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Genetic Studies on Mealiness, Dry Matter, Root Number and Fresh Root Yield, in Cassava (Manihot esculenta Crantz)

Isata Kamanda[1,2]*, Essie T Blay[2], Isaac K Asante[2], Agyemang Danquah[2], Beatrice E Ifie[2], Elizabeth Parkes[3], Peter Kulakow[3] and Abdul R Conteh[1]

[1]Sierra Leone Agricultural Research Institute, P. O. Box, 1313, Freetown, Sierra Leone

[2]West Africa Centre for Crop Improvement (WACCI), University of Ghana, Legon, Ghana

[3]International Institute Tropical Agriculture, PMB 5320, Oyo Road, Ibadan, Nigeria

ABSTRACT

Breeding for increased mealiness, number of roots, dry matter content and good fresh root yield enhancing the production of cassava to meet consumer acceptance for cassava storage root and its products has become the next challenge in cassava breeding in Sierra Leone. These traits are essential for cassava production as they are the most preferred traits for end-use consumption. Data were subjected to statistical analyses using SAS version 9.3. Analytical tools employed included general analysis of variance and diallel analysis of variance for combining abilities and estimates. The mean performance for number of roots per plant ranged from 4.85 to 2.50 for crosses IBA 120004 x I088693 and IBA120004 x TMEB1 with a grand mean of 3.59, while the mean performance for fresh root yield ranged from a highest of 0.80kg/plant, I9100416 x I088693 to 0.23kg/plant UBJ120003 x IBA 120004. Significant differences were observed among the 65 F1 crosses for dry matter ($P < 0.01$); number of storage roots per family and fresh root yield per family at $P < 0.05$. General combining ability (GCA) variance was significant only for fresh root yield per family at $P < 0.05$ whereas specific combining ability (SCA) variance were significant for dry matter ($P < 0.05$) and number of storage roots at $P < 0.01$ and fresh root yield at $P < 0.05$. High variability for different traits had also been reported in cassava. The mean FRSY and SRN at the seedling evaluation stage in this study were lower than those reported by Ojulong et al., Mtunda and Tumuhimbise et al., Highest magnitude of positive and significant SCA effects was shown by F1 progenies from crosses UBJ120003 x UCC2001(246), UBJ120003 x TMEB693, UBJ120003 x TMEB 419, UBJ120003 x MM961871, UBJ120003 x I088693, TMEB419 x I088747, TMEB419 x I011368, MM961871 x I9100416, IBA120004 x I088747, IBA 120004 x I088693, IBA961165 x I088693, IBA 961165 x I088693, and I9100416 x I088693. Combining ability analysis for storage root related traits at this early stage was possible because of the high SRN produced by the seedling plants ranging from 1 to 23 storage roots plant−1. his study clearly demonstrates that it is possible to conduct combining ability analysis for storage root related traits at the seedling stage of cassava breeding. This high SRN was attributed to the method that was used in raising seedlings combined with good growing conditions in Sierra Leone. Findings of this study also demonstrated that it is possible to simultaneously select for yield and quality traits, such as DMC at the seedling stage using simple statistical methods. It was also revealed that breeding strategies for crop improvement should exploit the advantage of both additive and non-additive gene action to be able to achieve the different levels of stages in improving most of these studied traits.

***Corresponding author**

Isata Kamanda, Sierra Leone Agricultural Research Institute, P. O. Box, 1313, Freetown, Sierra Leone and West Africa Centre for Crop Improvement (WACCI), University of Ghana, Legon, Ghana.

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Introduction

Breeding for increased mealiness, number of roots, dry matter content and good fresh root yield enhancing the production of cassava to meet consumer acceptance for cassava storage root and its products has become the next challenge in cassava breeding in Sierra Leone [1,2]. These traits are essential for cassava production as they are the most preferred traits for end-use consumption. Although other breeding mating designs had been successfully used for cassava, they are limited in that, they do not provide information for estimation of specific combining ability (SCA), which is important in the inheritance of key traits such as number of storage roots and fresh root yield [3-5]. Subsequent shifts in cassava breeding schemes have seen an increased production of full-sib progenies [4,6]. The selection of suitable parents and good mating designs are keys to successful breeding schemes.

The importance of mating designs in cassava breeding cannot be neglected as it provides information on the genetic control of the character under investigation, generates a breeding population to be used as a basis for the selection and development of potential varieties, estimating the genetic gain and provides information for evaluating the parents used in breeding program [7].The full-sib crossing schemes employ controlled pollinations, where selected mating designs are used to generate families from specific parental combinations, facilitating genetic studies alongside production of breeding populations with traits of interest [8,9].

The diallel mating design, particularly, has become popular for cassava breeding simply because it facilitates generation of useful information on genetics of key agronomic traits and allows identification of parents with superior combining ability for developing breeding populations [1,2,10-12]. It is this genetic information that guides breeders to deploy appropriate strategies for crop improvement [7,9].

Knowledge of general combining ability (GCA) of parental lines is particularly helpful for predicting genetic gains in a breeding program [13]. Hayman elaborated on the procedure for statistical analyses based on diallel data, which partitions total variation into GCA of the parents and SCA of crosses. Combining ability could be described as the relative potentials of an inbred line or a clone, when allowed to mate with another inbred line or clone, to transmit desirable traits or specific trait to the next generation [14]. It facilitates the prediction of the behavior of a line when exploited as a progenitor in a hybrid and compliments the selection of superior breeding lines for hybrid combination and for studying the nature of genetic variation). Griffing reported a method of analyzing combining abilities using the genetic estimates of the parent and hybrid components of diallel analysis through general and specific combining abilities [15]. Falconer and Mackay described general combining ability (GCA) as the mean performance of the progenitors in all its crosses and it is expressed as a deviation from the mean of all crosses [13]. This average behavior of parents in crosses (GCA), calculates the breeding value of a given genotype because of additive gene effects [3,16].

Specific combining ability (SCA) is described as the deviation of individual crosses from the average performance of parents, because of the presence of dominance effects. Understanding the expression of gene action would be important for formulating breeding techniques to generate and develop desired traits. Therefore, information on combining abilities is required to identify suitable and superior progenitors and genotypes which can be hybridized for the development of elite cultivars and progenies varieties that would ultimately ensure sustained production and productivity by subsistence farmers in Sierra Leone.

The cassava breeding programme in Sierra Leone has been evaluating half sib seeds and clones sourced from the cassava breeding unit in IITA. Ibadan. In Cassava breeding, various mating designs and arrangements are exploited by breeder to generate improved cassava genotypes or varieties. The present study is probably the first breeding research undertaken for Sierra Leone. Currently cassava varieties released in Sierra Leone are white or cream fleshed with little amount of high dry matter, mealiness and increased yield. To employ suitable breeding strategies for genetic improvement of economically important traits which are quantitatively inherited, diallel experimental design was used for this study.

The objectives of the study were to:

- Estimate the combining abilities of twelve cassava genotypes for mealiness, dry matter content, number of roots and fresh root yield.
- Determine the gene action for mealiness, dry matter content, number of roots and fresh root yield, and
- Identify and select superior families for the development of elite clones.

Materials and Methods

Establishment of Crossing block

The crossing block was established in May 2015/2016 in Ubiaja, Edo state, Nigeria. The soil within this location comprises sandy clay loam. Ubiaja has a bimodal rainfall pattern, with two distinct rainy seasons and dry seasons of nearly equal length. The peak rainfall occurs between April to May and September to November. Twelve cassava parents (Table 1) were selected based on mealiness, dry matter content, pest and disease resistance, plant architecture, flowering ability and fresh root yield from the IITA genetic gain as well as landraces from Ghana. The 12 genotypes were crossed in a 12 x 12 diallel mating design without reciprocals and selfs. Controlled pollinations were undertaken three months after planting. Hand weeding was performed as required. Controlled hand pollination was carried out according to the standard procedure described by Kawano total seeds obtained was 5,382 (Table 2)

Table 1: Twelve Cassava Genotypes used as Parents for F1 Progenies, their Pedigree and Important Traits

Genotype	Pedigree	Traits
IITA-TMS-IBA 120003		Vitamin A, early bulking, high root yield
UCC 20012 (246)		High dry matter/Mealy, resistant to ACMD, high root yield
IITA-TMS-IBA 693		High dry matter/Mealy, resistant to ACMD, high root yield
TMEB 419		High dry matter/Mealy, resistant to ACMD, high root yield
TMEB 1		High dry matter/Mealy, resistant to ACMD
MM96/8179		Zinc, high dry matter, resistant to ACMD, high root yield
IITA-TMS-IBA 120004	IBA011224 X IBA011368	Vitamin A, early bulking, high root yield
96/1165	O88/00210 HS	Iron, high dry matter, resistant to ACMD, high root yield
91/00416	91934 X 63397	Zinc, high dry matter, resistant to ACMD, high root yield
IITA-TMS-IBA088747	FBA-1 X 05/0561	Protein, resistant to ACMD, high root yield
IITA-TMS-IBA088693	05/0303 X 06/0657	Protein, resistant to ACMD, high root yield
IITA-TMS-IBA011368	940561 X 940263	Vitamin A, early bulking, high root yield
IBA - Ibadan; IITA- International Institute of Tropical Agriculture; TMS - Tropical Manihot Selection;		

NB- Parent1-UBJ120003: Parent2- UCC2001 (246): Parent3- TMEB693:Parent4- TMEB419: Parent5-TMEB1: Parent6- MM961781: Parent7-IBA120004: Parent8- I961165: Parent9- I9100416: Parent10 – I088747: Parent11-I088693: Parent12- I011368

Table 2: Seeds Obtained from 12 x 12 Half Diallel Cross of Cassava Genotypes and Number of Seeds Produced

Female	UB120003	UCC2001(246)	TMEB693	TMEB419	TMEB 1	MM961871	IBA120004	IBA961165	I9100416	I088747	I088693	I011368
Male												
UBJ120003		77	71	148	20	46		96	54	75	100	100
UCC2001(246)			13	148	10	29	93	150	95	100	150	151
TMEB693				151	30	76	78	59	44	150	90	75
TMEB419					21	29	75	70	35	98	75	7
TMEB1						75	23	64	38	100	250	86
MM961871							60	114	72	100	88	100
IBA120004								150	56	83	106	100
I961165									67	100	84	150
I9100416										21	45	18
I088747											143	200
I088693												124
I011368												

Seedling Nursery Evaluated at Foya Crop Site

A total of 40 seeds were randomly selected after germination test from each of the 65 F1 families or cross combination. Seeds were planted at a spacing of 0.30 cm x 1 m in June, 2016 in two replications at Foya crop site Njala, representing the transitional rain forest agro climatic zone in Sierra Leone for one cropping season (2016--2017). The trial was established in a randomize complete block design using serpentine design within the 2 replications in three blocks each. The 'Cocoa' cassava variety (an ACMV susceptible variety) was planted around the trial to ensure screening for ACMD. Fertilizer, NPK 20-10-10 was applied 8 weeks after planting at the recommended rate of 450 kg/ha. The blocks were separated by 2m alleys. The trial was conducted without supplementary irrigation, and field maintenance was undertaken throughout the period of evaluation as necessary.

Data Collection

At harvest data were collected on some yield related (Table 3) traits per the standard procedure outlined by Fukuda et al. (2010). Evaluation was done on 40 plants per family.

Table 3: Phenotypic Traits used in the Characterization of Cassava F1 Progeny

Traits	Procedure	Time of evaluation	Mode of Scoring	Remarks (phenotypic class)
Number of harvested roots per family	Record the number of roots harvested per plot of each clone.	12 MAP (at harvest)	count	Number of stand harvested and counted
Number of storage root	Record the number of plant stand harvested	12 MAP (at harvest	Count	Number of roots harvested and counted
Number of root per plant	The most frequent occurrence was observed and recorded.	12 MAP (at harvest)	Count	3 = small sized roots, 5= medium sized roots 7 = large sized roots
Fresh storage root weight	Roots were placed in a clean synthetic bag and weighed using a spring balance scale set to zero using the empty bag.	12 MAP (at harvest)	Weighing	Shoot fresh weight (stem and leaves)
Shoot weight (kg)	Shoots were tied with a twig and weighed using a spring balance scale set to zero.	12 MAP (at harvest)	Weighing	Harvested samples
Mealiness	Root was cooked for 25 minutes and a scale of 1,2, and 3 was used to screened the cooked samples	12 MAP (at harvest)	Hand screening	Harvested samples

MAP = Month After Planting

Dry matter content (DMC) expressed as a percentage was determined by selecting at least 3 storage roots from a bulk of storage roots of each plant. The roots were washed, peeled and sliced into piece. The sliced of the six fresh samples were weighed to obtain 100grams before drying for 48hours in an oven at 80°C. The dried samples were then reweighed to obtain the dry mass and the DMC was calculated as;

$$\text{DMC (\%)} = (\text{Oven dried root weight} / \text{Fresh root weight}) \times 100$$

Fresh root yield (FYLD in t ha^{-1})

Fresh root yield was estimated as from fresh storage root weight (FRW) for each family;

$$\text{FYLD (t ha}^{-1}\text{)} = \text{Fresh root weight} \times 10\,000$$

Mealiness

Mealiness is an important trait in breeding for quality assessment, it is a method used in assessing the cooking quality of mealy cassava genotypes. Mealiness was estimated following IITA standard laboratory procedure. Cassava stands with at least three roots were randomly selected from cross combinations. Samples were prepared by washing each root with clean water to remove all soil. The roots were peeled and washed again and then dried with paper towel. Each root was sliced into four equal parts. The sliced samples were placed into a pot when the temperature of the boiling water attained 100oC. The samples were cooked for 25 min on a gas cooker. A scale of 1 to 3 was used to assess mealiness, where 1 = 10-30% mealy, 2 = 40-60% mealy, and 3 = 70-100 mealy.

Data Analysis

Data were subjected to statistical analyses using SAS version 9.3. Analytical tools employed included general analysis of variance and diallel analysis of variance for combining abilities and estimates.

The general analysis of variance was used to test if the sources of variation had any significant influence on the character. Diallel analysis of variance for combining ability was performed using mean values, following Griffing 's Model I Method IV [15].

$$Y_{ijkl} = \mu + R_i + G_j + G_k + S_{jk} + E_{ijkl}$$

Where;

Y_{ijkl} = is the l-th observation of the i-th replication for the jk-th cross;

μ = is the overall mean;

R_i = is the fixed effect of the i-th replication, i=1 to b;

G_j or G_k = is the random general combining ability (GCA) effect of the j-th female or the k-th male ~Normally and Independently Distributed (NID) (0, σ2G), j, k=1 to p and j<k;

S_{jk} = is the random specific combining ability (SCA) effect of the j-th and the k-th parents (j≠ k) ~NID (0, σ2S);

E_{ijkl} = is the random within plot error term ~NID (0, σ2E)

Test of Significance for Combining Ability Effects

The t-test was applied to examine the effects of GCA and SCA at 0.05, 0.01 and 0.001 levels of probability. T statistic calculated for GCA effects and SCA effects are as follows:

GCA effects = GCA / S.E

SCA effects = SCA/ S.E

The distribution of crosses in relation to GCA and SCA effects were determined by denoting significant positive combining ability effects as high, non-significant as average and significant negative as low for characters studied (mealiness, dry matter content (DMC), number of storage roots and fresh root weight ha^{-1}) following the method described by Michael et al. and Akuwa [1,16].

Results

Mean Performances of Crosses for Number of Storage Roots Per Plant and Fresh Root Yield

Results in Table 1.4 shows mean performances of crosses for number of storage roots per plant and fresh root yield. The mean performance for number of roots per plant ranged from 4.85 to 2.50 for crosses IBA 120004 x I088693 and IBA120004 x TMEB1 with a grand mean of 3.59, while the mean performance for fresh root yield ranged from a highest of 0.80kg/plant, I9100416 x I088693 to 0.23kg/plant UBJ120003 x IBA 120004.

Table 4: Mean Performances of Crosses for Number of Roots Per Plant and Fresh Root Yield

Cross	Number of storage roots	Fresh root Yield (kg/plant)	Cross	Number of storage roots	Fresh Root Yield (kg/plant)
1x2	3.80	0.38	**4x8**	4.00	0.60
1x3	3.00	0.26	**4x9**	3.70	0.43
1x4	4.45	0.63	**4x10**	3.70	0.55
1x5	3.85	0.38	**4x11**	3.65	0.43
1x6	3.70	0.34	**4x12**	3.20	0.41
1x7	2.65	0.23	**5x6**	3.15	0.31
1x8	4.20	0.61	**5x7**	3.50	0.32
1x9	3.25	0.31	**5x8**	2.85	0.39
1x10	3.60	0.33	**5x9**	4.00	0.27
1x11	4.20	0.58	**5x10**	3.65	0.31
1x12	3.65	0.37	**5x11**	4.25	0.58
2x3	3.85	0.58	**5x12**	3.50	0.36
2x4	3.90	0.39	**6x7**	3.65	0.54
2x5	3.95	0.54	**6x8**	3.25	0.37
2x6	3.75	0.38	**6x9**	2.85	0.31
2X7	3.75	0.64	**6x10**	3.05	0.28
2x8	3.75	0.31	**6x11**	2.85	0.34
2x9	3.75	0.35	**6x12**	3.15	0.35
2x10	4.25	0.54	**7x8**	3.30	0.80

2x11	3.20	0.38	**7x9**	4.85	0.40
2x12	3.75	0.39	**7x10**	3.15	0.34
3x4	3.80	0.56	**7x11**	2.50	0.27
3x5	3.80	0.56	**7x12**	3.30	0.37
3x6	3.75	0.55	**8x9**	3.20	0.33
3x7	3.75	0.55	**8x10**	3.15	0.36
3x8	3.75	0.55	**8x11**	3.45	0.40
3x9	3.75	0.55	**8x12**	3.40	0.38
3x10	3.80	0.57	**9x10**	3.30	0.36
3x11	3.75	0.54	**9x11**	4.30	0.80
3x12	3.80	0.57	**9x12**	3.15	0.35
4x5	3.75	0.55	**10x11**	4.15	0.60
4x6	3.75	0.55	**10x12**	3.70	0.43
4x7	3.05	0.30	**11x12**	3.85	0.56
Grand mean				**3.59**	**0.44**
SE				**0.41**	**0.14**
LSD				**0.82**	**0.28**
CV				**11.5**	**31.9**

NB- Parent1-UBJ120003: Parent2- UCC2001 (246): Parent3- TMEB693:Parent4- TMEB419: Parent5-TMEB1: Parent6- MM961781: Parent7-IBA120004: Parent8- I961165: Parent9- I9100416: Parent10 – I088747: Parent11-I088693: Parent12- I011368

Mean Performances of Crosses for Mealiness and Dry Matter Content

Results in Table 5 shows mean performances of crosses for mealiness and dry matter content. The highest and lowest mean performance for dry matter content were recorded from crosses UBJ120003 x TME693 and UBJ120003 x TME419 respectively ranging from 51.60% to 23.55%, while the mean performance for mealiness ranged from 2.55 in IBA 120004 x I088747 to the lowest of 1.55 in IBA 961165 x I9100416.

Table 5: Mean Performances of Crosses for Mealiness and Dry Matter Content

Cross	Dry Matter content (%)	Mealiness	Cross	Dry Matter Content (%)	Mealiness
1x2	48.80	1.90	**4x8**	46.65	2.10
1x3	23.55	1.85	**4x9**	46.10	1.85
1x4	51.60	2.20	**4x10**	47.50	2.15
1x5	47.75	2.15	**4x11**	46.05	2.00
1x6	48.50	2.00	**4x12**	41.65	2.20
1x7	46.10	2.30	**5x6**	45.95	2.10
1x8	47.60	2.15	**5x7**	44.85	2.05
1x9	47.35	2.00	**5x8**	46.25	2.30
1x10	46.05	2.15	**5x9**	47.15	2.00
1x11	37.60	1.80	**5x10**	48.95	2.15
1x12	45.25	2.10	**5x11**	46.45	2.15
2x3	45.80	2.15	**5x12**	45.90	2.10
2x4	46.40	2.55	**6x7**	48.35	2.15
2x5	43.50	2.15	**6x8**	46.50	1.90
2x6	44.55	2.10	**6x9**	39.00	2.45
2X7	45.85	2.10	**6x10**	45.80	2.30
2x8	46.35	1.90	**6x11**	44.40	2.05
2x9	44.65	2.10	**6x12**	45.75	2.15
2x10	45.00	2.05	**7x8**	49.15	1.95
2x11	44.80	2.10	**7x9**	45.70	2.15
2x12	45.20	2.15	**7x10**	43.25	2.55
3x4	45.20	2.15	**7x11**	40.90	2.25

3x5	45.30	2.10	**7x12**	44.90	2.20
3x6	45.05	2.05	**8x9**	48.70	1.55
3x7	45.20	2.10	**8x10**	47.00	2.00
3x8	45.25	2.10	**8x11**	45.45	2.45
3x9	45.25	2.10	**8x12**	41.15	1.95
3x10	45.20	2.10	**9x10**	49.35	2.05
3x11	45.15	2.10	**9x11**	49.40	2.10
3x12	45.20	2.10	**9x12**	47.65	1.80
4x5	45.20	2.10	**10x11**	48.40	1.80
4x6	45.20	2.10	**10x12**	47.65	2.00
4x7	49.70	1.95	**11x12**	46.75	1.90
Grand mean				**45.57**	**2.09**
SE				**2.34**	**0.21**
LSD				**4.67**	**0.41**
CV				**5.1**	**9.9**

NB- Parent1-UBJ120003: Parent2- UCC2001 (246): Parent3- TMEB693:Parent4- TMEB419: Parent5-TMEB1: Parent6- MM961781: Parent7-IBA120004: Parent8- I961165: Parent9- I9100416: Parent10 – I088747: Parent11-I088693: Parent12- I011368

Estimates of General Combining Effect (GCA) and Specific Combining Effect (SCA)

Significant differences were observed among the 65 F1 crosses for dry matter ($P < 0.01$); number of storage roots per family and fresh root yield per family at $P < 0.05$. General combining ability (GCA) variance was significant only for fresh root yield per family at $P < 0.05$ whereas specific combining ability (SCA) variance were significant for dry matter ($P < 0.05$) and number of storage roots at $P < 0.01$ and fresh root yield at $P < 0.05$ (Table 6).

Table 6: Mean Squares of 12 x 12 Diallel of Measured Traits in Njala

Source	df	Dry Matter Content	Number of Storage Roots	Mealiness	Fresh Root Yield
Rep	1	60.01**	0.88	0.40**	1.17**
Cross	65	26.23**	0.39*	0.06	0.03*
GCA	11	11.63	0.21	0.05	0.04*
SCA	54	13.42*	0.19**	0.06	0.03*
Error	65	2.73	0.09	0.04	0.01

***, **: Significant at P <0.05 and P<0.01 respectively**

Estimates of General Combining Ability (GCA) Effects

Both significant positive and negative GCA effects were observed for the measured traits (Table 7). For dry matter content, eight (8) out of the 12 parents showed significant effect. Parent I088747 gave the highest positive and significant GCA effect (1.28) at $p < 0.01$. Of the remaining six parents with negative GCA effects for dry matter, parents (UBJ120003 and TMEB693) gave the highest negative but significant GCA effects -1.12 ($P < 0.05$) and -2.51 ($P < 0.01$)). For number of storage roots, significant GCA effects were recorded in four parents UCC2001 (246), TMEB693 MM961871 and I9100416). Parents UCC2001 (246) and TMEB693 showed positive significant effects while MM961871 and I9100416 had significant negative GCA effects at $p < 0.05$. For mealiness, only two parents (IBA120004, and I9100416) gave significant GCA effects with values of 0.08 and -0.08 at $p < 0.05$. For fresh root yield, three parents (UBJ120003, I088747 and I011368) with parent I088747 showed highly significant ($p < 0.01$) GCA effect. Two parents (TMEB693 and I088747), had positive significant values (0.10 and 0.06) at $p < 0.05$ and 0.01 respectively.

Table 7: Estimate of General Combining Ability of 12 Cassava Genotypes Evaluated in Njala

Parent	Dry Matter Content	Number of Storage Roots	Mealiness	Fresh Root Yield
UBJ120003	-1.12*	0.08	-0.04	-0.05*
UCC2001(246)	-0.04*	0.22*	0.03	0.00
TMEB693	-2.51**	0.22*	-0.01	0.10
TMEB419	0.99*	0.14	0.04	0.03
TMEB1	0.59**	-0.02	0.04	0.00
MM961871	-0.27	-0.23*	0.04	-0.05
IBA120004	0.38	-0.13	0.08*	0.00

I961165	0.87*	-0.02	-0.06	0.01
I9100416	0.9*	-0.16*	-0.08*	-0.04
I088747	1.28**	-0.07	0.03	-0.01
I088693	-0.60	0.15	-0.03	0.06**
I011368	-0.40	-0.09	-0.03	-0.04*
Se	0.52	0.08	0.03	0.02

*, **: Significant at P <0.05 and P<0.01 respectively, NB: Parent1-UBJ120003: Parent2-UCC2001 (246): Parent3-TMEB693:Parent4-TMEB419: Parent5-TMEB1: Parent6- MM961781: Parent7- IBA120004: Parent8-I961165: Parent9- I9100416: Parent10 – I088747: Parent11-I088693: Parent12- I011368.

Estimates of Specific Combining Ability (SCA) Effects

Table 8 and 9 shows the estimates of SCA effects. Some significant positive and negative SCA effects were obtained for measured traits. For dry matter content, SCA for hybrids from eleven crosses 1x7, 1x4, 1x6, 1x11, 3x10, 4x 12, 6x9, 7x10, 7x11,8x11, 8x12 and 9x11were significant. Progenies from cross 1x 4 had the highest positive significant SCA value (6.14), while progenies from cross 1x3 had the highest significant negative value (-18.39) at p < 0.01 respectively. For number of storage roots, eleven cross progenies (1x2, 1x4, 1x7, 1x8, 2x7, 2x8, 4x7, 5x8, 7x8, 7x12 and 9x11) had SCA effects. F1 progeny from 7x8 had the highest positive significant value (1.41), while progeny from cross 7x11 had the highest negative significant value (-1.11) at p < 0.01 respectively. For mealiness, six progenies 2x4, 6x9, 7x10, 8x9, 8x11 and 10x11 recorded positive or negative significant effects, with F1 progeny of cross 8x11 having the highest positive significant value (0.45) and progeny cross of 8x9 having the highest negative significant value (-0.39) at p < 0.05 and 0.01 respectively. In the case of fresh root yield, eight crosses (1x3, 1x4, 1x 8, 2x7, 5x8, 7 x8, 7x11 and 9x11) showed significant SCA effects. The progeny from cross 7x8 gave the highest positive significant value (0.35), while F1 progeny from cross 7x11 gave the lowest negative significant value (-0.23) at p < 0.05.

Table 8: Estimate of SCA for no of Roots and Fresh Root Yield of 65 Diallel Crosses Evaluated in Njala

Cross	No of Storage Roots	Fresh Root Yield	Cross	No of Storage Roots	Fresh Root Yield
1x2	-0.1	-0.02	**4x8**	0.28	0.12
1x3	-0.80*	-0.23*	**4x9**	0.13	-0.01
1x4	0.63*	0.20*	**4x10**	0.03	-0.03
1x5	0.19	-0.02	**4x11**	-0.24	-0.12
1x6	0.26	0.12	**4x12**	-0.45	-0.12
1x7	-0.89**	-0.17	**5x6**	-0.19	-0.06
1x8	0.54*	0.20*	**5x7**	0.06	-0.04
1x9	-0.26	-0.05	**5x8**	-0.70*	-0.18*
1x10	-0.01	-0.06	**5x9**	-0.36	-0.09
1x11	0.37	0.12	**5x10**	0.15	0.12
1 x12	0.06	0.02	**5x11**	0.53	0.09
2x3	-0.09	0.04	**5 x 12**	0.02	-0.03
2x4	-0.06	-0.08	**6x7**	0.42	0.16
2x5	0.16	0.10	**6x8**	-0.09	-0.03
2x6	0.17	-0.01	**6x9**	-0.34	-0.04
2X7	0.57*	0.20*	**6x10**	-0.44	-0.1
2x8	-0.59*	-0.15	**6x11**	-0.36	-0.11
2x9	0.1	-0.05	**6 x12**	0.03	0.01
2x 10	0.01	0.11	**7x8**	1.41**	0.35**
2 x11	-0.21	-0.13	**7x9**	0.25	0.07
2x12	0.03	-0.01	**7x10**	-0.24	-0.09
3x4	-0.07	-0.01	**7x11**	-1.11**	-0.23*
3x5	0.09	0.03	**7x12**	-0.07	-0.03
3x6	0.26	0.07	**8x9**	-0.21	-0.09
3x7	0.16	0.02	**8x10**	-0.35	-0.09
3x8	0.05	0.11	**8x11**	-0.27	-0.11
3x9	0.19	0.04	**8x12**	-0.08	-0.03
3x10	0.15	0.04	**9x10**	-0.06	-0.04

3x11	-0.12	-0.06	**9x11**	0.72*	0.34**
3x12	0.17	0.07	**9x12**	-0.19	-0.01
4x5	0.03	0.09	**10x11**	0.48	0.11
4x6	0.25	0.13	**10x12**	0.27	0.04
4x7	-0.56*	-0.17	**11x12**	0.2	0.1
SE	0.27	0.09	**SE**	0.27	0.09

***, ** Significant at P<0.005and P< 0.001 respectively**
NB- Parent1-UBJ120003: Parent2- UCC2001 (246): Parent3- TMEB693:Parent4- TMEB419: Parent5-TMEB1: Parent6- MM961781: Parent7-IBA120004: Parent8- I961165: Parent9- I9100416: Parent10 – I088747: Parent11-I088693: Parent12- I011368

Table 9: Estimate of SCA for Dry Matter Content and Mealiness of 65 Diallel Crosses Evaluated in Njala

Cross	Dry Matter	Mealiness	Cross	Dry Matter	Mealiness
1x2	4.38*	-0.18	**4x8**	-0.79	0.04
1x3	-18.39**	-0.19	**4x9**	-1.36	-0.19
1x4	6.14**	0.11	**4x10**	-0.35	-0.01
1x5	2.69	0.06	**4x11**	0.07	-0.1
1x6	4.26*	-0.09	**4x12**	-4.49**	0.11
1x7	1.37	0.17	**5x6**	0.32	-0.06
1x8	2.26	0.16	**5x7**	-1.58	-0.15
1x9	1.99	0.03	**5x8**	-0.79	0.24
1x10	0.3	0.07	**5x9**	0.08	-0.04
1x11	-6.26**	-0.22	**5x10**	1.49	-0.01
1 x12	1.21	0.08	**5x11**	0.87	0.05
2x3	2.78	0.04	**5 x 12**	0.15	0.01
2x4	-0.12	0.39**	**6x7**	2.73	-0.05
2x5	-2.62	0	**6x8**	0.27	-0.16
2x6	-0.75	-0.05	**6x9**	-7.24**	0.41**
2X7	0.05	-0.09	**6x10**	-0.83	0.14
2x8	-0.05	-0.15	**6x11**	-0.35	-0.05
2x9	-1.78	0.07	**6 x12**	0.82	0.06
2x 10	-1.81	-0.1	**7x8**	2.44	-0.15
2 x11	-0.13	0.01	**7x9**	-1.03	0.07
2x12	0.09	0.07	**7x10**	-3.87*	0.35*
3x4	1.14	0.03	**7x11**	-4.34*	0.11
3x5	1.64	-0.02	**7x12**	-0.51	0.07
3x6	2.21	-0.07	**8x9**	1.35	-0.39**
3x7	1.87	-0.06	**8x10**	-0.73	-0.06
3x8	1.31	0.08	**8x11**	-0.4	0.45**
3x9	1.29	0.1	**8x12**	-4.87**	-0.04
3x10	0.85	-0.01	**9x10**	1.59	0.01
3x11	2.68	0.05	**9x11**	3.52*	0.12
3x12	2.56	0.05	**9x12**	1.6	-0.17
4x5	-1.96	-0.06	**10x11**	2.13	-0.29*
4x6	-1.14	-0.06	**10x12**	1.21	-0.09
4x7	2.86	-0.25	**11x12**	2.19	-0.13
SE	1.49	0.13	**SE**	1.49	0.13

***, ** Significant at P<0.005and P< 0.001 respectively**
NB- Parent1-UBJ120003: Parent2- UCC2001 (246): Parent3- TMEB693:Parent4- TMEB419: Parent5-TMEB1: Parent6- MM961781: Parent7-IBA120004: Parent8- I961165: Parent9- I9100416: Parent10 – I088747: Parent11-I088693: Parent12- I011368

Discussion

Diallel analysis for the twelve parents and their F1 progenies evaluated in a seedling nursery trial confirmed that the progenies were significantly different for all the traits revealing the genetic diversity existing among the parents and hence F1 progenies. This predicts the opportunity to make progress with selection. A segregating cassava population comprising of 65 families from a 12 x 12 diallel without reciprocals was tested in the study.

High variability for different traits had also been reported in cassava [1,11]. The mean FRSY and SRN at the seedling evaluation stage in this study were lower than those reported by Ojulong et al., Mtunda and Tumuhimbise et al., [2]. The higher values for these two traits reported by the previous studies cited by the two researchers above may be attributed to the technique that was used for germinating botanical their seeds. Their botanical seeds were germinated in plastic bags and the resulting seedlings with undamaged roots were transplanted to the field. Ceballos et al., indicated that cassava seeds germinated in seedling containers and later transplanted as seedlings to the field often do not develop taproot and that the mature plants that develop from such seedlings are like the plants derived from stem-cuttings in storage root formation [3]. Generally, it was observed from this study that there were significant GCA and SCA effects for the traits studied revealing that the inheritance of these traits had both additive and non-additive gene actions conferring the inheritance of these studied traits.

This is an indication that breeding strategies for the improvement of fresh root yield may exploit the advantage of both additive and non-additive gene action. SCA variance was slightly higher than GCA variance for dry matter but higher magnitude of GCA variance was observed for fresh root yield and number of roots. Contrasting findings were reported from Akuwa, for which he concluded that the propondence on the inheritance of fresh root yield based on non-additive gene action [1].

Fresh root yield had significant GCA effects, suggesting that the inheritance of this trait is largely under the control of additive gene action hence in making selection from such crosses, larger portion of the improvement would be expected to come from the GCA with relatively small contribution from the SCA. This disagrees with findings reported by Calle et al., Zacarias and Labuschagne. Kulembeka et al., and Esuma et al. [8,10,12]. The contrasting findings from this study and from other reports may be attributed to the differences in the genotypes used in the crosses as well as differences in the environment under which the different studies were conducted.

General combining ability effects measure the performance of parents in relation to one another [1]. Significant positive values were denoted as high GCA; non-significant as average while significant negative effect was regarded as low for the traits evaluated. Highest positive and significant GCA in Parent 10 (I088747) for dry matter means that this genotype was the best general combiner and a superior genotype as presented for dry matter while, Parents 1 (UBJ120003) and 3 (TMEB693) which had negative but significant GCA effects may be regarded as very poor general combiners for dry matter because of their low performance among the set of parents. For number of roots, Parents 2 (UCC2001 (246) and 3 (TMEB693) were best general combiners; Parent 7 (IBA120004) was the best combiner for mealiness; and for fresh root yield, Parent 11 (I088693) was observed as the best general combiner.

The specific combining ability (SCA) effects measures distributive performance of crosses based on their parental GCA effect [1]. Estimates of the SCA effects also varied both in magnitude and direction. Analysis of SCA showed that families developed from parents with contrasting GCA effects for traits, quite often had correspondingly high and significant SCA effects, suggesting that specific combinations of alleles were important in controlling traits or that there could be some interlocus gene interaction.

Highest magnitude of positive and significant SCA effects was shown by F1 progenies from crosses UBJ120003 x UCC2001(246), UBJ120003 x TMEB693, UBJ120003 x TMEB 419, UBJ120003 x MM961871, UBJ120003 x I088693, TMEB419 x I088747, TMEB419 x I011368, MM961871 x I9100416, IBA120004 x I088747, IBA 120004 x I088693, IBA961165 x I088693, IBA 961165 x I088693, and I9100416 x I088693.

For dry matter, it confirmed that UBJ120003 x TMEB 419 FI cross was the best specific combiner and superior genotype for dry matter while, progeny from cross MM961871 x I9100416 which gave the highest negative but significant SCA effect is considered as a very poor specific combiner for dry matter. Progeny from crosses with positive significant effects can be selected for development of elite clones for dry matter. For number of roots, F1 progeny from cross IBA120004 x IBA 961165 was the best combiner, for mealiness, while progenies from crosses IBA120004 x IBA961165 and IBA 961165 x I088693 had the best SCA for fresh root yield.

Combining ability analysis for storage root related traits at this early stage was possible because of the high SRN produced by the seedling plants ranging from 1 to 23 storage roots plant−1. This study clearly demonstrates that it is possible to conduct combining ability analysis for storage root related traits at the seedling stage of cassava breeding. This high SRN was attributed to the method that was used in raising seedlings combined with good growing conditions in Sierra Leone.

However, in some cases, parents with best GCA effects did not necessarily produce best progeny for the respective traits, implying that the GCA of a given progenitor did not predict well the performance of a given progeny. Combining ability analysis at the seedling stage cannot be undertaken in areas where storage root development by seedlings is poor and in fields where variability is high. Findings of this study also demonstrated that it is possible to simultaneously select for yield and quality traits, such as DMC at the seedling stage using simple statistical methods. It was also revealed that breeding strategies for crop improvement should exploit the advantage of both additive and non-additive gene action to be able to achieve the different levels of stages in improving most of these studied traits.

Conclusion

A high degree of variation was detected among individual genotypes and families for all traits studied, indicating potential for recurrent selection and improvement. The highest general combiners were Parent 10 (I088747), Parent 2 (UCC2001 (246)), Parent7 (IBA120004) and Parent 11 (I088693) for dry matter content, number of storage roots, mealiness and fresh root yield respectively whereas the lowest specific combiners were UBJ120003 x I088747, UBJ120003 x MM961781, UCC2001 (246) x IBA120004 and UCC2001 (246) x TMEB1 for number of storage roots, fresh root yield, dry matter content and mealiness. For dry matter and number of storage roots recurrent selection method would be efficient. Following hybridization of the selected parents, the non-additive gene effects that predominate in some traits could be "captured" or fixed in subsequent generations by exploiting the vegetatively propagatable nature of cassava.

This study could be utilized as a model for reducing the potential loss of useful genetic data and breeding material, subsequently improving the effectiveness and efficiency of the standard cassava breeding cycle. We, however, acknowledge the limitation of one-year data in this study, and therefore emphasize that these results might not be very conclusive. In view of enhancing or maximizing the potential of cassava production and cassava products, significant progress in increasing these farmer preferred traits which include mealiness, dry matter, and fresh root yield can become successful through appropriate breeding techniques. This result however confirmed that among the cross, families UBJ120003 x TMEB419, IBA 120004 x IBA 961165, IBA961165 x I088693 and IBA120004 x IBA961165 show high potential for exploitation in breeding for multiple important economic traits [17].

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