



Phenotypic divergence among wine grape accessions in the semi-arid region of Brazil

Rita Mércia Estigarribia Borges^{1*}, Elainei Oliveira dos Santos Alves², Nadja Pollyanna da Silva Gonçalves¹, Ana Patrícia de Oliveira Gomes¹, Daniela Correia Leite Andrade¹, and Teresinha Costa Silveira de Albuquerque³

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ABSTRACT - *The objective was to estimate the phenotypic divergence in wine grapes based on 11 agronomic variables. Two contrasting groups, both for white as for red grapes, were formed by principal component analysis. In white grapes, greatest divergence was observed in the accessions Baco Blanc, Campanário and Palomino. In red grapes, the most divergent were Aramon and Tannat; Castelão and Mars. The standardized Euclidean distance indicated 52.4 and 40.0% white and red grape accessions, respectively, with means exceeding the overall mean. By UPGMA, four major groups were formed for white and red grapes. Both principal component analysis and UPGMA showed that the genealogy of the accessions Petite Sirah FR and Petite Sirah RS is similar. The accessions with most divergence in the traits studied should be used to produce hybrids, as well as for selection of accessions with a view to regional wine making.*

Key words: *Vitis vinifera* L., genetic resources, grape descriptors.

INTRODUCTION

For the use of germplasm in breeding programs, information on the accessions contained in a collection or database must be available. The study of phenotypic divergence among accessions of a genebank is based on alterations observed in morphological and agronomic traits of plants, due to both the genetic variability of the genotypes under study, and the influence thereon of environmental factors, mainly of climate (This et al. 2006).

The use of the multivariate analytical methodology in genebank management allows the estimation of phenotypic divergence in accessions and the establishment of strategies for information organization that will value up the use of germplasm in breeding programs (Assis et

al. 2002, Moura 2003, Sudré et al. 2005, Oliveira et al. 2003). This information on the potential of parents for use in hybridization and that can indicate possible duplicate accessions in germplasm collections is of great importance for plant breeding (Nass 2001).

Currently, the grapevine genebank of Embrapa Tropical Semi-Arid contains 231 accessions, among these cultivars of table grapes, wine grapes and grapes for juice and rootstocks. The characterization of the accessions of the grapevine genebank has been studied since the eighties, however, the genotypic and phenotypic divergence of grape accessions has only recently been assessed (Borges et al. 2008, Leão et al. 2008). The study of 73 wine grape accessions and cultivars in the valley of the lower course of the São Francisco river, Brazil, that make up the

¹ Embrapa Semiárido, BR 428, km 152, Zona Rural, C.P. 23, 56.300-970, Petrolina, PE, Brazil. *E-mail: rmborges@cpatsa.embrapa.br.

² Universidade Estadual de Santa Cruz, Departamento de Genética, Campus Soane Nazaré de Andrade, Rodovia Ilhéus-Itabuna, km 16, 45.662-000, Ilhéus, BA, Brazil.

³ Embrapa Roraima, Rodovia BR-174, km 8, Distrito Industrial, 69.301-970, Boa Vista, RR, Brazil.

genebank was only intensified in recent years, due to the implementation of six wineries in the region. Until 2000, the wine production in Brazil had been practically restricted to the state of Rio Grande do Sul. The importance of characterizing morphological and agronomic traits to identify wine grape cultivars that are fully adapted to the semi-arid environment and capable of producing wines with superior organoleptic qualities is unquestioned. Studies of this nature are performed both to define the importance of local varieties for making wines with the characteristics of a particular region (Failla et al. 2007) or to define the existing dissimilarities in genebanks (Martinez and Martinez 2007).

The aim of this study was to estimate the phenotypic divergence in 43 red and white grape accessions (*Vitis vinifera* L.) from the genebank of Embrapa Tropical Semi-Arid, using 11 quantitative variables.

MATERIAL AND METHODS

In this study, 22 accessions of white and 21 of red grapes for wine production from the genebank of the Embrapa Tropical Semi-Arid (Table 1), maintained in the Campo Experimental of Mandacaru, Juazeiro, BA (lat 9° 24', long 40° 26', 375 m asl), with hot and dry tropical climate. The mean annual temperature is 23.6 °C, relative humidity 67.1% and mean annual rainfall 455 mm. The soils at the site are classified predominantly as Vertisols.

Phenotypic dissimilarities were estimated in four crop cycles in the years 2005 and 2006, evaluating the four plants that make up the sample of each accession based on 11 traits: mean plant yield (g); number of bunches (mean of four plants); mean weight of five bunches (g) (mean of five bunches per plant, collected at random); mean bunch length (cm); mean bunch diameter (cm); mean berry weight (g) (mean of 10 berries per bunch, randomly collected in the bunches sampled); mean berry length (cm) (mean of 10 berries per bunch, randomly collected in the bunches sampled); mean berry diameter (cm) (mean of 10 berries per bunch, randomly collected in bunches sampled); physico-chemical characters, defined as total soluble solids (⁰Brix) with a sample of 10 bunches of five berries per plant; total acidity (TA) by titration with NaOH; and the ratio TSS/TTA.

To estimate the genetic diversity, we used the principal component analysis and mean Euclidean distance calculated from data obtained, standardized based on the eight selected descriptors, and methods proposed by Cruz

and Regazzi (1994) for accessions without randomization and local control. Software Genes (Cruz 2006) was used for data analysis.

The symmetric matrices generated by the distances between pairs of accessions were used for clustering by the hierarchical method (UPGMA), identifying the dissimilarities for the two groups of accessions under study, white and red grapes.

RESULTS AND DISCUSSION

The phenotypic divergence among accessions was studied based on the results obtained by principal component analysis (Table 2 and Figure 1) and dendrogram (Figure 2).

One of the goals of the use of principal components in studies of genetic divergence is to evaluate the dissimilarity of accessions in a scatter plot (Cruz and Regazzi 1994), using the first components as axes of reference. This permits a good approximation of the performance of plants grouped in an *n*-dimensional space. In the principal component analysis of white grapes, 73% of the total available variation was explained by the third component, adjusting the three-dimensional imaging (Figure 1A). Two contrasting groups of accessions were formed: group I accessions of Gewürztraminer, Italic Riesling, Semillon and Sylvaner. Group II accessions of Laparo, Malvasia, Muscat, Muscat Canelli and Seara Nova. The other accessions were located separately (Figure 1A). Greatest divergence was observed in the accessions Baco Blanc, Palomino and Belfry (Figure 1A). The variables with greatest participation in genetic diversity were the ratio TSS/TTA, mean berry length and mean bunch weight, with 40, 21.59 and 11.41% of relevance, respectively, for the variability among the accessions (Table 2). In the analysis of red grapes, the first three components explained 79.59% of the total variation available (Table 2). In the graphic dispersion analysis, the formation of two contrasting groups was also observed (Figure 1B): group I accessions of Angelote, Royalty, Ruby Cabernet, Sangiovese, and Tampa, group II accessions Grand Noir, Petite Sirah FR and Petite Sirah RS. The isolated accessions were Aramon, BRS Lorena, Cabernet Sauvignon, Carignane, Castelão, Gamay, Gamay Beaujolais, Grand Noir, Grenache, Mars, Periquita, Souzao, Tannat, and Tibouren. The variables that contributed most to the divergence were mean berry diameter, berry weight and TSS/TTA ratio, with percentages of 36.6, 27.3 and 14.5% of the variability among accessions, respectively (Table 2). The

Table 1. Identification of accessions of the grapevine genebank of Embrapa Tropical Semi-Arid

| White grape genotypes | | Red grape genotypes | |
|-----------------------|--|-----------------------|--|
| *Code of accessions | Parents | Code of accessions | Parents |
| 1. Altesse | NIP | 1. Angelota | NIP |
| 2. Baco Blanc | Folle Blanche x Noah ¹ | 2. Aramon | NIP |
| 3. Campanário | Camarate Preto x Fernão Pires ¹ | 3. BRS Lorena | Malvasia Bianca x Seyval ⁴ |
| 4. Chenin Blanc | NIP | 4. Cabernet Sauvignon | Sauvignon Blanc x Cabernet Franc ² |
| 5. Colombar | Gouais Blanc x Chenin Blanc ² | 5. Carignan | NIP |
| 6. Feher Szagos | NIP | 6. Castelão | NIP |
| 7. Gewürztraminer | Clone of Traminer ⁵ | 7. Gamay | clone of Pinot Noir ³ |
| 8. Lassif | NIP | 8. Gamay Beaujolais | clone of Pinot Noir ³ |
| 9. Malvasia de Lapari | Malvasia Bianca x Seyval ⁵ | 9. Grand Noir | Aramon x Petit Bouschet ³ |
| 10. Moscatel | NIP | 10. Grenache | Alicante Bouschet x Cannonau ⁴ |
| 11. Moscato Canelli | NIP | 11. Mars | Island belle x A1339 ¹ |
| 12. Palomino | NIP | 12. Periquita | NIP |
| 13. Regner | Lugliencia Bianca x Gamay Precoce ¹ | 13. Petite Sirah FR | Peloursin x Syrah ³ |
| 14. Riesling Itálico | NIP | 14. Petite Sirah RS | Peloursin x Syrah ³ |
| 15. Sauvignon Blanc | NIP | 15. Royalty | Alicante Ganzin x Trouseau ³ |
| 16. Seara Nova | Diagalves x Fernão Pires ¹ | 16. Ruby Cabernet | Carignan x Cabernet Sauvignon ³ |
| 17. Sémillon | NIP | 17. Sangiovese | Ciliegiolo × Calabrese di Montenuovo ⁴ |
| 18. Siegerrebe | Madeleine Angevine x Traminer Rot ¹ | 18. Souzao | NIP |
| 19. Sylvaner | Oesterreichisch weiss x Traminer ¹ | 19. Tampa | <i>Vitis smalliana</i> O.P. x Niagara ⁵ |
| 20. Trebbiano Toscano | NIP | 20. Tannat | NIP |
| 21. Ugni Blanc | NIP | 21. Tibouren | NIP |
| 22. Verdea | NIP | | |

* Numbering used for the identification of the accessions in the dispersion diagram, in the principal component analysis. NIP: non-identified parent; ¹Vitis International; ² Bowers et al (2000); ³ Hawkins (2007); ⁴ Vouillamoz et al (2007); ⁵ European Vitis Database (2007).

Table 2. Variance of each principal component and its relevance in comparison with the total variance

| Principal component | White grape genotypes | | Red grape genotypes | |
|---------------------|-----------------------|-------------------------|---------------------|-------------------------|
| | Variance (%) | Accumulated variance(%) | Variance (%) | Accumulated variance(%) |
| 1 | 40.00 | 40.00 | 37.67 | 37.67 |
| 2 | 21.59 | 61.59 | 27.39 | 65.06 |
| 3 | 11.41 | 73.00 | 14.53 | 79.59 |
| 4 | 9.48 | 82.48 | 8.84 | 88.43 |
| 5 | 5.61 | 88.09 | 3.89 | 92.32 |
| 6 | 5.06 | 93.15 | 2.75 | 95.07 |
| 7 | 3.00 | 96.15 | 2.41 | 97.48 |
| 8 | 2.38 | 98.53 | 1.36 | 98.84 |
| 9 | 0.67 | 99.20 | 0.61 | 99.45 |
| 10 | 0.52 | 99.72 | 0.40 | 99.85 |
| 11 | 0.28 | 100.00 | 0.15 | 100.00 |

greatest differences were observed among the pairs of accessions Aramon and Tannat and Castellán and Mars (Figure 1B).

In a comparison of the results obtained with genealogy, the parents of a great part of the accessions could not be identified (Table 1), complicating the comparison of group formation and the relationship of the members of the groups formed with their respective parents. This et al. (2006) mentioned three processes of significant impact on the

development of grapevines: sexual reproduction, vegetative propagation and somatic mutations. Still, the authors report that due to the widespread use of *Vitis vinifera* in the worldwide wine industry, the species has undergone processes of domestication and changes occurred in morphological characters. However, for genotypes for wine production, some cultivars predominate, e.g., Sauvignon Cabernet and Petite Sirah. According to Hawkins (2007), these varieties are considered old grape varieties, mostly related to a particular region, producing quality wines with defined local characteristics. The existing variations resulted in the emergence of clones. Synonymy was observed in white grapes, which are part of the same similarity group of accessions Gewürztraminer, Traminer and Sylvaner clone (Table 1). In red grapes, the accessions Petite Sirah FR and Petite Sirah RS belong to the same group (Figure 1B), probably because these clones constitute variations within the variety. Studies of morphological characters contribute to demonstrate the diversity in germplasm of *Vitis vinifera* (Martinez and Martinez 2007). A similar study was conducted by Borges et al. (2008) with grapes for

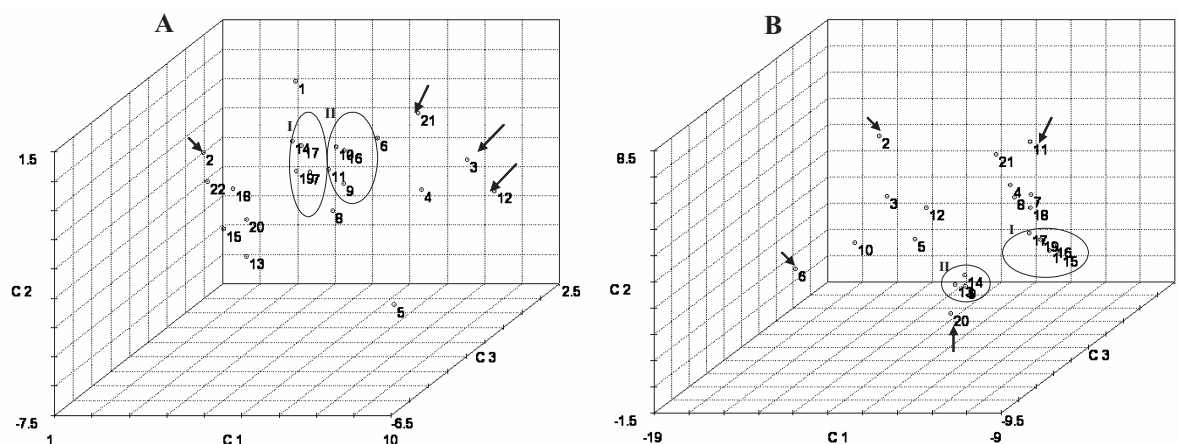


Figure 1. Dispersion diagram drawn from the component scores 1, 2 and 3 in the principal component analysis. **A.** Formation of divergence groups of white grape genotypes: I. Gewürztraminer, Riesling Itáliaico, Sémillon, Sylvaner; II. Malvasia de Lapari, Moscatel, Moscato Canelli, Seara Nova. Arrows show the most divergent accessions. **B.** Formation of divergence groups of red grape genotypes: I. Angelota, Royalty, Ruby Cabernet, Sangiovese, Tampa; II. Grand Noir, Petite Sirah FR, Petite Sirah RS. Arrows show the most divergent accessions.

fresh consumption from the genebank of Embrapa Tropical Semi-Arid.

The dissimilarity measures were determined by analysis of the mean Euclidean distance, where, for white grapes, the minimum and maximum dissimilarities were 0.28 in the accessions Moscato Canelli and Seara Nova, and 2.41 in Altesse and Colombard, respectively, with an overall mean estimate of 1.35. These results indicate that the last two accessions in this analysis are the most divergent. In the group of red grapes, the minimum dissimilarity value between the accessions Gamay and Gamay Beaujolais was 0.40 and the maximum for Castelão and Royalty 2.51, indicating greatest divergence. The average value was 1.35. The means of the estimates of 11 white grape accessions (52.38%) and of eight red grape accessions (40%) exceeded the overall mean. The concentration of overall means of accessions above the overall mean of estimates obtained by mean Euclidean distance indicates intermediate levels of phenotypic divergence for the characters studied and the need to increase the variability through the introduction of new accessions. The existing variability can however be exploited in breeding programs of grapevine for quality wine production.

The cluster analysis UPGMA, based on dissimilarity estimates of the group of white grapes, indicated the formation of four major groups, namely: I) Moscato Canelli, Seara Nova Sylvaner, Sémillon, Moscatel, Feher Szagos, Ugni Blanc, Altesse and Riesling Itáliaico; II) Sauvignon Blanc, Trebbiano Toscano, Regner, Baco Blanc, Siegerrebe, Verdea, Chenin Blanc, Malvasia de Lapari, Lassif; III)

Gewürztraminer and IV) Campanário, Palomino and Colombard (Figure 2A). No relationship was found between the groups formed and genealogy. For the group of red grapes, four groups were formed: I) Gamay, Gamay Beaujolais, Cabernet Sauvignon, Ruby Cabernet, Sangiovese, Mars, Angelota, Royalty, Souzao, Carignan, Periquita, Petite Sirah FR, Petite Sirah RS, Grand Noir, Tannat, Tampa; II) Tibouren; III) Aramon, BRS Lorena; IV) Castelão and Grenache (Figure 2B). As in principal component analysis, the UPGMA analysis showed that the genealogy of the accessions Petite Sirah FR and Petite Sirah RS is similar (Figure 2B). The same was observed for the accessions Beaujolais Gamay and Gamay, which are clones of iPinot Noir (Table 1). Comparing the phenograms, greater dissimilarity was observed in the group of red grapes, as the formation of a large number of subgroups showed (Figure 2B).

Finally, the results obtained in principal component analysis indicated that the most divergent accessions were Baco Blanc and Palomino, for white grapes, and Castellán and Mars for the group of red grapes. By the mean Euclidean distance for the two groups, the high concentration of accessions with a higher mean of estimates between pairs of accessions than the overall mean of estimates (52.38 and 40% for white and red grapes, respectively), is a strong indicator of the need to broaden the genetic diversity in the grapevine genebank of Embrapa Tropical Semi-Arid. By UPGMA clustering, four large groups were formed, both of white as of red grapes. In white grapes, similarity was found between the accessions Petite Sirah FR and

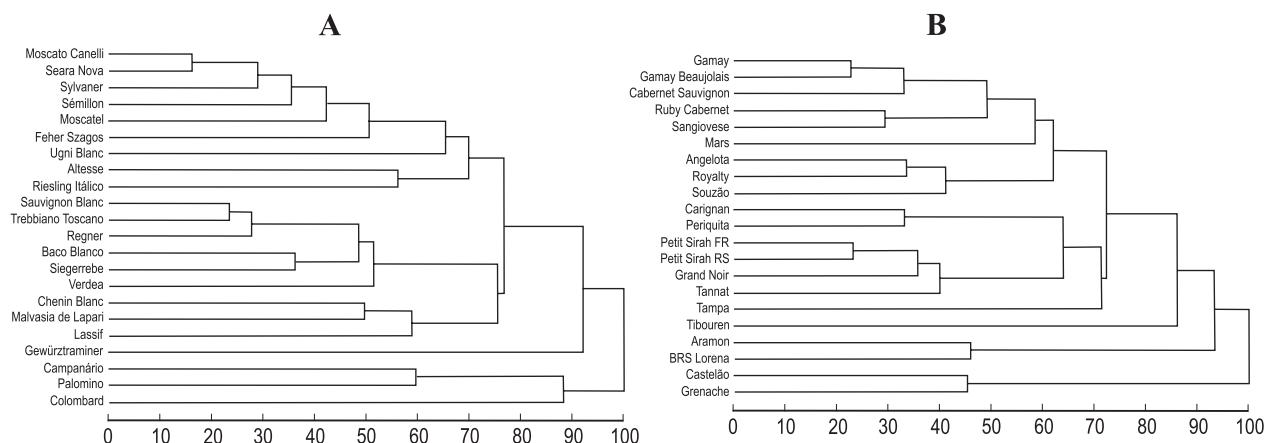


Figure 2. Dendrogram obtained by the UPGMA clustering based on the phenotypic dissimilarities **A.** 22 white grape genotypes for wine production; **B.** 21 red grape genotypes for wine production.

Petite Sirah RS and Gamay and Gamay Beaujolais. The dissimilarity was greater in the group of red grapes due to the formation of a large number of subgroups.

Studies of divergence provide parameters for the identification of suitable parents for hybrid populations. According to Dias (1994), establishing efficient criteria for the identification of divergent parents for hybridization translates into savings in manpower and costs. Multivariate analyses are important tools for this identification and, in the case of the grapevines evaluated in this study, the identification of divergent accessions means the possibility of future work towards the establishment of grape hybrids

for winemaking. Our results also demonstrated that these accession are well-adapted and can be grown under semi-arid conditions that may contribute to the production of local quality wines, representing the region of the São Francisco river valley.

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Divergência fenotípica entre acessos de uvas de vinho no semiárido brasileiro

RESUMO - *Objetivou-se estimar a divergência fenotípica em uvas para a elaboração de vinhos baseada em onze variáveis morfoagronômicas. A análise por componentes principais mostrou a formação de dois grupos contrastantes, tanto para uvas brancas quanto para uvas tintas. Nas uvas brancas, maior divergência foi observada entre os acessos Baco Blanc, Campanário e Palomino. Nas uvas tintas, os mais divergentes foram Aramon e Tannat; Castelão e Mars. A distância euclidiana revelou 52,4 e 40,0% de acessos com média acima da média geral para brancas e tintas, respectivamente. No UPGMA, formaram-se quatro grandes grupos para uvas brancas e tintas. Em relação à genealogia, tanto a análise por componentes principais quanto por UPGMA, ficou demonstrado que os acessos Petite Sirah FR e Petite Sirah RS são similares. Os mais divergentes para os caracteres estudados devem ser utilizados para a obtenção de híbridos, bem como para a seleção de acessos visando a elaboração de vinhos regionais.*

Palavras-chave: *Vitis vinifera* L., recursos genéticos, descritores de uva.

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