

# Genetic Divergence in Clones of *Coffea canephora* Variety Conilon by Different Methods of Multivariate Analysis

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## SUMMARY

The objective of this work was to study by different methods of multivariate analysis the genetic divergence of forty genotypes of conilon coffee of the Coffee Genetic Improvement Program of the Capixaba Institute of Research - Incaper. In the analysis of dissimilarity, evaluated by the generalized distance of Mahalanobis, the genotypes most dissimilar were ES 318 and ES 01 in Sooretama, and ES 309 and ES 315 in Marilândia, Those most similar were ES 330 and ES 336 in Sooretama and ES 324 and ES 333 in Marilândia. In the study of clustering by the technique of Tocher, the genotypes were distributed in ten groups in Sooretama and five in Marilândia. In both locations there was good agreement in the disposition of the genotypes, in amount of genetic divergence, when the hierarchical nearest neighbor method and the method of Tocher were used. We verified good genetic divergence among the clones for the different biometric methodologies studies. The results obtained, associated to the main agronomic characteristics evaluated, were important for the strategies addressing genetic improvement through sexual and asexual reproduction and propagation. The clones ES 01, ES 308, ES 309, ES 311, ES 321, ES 327, ES 328, ES 329, ES 330 and ES 337 are promising clones to be maintained and used in the Program of Improvement.

## INTRODUCTION

The conilon of the *Coffea canephora* species has great economic and social importance in the State of Espírito Santo. This State, in 2007, produced 73% of the conilon coffee of Brazil (7,5 million processed sacks). The Capixaba Institute of Research (Incaper) has been conducting a research program in genetic improvement with this species since 1985. As applied results of this program, newly developed seeds and seedlings of six conilon varieties were made available to the producers from the state of Espírito Santo (Ferrão et al., 2007).

The study of genetic divergence is of great importance in a genetic improvement program, because, biometric techniques with the use of multivariate analyses, diallelic analyses and, or, molecular, are decisive tools in the identification of promising parents and with complementarity of hybridization, in the quantification of genetic variability of the genetic material studied, in the grouping of genotypes more similar aiming at the formation of synthetic varieties in the identification of the importance of each characteristic in the process of selection and also in the availability of information about the available genetic resources in the program and in the exchange of genetic material ( Ferrão et al., 2007).

The objective of this work was to study by different methods of multivariate analysis the genetic divergence of forty genotypes of conilon coffee of the Coffee Genetic Improvement Program of the Capixaba Institute of Research - Incaper.

## MATERIALS AND METHODS

The studies were carried out during the period of 1996 to 2002, in Sooretama and Marilândia, in Espírito Santo, Brazil, for fourteen characteristics. The experiments were installed in random blocks with four repetitions and spacing of 3.0 x 1.5 m. The statistical and biometric analyses utilized were: dissimilarity evaluation, distance of Mahalanobis, Tocher group and graphic representation of the genotypes for the technique of variable canonical. For those statistical and biometric analyses were utilized the Genes program (Cruz, 2001).

## RESULTS AND DISCUSSION

In the analysis of dissimilarity, evaluated by the generalized distance of Mahalanobis, the genotypes most dissimilar were ES 318 and ES 01 in Sooretama, and ES 309 and ES 315 in Marilândia. Those most similar were ES 330 and ES 336 in Sooretama and ES 324 and ES 333 in Marilândia.

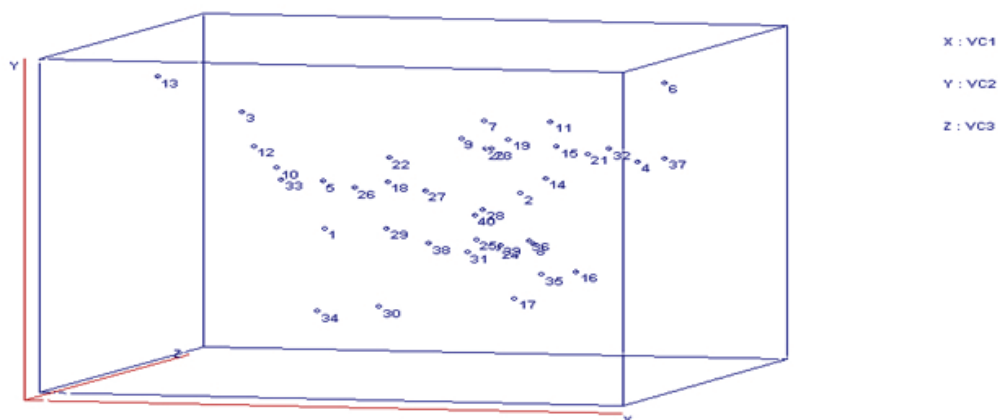
**Table 1. Grouping, by the Tocher method, of 40 genotypes conilon coffee based on the dissimilarity expressed by the generalized distance of Mahalanobis estimated from 14 characteristics, at Sooretama and Marilândia, ES.**

Groups	Genotypes in Sooretama	Genotypes in Marilândia
I	7(ES 312) 19(ES 324) 20(ES 325) 23(ES 328) 9(ES 314) 14(ES 319) 21(ES 326) 11(ES 316) 15(ES 320) 2(ES 307) 27(ES 332) 40(VSM-T <sub>5</sub> ) 28(ES 333) 18(ES 323)	19(ES 324) 28(ES 333) 29(ES 334) 40(VSM-T <sub>5</sub> ) 39(VCP-T <sub>4</sub> ) 25(ES 330) 20(ES 325) 36(ES 36-T <sub>1</sub> ) 14(ES 319) 9(ES 314) 8(ES 313) 21(ES 326) 2(ES 307) 7(ES 312) 15(ES 320) 18(ES 323) 11(ES 316) 31(ES 336) 30(ES 335) 17(ES 322) 35(ES 340) 23(ES 328) 5(ES 310) 26(ES 331) 27(ES 332) 24(ES 329) 1(ES 306) 34(ES 339)
II	25(ES 330) 31(ES 336) 38(ES 23-T <sub>3</sub> ) 29(ES 334) 8(ES 313) 24(ES 329) 39(VCP-T <sub>4</sub> ) 16(ES 321) 17(ES 322) 35(ES 340)	6(ES 311) 32(ES 337) 37(ES 01-T <sub>2</sub> ) 4(ES 309) 16(ES 321)
III	22(ES 327) 26(ES 331) 5(ES 310) 12(ES 317)	3(ES 308) 33(ES 338) 13(ES 318) 12(ES 317) 22(ES 327)
IV	10(ES 315) 33(ES 338)	38(ES 23-T <sub>3</sub> )
V	30(ES 335) 34(ES 339)	10(ES 315)
VI	4(ES 309) 32(ES 337)	
VII	6(ES 311) 37(ES 01-T <sub>2</sub> )	
VIII	3(ES 308) 13(ES 318)	
IX	1(ES 306)	
X	36(ES 36-T <sub>1</sub> )	

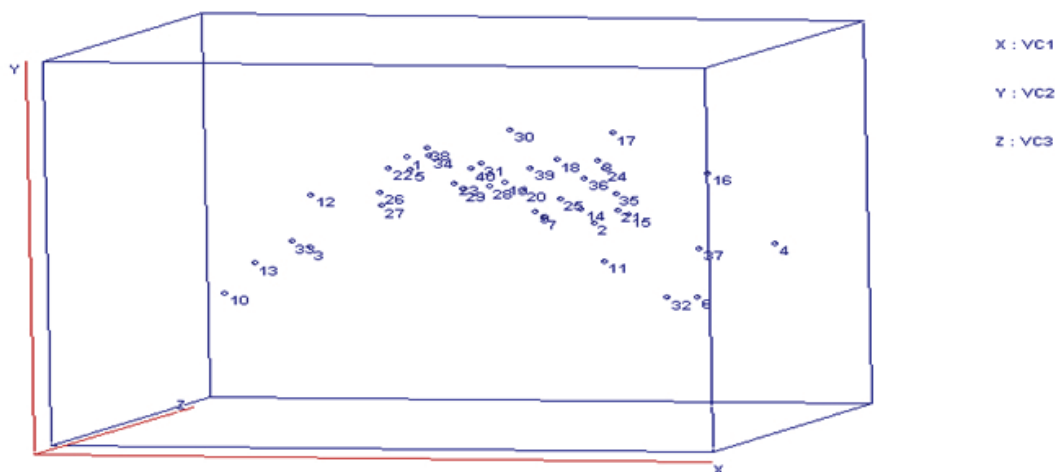
In the study of clustering by the technique of Tocher, the genotypes were distributed in ten groups in Sooretama and five in Marilândia. In both locations there was good agreement in the disposition of the genotypes, in amount of genetic divergence, when the hierarchical nearest neighbor method and the method of Tocher were used (Table 1).

By graphical dispersion with the technique of canonical variables, the clones most divergent in Sooretama were ES 318, ES 311, ES 308 and ES 01, and in Marilândia, ES 315, ES 318,

ES 338, ES 317, ES 309, ES 337 and ES 321. In Sooretama, by canonical analysis, 80.59% of the total variance was explained by the first three discriminate canonical functions with variances of 39.42%, 29.94% and 11.23%, respectively, while in Marilândia the first three canonical functions accounted for 77.70% of the total variance, with variances of 50.51%, 16.35% e 10.81%, respectively (Figure 1 and 2).



**Figure 1. Three-dimensional graph of the dispersion of 40 genotypes of conilon coffee in relation to the canonical variables VC<sub>1</sub>, VC<sub>2</sub> and VC<sub>3</sub>, in Sooretama, ES.**



**Figure 2. Three-dimensional graph of the dispersion of 40 genotypes of conilon coffee in relation to the canonical variables VC<sub>1</sub>, VC<sub>2</sub> and VC<sub>3</sub>, in Marilândia, ES.**

## CONCLUSIONS

We verified good genetic divergence among the clones by the different biometric methods studied. The results obtained, associated to the main agronomic characteristics evaluated, were important for directing strategies of genetic improvement through sexual and asexual reproduction and propagation.

The clones ES 01, ES 308, ES 309, ES 311, ES 321, ES 327, ES 328, ES 329, ES 330 and ES 337 are promising clones to be maintained and used in the Program of Improvement.

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