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A Dense SNP-Based Genetic Linkage Map Of Grapevine (*Vitis Vinifera* L.) Anchored To The Sequenced Genome Of Pinot Noir

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Given its cultural and economic importance, wine grape is an obvious candidate for the first woody crop to have its genome deciphered. Here we present the construction of a dense genetic map for the genus *Vitis* and, for the first time, its physical anchor to the sequenced genome of *Vitis vinifera* cv. Pinot Noir. In the mean time our research focused with the multiple goals of genome assembly, gene identification and annotation, and identification of a maximum number of polymorphisms. Pinot Noir is highly polymorphic with two clearly distinguishable haplotypes revealing several million SNPs and small indels. Based on a conservative estimate, 451,190 new SNPs and 67,580 new In/dels were revealed during the genome construction. This represents a substantial resource for molecular breeding programs, as well as trait and QTL marker association. A total coverage of 7 genome equivalents of libraries of ascending size, coupled with systematic highly parallel automated primer walking allowed us to create an effective genome sequence and assembly of grape. Two BAC libraries and a fosmid library were end-sequenced to assemble large meta-contigs. Polymorphisms discovered by assembling the two haplotypes of the Pinot Noir genome were used to develop markers for each meta-contig to correlate them with linkage groups. All the markers with associated sequence, that were well ordered on the genetic map, were used to order and to orient meta-contigs on the appropriate linkage groups. Region-dependent estimations of physical and recombinational distance are also presented.

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