

P8 – Genetic diversity and population structure in Brazilian grapevine hybrids

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Abstract

The grapevine breeding program has been developed at the Agronomic Institute (IAC) since the 1940s to develop new cultivars adapted to the climatic conditions of Brazil. More than 2,000 crosses were carried out over 50 years, using 850 genotypes as parents. However, among the thousands of hybrids developed by the program, only 130 are still maintained in the IAC grapevine germplasm collection. Little is known about its genetic makeup and usefulness for the current breeding program. The present study evaluates the genetic diversity and population structure of these 130 Brazilian grapevine hybrids using 17 highly polymorphic microsatellite markers. A total of 202 alleles were obtained, and high expected heterozygosity was identified (0.81). The STRUCTURE analysis indicated that the hybrids represent three distinct genetic clusters. Based on a membership probability threshold of 0.70, 28 hybrids were assigned to cluster 1, 45 hybrids were assigned to cluster 2, and 44 hybrids were assigned to cluster 3. Thirteen hybrids did not sort to defined clusters and were assigned to the admixed group. The discriminant analysis of principal components (DAPC) showed several similarities to those achieved by STRUCTURE, and both analyses showed the same pattern of clustering. The genetic groups were based mainly on the use and combination of parental groups. In cluster 1 were allocated wine hybrids obtained by crossing Seibel hybrids with *V. vinifera* wine cultivars. Cluster 2 was formed by table grape hybrids obtained through crosses with fine muscat grapes. In cluster 3 there was no clear discrimination based on human usage, hybrids for wine, table, and rootstock are found in this group. However, all hybrids of this group have in common the presence of wild *Vitis* in their genealogy. The molecular characterization of this breeding hybrids bank collection contributes to understanding the genetic basis of the genotypes, guiding the efficient exploitation of available genetic diversity. These results could be applied to other breeding programs and assist in the selection of parents, management of the breeding collection, and conservation of the grapevine genetic resources.

Keywords: SSR markers, genetic resources, plant breeding, *Vitis* spp., grape