

Inheritance of agronomically relevant traits in cassava



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Introduction

Cassava (*Manihot esculenta* Crantz), along with maize, sugarcane and rice constitute the most important sources of energy in the diet of most tropical countries of the world. Currently cassava is an important crop in regions at latitude lower than 30° from sea level up to 1800 meters above sea level. Although its most common product is the starchy root, the foliage has an excellent nutritional quality for animal and human consumption and offers great potential. Cassava is the fourth most important basic food after rice, wheat and maize and is a fundamental component in the diet of million of people.

However, in spite of its importance of this crop, very little progress has been done to understand the inheritance of traits with agronomic relevance. Very few articles regarding the inheritance of quantitative traits have been published (Easwari *et al.* 1995; Easwari and Sheela, 1993; 1998). Cassava shows in this regard a unique because a molecular map has been already developed (Fregene *et al.* 1997) and yet very little knowledge based on traditional genetics has so far been produced.

Objective

The objective of this study was to obtain information on the inheritance of traits with agronomic relevance in cassava so that a more scientifically based approach for improving them could be implemented.

Materials and methods

Three sets of clones, adapted respectively to sub-humid, acid-soil savannas and mid-altitude valleys, were selected as parents of three different diallel studies (9 or 10 parents). Each F1 cross was represented by 30 clones. Trials were planted with three replications in two representative locations. Experimental plots included 30 plants (one plant per each of the 30 clones making up each F1 cross). Each clone was represented by six plants planted in the three replications, within each of the two locations. Because of the particular design of these experiments, both between and within family genetic variation could be estimated. However, only between-family variation is analyzed herein. The analysis of variance follows the method proposed by Griffing (1956). Genotypes and environments were considered fixed and random effects, respectively.

Results

The most relevant results are summarized in **Table 1**. Analysis of variance (combined across the two locations used for each type of environment) showed highly significant genotype x environment interaction for most variables studied.

There was a clear consistency in the relative proportion of the sum of squares due to genetic effects explained by general (GCA) and specific (SCA) combining ability effects across the three diallel studies. On average, about 49% of the cross sum of squares for fresh root yield, was explained by GCA. For harvest index, GCA explained about 60% of the cross sum of squares. For dry matter content, height of first branching and plant type score GCA effects were much more important, explaining from 70-75 % of the crosses sum of squares. Plant health variables: reaction to super-elongation disease (SED), white flies, thrips and mites (**Table 2**) showed the highest impact of GCA effects explaining from 82 to 86% of the cross sum of squares.

Table 1. Analysis of variance of three different diallel studies with mean squares for crosses, general (GCA) and specific (SCA) combining ability effects and their respective interaction with the environment.



Table 2. Mean squares for crosses, general (GCA) and specific (SCA) combining ability effects from the analysis of variance for traits related to plant health. With the exception of thrips all variables were evaluated in single locations.



Conclusions

GCA and SCA effects were the main source of variation among crosses means for fresh root yield and harvest index; whereas for dry matter content, height of first branching, plant type score the GCA effects were much more important than SCA effects. For plant health variables (reaction to super-elongation disease, white flies, thrips and mites) the GCA effects were the principal source of variations among crosses means.

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