Evaluation of genetic dissimilarity in a segregating wine grape population

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ABSTRACT. This study examined the genetic diversity present in a population obtained by crossing two very distinctive varieties of wine grapes (142 progeny from a Riesling x Cabernet Sauvignon cross, including both parents, created at the University of California). The following list of morphological characters were evaluated and found to segregate in this population: cluster weight, cluster length, presence or absence of cluster wings, cluster wing length, number of berries, cluster density (CD), and berry weight. The following juice parameters were also measured: °Brix, pH, total phenolics, and titratable acidity. Genetic diversity within this population was estimated through multivariate methods that utilized the Gower index of dissimilarity and UPGMA clustering. The correlations between traits and relative contribution of each variable were also compared. Eleven groups of progeny were distinguished into categories with low, intermediate and high values for cluster weight and cluster density, and low and high values for total phenolics. An inverse correlation was detected between the variables related to production and those related to the quality of the fruit. Principal components analysis demonstrated that all variables examined in this study are important for the correct discrimination of optimal

genotypes in this population. These statistical tools can be used to select individuals with the greatest potential for producing high-quality wines.

Key words: Grape breeding; Principal components analysis; Fruit quality; Multivariate analysis