## A breeding program for training exercises

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.

Traditionally in CIAT headquarters at Palmira, the progenies generated from the crossing blocks (F1) were planted in screen houses 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 were 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 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 allow 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. (1)



<sup>1)</sup>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. This sequence corresponds to the generic steps which might appear in a typical Cassava breeding project. The details are no meant to be a recommendation of how to conduct a breeding project, only examples of steps which might be involved in some sequence. The tutorial is meant to indicate how such steps could be accomplished with the help of the BMS.

| Import Parental List      | Set of 6 female parents and 7            | There where will be two lists   |
|---------------------------|--|---------------------------------|
| MALE2014                  | male parents (some repeated)             | created. One for female         |
| FEMALE2014                | with high protein content and            | parents and another one for     |
|                           | CMD Resistance                           | male parents                    |
| F1 Nursery                | F1's planted                             | 26 crosses made from the        |
| NR2014F1                  |  | female and male parents         |
| <b>Clonal Propagation</b> | 200 Plants Developed through             | Derive 200 Plants from the F1   |
| NR2014C1                  | clonal propagation                       | through clonal propagation      |
| Selected Clones           | <b>25</b> selected from the initial list | Select 25 individuals from the  |
| NR2015V1                  | of clones                                | initial clones for traditional  |
|                           |  | clonal increase                 |
| Field Trial               | The selected clones will be              | There will be 2 locations and 3 |
| TR2015V1                  | tested in the field for                  | reps in a RCBD design           |
|                           | evaluation                               |                                 |

## (1): A NEW EVALUATION SCHEME FOR CASSAVA BREEDING AT CIAT.

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