A NEW EVALUATION SCHEME FOR CASSAVA BREEDING AT CIAT

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ABSTRACT

One of the most important questions to be answered in plant breeding relates to the parents to be used in the generation of new germplasm. This is particularly true for cassava, given the time required to evaluate segregating progenies and the large genetic variation generated with each cross due to the highly heterozygous nature of the crop. In the past, cassava breeding at CIAT focused on properly identifying the best clones, from large, segregating progenies. However, the process was not designed to take advantage of all the potential information that could be generated. Significant steps have recently been taken at CIAT to modify the evaluation scheme, particularly during the first clonal evaluation stage, with the following objectives: a) obtain information that allows an approximation to the general combining ability of progenitors; b) shorten the length of the evaluation process; c) improve the probabilities of identifying superior germplasm; and d) detect new potential traits that can be incorporated into the selection criteria. The modifications have been implemented and improved during the past three years. The new breeding scheme has already produced important benefits. Parents are currently selected based on the quality of progenies they produce. Leaf retention at five month of age and in the absence of biotic or abiotic stresses, has proven to have a large effect on root yield. The evaluation cycle has been shortened by 16 months, and it is expected that the new scheme is more efficient in identifying superior germplasm.

INTRODUCTION

Cassava germplasm development at CIAT is centered on the development of improved gene pools for specific edapho-climatic zones with importance for cassava production. The most relevant ecosystems are the semi-arid and sub-humid tropics, for which the majority of efforts are devoted. The main selection activity is conducted in sites selected to represent the conditions of the target ecosystem. For each zone, a recurrent selection program with a progressive set of stages is followed. As the stages progress, more emphasis is given to traits of lower heritability, because more planting material for each genotype is available, and the evaluation can be conducted in bigger plots with replications. Certain selection criteria are of general importance across ecosystems (i.e. yield potential, dry matter content), while others are specific for each ecosystem (i.e. specific pests and/or diseases).

The traditional evaluation and selection procedure has a few important drawbacks: a) breeding cycles were long; b) no data was taken at the early stages to allow estimates of general combining ability effects of the progenitors employed; and c) it took several steps in the selection process until replicated evaluations could be performed. Cassava has unique opportunities to increase its relevance in tropical agriculture and agro-industries. To take advantage of these opportunities a more dynamic and efficient breeding scheme is required to meet the new demands on this crop. This article describes the modifications introduced into the cassava breeding scheme at CIAT and some of the initial observations made upon their implementation.

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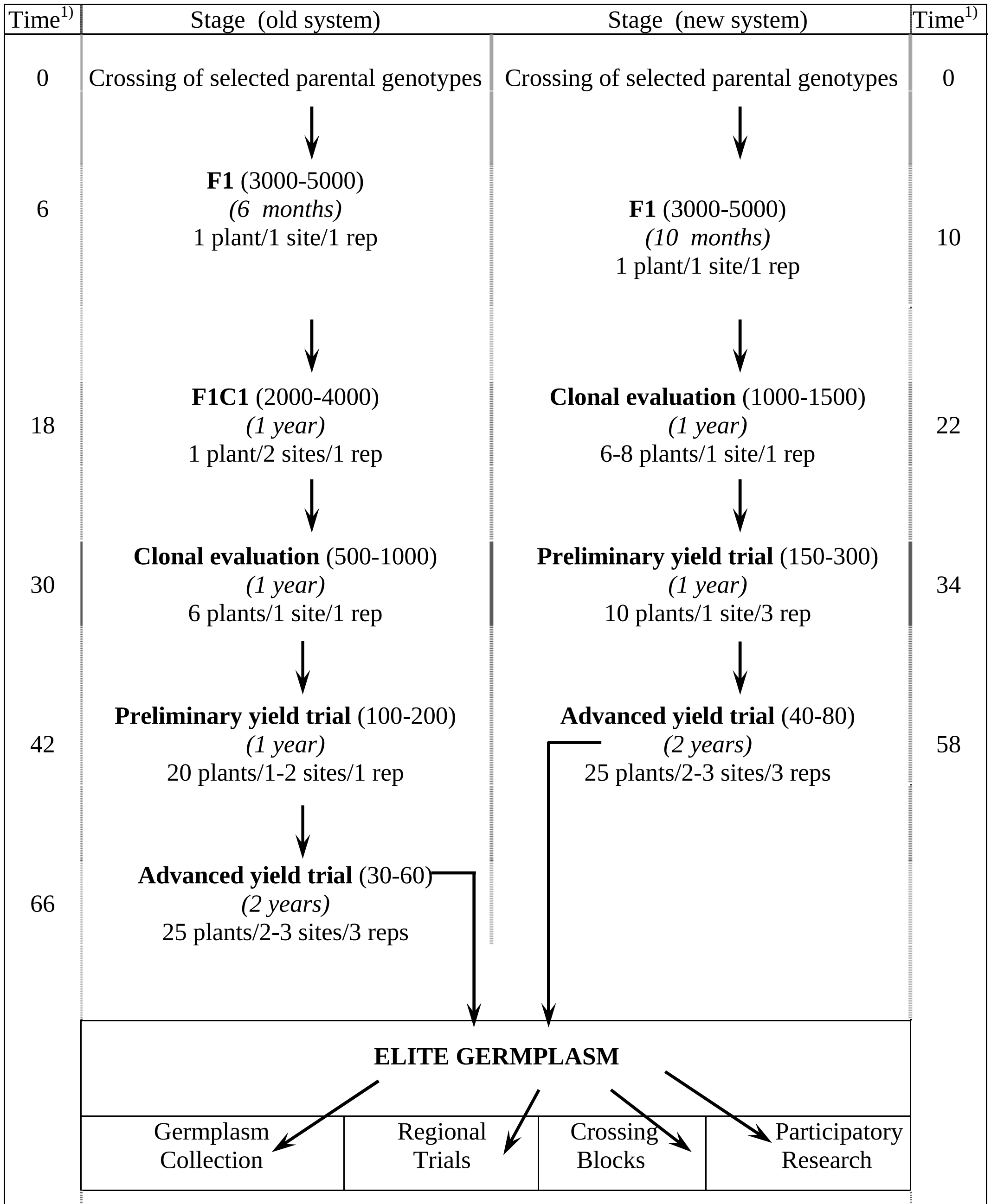
MATERIALS AND METHODS

1. Modifications in the evaluation scheme

Traditionally in CIAT headquartes at Palmira, the progenies generated from the crossing blocks (*F1*) were planted in screenhouses and the seedlings transplanted to the field after two months **(Figure 1).** At six months after planting, two stakes were harvested from each plant and given a consecutive number according to the plant. One of the stakes was planted at CIAT-Palmira, the other was planted at the main selection site (*F1C1*). Selection was conducted at harvest on individual plants at the main selection site. Planting material taken from the selected genotypes, but using the replicated source at CIAT-Palmira, was used subsequently to establish a non-replicated, 6-plant plot, at the main selection site (*Clonal Evaluation*). Evaluation was done using three central plants. The remaining three plants were used as source of planting material which now started to originate at the selection site. The following stage (*Preliminary Yield Trial)* was planted in non-replicated 20-plant plots. Evaluation was done on the central six plants, and the remaining 14 outside plants were left as source of stakes. Selected genotypes were then passed to the *Advanced Yield Trials* at one or two sites, with three replications of 25-plant plots. Genotypes selected over 2 consecutive years at the *Advanced Yield Trial* level were considered as "*elite genotypes*" and incorporated in the germplasm collection and the crossing blocks. Since each year a new breeding cycle was initiated, all the stages were simultaneously being conducted in each site **(Figure 1)**.

Some modifications to the traditional scheme have now been introduced. A major constraint of the traditional evaluation methodology was that the first three stages of selection (*F1C1*, *Clonal Evaluation,* and *Preliminary Yield Trial*) were based on non-replicated plots. In addition, large amounts of material was maintained at headquarters just to have duplicates of the very few materials that would eventually reach the status of *"elite genotype"* in each selection cycle. The changes introduced will speed up the selection process, allow for the evaluation of larger number of progenies and, hopefully, will increase the efficiency of the selection process. The main changes are as follows:

1) The *F1* plants are grown for ten months rather than six. At that age they produce up to 8-10 stakes. The stakes are then sent to the proper evaluation site for the *Clonal Evaluation*. This implies that the *F1C1* stage is eliminated and that no duplicate of each genotype is maintained at CIAT headquarters.
2) The *Clonal Evaluations* are based on up to eight plants, rather than six as before. An important modification for the sub-humid environment is that most measurements in the *Clonal Evaluation* are carried out in two stages: at the normal harvest time only two plants are harvested to measure % of dry matter in the roots. This trait varies considerably with the time of harvest and age of the plant. Therefore, to estimate it correctly, the plants need to be harvested at the proper time. The remaining six plants of each plot are harvested just prior to normal planting time (one week before) and yield potential is measured again. A few other traits are also measured or estimated (using visual scores): plant architecture, foliar health (for insects and diseases separately), above-ground biomass (for measuring harvest index), and root aspect. A



[1)]Time in months after germination of botanical seed.

Figure 1. Basic cassava breeding schemes applied for each of the priority ecosystems. On the right is the new scheme currently under implementation. Later stages of selection are made following the old system.

selection index was used to make an efficient and fast selection of the approximately 1000-2000 genotypes evaluated at this stage, for each ecosystem.

3) The changes described above allows taking stakes from no less than six plants (except for those cases where stakes did not germinate or plants died), rather than three, as in the past. For eco-regions different from the sub-humid environment, only one harvesting is carried out using all the available plants (seven).

The six plants harvested at the second harvest time, produced no less than 30 cuttings, which were used for the first replicated trial based on three replications and two row plots with ten plants per plot. It is recognized that this evaluation results in some competition effect among neighboring plots. However, it is hoped that the number of replications will neutralize most of these effects. Also, row spacing between plots was increased and the plant to plant distance within the plot reduced. This maintained the density unchanged, while favoring competition among plants from the same genotype.

4) A final important modification to the evaluation process is that data was taken and analyzed for all the progenies evaluated. In the past, data was taken only for those families that went beyond the *Clonal Evaluation* stage. Therefore it was difficult to estimate *combining ability effects* of parental materials, because most of the crosses did not produce balanced data (many progenies had been discarded in the field before any data was taken). The changes introduced allows us to base the selection of the parental materials on its breeding value (related to *general combining ability*) rather that its performance *per se*, or empirical appreciation of their potential as progenitor.

2. Description of the selection index used to facilitate the selection process

A selection index (**SI**) is just a way to simplify the selection process. Once all data from an evaluation is taken and downloaded into a computer file, the **SI** summarizes all the relevant information in a single number. The data set can then be ranked from the highest **SI** to the lowest. In this way, the best germplasm concentrate in the top of the file. Having the best materials grouped together facilitates the analysis of each individual genotype for a final selection. It should be emphasized that **SI** does not provide any new information and does not improve the quality of the data either. So, cassava breeding remains hard work and a demanding activity in the field. What the **SI** does is to facilitate the analysis of the data obtained.

The **SI** integrates, in a single number, the information from several variables that the breeder renders as important. Generally, three to five variables are included. Too many variables in the **SI** should be avoided, because the progress for each individual trait decreases when the simultaneous improvement of numerous traits is expected. So, the first element that defines the **SI** is the variables to be included:

$$\mathbf{SI_{.}: X_{1.} + X_{2.} + X_{3.} + \ldots + X_{n.}}$$

where $\mathbf{X_{1.}}$ refers to the first variable in the **SI** (for example fresh root yield), $\mathbf{X_{2.}}$ refers to the second variable (for example dry matter content), and so on. For each case, there is a dot as a reminder that each genotype has its own **SI** value.

The procedure to define a **SI** requires some weights for each variable to be included (Baker, 1986). Some variables are more important than others: the higher the relevance of the variable, the higher the weight it will have in the index. The relative importance of each variable depends on each breeder's criteria. The **SI** used at CIAT in Colombia does not necessarily have to be used by other cassava breeders. A particular **SI** can be defined for each region, particular end use, or breeder's preferences and/or priorities.

A second element in the **SI** is the relative weight that each variable will have in the **SI**. There are numerous criteria to define weights (Baker, 1986). In some cases an economic value for each trait is used. In other cases the heritability of the trait contributes to the definition of its weight in the **SI**. Furthermore, genetic correlations among variables can also be considered. In the example below, a weight based on the breeder's judgement is used. It is assume that the simplicity of the proposed method, although not scientifically precise or sophisticated, is very appealing. The formula for the **SI**, therefore, evolves to be as follows:

$$\mathbf{SI_{.}: (X_{1.} \times W_1) + (X_{2.} \times W_2) + (X_{3.} \times W_3) + \ldots + (X_{n.} \times W_n)}$$

Where $\mathbf{W_1}$, $\mathbf{W_2}$, $\mathbf{W_3}$, … $\mathbf{W_n}$ are the respective weights for each variable.

The **SI**, as developed, is already complete. There is, however, an additional point to explain before applying the procedure. In the last equation, it should be clear, **SI** is a linear function of the **n** variables included in the formula. One problem that this **SI** presents is the issue of units. Different variables are measured in different units: fresh root yield will be around **30** t/ha, number of commercial roots may be around **6** per plant, and harvest index is around **0.60**. The fact that each variable is measured in different units, with large differences in their magnitude creates a problem because those variables measured in higher magnitude would have a higher weight in the definition of the **SI**. This problem can be solved if the variables are standardized, using the classical statistical formula (Steel and Torrie, 1960):

$$\mathbf{X_{i.}' = (X_{i.} - \mu) / St. Dev.}$$

where $\mathbf{X_{i.}'}$ is the standardized value, $\mathbf{X_{i.}}$ is the original value, μ is the mean of the population, and **St. Dev.** is the standard deviation for the variable analyzed. The standardization procedure changes the units of a given variable (t/ha, %, etc.) into units of standard deviation. After the variables are standarized they should have a mean of zero and a standard deviation of one.

After the **SIs** are calculated, the results are analyzed and eventually some adjustment on the weights are made. In other words, the results of a given **SI** may give too much emphasis to dry matter content and not enough to plant type, for example. So the analysis is a dynamic process involving a few iterations until the desirable results are obtained. The selection index used at CIAT for the sub-humid environment is:

SI = (FRY x 10) + (DMC x 8) - (PTS x 5) + (HI x 5)

where **FRY** means Fresh Root Yield, **DMC** is Dry Matter Content, **PTS** stands for Plant Type Score, and **HI** represents Harvest Index. The weights used for each variable were 10, 8, 5, and 5, respectively. These weights are the result of a subjective process by the breeder. As said above, each breeding program will have its own weights, addressing its own priorities.

It should be clarified why in the formula, the value for **PTS** (plant type score) is negative. The reason is simple: the best plant type is rated 1, and the worst is rated as 5. In this case, the index should “reduce the expression” of the variable, because the best material are those with a low score. By utilizing the negative sign the formula will automatically give preference to those materials having negative standardized values, which are those with a low score.

Once the **SI** value for each genotype has been obtained the entire data set can be ordered by the **SI** variable. Most of the superior clones will be on top (or the bottom, depending on how the ranking is made) of the file. It is then **highly** advisable for the breeder to carefully analyze the results, because it is frequent to still find a few undesirable clones among the ones favored by the index.

3. The capacity to maintain high dry matter content at the onset of the rainy season

In the North Coast of Colombia, the *Clonal Evaluation Trial* was handled in a particular fashion. Because of the bimodal distribution of rainfall, with the rainy season starting towards the end of April to early May, cassava is traditionally harvested in February or March. Plants harvested at this time cannot be used as seed source because the stakes deteriorate by the time the rains arrive in May. Consequently, the *Clonal Evaluation Trial* used to be evaluated during the dry season, using three plants. The remaining three plants were left as seed source, being cut in May. When the rains arrive, the cassava plant reinitiates its growth, thus extracting energy that had been accumulated in the roots. As a consequence, dry matter content drops to the extent that starch and chip-drying industries usually either reject the roots or pay low prices for them.

The *Clonal Evaluation Trial* was modified by increasing the number of plants representing each clone to eight. Of these eight plants, two were harvested in March, to measure dry matter content during the optimal time for taking this measure. The remaining six plants stayed in the field until the rains arrived and were finally harvested in mid-May, when root yield and dry matter content were measured again. Despite the duplication of work, it was hoped that this procedure would allow for the identification of clones with capacity to maintain high dry matter content even after the arrival of the rainy season. It should be pointed out that an important modification introduced in the new selection system is that the *F1C1* stage has been eliminated and the first stage of selection is now the *Clonal Evaluation Trial*. In addition to the modifications introduced into these trials mentioned above, there is another major change: since no selection has been made previously, the new *Clonal Evaluations* are much richer regarding genetic variability.

In this paper the results of the *Clonal Evaluations* conducted in the Sub-humid environment of Colombia's north coast and harvested in 2001 and 2002 are presented to illustrate the advantages of the new evaluation scheme.

RESULTS

1. The use of the selection index and availability of data from all clones evaluated

Table 1 presents the results from the *Clonal Evaluation Trial* harvested early in 2002. The trial included the evaluation of 1967 clones from a total of about 52 full-sib families. The codes for identifying full-sib families changed this year from CM to GM, because the CM code already reached the number 10,000. The information provided in this table is very valuable because it offers balanced data about the general performance of each family. This data, in turn, is useful for identifying parents that tend to produce superior performing progenies (≈ breeding value).

For instance, family CM9923 was composed of 34 clones of which 24 were selected (70.6%). The average of selected clones across the evaluation was 16%. It is obvious therefore that this family showed an outstanding performance. In contrast, full-sib family GM281 had 39 clones of which none were selected. Furthermore, it is clear that family GM281 has very low dry matter content (23.0%) and low root yield (14.0 t/ha). On the other hand CM9923 had much higher root yield (32.2 t/ha) and dry matter content (31.2%), as well as excellent plant type (2.03).

Once the information of each family is consolidated, some conclusions can be drawn from their respective progenitors. Moreover, because a given clone participates as progenitor in more than one family, very reliable information about the progeny of each progenitor can be produced to feed back into the breeding process **(Table 2)**. Those clones with superior progenies are maintained and those with mediocre ones are eliminated.

2. Improving dry matter content upon the arrival of the rains

The new procedure for the *Clonal Evaluation* permits measuring dry matter content in each clone on two occasions: during the dry season (March) and after the rains arrive (May). **Figure 2** illustrates the relationship between dry matter content in March and that in May for the 1,350 genotypes harvested during 2001.

From the information provided in **Figure 2**, it can be concluded that a relationship exists between the two sets of dry matter contents, corroborated by a correlation coefficient of 0.689. However, observations made in March do not allow to predict with precision those materials that will present high dry matter content in May. For example, clone "A" in **Figure 2** had high dry matter content in March (> 40%), but very low content in May (< 25%). In contrast, clone "B" showed a mediocre performance in March (< 35%), but it was outstanding (about 37.5%) after the rains arrived in May.

Table 1. Results (averages for each full-sib family) from the Clonal Evaluation Trial harvested in 2002 in Santo Tomás, Atlántico Colombia, with 1967 clones.

Family	Size[1)]	Selec. clones (%)	Clones w/fol. retent. (%)	Fresh root yield (t/ha)	Dry matter content (%)	Plant type (1-5)	HI (0-1)	Select. Index	Family	Size[1)]	Selec. clones (%)	Clones w/fol. retent. (%)	Fresh root yield (t/ha)	Dry matter content (%)	Plant type (1-5)	HI (0-1)	Select. Index
CM 8209	70	11.0	8.6	22.2	29.8	2.69	0.51	-3.0	GM 236	36	11.0	30.6	24.2	29.6	2.65	0.65	5.9
CM 9106	5	20.0	40.0	21.4	28.0	2.90	0.65	-2.2	GM 237	2	0.0	0.0	3.4	21.1	4.75	0.36	-61.9
CM 9148	31	3.0	9.7	20.8	28.9	3.24	0.53	-9.0	GM 238	52	17.3	23.1	30.0	28.1	3.21	0.66	5.3
CM 9178	40	4.9	27.5	20.8	28.9	3.01	0.57	-5.6	GM 239	16	37.5	50.0	28.0	31.1	2.34	0.57	11.3
CM 9703	18	0.0	11.1	21.4	29.6	3.03	0.56	-4.2	GM 246	42	14.3	16.7	25.5	29.9	2.61	0.61	6.3
CM 9907	50	28.0	18.0	28.4	28.9	2.58	0.64	9.1	GM 247	16	37.5	37.5	22.2	29.6	2.81	0.67	3.2
CM 9921	15	40.0	33.3	26.5	31.8	3.03	0.65	9.76	GM 248	27	18.5	25.9	23.6	28.3	2.91	0.69	2.5
CM 9923	34	70.6	17.3	32.2	31.2	2.03	0.59	19.2	GM 249	43	16.8	46.5	22.1	30.7	2.81	0.54	-0.5
CM 9926	21	19.0	19.1	30.9	28.5	3.00	0.67	9.2	GM 250	29	10.3	10.3	25.7	29.6	2.78	0.58	3.2
CM 9945	25	4.0	28.0	19.7	29.5	3.46	0.64	-5.4	GM 252	21	4.8	19.5	21.9	27.4	3.12	0.63	-5.7
CM 9946	8	42.9	37.5	23.1	30.8	2.31	0.54	4.5	GM 253	57	3.5	52.6	22.0	30.2	2.90	0.56	-1.4
CM 9949	35	11.0	28.6	22.6	28.4	2.71	0.54	-4.1	GM 255	31	9.7	0.0	24.8	28.1	2.77	0.52	-3.6
CM 9952	41	17.0	7.3	29.7	26.3	2.88	0.64	3.7	GM 258	29	17.2	44.8	24.9	29.6	2.97	0.60	1.8
CM 9954	15	6.7	26.7	25.5	28.7	1.57	0.51	6.66	GM 259	55	21.8	1.8	26.7	27.7	2.70	0.63	3.4
CM 9957	47	23.4	6.4	26.3	30.8	2.59	0.58	10.0	GM 262	62	16.4	53.2	24.6	28.3	2.62	0.59	0.7
CM 9958	59	35.6	22.0	27.0	30.6	2.28	0.58	9.95	GM 266	61	6.6	32.8	23.4	28.3	2.75	0.58	-1.5
CM 9966	44	16.0	22.7	26.1	28.6	2.69	0.59	2.3	GM 273	28	17.9	0.0	26.6	29.6	2.75	0.62	6.2
GM 210	15	0.0	20.0	18.2	30.1	3.13	0.51	-9.67	GM 274	16	12.5	50.0	27.0	30.3	2.69	0.55	5.2
GM 211	71	11.3	18.3	20.7	31.0	2.87	0.52	-3.1	GM 280	9	0.0	0.0	9.31	25.3	3.33	0.57	-27.3
GM 212	56	1.8	16.1	20.4	31.8	3.05	0.48	-4.7	GM 281	39	0.0	18.0	14.0	23.0	3.04	0.62	-22.7
GM 213	79	7.6	1.3	20.7	28.4	2.51	0.51	-5.7	GM 282	76	2.6	56.6	19.4	27.2	2.82	0.59	-8.4
GM 214	67	12.0	0.0	21.3	31.1	2.63	0.51	-0.71	GM 287	24	8.3	29.2	24.3	27.4	3.08	0.63	-2.5
GM 215	37	5.4	10.8	20.6	28.6	2.82	0.54	-6.62	GM 288	46	26.0	32.6	27.4	29.5	2.63	0.58	6.1
GM 216	29	3.4	27.6	17.0	26.1	2.53	0.42	-18.8	GM 290	66	44.0	40.9	32.7	29.0	2.77	0.65	12.8
GM 217	57	8.8	5.3	20.4	27.9	2.75	0.57	-6.5	GM 291	31	12.9	12.9	26.7	26.6	2.95	0.70	2.4
GM 218	30	6.7	63.3	21.8	31.2	2.93	0.52	-1.8	GM 302	53	26.4	24.4	27.4	29.2	2.75	0.56	3.4

[1)] Size: Number of clones from each full-sib family. **Selec. clones**: Proportion of clones from the family selected using the selection index criteria. **Clones w/fol. retent.:** Proportion of clones from a given family exhibiting foliar retention. **Dry mat. cont.:** Dry matter content (%) in the roots measured after the arrival of the rains. **Plant type:** 1= Excellent and 5= Very Undesirable. **HI:** Harvest Index. **SI**: Selection Index

Based on these data, 20 clones were selected in 2001 not only for their high dry matter content, but also because their DM content decreased little upon the arrival of the rains. These 20 clones were planted again and harvested in May 2002. Dry matter content values in 2001 and 2002 had a good correlation (0.65), confirming that this trait has relatively high heritability, and that the selection scheme as the one implemented is likely to be successful.

Table 2. Progenitors that generated the families listed in Table 1 and general performance of their progenies pooling together data from all the families where they participated.

Progenitor	Number of clones generated	% of clones selected
CM 523-7	511	6.80
CM 6754-8	231	16.45
CM 8027-3	318	23.10
SM 805-15	289	9.24
SM 1219-9	465	13.19
SM 1411-5	305	25.70
SM 1565-17	399	12.24
SM 1657-12	155	13.20
SM 1665-2	400	15.43
SM 2192-6	465	19.24
Rayong 60	394	15.16
Total	**3932**	**-**
Mean	**-**	**15.43**

3. Importance of leaf retention

Another significant result obtained from the *Clonal Evaluation* harvested in 2001 was the observation that some genotypes had the capacity to retain leaves for longer periods during plant growth observed by the end of October. At that time, the crop was 5½ months old and a differential capacity to retain leaves was already obvious. Although in most materials (1,225 or 90.7%), leaf abscission had already occurred in the lower 2/3 of the plant, the remaining 125 clones (or 9.3%) had still retained their leaves **(Figure 3)**. Leaf retention capacity was recorded at that time.

Table 3 presents the averages of different traits for the 1,225 clones that did not retain their leaves and for the 125 that did. The notable difference observed between the performances of the two groups suggest that the capacity to retain leaves at five months of age (at a time when no marked water stress has yet occurred in the region) has, indeed, a profound effect on overall performance measured at ten months of age. The materials that retained leaves yielded, on average, 26% more fresh roots (24.96 *versus* 19.75 t/ha), which represents an addition of about 2 t/ha of dry matter. Furthermore, leaf retention was also observed to associate with higher dry matter content (between 1% and 2% more, depending on when it was measured) and with a higher harvest index (by about 10%). These results are significant in that a trait has been identified that is most likely to be of high heritability (i.e., easy to select and fix in populations adapted to sub-humid conditions) and has a positive effect on the agronomic performance of cassava in this region.

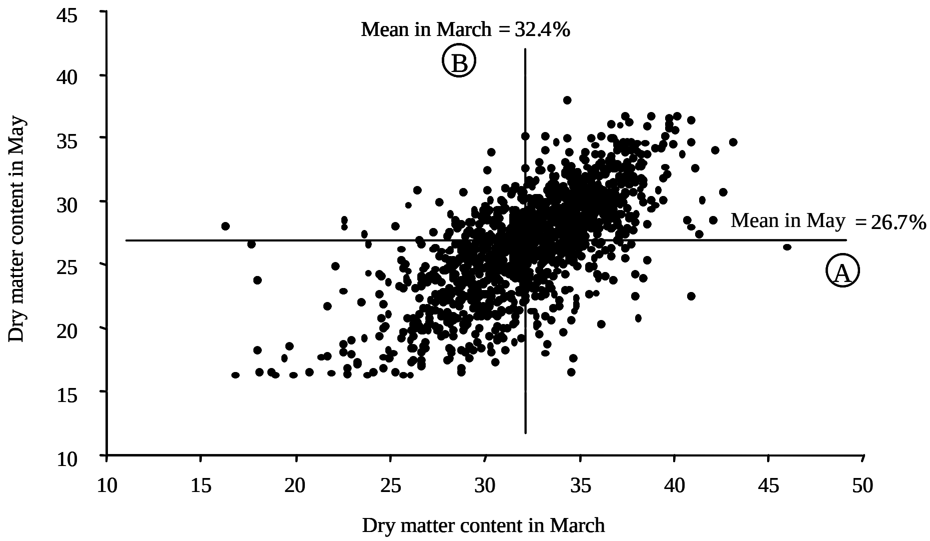


Figure 2. Dry matter content (%) measured for 1,350 genotypes in March and again in May, 2001. Clones A and B are discussed in the text.

Figure 3. Differences in leaf retention as observed in the Clonal Evaluation at Santo Tomás, Department of Atlántico, Colombia. At 5½ months, some families were retaining leaves while others had significant leaf fall.

Table 3. Effect of leaf retention in 5½-month-old cassava on traits measured five months later (at harvest) in the *Clonal Evaluation* in Santo Tomás, Department of Atlántico, Colombia in 2001.

Leaf retention	Dry matter content (%)		Harvest index (0 to 1)		Fresh root yield (t/ha)		Dry matter yield (t/ha)		Fresh root yield[1] (t/ha)
	March	May	March	May	March	May	March	May	
Yes	32.15	28.51	0.55	0.50	27.05	24.12	9.16	6.95	24.96
No	31.48	26.27	0.48	0.44	21.91	18.89	7.08	5.10	19.75

1) Weighted average of fresh root yields taking into account the number of plants harvested in March and May.

The positive effects of leaf retention on the general performance of cassava was predicted earlier by Cock and co-workers (1979). These results confirmed the predictions based on theoretical models and have been further confirmed with other evaluations whose results are not presented here. The distinctive variation for leaf retention was apparent because a large number of clones (new *Clonal Evaluation*) were represented by eigth rather than one plant per genotype (old *F1C1* stage).

CONCLUSIONS

The main advantages of the new evaluation scheme can be summarized as follows:

- The duplication of materials maintained at CIAT headquarters is avoided until they reach status of "elite genotype".
- The selection of a large number of segregating progenies, at the *F1C1* stage, which was based on single plant observations, is avoided.
- The time required to reach the stage of replicated trials is minimized.
- The total length of each cycle of selection is reduced by almost a year.
- Data records will allow for selecting parental material based on *general combining ability*.
- The total cost for each cycle of selection should be reduced.
- Selection will be less subjective by using appropriate selection index specifically developed for that purpose.
- Genetic differences among clones are much more apparent in the *new Clonal Evaluation* than in the old *F1C1* stage.
- For environments with rains concentrated in one season, there is a possibility of selecting clones able to maintain high dry matter upon the arrival of the rains.

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