Genetic diversity in yellow passion fruit populations

Alexandre Pio Viana[1*], Telma Nair Santana Pereira[1], Messias Gonzaga Pereira[1], Margarete Magalhães de Souza[1], José Francisco Martinez Maldonado[2], and Antônio Teixeira do Amaral Júnior[1]

ABSTRACT - *The genetic diversity in yellow passion fruit genotypes from populations of different origins (Campos dos Goytacazes, Itaperuna and São Francisco de Itabapoana , Rio de Janeiro State, Brazil), was quantified. The following traits were evaluated in two environments (Macaé and Campos dos Goytacazes): fruit weight, mean number of fruits, fruit length, equatorial fruit diameter, rind thickness, brix content, acid content, juice yield. The evaluation of the genotypes cultivated in Macaé resulted in the formation of groups according to the origin of the accessions. The accessions collected in Itaperuna and in Campos dos Goytacazes performed better than those collected in São Francisco do Itabapoana. A consistent and similar pattern was observed in the analysis of the environment Campos dos Goytacazes, indicating that the accessions grown in São Francisco do Itabapoana represent genomes with inadequate traits for local producers.*

Key words: *Passiflora* sp, multivariate analysis, genetic diversity.

INTRODUCTION

Yellow passion fruit (*Passiflora edulis* f. *flavicarpa* Deg.) is a fruit species of great economic importance, which has, nonetheless, rarely been investigated in studies of applied genetic improvement. For the establishment of such studies, it is very importance to investigate the genetic structure of wild and cultivated populations to identify promising parents that can generate sufficiently heterotic hybrids which in turn result in superior segregating genotypes, allowing a more effective genetic improvement program for the crop.

Several multivariate methods, such as the Principal components, Canonical variables and the Cluster analyses can be used to predict genetic divergence. The choice of the method depends on the precision the breeder desires, as well as the ease of analysis and data acquisition (Cruz and Regazzi 2001).

In respect of improvement programs, Falconer (1987) underlines that when genotypes are evaluated in more than one environment to quantify the diversity in the interaction, differences in performance can mean different clusters. Since the accessions were developed in dynamic systems, their response to environmental variations is generally differentiated. The genotype x environment interaction is a constant challenge for breeders in view of the complications it entails in the selection of accessions evaluated in different environments. The greater the genetic diversity among genotypes and environments, above all in environments with considerable temperature and precipitation variations, the greater the importance of the interaction (Borém 1997). So, evaluations of the

[1] Universidade Estadual do Norte Fluminense - UENF, Avenida Alberto Lamego, 2000, 28.015-610, Campos dos Goytacazes, RJ, Brasil. *E-mail: pirapora@uenf.br
[2] Empresa de Pesquisa Agropecuária do Estado do Rio de Janeiro - PESAGRO, 27.901-970, Macaé, RJ. Brasil

genetic diversity in more than one environment can therefore shed light on the performance of genotypes, with consequent influence on their performance in future improvement programs.

Notwithstanding the importance, few evaluation studies on heterotic groups of yellow passion fruit, using multivariate statistical techniques, have so far aimed at the indication of crossings for future improvement programs of the crop. To date, studies have focused on genetic parameters (Viana et al. 2004), correlations between traits (Viana et al. 2003) besides related species and their reproductive traits (Meletti et al. 2003, Viana et al. 2003, Souza et al. 2003, 2004).

This study targeted to quantify the genetic diversity in yellow passion fruit accessions collected in the regions Norte and Noroeste Fluminense of the state of Rio de Janeiro, to identify superior genotypes that could be used in a regional improvement program for the crop.

MATERIAL AND METHODS

Accessions

Three populations of yellow passion fruit, identified in the county of São Francisco de Itabapoana, Itaperuna and Campos dos Goytacazes (north and northwest of the Rio de Janeiro State) were sampled. Sampling was based on the technology level of the farms at these locations. Five plants per population were randomly picked. These plants were vegetatively propagated to obtain genetically identical plants for field evaluations.

Stem cuttings of the 20 genotypes (Table 1) were collected, cut to a length of 20 cm, with one pair of half leaves not treated with any growth regulator and planted in rooting beds of coarse sand, in March and April 2000. During the rooting period, the cuttings were irrigated twice a day. By the end of July, the rooted cuttings were transferred to polyethylene bags (7 x 15 cm) filled with Plantmax substratum. Forty days after planting, the acclimatized plantlets were transplanted to the field.

Field trial

The plants were cultivated along a wire system, supported by a single wire (nr.12) at a height of 1.80 meters from the ground. The statistical design was arranged in random blocks with three replications. Experiments were installed in two environments in September 2000, one in Campos dos Goytacazes, at the Escola Agrícola Antônio Sarlo, and the other in Macaé, at the experimental station of fruit crops of the PESAGRO-RIO.

Table 1. Identification of genotypes of yellow passion fruit (*Passiflora edulis* f. *flavicarpa*) by the index number of the Passiflora collection of the UENF and place of origin

Genotype	Index nr.	Origin
01	UENF 1505	São Francisco do Itabapoana
02	UENF 1506	São Francisco do Itabapoana
03	UENF 1507	São Francisco do Itabapoana
04	UENF 1508	São Francisco do Itabapoana
05	UENF 1509	São Francisco do Itabapoana
06	UENF 1510	São Francisco do Itabapoana
07	UENF 1511	São Francisco do Itabapoana
08	UENF 1512	São Francisco do Itabapoana
09	UENF 1513	São Francisco do Itabapoana
10	UENF 1514	São Francisco do Itabapoana
11	UENF 1515	Itaperuna
12	UENF 1516	Itaperuna
13	UENF 1517	Itaperuna
14	UENF 1518	Itaperuna
15	UENF 1519	Itaperuna
16	UENF 1520	Campos dos Goytacazes
17	UENF 1521	Campos dos Goytacazes
18	UENF 1522	Campos dos Goytacazes
19	UENF 1523	Campos dos Goytacazes
20	UENF 1524	Campos dos Goytacazes

Evaluated traits

To evaluate the genetic diversity through morpho-agronomic traits, the genotypes were sampled thrice in three months (beginning in January, 2001, and continued in February and March). The number of fruits obtained per genotype in each sampling was variable since only ripe fruits were collected.

The evaluated traits were the following: a) mean number of fruits (NF): the number of green fruits per plot was counted in the first flowering in January. The values were divided by the number of plants, calculating the mean number of fruits per plant in the plot; b) the fruit weight (FW) was obtained by weighing the ripe fruits on an OHADUS, model TP 4000D, electronic scale (capacity of 4.0 kg and precision of 0.01 g); c) the fruit length (FL) was obtained by measuring the fruits lengthwise (longitudinal) by a pachymeter; d) the equatorial fruit diameter (FD) was obtained by measuring the fruit width (transversal) by a pachymeter; e) the rind thickness (RTh) was determined

by measuring the outer rind in the mid part of the transversally cut fruits, at the point of greatest diameter, by a pachymeter; f) the degrees brix were obtained by refractometry, by a portable refractometer ATAGO N1, with readings in a range of 0 to 32^0 degrees brix. The readings were performed in pulp juice samples, extracted by manual pressing and filtered through nylon mesh; g) the titratable acidity contents were determined in a 10 ml juice sample to which three drops of 1% phenolphthalein indicator were added, and then titrated, under agitation, with NaOH solution at 0.1 N, standardized beforehand with potassium biphtalate; and h) the percentage of juice was computed by the difference between fruit weight and weight of the extracted juice, based on values of two, three or four fruits.

Statistical analyses

The data were subjected to analysis of variance and cluster analysis, using the hierarchical method of the Nearest Neighbor and Tocher, based on Mahalanobis's generalized distance. The relative contribution of the traits to the discrimination of variability in the accessions was evaluated by the method of Singh (1981). The genetic diversity was further evaluated by Canonical variables, using the software Genes (Cruz 2001).

RESULTS AND DISCUSSION

The mean squares showed significant differences by the F test among the traits under study (Table 2) for the effect of environments on the genotype x environment interaction. Significant differences were observed for the traits number of fruits (NF), fruit length (FL), rind thickness (RTh), and fruit weight (FW) in both study environments

(Campos dos Goytacazes and Macaé). These traits presented a coefficient of variation of 18.00, 6.36, 19.18, and 14.89%, respectively. For all study traits the coefficients of variation were low, indicating an effective data acquisition. No significant differences were observed among genotypes for the traits equatorial fruit diameter (FD), brix content, acid content and percentage of juice.

Individual analyses are of great importance, since they allow the evaluation of the genetic variability and the discrepancies between the residual variances in each environment. In Macaé significant differences were observed by the F test regarding fruit number, length, weight and equatorial fruit diameter as well as rind thickness and brix content. In relation to the acidity content and juice percentage no significant differences were observed. In Campos dos Goytacazes, significance by the F test was verified for the traits fruit number, length, weight, equatorial fruit diameter and rind thickness. No significant differences were observed by the F test for degrees brix and acidity contents and juice percentage. The experimental variation coefficients were 8.36, 16.37 and 17.48%, respectively.

The Nearest neighbor method resulted in the formation of groups according to the evaluated traits. For the environment Macaé the formation of six groups was observed (Figure 1), based on the differences in the dendogram, more specifically, for the magnitude of 30% of the maximum distance (25): group 1, formed by genotype 1, group 2 formed by six genotypes (10, 11, 20, 12, 15, 14, and 16); group 3 with four genotypes (4, 18, 19 and 13); group 4 with two genotypes (9 and 17), group 5 formed by a single genotype (8) and group 6 with five genotypes

Table 2. Summary of analyses of variance for eight traits for evaluated in passion fruit genotypes in two environments (Macaé and Campos dos Goytacazes counties)

Sources of variation	df	NF[1]	FL[2]	FD[3]	RTh[4]	FW[5]	Brix content	Acidity content	percentage of juice
Block/Environments	4								
Genotypes	19	162.95**	123.87**	108.78	4.57**	4458.7**	2.54	0.51	30.51
Environments	1	20.00	153.81**	0.31	0.003	26.60	30.50**	0.31	259.04*
G x E	19	12.86**	21.25	58.79**	1.49	1347.1*	1.65	0.41	52.62
Error	76	2.91	30.74	20.18	0.59	737.89	1.02	0.29	33.58
Mean		9.47	87.08	77.86	4.00	182.42	14.42	3.65	34.58
Cve(%)		18.00	6.36	5.77	19.18	14.89	7.03	14.97	16.75

[1]NF: number of fruits; [2]FL: fruit length; [3]FD: equatorial fruit diameter; [4]RTh: rind thickness; [5]FW: fruit weight
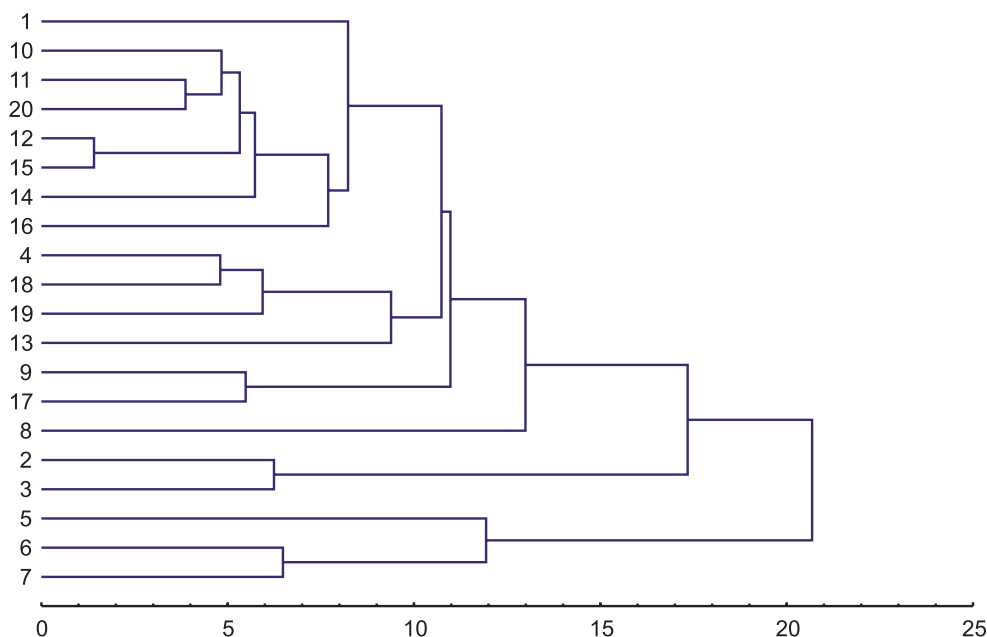* P < 0.05, ** P< 0.01

Figure 1. Nearest neighbor dendrogram from Mahalanobis' distances based on eight traits of 20 passion fruit genotypes evaluated in Macaé. Genotypes are coded as in Table 1

(2, 3, 5, 6, and 7). The genotypes that made up the first two groups were those of superior performance by the analysis of the phenotypic means of the trait number of fruits. Group 1 achieved a mean yield of 14, and group 2 a mean yield of 12 fruits. For the trait fruit weight, group 1 presented a mean weight of 204.98 g and group 2 a mean fruit weight of 161.12 g, compared with the other genotypes. The genotypes that constituted the other three groups were from São Francisco do Itabapoana, which, in this study, performed worst for the variable mean number of fruits, varying from 6 to 7 fruits, and fruit weight varying between 140 and 150 g.

Five groups were formed with data from Campos dos Goytacazes (Figure 2) based on the formation of groups at 62% of the maximum distance (18): group 1, formed by eight genotypes (1, 8, 14, 20, 12, 13, 15 and 10); group 2, by seven genotypes (2, 3, 5, 4, 9, 18, and 16); group 3, formed by genotype 17, group 4 and the 5, formed by two genotypes each (6, and 7, and 11 and 19 respectively).

The groups distinguished superior and inferior accessions in a consistent pattern, in respect of the most important traits (number of fruits and fruit weight). For the trait number of fruits group 1 presented a mean of 13.0 fruits per plant, group 2, 5.0 fruits per plant and groups 3

and 4 each 3 fruits per plant. In relation to the mean fruit weight, group 1 attained 193.38 g, group 2 fruits of 171.55 g and groups 3 and 4 a mean weight of 140.0 g. It is possible that the genotypic inferiority of the accessions from São Francisco do Itabapoana was a consequence of the low technological level used in successive cultivation cycles. They are possibly populations which, over the years of cultivation, underwent a selection favoring genotypes that are more resistant against adverse conditions, but little productive.

By the results of the Tocher cluster, eight accession groups were formed in the environment Macaé. Group 1 contained 35% of the accessions, the best performing plants, mostly, for the traits number of fruits and fruit weight (12, 15, 11, 14, 20, 10, and 1). Group 2 allocated the plants 4, 18, 19, 16, and group 3 the plants 9, 17. These three groups joined the genotypes of greatest interest, which presented the best performance in the evaluated traits and therefore carry the greatest potential for success in the establishment of superior populations in improvement programs. Viana et al. (2004) worked with the same populations and observed heritability of about 92% for the trait number of fruits, which justifies the application of simple selection methods with satisfactory gains. Groups 4 and 5 allocated plants whose traits presented intermediate
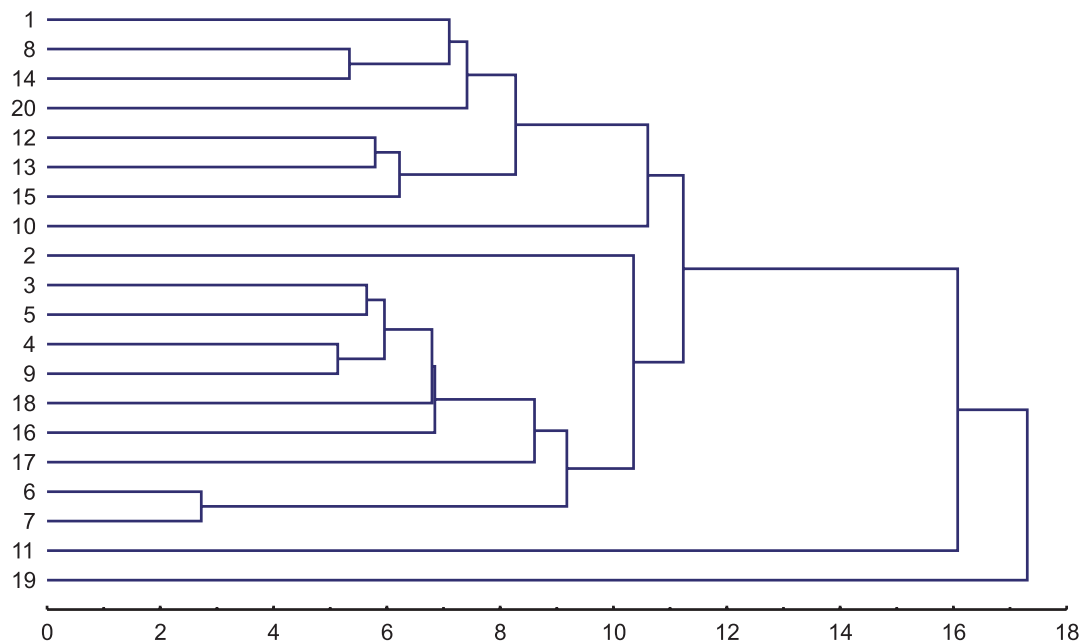
Figure 2. Nearest neighbor dendrogram from Mahalanobis' distances based on eight traits of 20 passion fruit genotypes evaluated in Campos dos Goytacazes. Genotypes are coded as in Table 1

values, from the population of São Francisco de Itabapoana (2, 3) and (6, 7), respectively. Groups 6 and 7 clustered the plants 5 and 8 with lower values for the evaluated traits. Group 8 was formed solely by genotype 13.

A similar cluster pattern was verified for the environment Campos dos Goytacazes. Group 1 contained 40% of the accessions, with the genotypes of inferior performance for the evaluated traits (6, 7, 5, 3, 4, 18, 16, 9), which belong to the populations of São Francisco do Itabapoana and Campos dos Goytacazes. Group 2 united the genotypes that performed well for the evaluated traits (8, 14, 20, 10). Group 3 clustered genotypes 12, 13 and 15.

Group 4 contained only plant 11, which presented high phenotypic values for the traits juice yield (mean of 35%) and equatorial fruit diameter (mean of 82 mm). It would be auspicious to work with genotypes that contain such traits in equilibrium, aiming at simultaneous gains for equatorial fruit diameter and juice yield, according to a study developed by Viana et al. (2003). The authors observed high canonical correlations between these groups of traits, with high magnitudes and a positive signal. Group 5 contained genotype 19, and groups 6, 7 and 8, respectively, genotypes 1, 17 and 2.

The distribution of plants into groups provides an important piece of information for genetic plant

improvement. It supports the selection of genotypes for hybridization programs, where crossings between superior genotypes and of distinct groups must be given priority since the expression of heterosis is function of the genetic distance between plants. For the environment Macaé the first two Canonical variables explained about 77.27% of the total variation, respectively, 63.36% for the first and 13.91% for the second.

To have a negligible distortion in the transposition of an n-dimensional to a two or three-dimensional space, the first two Canonical variables must explain at least 80% of the existing variation; otherwise a third variable must be included in the study (Cruz and Regazzi 2001). In the present study the first three Canonical variables were sufficient to explain 88.51% of the total variation for the environment Macaé, while for the environment Campos dos Goytacazes, the first two Canonical Variables were sufficient to explain 80.31% of the existing variation.

The genotypes followed a similar and consistent distribution in relation to the other methods used to analyze genetic divergence (Figure 3). Genotypes 1, 10, 11, 12, 13, 14, 15, 16, and 20 formed a group, probably by the superior performance in relation to the other genotypes under study. Genotypes 5, 7, 6, and 2 formed another group which expressed their similarity and inferior performance in
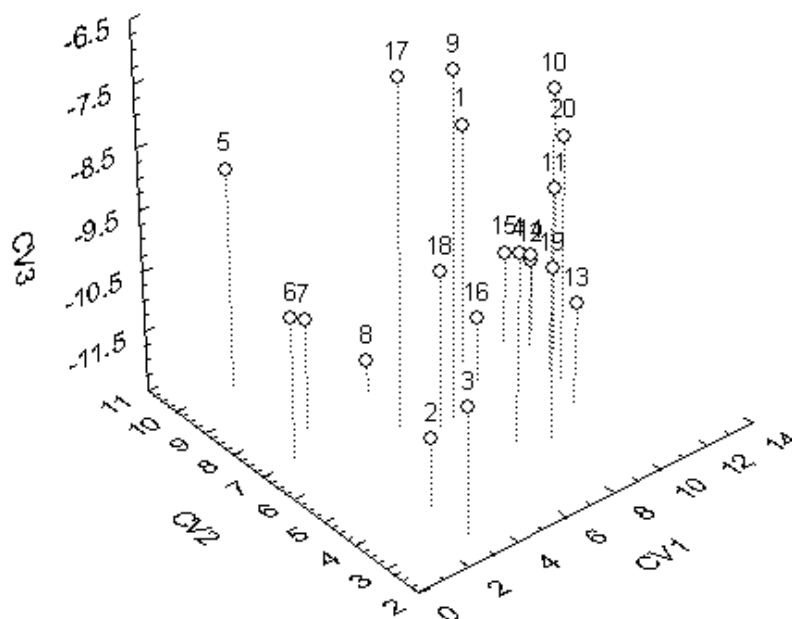
Figure 3. Canonical variable plot related to eight traits evaluated in 20 passion fruit genotypes in Macaé

relation to the others. These plants were collected in São Francisco de Itabapoana, where the production conditions and use of technology favor the choice of drought-resistant, though little productive plants. Another group formed in the analysis of graphic dispersion united the genotypes 4, 8, 9, 17, 18 and 19, which were grouped similarly by the other methods as well.

For the environment Campos dos Goytacazes (Figure 4), the distribution of the genotypes was similar to the cluster. In this environment, the genotypes 15, 12, 13, 11, the most promising for use in improvement programs, are near to each other. Genotypes 1, 8, 10, 14, 19, and 20 were also close, forming a well-performing group. The other groups contained the genotypes 18, 16, 3, 9, 4 and 17 and, an inferior group, the genotypes 2, 5, 6 and 7.

In the environment Macaé the trait number of fruits contributed with 68.15% to the existing variation between the accessions, in second place with 11.04% was the variable rind thickness, fruit weight contributed with 5.61% and the others contributed with 15.20% to the remaining variation by the method of Singh (1981).

For the environment Campos dos Goytacazes, the variable number of fruits accounted for 58.10% of the existing variation between the accessions, in second place with 13.54% was the trait rind thickness, fruit weight contributed with 7.81% and the others

contributed with 20.55% to the remaining variation, evidencing the importance of the three traits, number of fruits, rind thickness and fruit weight in studies of this nature with passion fruit.

The conclusion was drawn that the populations from Itaperuna and Campos dos Goytacazes have the greatest potential for selecting parents for an improvement program with the crop. This conclusion was based on the fact that the population from Campos dos Goytacazes is selected plant material, by the company Maguari, provenient from the Triângulo Mineiro, probably with a higher concentration of favorable genes for the traits of interest. The population from Itaperuna on the other hand came from farms on which technology was used, besides seed selection of superior plants from commercial plantations for the production of new plantlets. In turn, the populations of São Francisco do Itabapoana came from farms where no technology at all had been applied to achieve superior yields.

CONCLUSIONS

Superior populations were identified, with possibilities of use in the improvement program that will be set up at the Darcy Ribeiro North Fluminense State University.
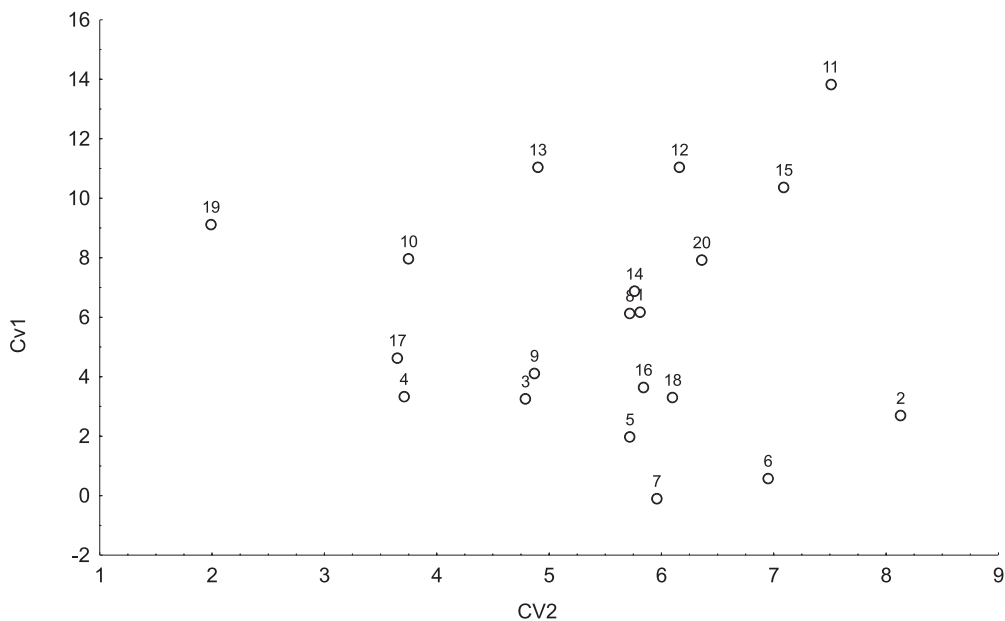
Figure 4. Canonical variable plot related to eight traits evaluated in 20 passion fruit genotypes in Campos dos Goytacazes

The analysis of the groups formed identified regionally adapted genotypes from the population of São Francisco do Itabapoana, which were low- yielding regarding agronomical traits but have a potential for use in passion fruit improvement.

The populations from Itaperuna and Campos dos Goytacazes performed best and were selected for the establishment of segregating superior genotypes in advanced generations of improvement in the North of Rio de Janeiro State, Brazil, besides the direct use of some genotypes in a recombination program of the involved accessions.

Diversidade genética em populações de maracujazeiro amarelo

RESUMO - *A diversidade genética em maracujazeiro amarelo foi quantificada por meio da coleta de genótipos em populações de diferentes procedências (Itaperuna, São Francisco do Itabapoana e Campos dos Goytacazes), avaliando-se, em dois ambientes (Macaé e Campos dos Goytacazes), as características: peso de fruto, número médio de frutos, comprimento e diâmetro equatorial dos frutos, espessura de casca, teor de graus brix, teor de acidez, rendimento de suco. A avaliação dos genótipos cultivados em Macaé revelou a formação de grupos de acordo com a origem dos acessos, sendo que os acessos coletados em Itaperuna e em Campos dos Goytacazes se mostraram superiores aos coletados em São Francisco do Itabapoana. Um padrão consistente e similar foi observado pela análise do ambiente Campos dos Goytacazes, indicando que os acessos cultivados em São Francisco do Itabapoana podem constituir genomas com características inadequada aos produtores daquele município.*

AP Viana et al.

REFERENCES

Borém A (1997) **Melhoramento de plantas**. Editora UFV, Viçosa, 547p.

Cruz CD and Regazzi AJ (2001) **Modelos biométricos aplicados ao melhoramento genético**. Editora UFV, Viçosa, 390p.

Cruz CD (2001) **Programa Genes versão windows: aplicativo computacional em genética e estatística**. Editora UFV, Viçosa, 648p.

Falconer DS (1987) **Introdução à genética quantitativa**. Editora UFV, Viçosa, 279p.

Meletti LMM, Bernacci LC, Soares-Scott MD, Azevedo Filho JA and Martins ALM (2003) Variabilidade genética em caracteres morfológicos, agronômicos e citogenéticos de populações de maracujazeiro-doce. **Revista Brasileira de Fruticultura 25**: 275-278.

Sousa MM, Pereira TNS, Viana AP, Messias GP, Bernacci LC, Sudré CP and Silva L (2003) Meiotic irregularities and pollen viability in *Passiflora edmundoi* Sacco (Passifloraceae). **Caryologia 56**: 453-51.

Sousa MM, Pereira TNS, Viana AP, Messias GP, Amaral Júnior AT and Madureira HC (2004) Flower receptivity and fruit characteristics associated to time of pollination in yellow passion fruit *Passiflora edulis* sims f. *falvicarpa*. **Scientia Horticulture 1**: 1-13.

Sousa MM, Palomino G, Pereira TNS, Messias GP and Viana AP (2004) Flow cytometric analysis of genome size variation in some Passiflora species. **Hereditas 1**: 1-8.

Viana AP, Pereira TNS, Pereira MG, Souza MM, Maldonado FM and Amaral AT (2003) Diversidade genética entre genótipos comerciais de maracujazeiro amarelo (*Passiflora edulis* f. *flavicarpa*) e entre espécies nativas de Passiflora determinada por marcadores RAPD. **Revista Brasileira de Fruticultura 25**: 489-493.

Viana AP, Pereira TNS, Pereira MG, Amaral Júnior AT, Souza MM and Maldonado JFM (2004) Parâmetros genéticos em populações de maracujazeiro amarelo. **Revista Ceres 51**: 541-551.

Viana AP, Pereira TNS, Pereira MG, Souza MM, Maldonado JFM and Amaral Júnior AT (2003) Simple and canonic correlation between agronomical and fruit quality traits in yellow passion fruit (*Passiflora edulis* f. *flavicarp*) populations. **Crop Breeding and Applied ABiotechnology 3**: 133-140.

Singh D (1981) The relative importance of characters affecting genetic divergence. **The Indian Journal of Genetics and Plant Breeding 14**: 237-245.