

GBS assaying of F1 population obtained from self-pollination of muscadine grapevine cv. Dixie (*Muscadinia rotundifolia* Michaux.)

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Since phylloxera and mildew were brought from North America to Europe in the second half of the 19th century, breeders around the world have been introducing resistance genes from American and Asian wild species into the gene pool of European grapevines. During this time, significant success was achieved, and new varieties were obtained that give high quality vines and have a high degree of resistance to powdery mildew. Sources of pathogen resistance genes were mostly *Vitis* species from North America (*V. riparia*, *V. labrusca*, *V. aestivalis* and *V. berlandieri*) and, more recently, the Far East species (*V. amurensis*). All these sources provide only partial resistance of the cultivated grapevine, while loci introgressed from *Vitis* (*Muscadinia*) *rotundifolia* confer complete resistance to pathogens in all studies known to date. Recently, a high-resolution genetic map conferring 2069 SNP markers has been published for the *Muscadinia rotundifolia* (cv Traished), after GBS (Genotyping-By-Sequencing) assaying of two populations of F1 hybrids.

Only one variety of *M. rotundifolia* (cv Dixie) was introduced in Russia, where it has been successfully propagated in Krasnodar region and Crimean Peninsula. There, cv. Dixie bears fruit annually as a result of self-pollination, providing a natural source of F1 hybrids. Evaluating of the F1 hybrid population revealed biological variability of some morphological traits, e.g., grown power, weight and shapes of berries.

In this study we present result of GBS assaying of 134 F1 hybrids obtained from self-pollination of cv. Dixie. Number of detected heterozygous loci and general heterozygosity level is described. During self-pollination of Dixie variety, the process of formation of female and male gametes occurs leading to recombination events and producing new combinations of homozygous and heterozygous loci, different from the parent genotype. Counting the frequency of such recombination events between heterozygous loci in a population of Dixie F1 hybrids allowed us to calculate the genetic distances between SNP markers and construct a linkage map.

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