BIOLOGIA PLANTARUM 46 (2): 217-222, 2003

# Phenetic relationship of rubber tree clones

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## Abstract

Twenty clones of the breeding population of *Hevea brasiliensis* were evaluated for phenetic diversity. The test-clones included six clones developed in Nigeria, ten Malaysian clones, two clones from Indonesia and a clone from each of Brazil and Sri Lanka. Data collected on fifteen seed characters in 1998 and 1999 were utilized for multivariate analysis. Cluster analysis of data matrix of clonal mean seed characters was conducted to produce principal component axes, dendrograms and Tocher's clusters in 1998, 1999 and the combined data. There was taxonomic isolation of the recent collection from Brazil (IAN 710) from the other clones that are either members or descendants of the Wickham collection of 1876. There was a continuum of phenetic diversity from the highly divergent to the closely related pairs of clones. The highly divergent clones are expected to produce heterotic progenies in crosses while crosses among clones with close phenetic similarity should be avoided. This will guide against inbreeding depression and genetic erosion.

*Additional key words*: *Hevea brasiliensis*, multivariate analysis, seed characters.

## Introduction

The domestication of *Hevea* started in the 19th century. *Hevea* is native to the Amazon basin in South America and the pioneering effort of its spread from the centre of origin was in 1876 by Sir Wickham. The Wickham collection was the main germplasm for genetic improvement of *H. brasiliensis* in south-east Asia and in Africa. To date, the Wickham germplasm and its descendants provide most of the parents-in-crosses for genetic improvement of *H. brasiliensis*.

However, there are signs of a reduction in the progress of yield improvement while there is incidence of 'new' diseases of *H. brasiliensis* (Verghese *et al.* 1994). This has given cause for concern about the phenetic diversity of *H. brasiliensis* available to farmers and for the purpose of genetic improvement. Presently, the breeding population of *H. brasiliensis* consists of selected primary clones of the Wickham collection and the 2 - 3 generations of crosses among members of the Wickham collection. Hence, the objectives of this study, which are to evaluate the phenetic relationship of clones of the breeding population of *H. brasiliensis* in Nigeria and provide a guide to continued use of the clones in crosses.

## Materials and methods

**Plants:** Twenty clones that constitute *Hevea brasiliensis* (H.K.B.) Muell. Arg. breeding population in Nigeria were evaluated at the Rubber Research Institute of Nigeria (RRIN), Benin City. The test-clones included six RRIN developed clones (NIG 800 to NIG 804 and NIG 810), ten Malaysian clones (RRIM 501, RRIM 513, RRIM 600, RRIM 614, RRIM 623, RRIM 628, RRIM 707, PB 5/51, PB 217 and GT 1), two clones (PR 107 and TJIR 1) from Indonesia, IAN 710 from Brazil and RRIC 45 from Sri Lanka. The clones were planted in 1983 and evaluated for fifteen seed/pollination characters in 1998 and 1999. There were thirty trees per clone.

**Data collection:** In each year, hand pollination by selfing was carried out, as described by Onokpise (1976), in each clone in March by introducing pollen grains of a male flower to the stigma of a flower that is borne on the same inflorescence as the male flower. In order to exclude

*Received* 7 May 2001, *accepted* 27 March 2002.
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foreign pollen, the tip of the petal column, housing the stigma, was covered by cotton wool and held in place by sticky latex. Data were subsequently collected and recorded as percentage fruit set, pod maturity and seed germination. Percentage pod maturity was calculated as proportion of flowers pollinated and proportion of fruit set. At pod maturity, pods were harvested and seeds were removed from the pods. A sample of one hundred seeds was randomly obtained for each clone and evaluated for seed length, width, mass, volume, kernel mass, shell mass, mass ratios of seed/kernel, seed/shell and kernel/shell, and ratios of seed length/width, mass/volume. Seed length and width were taken using vernier callipers. Seed volume was recorded as the volume of water displaced in a measuring cylinder.

**Data analysis:** Multivariate analysis was conducted on the separate data sets of clonal means obtained in 1998, 1999 and combined data using *SPSS 7.5 for Windows* statistical software. There was cluster analysis with ordination of test-clones on principal component axes (PCA), dendrograms and Tocher's method (Singh and Chaudhaury 1977, Matus *et al.* 1999).

## Results

Principal component axes 1 (PCA 1) had relatively high contribution to variation with 34.83, 95.34 and 96.93 % variance in 1998, 1999 and combined data respectively (Table 1). PCA 2 had significant contribution to variation at 24.71 % variance in 1998 (Table 1) and only seed characters were of phenetic value (Table 2). The characters that were closely associated with the variation due to the significant PCA in 1998, 1999 and combined data were seed mass, seed volume and kernel mass (Table 2). Among the six basic characters, seed mass, volume and kernel mass had relatively high standard error (Table 2). The ratio of seed mass/volume was of phenetic importance in 1998 and combined data while seed length, shell mass and mass ratios of seed/kernel, seed/shell and kernel/shell had relatively high phenetic value in 1998 (Table 2).

Following the ordination of the twenty *Hevea* clones on principal components 1 and 2, there were six clusters in 1998 (Fig. 1, Table 3), five clusters in 1999 (Fig. 2, Table 3) and four clusters in combined data (Fig. 3, Table 3). The ordination of the test – clones on PCA 1 and 3 in 1998, produced seven clusters (Fig. 1, Table 3). There was consistent close clustering of GT 1 and

Table 1. Percent variance (PV) and cumulative variance (CV) [%] of the first five principal component axes (PCA) of seed characters of *Hevea* in 1998, 1999 and combined data (* - PCA account for > 20 % of total variance).

| PCA | 1998 | | 1999 | | Combined data | |
|---|---|---|---|---|---|---|
| | PV | CV | PV | CV | PV | CV |
| 1 | 34.83* | 34.83 | 95.34* | 95.34 | 96.93* | 96.93 |
| 2 | 24.71* | 59.54 | 2.96 | 98.30 | 2.43 | 99.36 |
| 3 | 13.19 | 72.73 | 1.12 | 99.42 | 0.35 | 99.71 |
| 4 | 9.17 | 81.90 | 0.55 | 99.97 | 0.24 | 99.95 |
| 5 | 6.86 | 88.76 | 0.02 | 99.99 | 0.03 | 99.98 |

Table 2. Component score coefficient of the descriptors in each of the significant principal component axes (PCA) and standard error of the mean of seed characters of *Hevea* in 1998, 1999 and combined data (* - characters with component score deviation ≥ 0.15).

| Descriptors | Component score coefficient | | | | Standard errors | | |
|---|---|---|---|---|---|---|---|
| | 1998 (PCA1) | 1998 (PCA2) | 1999 (PCA1) | combined (PCA1) | 1998 | 1999 | combined |
| Seed length [cm] | 0.077 | -0.195* | 0.111 | 0.048 | 0.03 | 0.02 | 0.02 |
| Seed width [cm] | 0.100 | -0.129 | 0.086 | 0.059 | 0.02 | 0.02 | 0.02 |
| Seed mass [g] | 0.156* | -0.140 | 0.157* | 0.204* | 0.11 | 0.12 | 0.09 |
| Seed volume [$cm^3$] | 0.170* | -0.054 | 0.148* | 0.184* | 0.11 | 0.12 | 0.08 |
| Kernel mass [g] | 0.080 | 0.232* | 0.151* | 0.183* | 0.11 | 0.07 | 0.06 |
| Shell mass [g] | 0.174* | 0.005 | 0.095 | 0.135 | 0.10 | 0.08 | 0.07 |
| Seed length/width | 0.016 | -0.114 | 0.060 | -0.007 | 0.01 | 0.01 | 0.01 |
| Seed/kernel mass | -0.023 | -0.221* | -0.110 | -0.124 | 0.46 | 2.00 | 0.01 |
| Seed/shell mass | -0.148* | 0.093 | 0.100 | -0.040 | 1.03 | 0.15 | 0.55 |
| Kernel/shell mass | -0.149* | 0.096 | 0.138 | -0.026 | 1.02 | 0.06 | 0.54 |
| Seed mass/volume | 0.112 | 0.199* | 0.100 | 0.191* | 0.03 | 0.03 | 0.02 |
| Fruit set [%] | 0.088 | 0.042 | -0.067 | -0.074 | 0.08 | 0.05 | 0.05 |
| Matured pods [% of flowers] | 0.129 | 0.017 | -0.059 | -0.110 | 0.07 | 0.06 | 0.07 |
| Matured pods [% of fruit set] | 0.058 | -0.119 | -0.039 | -0.077 | 0.09 | 0.06 | 0.04 |
| Seed germination [%] | -0.010 | 0.055 | - | - | 0.08 | - | - |

Table 3. Clusters of twenty *Hevea* clones using principal component axes, dendrograms and Tocher's method.

| Clone | PCA1×PCA2 1998 | PCA1×PCA3 1998 | PCA1×PCA2 1999 | PCA1×PCA2 combined | Dendrogram 1998 | Dendrogram 1999 | Dendrogram combined | Tocher method 1998 | Tocher method 1999 | Tocher method combined |
|---|---|---|---|---|---|---|---|---|---|---|
| GT 1 | 5 | 5 | 2 | 1 | 1 | 3 | 1 | 1 | 5 | 1 |
| PB 5/51 | 5 | 6 | 3 | 1 | 1 | 2 | 1 | 6 | 3 | 5 |
| RRIM 501 | 5 | 4 | 4 | 2 | 1 | 2 | 2 | 7 | 3 | 2 |
| RRIM 623 | 5 | 4 | 2 | 1 | 1 | 3 | 1 | 1 | 4 | 1 |
| RRIM 707 | 4 | 7 | 1 | 3 | 4 | 1 | 3 | 4 | 1 | 3 |
| RRIM 600 | 5 | 6 | 3 | 4 | 1 | 2 | 3 | 5 | 2 | 3 |
| TJIR 1 | 5 | 5 | 1 | 2 | 1 | 2 | 2 | 1 | 3 | 2 |
| PR 107 | 4 | 7 | 3 | 2 | 4 | 2 | 2 | 3 | 3 | 2 |
| RRIM 628 | 5 | 4 | - | - | 1 | - | - | 1 | - | - |
| RRIC 45 | 3 | 5 | 1 | 2 | 1 | 1 | 2 | 1 | 1 | 4 |
| NIG 801 | 2 | 6 | 1 | 3 | 2 | 1 | 3 | 2 | 1 | 4 |
| RRIM 614 | 1 | 4 | 4 | 3 | 2 | 1 | 3 | 8 | 6 | 3 |
| IAN 710 | 6 | 3 | 5 | 2 | 5 | 4 | 2 | 1 | 7 | 2 |
| NIG 800 | 2 | 5 | 3 | 1 | 2 | 2 | 1 | 2 | 2 | 1 |
| PB 217 | 3 | 5 | 3 | 2 | 1 | 2 | 2 | 1 | 1 | 2 |
| NIG 810 | 2 | 1 | - | - | 3 | - | - | 1 | - | - |
| NIG 802 | 2 | 4 | 2 | 2 | 2 | 3 | 2 | 9 | 5 | 4 |
| NIG 804 | 2 | 2 | 2 | 1 | 2 | 3 | 1 | 1 | 2 | 1 |
| NIG 803 | 2 | 5 | 3 | 3 | 2 | 2 | 3 | 1 | 2 | 3 |
| RRIM 513 | - | - | 2 | - | - | 3 | - | - | 4 | - |

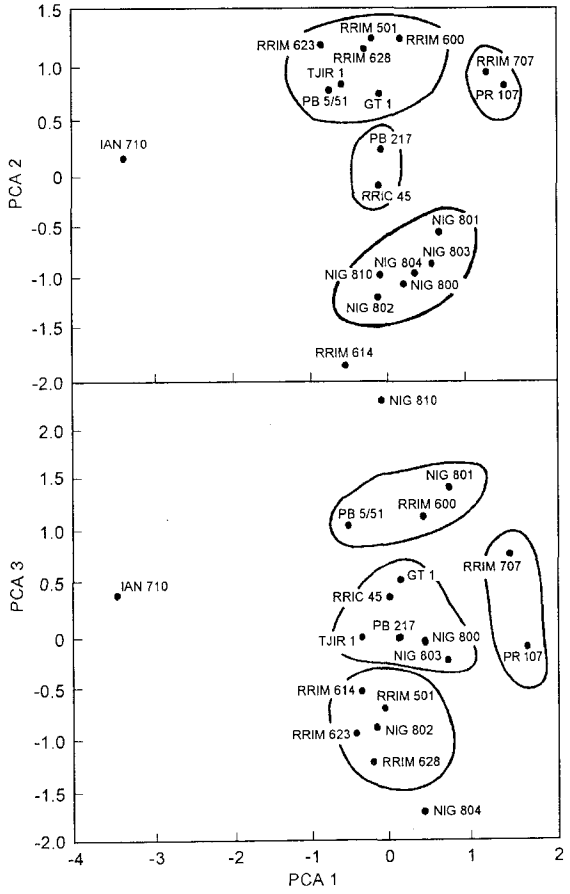


Fig. 1. The ordination of 19 *Hevea* clones on principal component axis (PCA) 1 and each of PCA 2, PCA 3 from cluster analysis of 1998 data.

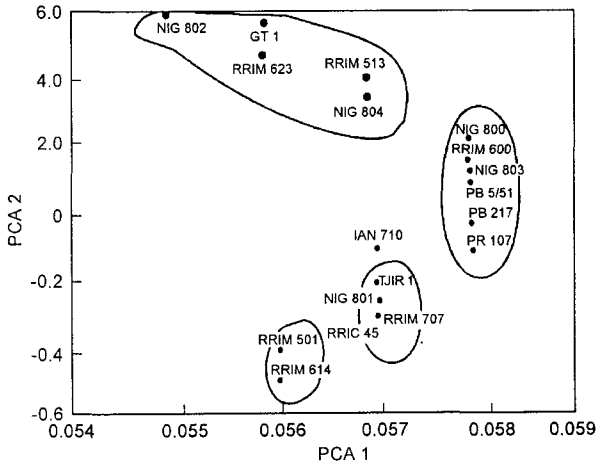


Fig. 2. The ordination of 18 *Hevea* clones on principal component axis (PCA) 1 and 2 from cluster analysis of 1999 data.

RRIM 623, TJIR 1 and RRIC 45 in 1998, 1999 and combined data (Table 3). Also, there was consistent divergence of fifty bi-clonal combinations (Table 4). Among these, RRIM 707, RRIM 614 and IAN 710 exhibited phenetic divergence from ten other clones and NIG 804 was divergent from nine clones (Table 4).

Based on the dendrograms, there were five, four and three clusters in 1998, 1999 and combined data respectively (Figs. 4, 5, 6, Table 3). There was phenetic similarity of GT 1 with RRIM 623; RRIM 501 with TJIR 1 and PB 217; NIG 801 with RRIM 614 (Table 3). Phenetic divergence of forty-three bi-clonal combinations was obtained (Table 4). IAN 710 was divergent from ten

clones while RRIM 707, NIG 801, RRIM 614 and NIG 804 were each divergent from eight clones (Table 4).

In the Tocher's clustering method, there were nine, seven and five clusters in 1998, 1999 and combined data respectively. There was no consistent similarity of clones across 1998, 1999 and combined data (Table 3). There were eighty divergent pairs of clonal combinations with divergence of NIG 802 from fifteen clones, PB 5/51 and RRIM 614 from thirteen clones and NIG 801 from twelve clones (Table 4).

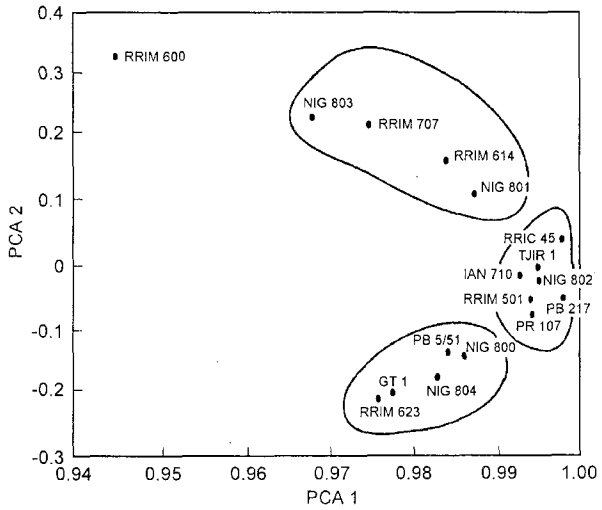


Fig. 3. The ordination of 17 *Hevea* clones on principal component axis (PCA) 1 and 2 from cluster analysis of combined data.

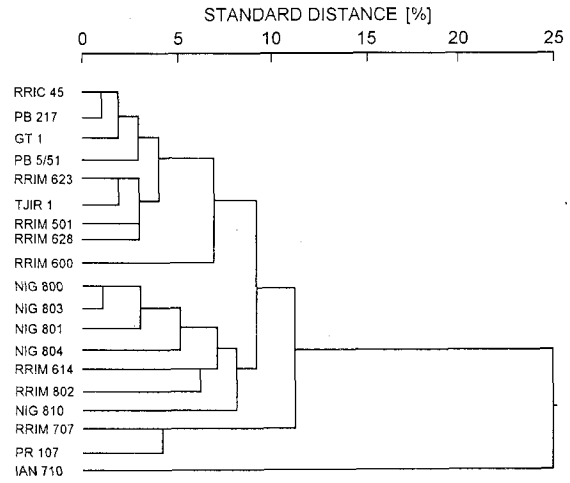


Fig. 4. Dendrogram of 19 *Hevea* clones from cluster analysis of seed characters in 1998.

Considering the three clustering methods, there was phenetic similarity between GT 1 and RRIM 623, TJIR 1 and RRIC 45 and among RRIM 501, TJIR 1 and PB 217 (Table 4). Phenetic divergence across the three clustering methods was an indication of high phenetic divergence of bi-clonal combinations. In this case, maximum divergence was exhibited by RRIM 707, RRIM 614 and IAN 710 whereby each clone was divergent from six clones. NIG 801, PB 5/51 and PR 107 were divergent from five, four and three clones respectively (Table 4). RRIM 501, NIG 802 and NIG 804 were each divergent from three clones, GT 1 and NIG 800 were each divergent from two clones, RRIM 623, TJIR 1 and PB 217 were divergent from a clone each (Table 4). With divergence of pairs of clones in any two clustering methods, there was medium divergence. Examples of such clonal combinations are: GT 1 from RRIM 707, PR 107 and IAN 710, PB 5/51 from NIG 801, *etc.*

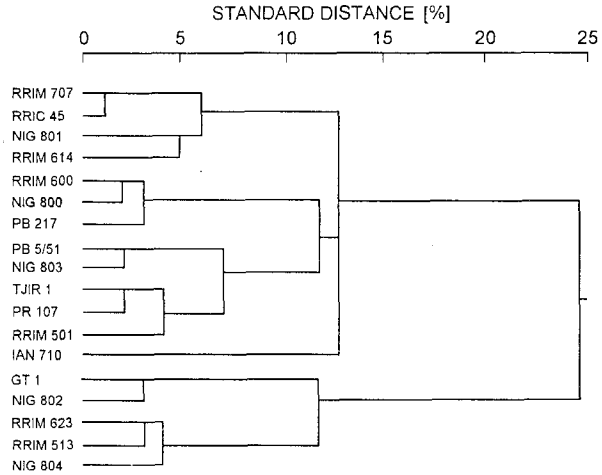


Fig. 5. Dendrogram of 18 *Hevea* clones from cluster analysis of seed characters in 1999.

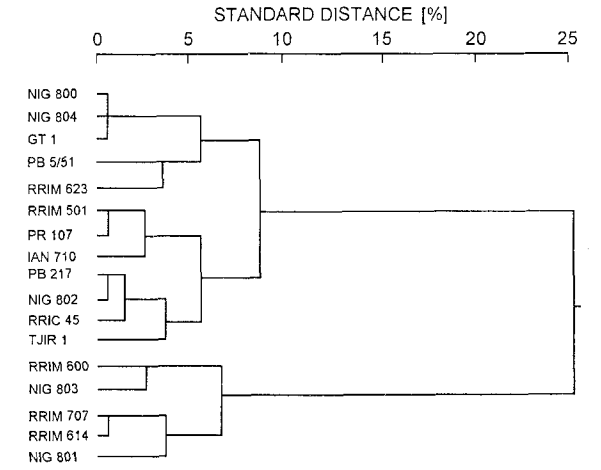


Fig. 6. Dendrogram of 17 *Hevea* clones from cluster analysis of seed characters in combined data.

Table 4. Phenetic divergence (x) and similarity (√) of *Hevea* clones based on principal component axes (P), dendrograms (D) and Tocher's (T) method.

| Clone | | PB 5/51 | RRIM 501 | RRIM 623 | RRIM 707 | RRIM 600 | TJIR 1 | PR 107 | RRIC 45 | NIG 801 | RRIM 614 | IAN 710 | NIG 800 | PB 217 | NIG 802 | NIG 804 | NIG 803 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GT 1 | P | = | = | √ | x | = | ≈ | x | = | x | x | x | = | ≈ | = | = | = |
| | D | = | = | √ | ≈ | = | ≈ | = | = | x | x | x | = | = | = | = | x |
| | T | x | x | = | x | x | ≈ | x | = | x | x | = | = | = | x | = | ≈ |
| PB 5/51 | P | | = | = | x | = | ≈ | x | = | = | x | x | = | = | x | = | = |
| | D | | ≈ | = | x | = | ≈ | = | = | x | x | x | = | = | x | = | = |
| | T | | = | x | x | x | ≈ | = | x | x | x | x | x | x | x | x | x |
| RRIM 501 | P | | | = | x | = | = | = | = | x | = | = | x | = | = | x | x |
| | D | | | = | x | = | √ | = | = | x | x | = | = | √ | = | x | = |
| | T | | | x | x | x | ≈ | = | x | x | x | = | x | = | x | x | x |
| RRIM 623 | P | | | | x | = | ≈ | x | x | x | = | x | = | x | = | = | x |
| | D | | | | = | = | ≈ | = | = | x | x | x | = | = | = | = | x |
| | T | | | | x | x | ≈ | x | = | x | x | = | = | = | x | = | = |
| RRIM 707 | P | | | | | x | ≈ | = | = | = | = | x | x | x | x | x | = |
| | D | | | | | = | x | = | = | = | = | x | x | x | x | x | = |
| | T | | | | | = | x | x | = | = | = | x | x | = | x | x | = |
| RRIM 600 | P | | | | | | ≈ | = | x | = | x | x | = | = | x | x | = |
| | D | | | | | | ≈ | = | = | = | = | x | = | = | x | x | = |
| | T | | | | | | x | x | x | x | = | x | = | x | x | = | = |
| TJIR 1 | P | | | | | | | = | √ | = | x | = | = | = | = | x | = |
| | D | | | | | | | = | = | x | x | = | = | √ | = | x | = |
| | T | | | | | | | = | = | x | x | = | x | = | x | = | = |
| PR 107 | P | | | | | | | | = | x | x | = | = | = | = | x | = |
| | D | | | | | | | | = | x | x | = | = | = | = | x | = |
| | T | | | | | | | | x | x | x | = | x | = | x | x | x |
| RRIC 45 | P | | | | | | | | | = | x | = | = | = | = | x | = |
| | D | | | | | | | | | = | = | = | x | = | = | x | x |
| | T | | | | | | | | | = | x | = | x | = | x | = | = |
| NIG 801 | P | | | | | | | | | | = | x | = | x | = | = | = |
| | D | | | | | | | | | | √ | x | = | x | = | = | = |
| | T | | | | | | | | | | x | x | x | = | = | x | x |
| RRIM 614 | P | | | | | | | | | | | x | x | x | = | x | = |
| | D | | | | | | | | | | | x | = | x | = | = | = |
| | T | | | | | | | | | | | x | x | x | x | x | = |
| IAN 710 | P | | | | | | | | | | | | x | = | = | x | x |
| | D | | | | | | | | | | | | x | = | = | x | x |
| | T | | | | | | | | | | | | x | = | x | = | = |
| NIG 800 | P | | | | | | | | | | | | | = | = | = | = |
| | D | | | | | | | | | | | | | = | = | = | = |
| | T | | | | | | | | | | | | | x | x | = | = |
| PB 217 | P | | | | | | | | | | | | | | = | x | = |
| | D | | | | | | | | | | | | | | = | x | = |
| | T | | | | | | | | | | | | | | x | = | = |
| NIG 802 | P | | | | | | | | | | | | | | | = | = |
| | D | | | | | | | | | | | | | | | = | = |
| | T | | | | | | | | | | | | | | | x | x |

## Discussion

Morphological features have been used in taxonomic studies in *Allium sativum* (Matus *et al.* 1999), *Hevea brasiliensis* (Alika 1991), *Dioscorea* species (Cruz 1999) and several other crop species (Singh *et al.* 1998, Wahi and Kher 1991). In *Hevea brasiliensis,* similarity in phenetic relationship of clones based on morphological features and enzyme analysis has been reported (Chevallier 1988, Omokhafe 1991). The use of selfed seeds, in this study, eliminates bias often associated with inconsistent cross-compatibility as reported by Onokpise (1976).

The taxonomic importance of seed mass, seed volume and kernel mass in this study is in agreement with previous report of Alika (1991). Fortunately, seed and

kernel masses are also important economic characters in terms of seed utilisation (Patil 1990). The taxonomic importance of these characters is therefore, not at the expense of their economic importance.

The taxonomic isolation of IAN 710 (which is a recent collection from Brazil) from other clones of the Wickham collection is evidence of the genetic differentiation of the Wickham collection. This is expected as the Wickham collection has gone through natural and artificial selection as migrant population in Africa and Asia for more than a century. This feature has also been reported in *Pennisetum* (Balma *et al.* 1996). The taxonomic isolation of IAN 710 implies that it can serve as a good general combining parent for development of vigorous and high latex yielding clones.

A comparison of the heterotic effects of *Hevea* clones in crosses and phenetic divergence revealed a positive relationship between phenetic divergence and heterosis for latex yield (Alika 1982, Omokhafe and Ugwa 1997). In this regard, clones that manifest a wide disparity of phenetic divergence will produce off-springs whose mean performance will be higher than the parental means. Among the highly divergent clones, as obtained in this study, are RRIM 707 and each of PB 5/51, RRIM 501, IAN 710, NIG 800, NIG 802 and NIG 804, RRIM 614 and each of GT 1, PB 5/51, TJIR 1, PR 107, IAN 710 and PB 217, IAN 710 and each of PB 5/51, RRIM 600, NIG 800 and NIG 801. The clones of medium phenetic divergence are likewise, expected to produce heterotic progenies.

Clones of close phenetic similarity will be avoided in crosses to guide against inbreeding depression. In this regard, crosses between GT 1 and RRIM 623, TJIR 1 and RRIC 45 and crosses among RRIM 501, TJIR 1 and PB 217 should be avoided. The phenetic similarity of TJIR 1 and RRIC 45 provided evidence of filial relationship between the clones. RRIC 45 is a progeny of RRIC 8 × TJIR 1 (RRIN 1968) and RRIC 45 was found to be phenetically close to TJIR 1. This relationship suggests that where it is not possible to determine phenetic relationship prior to use of clones in crosses, the knowledge of the lineage of the clones can serve as a guide.

Among the three clustering techniques (principal component axes, dendrograms and Tocher's method), the Tocher's method followed the scattering principle as it had no evidence of phenetic similarity. This is a feature of the Tocher's method and a similar observation was reported in *Gherbera* and *Dahlia* species by Wahi and Kher (1991).

In conclusion, there is evidence of phenetic diversity of clones of the *Hevea* breeding population in Nigeria. For effective utilization of the available diversity, the crosses among the highly divergent clones is recommended while crosses among closely related clones should be avoided.

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