution of such maps is limited by the dimension of the segregating population. Unfortunately, biological and reproductive characteristics of grape do not allow easily producing and analyzing large populations required for high-resolution linkage maps. For this reason, it would be useful to develop mapping approaches not strictly dependent on meiotic recombination events to build high-resolution maps to be used in assisting the assembly of physical maps. In this line of action, we propose the application of Haploid Polymerase (HAPPY) mapping technique to the construction of a high-resolution linkage map in grape. This method has been tested with success in human and fungi, allowing map resolutions equivalent to that obtainable with *radiation hybrids* (in the order of hundreds of Kb). HAPPY mapping approach is based on analyzing the segregation of markers amplified from high molecular weight genomic DNA artificially “segregated” by limiting dilution into sub-haploid samples. After random breakage of genomic DNA and size selection of fragments, DNA aliquots are opportunely arranged to generate a mapping panel where every sample contains a casual sub-aliquot of the genome (about 0.7 equivalent genomes). Sub-fractions are tested by PCR for the presence of specific genes or markers. Co-segregation frequencies, reflecting the physical proximity between any pair of markers, allow a map to be computed.

In particular, here we discuss the set up of a grape (Pinot Noir, clone ENTAV115) HAPPY map at a resolution of 0.8-1.6 Mb. Specific primers are being designed on available genomic and BAC-end sequences, corresponding to a minimum of 1,200 markers that will be scored on the mapping panel. The resulting HAPPY map will be used to assist the assembly of the physical map currently being produced by fingerprinting of the same BAC library.