

## Genetic dissimilarity in cassava clones determined by multivariate techniques

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**ABSTRACT** - The genetic dissimilarity in 15 cassava clones was evaluated based on seven morpho-agronomic traits and multivariate procedures, aiming to select the most divergent and best in an approach to future hybridizations. The experiment was carried out in 2003/2005, in random blocks, with three replications. Based on the matrix of Mahalanobis' generalized distance, the clones were grouped as related to similarity, using the algorithms of Tocher and Nearest neighbor. The relative importance of the traits was also evaluated. The multivariate techniques were concordant in the study of genetic dissimilarity and efficient in grouping clones with short genetic distance. The following traits contributed most to the genetic diversity: total weight of the aerial part, root diameter, root weight, length of tuber roots and harvest index.

**Key words:** Mahalanobis' distance, *Manihot esculenta*, multivariate techniques.

### INTRODUCTION

The genetic diversity of Cassava is wide, but few are the varieties with a satisfactory combination of traits of agronomic interest. Only an adequate selection of the parents, followed by recombinations, can eventually obtain high heterosis or transgressive segregation (Araújo et al. 2002), which will make significant gains in terms of yield, quality and resistance to pests and diseases possible (Fukuda 1996).

It is essential to study the genetic divergence to identify parents of future superior clones (Oliveira et al. 2003), be it by detecting plants with maximal genetic divergence and good performance *per se* or by identifying plants with high genetic similarity. The former would permit the development of high-yielding uniform commercial cultivars and the latter can be used in bi or multiparental crosses (Silva et al. 2002).

According to Cruz and Regazzi (2001), the divergence has been evaluated by biometric techniques based on the quantification of heterosis or by predictive methods. These are based on morphological, physiological and agronomic differences of the parents.

Among the predictive methods are those that quantify genetic diversity by dissimilarity measures (Carvalho et al. 2003), e.g., the generalized distance of Mahalanobis.

Multivariate techniques have been used for quantitative as well as for qualitative traits, of which we cite the Tocher optimization and nearest neighbor methods and the approach of estimation of the relative importance of the evaluated traits (Machado et al. 2002). The criterion used to choose the ideal method depends on the data set, on the accuracy and on the analysis to be performed (Cruz and Regazzi 2001).

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Several studies report the use of multivariate techniques to determine genetic diversity (Vidigal et al. 1997, Peroni et al. 1999, Carvalho et al. 2003, Araújo et al. 2002, Sudré et al. 2005)

The purpose of this study was to quantify the genetic dissimilarity in 15 cassava clones by multivariate techniques, to identify the most promising ones for later hybridizations.

## MATERIAL AND METHODS

### Field experiment

The study was conducted in an experimental area of the Universidade Federal de Lavras, in Lavras, Minas Gerais, (lat 21° 14' 30" S, long 45° 00' 10" W, 900 m asl). The regional climate is classified as mesothermic, Cwa, (Köppen), with a mean annual temperature of 19.3 °C and mean precipitation of 1.411 mm, of which 65 - 70% is concentrated between December and March (Brazil 1992). The soil of the experimental area was classified as typic dystroferic Red Latosol, (Embrapa 1999).

The stem cuttings, approximately 15 to 20 cm long, with a diameter of 2.5 cm and 5 - 7 buds, were planted in a 10 cm deep furrow, in December 2003. The experimental plots consisted of 4 rows with 10 plants, spaced at 1.0 x 0.6 m. Sixteen plants of the two center rows were evaluated (eliminating the utmost plant on either end of each row) using a random block design with three replications. Plants were harvested 18 months after sowing.

At the installation of the experiment, 80 kg ha<sup>-1</sup> P<sub>2</sub>O<sub>5</sub> were applied, according to the recommendations of the CFSEMG (Commission of Soil Fertility of the State of Minas Gerais 1999).

### Evaluated traits

The treatments consisted of 15 cassava clones. Of these, 11 are commercially used (IAC 576-70, IAC 12, IAC 13, IAC 14, IAC 15, Ouro do Vale, Baiana, Baianinha, Mocotó, Fibra) and 4 are new clones (UFLA E, UFLA F, UFLA G, UFLA H, and UFLA J), obtained by polycrosses in the Cassava Breeding program of the Agriculture Department of the Universidade Federal de Lavras.

Botanic agronomical descriptors were used as proposed by Fukuda and Guevara (1998).

- total weight of the aerial part (WA): weight of aerial plant part per plot, in Mg ha<sup>-1</sup>.

- mean yield of tuber roots (WR): weight of roots per plot, in Mg ha<sup>-1</sup>.

- Yield of commercial tuber roots (WC): weight of the commercially used roots per plot, in Mg ha<sup>-1</sup>.

- Mean length of tuber roots (LR): Mean root length of a plot, measured at harvest, in cm.

- Mean diameter of tuber roots (DR): Mean root diameter of a plot, measured in the middle of the roots, in cm.

- Mean number of tuber roots per plant (NR): Mean number of roots per plot at harvest.

- Harvest index (HI): obtained by the ratio of the reserve root weight and the total plant weight (roots + aerial part).

### Statistical analyses

A univariate analysis of variance was performed with the data and then multivariate techniques of clustering were applied.

Firstly, the dissimilarity was estimated based on Mahalanobis' generalized distance ( $D_{ii}^2$ ) between clones  $i$  and  $i'$ . Thereafter, based on the distance matrix, the clones were grouped by the Tocher optimization method. This led to the establishment of groups, with homogeneity within and heterogeneity among groups, based on the criterion that the intragroup are smaller than the intergroup distances. Moreover, the hierarchical nearest neighbor method and projections of the distances onto the plane were used (Cruz and Regazzi 2001).

The relative contribution to diversity of the traits was evaluated by the method of Singh (1981), based on Mahalanobis' generalized distance. All statistical analyses were performed using software Genes (Cruz 2001).

## RESULTS AND DISCUSSION

The tuber root yields of the clones UFLA H, IAC 576-70 and Mocotó were highest (Table 1). The low productivity of the clones Ouro do Vale and Baiana, in an 18-month cycle, was as result of the high incidence of bacteriosis in these cultivars. Although the disease was not quantified in the other clones, considerable losses were detected in the case of these two.

The same tendency was observed in the commercial tuber root yield as in the tuber yield (Table 1). In the evaluation after 18 months, the clone performance was verified in similar conditions as those

**Table 1.** Means of traits evaluated in 15 cassava clones

Accessions	WR (Mg ha <sup>-1</sup> )	WC (Mg ha <sup>-1</sup> )	HI %	LR (cm)	DR (cm)	NR	WA (Mg ha <sup>-1</sup> )
IAC 576 - 70	61,42a	49,97a	0.63a	25.75c	5.78a	5.4a	35,09b
IAC 12	43,35b	35,20b	0.58a	23.50c	6.38a	6.71a	32,30b
IAC 13	36,86b	31,87b	0.62a	26.13c	5.43b	4.41b	21,47c
IAC 14	33,15b	29,92b	0.58a	23.78c	5.84a	4.32b	23,05c
IAC 15	28,75b	19,35b	0.64a	19.39c	5.51b	3.93b	16,78c
Fibra	28,59b	20,67b	0.47b	18.58c	5.09b	5.8a	34,43b
UFLAF	36,60b	29,99b	0.36b	23.40c	5.27b	6.22a	64,72a
OURO do VALE	15,67b	9,20b	0.44b	18.61c	4.57b	4.08b	19,05c
Baiana	20,17b	15,70b	0.55a	22.19c	5.26b	3.40b	16,47c
Baianinha	35,97b	30,38b	0.57a	25.20c	5.02b	6.00a	25,97c
Mocotó	51,74a	44,72a	0.58a	22.42c	5.74a	7.66a	35,53b
UFLAE	36,73b	32,52b	0.51b	30.63b	5.18b	4.36b	34,81b
UFLAG	40,82b	36,70b	0.44b	29.27b	5.22b	5.25a	49,69a
UFLAH	66,96a	65,52a	0.53a	38.22a	6.06a	4.93b	57,79a
UFLAJ	29,35b	21,65b	0.42b	20.89c	4.83b	5.66a	39,44b

Means followed by the same letters did not differ from each other at 5% probability by the Scott - Knott test

on the farms, taking the farmers' preference for longer cycles or for two vegetative cycles into consideration (Vidigal Filho et al. 2000).

The harvest indices of the clones IAC 12, IAC 13, IAC 14, IAC 15, IAC 576-70, UFLA H, Baiana, and Baianinha were higher than of the other evaluated and exceeded 50%, a value considered satisfactory. According to studies carried out by Fukuda (1996), there is a positive correlation between the harvest index and root production. The harvest index should therefore be used complementary in the selection of cultivars. The harvest index expresses the percentage that represents the root weight compared with the total plant weight. Vidigal Filho et al. (2000) demonstrated that the superiority of cultivar Fécula Branca over the others was attributable to the higher harvest index and higher yield, as observed for clone UFLA H as well.

Clone UFLA H was also superior in terms of tuber root length (Table 1). The clones UFLA E and UFLA G were longer than the others, and only shorter than clone UFLA H. Although a greater root length is desirable as an essential yield component, one must take into account that this trait can be a drawback at harvest, making the harvest more labor-intensive and increasing chances of mechanical root damage.

The tuber root diameter was greatest in the clones IAC 12, UFLA H, IAC 14, IAC 576-70 and Mocotó (Table 1). The root number per plant was highest in the cultivars IAC 57670, IAC 12, Fibra, UFLA F, Baianinha,

**Table 2.** Clusters formed based on the Tocher optimization method, considering 15 accessions of cassava evaluated by seven agronomic traits

Groups	Clones
I	BAIANA, IAC 14, IAC 13, IAC 15, and IAC 12
II	UFLA E, UFLA G, BAIANINHA, UFLA J, FIBRA and MOCOTO
III	OURO do VALE
IV	UFLA F
V	IAC 57670
VI	UFLA H

Mocotó, UFLA G and UFLA J (always more than five). This performance did however not correspond to the root yield.

Regarding the aerial part, the yield of the clones UFLA F (64.72 t ha<sup>-1</sup>) UFLA H (57.79 Mg ha<sup>-1</sup>) and UFLA G (49.69 Mg ha<sup>-1</sup>) was similar and exceeded the other clones (Table 1).

To determine the divergence, the genetic distances between the clones were initially estimated by the Generalized Distances of Mahalanobis.

The maximal value of the amplitude of the distances between the accessions IAC 15 and UFLA H was 58.4384, which allows the conclusion, in genetic terms, that these clones are most divergent, while the accessions IAC 14 and Baiana were the most similar (minimal value of 3.3865).

These results indicate that the most divergent clones can be used in future crosses. It is worth highlighting that

the greatest distances of  $D^2$  between all possible combinations of each one of the clones under study were found among combinations of the accessions UFLA H and IAC 12, accounting together for 80% of the greatest distances obtained by the combinations.

According to Dias et al. (1997), previous knowledge on the pairs of parents of greatest divergence greatly facilitates the definition of the hybridization process, by making the choice of the most divergent pairs for the generation of more heterotic hybrids possible.

The grouping by the Tocher method formed six dissimilarity groups (Table 3). Group I was the largest, with the clones Baiana, IAC 14, IAC 13, IAC 15 and IAC 12; Group II contained clones UFLA E, UFLA G, Baianinha, UFLA J, Fibra and Mocotó and the groups III, IV, V and VI the clones Ouro do Vale, UFLA F, IAC 57670 and UFLA H, respectively.

The inter and intragroups distances are presented in Table 4. The similarity was greatest in Group I, with a mean distance between accessions of 9.09. Group II contained the most divergent clones, with a mean intragroup distance of 10.02. The other groups were formed by only one clone. The most divergent pairs with good agronomic traits are therefore the ones that should be used in crosses for hybrids.

On the other hand, information on the most similar pairs is useful in programs involving backcrosses, where the use of similar parents, differentiated basically by the allele to be transferred, makes the recovery of the recurrent parent possible.

In relation to the intergroup distances, it may be stated that the Groups I and VI (44.9944); III and IV (45.7308); III and VI (52.6679) were the most divergent. The intragroup were shorter than the intergroup distances, as presumed in the Tocher method (Cruz and Regazzi 2001).

For the establishment of the dendrogram by the

**Table 4.** Clusters formed by the Tocher optimization method, considering 15 cassava clones evaluated by 7 and 5 agronomic traits (I and Ia)

Groups	Clones
I	BAIANA, IAC 14, IAC 13, IAC 15, and IAC 12
Ia	IAC 57670, MOCOTÓ, IAC 13, BAIANINHA and FIBRA
II	UFLA E, UFLA G, BAIANINHA, UFLA J, FIBRA and MOCOTÓ
Iia	BAIANA, IAC 14, IAC 15 and IAC 12
III	OURO DO VALE
IIIa	UFLA E, UFLA G and UFLA J
IV	UFLA F
IVa	UFLA H
V	IAC 57670
Va	OURO
VI	UFLA H
VIa	UFLA F

nearest neighbor method, percentages of the distances between clones were represented on the x axis and the 15 clones on the y axis.

According to Cruz and Regazzi (2001), this method is subjective; the authors highlight the importance of using other methods due to this subjectivity.

Abrupt changes as well as the knowledge on the clones were considered in the dendrogram to define the groups.

A cut at about 55% distance resulted in the formation of six groups, which coincided with those formed by the Tocher method.

The clone distances were projected in a diagram to make a visualization of the results possible by converting the dissimilarity measures into scores related to the two variables X and Y. The results observed in Figure 2 did not agree with those obtained by the Tocher or by the nearest neighbor method. Four groups were formed and the distances projected on the plan: one

**Table 3.** Mean intra and intercluster distance of cassava accessions based on the Tocher clustering method, in an evaluation of seven agronomic traits

Clusters	I	II	III	IV	V	VI
I	<b>9.0967</b>	24.6607	35.2884	39.8110	24.0217	44.9944
II		<b>10.0232</b>	17.5465	20.001	22.8349	25.5424
III			-	45.7308	30.0201	52.6679
IV				-	42.9951	29.0199
V					-	22.7603
VI						-

Distances in bold represent mean intra-cluster distances and the others mean inter-cluster distances

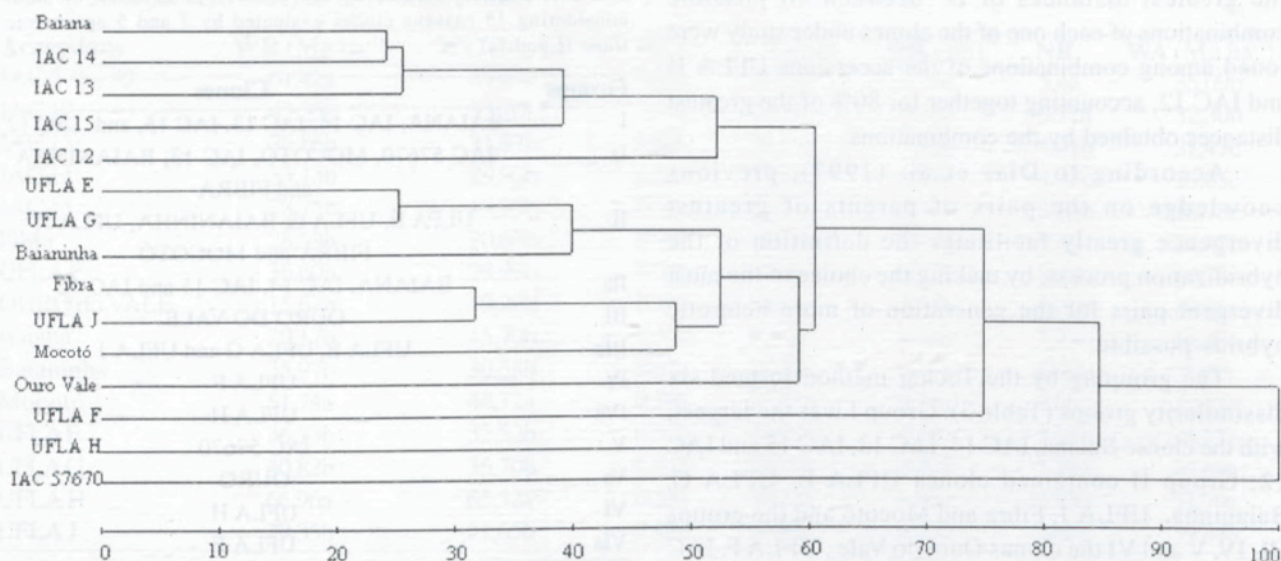


Figure 1. Dendrogram of genetic dissimilarity of 15 *Manihot esculenta* accessions, based on the nearest neighbor method, using seven agronomic traits

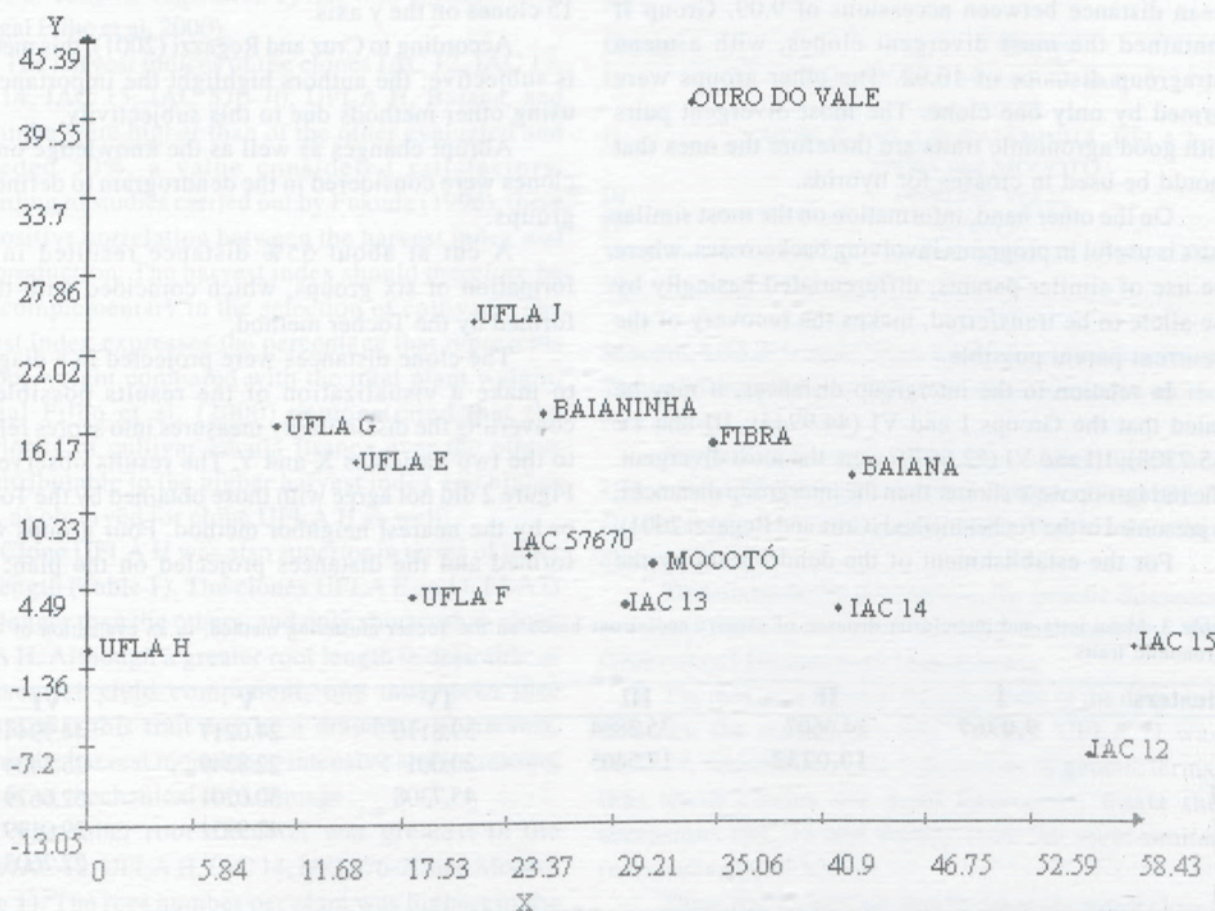


Figure 2. Projection of the distances of 15 cassava accessions

larger group, containing the clones Baiana, IAC 14, IAC 13, FLA E, UFLA G, Baianinha, UFLA J, UFLA F, IAC 57670, Fibra and Mocotó, one group formed by clones IAC 15 and IAC 12, and two other groups formed by the clones Ouro do Vale and UFLA H, respectively.

The traits that contributed most to the diversity were tuber root diameter (24.77%), total weight of the aerial part (24.36%), harvest index (14.01%) and weight and length of tuber roots (13.53 and 13.13%).

The grouping analysis by the Tocher method based on only these variables formed six groups, which were however not concordant with those formed considering all study traits (Table 4).

Group Ia was formed by clones Baianinha, Fibra,

Mocotó, IAC 57670 and IAC 13. Comparatively, the first three clones were grouped in the same group as in the previous clustering.

Group IIa was also formed by clones that coincided with the formation of the first clustering.

After discarding the variables that contributed least to the genetic diversity, three clones of very similar morphological and agronomical traits, UFLA E, UFLA G and UFLA J were grouped in group IIIa. The other groups IVa, Va and VIa were arranged in a new order, whereas the plants they contained were the same.

The dendrogram allowed the establishment of five groups that coincided with the plants representing each group by the Tocher method (Figure 3).

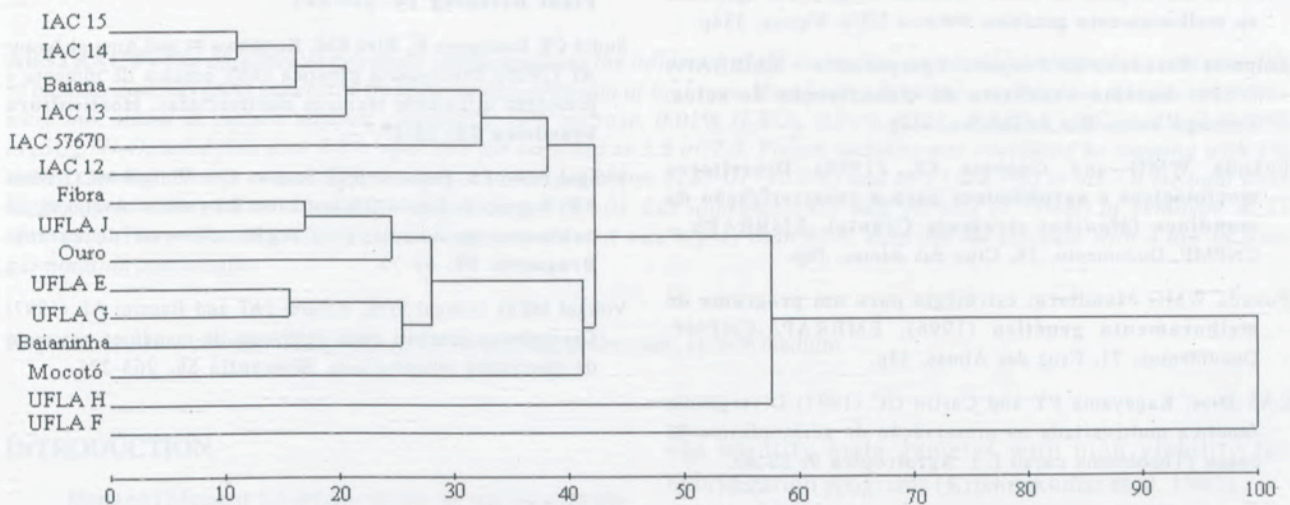


Figure 3. Dendrogram of genetic dissimilarity in 15 *Manihot esculenta* accessions, based on the nearest neighbor method, using five agronomic traits

## Aplicação de técnicas multivariadas na determinação da dissimilaridade genética entre clones de mandioca

**RESUMO** - Avaliou-se a dissimilaridade genética entre 15 clones de mandioca por meio de sete características morfo-agronômicas e da utilização de procedimentos multivariados, visando selecionar os mais divergentes e superiores para o direcionamento de hibridações futuras. O experimento foi conduzido em 2003/2005, em blocos ao acaso com três repetições. A partir da matriz de distância genética generalizada de Mahalanobis, os clones foram agrupados em função da sua similaridade, usando-se os algoritmos de Tocher e do Vizinho mais Próximo. Também se avaliou a importância relativa dos caracteres. As técnicas multivariadas foram concordantes no estudo da dissimilaridade genética e eficazes em agrupar clones com pequena distância genética. As características que mais contribuíram para a diversidade foram o peso total da parte aérea, o diâmetro, o peso e o comprimento de raízes tuberosas e o índice de colheita.

**Palavras-chave:** *Manihot esculenta*, técnicas multivariadas, distância de Mahalanobis.

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