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Estimates of Genetic Components for Yield and Quality of Cassava (*Manihot esculenta* Crantz) Genotypes at Jimma, Southwest Ethiopia

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ABSTRACT

Despite its multi-directional importance and utility, only limited research efforts have been oriented towards cassava improvement in Ethiopia. The yield potential of cassava is not being fully appreciated. Apart from the yield gap, HCN content of cassava is also a serious limitation for consumption. In respect to this 64 cassava accessions introduced from IITA were planted at JARC in 8×8 simple lattice design with the objective of to determine extent of genetic variability with respect to different quantitative traits during 2012/13 cropping season. The minimum descriptor lists implemented by IITA were adopted in the study. Analysis of variance showed significant difference among the accessions for all traits except leaf width. Wide range of variation in shoot and root traits, with relatively high storage root, dry matter content, starch yield and low HCN content was observed among the introduced accessions. High genotypic coefficient of variation coupled with high heritability and genetic advance as percent of mean was found for height to first branch, length of commercial storage root number (>20 cm), fresh storage root weight, above ground biomass yield and harvest index. These combinations of traits could be used as a more reliable index for simple selection in cassava. The present study indicated a considerable amount of variability for the majority of the characters of interest in cassava along with the preferred yield and quality for utilization. However, since most of the traits could be affected by environment and the stage of harvesting. Therefore, confirmation of genotype by environment interaction and stage of harvesting with complementing of the conventional characterization approach through advanced tools of molecular approaches are suggested.

Key words: Cassava, genetic advance, genetic variability, genotypic coefficient of variation, heritability, hydrogen cyanide

INTRODUCTION

Cassava (*Manihot esculenta* Crantz) is a dicotyledonous, diploid chromosome number (2n = 36) which belonging to *Euphorbiaceae* family. The geographical origin was long debated, although it is now thought to derive from a major center of diversity of the 98 *Manihot* species in Central Brazil (Allem, 2002; Nassar, 2002). It was widely distributed around the world between the 16th and 19th centuries by European explorers due to its recognition and value as a food and cash crop (Allem, 2002). Nowadays, cassava was cultivated in all the tropical countries of the world, including some isolated and remote islands of the Pacific (Scott *et al.*, 2000). According to Dejene (2006) it was introduced to Ethiopia in the 19th century and cultivated extensively in the southern and south-western parts.

The aggregate world cassava production in 2011 was 262.4 mt from an area of 2.1 million ha of land, The African share was about 149.5 mt from an area of 1.3 million ha. Nigeria, Indonesia, Brazil and Thailand are the predominantly cassava producers in that order. The crop is the 3rd most important root crop next to potato and sugar beet. In 2009, the food supply quantity was around 95 mt (FAOSTAT., 2012) and cassava contributed significantly to the nutrition and livelihood of 800 million people around the world in approximately 80 countries (FAO., 2000; Lebot, 2009). Apart from human food, cassava serves as an important animal feed and is considered as tropical alfalfa (Kim *et al.*, 2008) and it is also vital as industrial raw material (Tonukari, 2004). Furthermore, it is a major staple crop and tolerance to erratic weather conditions that makes the crop an important part of the solution to improving food security in times of climate change (Liu *et al.*, 2008).

High root yield per unit area, protein and dry matter content, starch and flour contents (>30%) and low HCN content in fresh roots (<50 ppm) was the predominantly improvement aims in cassava (Jennings and Iglesias, 2002). Despite its multi-directional importance and utility, only limited study efforts have been oriented towards cassava improvement in Ethiopia. Towards this effort, Amsalu (2006) characterized some cassava cultivars and studied the genetic diversity of introduced and locally collected cassava genotypes. Among the accessions introduced from IITA, Nigeria only 2 accessions (44/72 Red and 104/72 Nigeria Red) were the only officially released as varieties in the name Kello and Qulle, respectively (IITA., 2012). Apart from limited or lack of improved variety and yield gap, cyanogenic potential of cassava is a serious limitation for human and animal consumption. In southern Ethiopia, health problems such as nausea, vomiting, distress in abdomen, blotting, weakness, headache and dizziness are common which commonly occur mainly on children and seldom on adults when cassava is consumed frequently (Abuye *et al.*, 1998). Therefore, to alleviate this limiting factor there is an urgent need to screen for low HCN varieties.

Therefore, determining of the genetic variability is essential for conservation of genetic resources and crucial in breeding to identify and develop new cassava varieties to be used as targets for efforts in yield improvement that meet the demands of producers (Rubaihayo *et al.*, 2001). Generally, genetic variability parameters including a genetic coefficient of variation, heritability estimates and genetic advance are absolutely necessary to start efficient breeding programs (Atta *et al.*, 2008). Consequently the introduced cassava genotypes from IITA was need detailed characterization in respect of the above challenges. In order to pave the way for genetic improvement of the crop the present study was proposed with the objectives of determine the extent of genetic variability based on quantitative traits.

MATERIALS AND METHODS

The experiment was conducted during July 11-2012 to December 16-2013 at Jimma Agricultural Research Center. A total of 64 cassava accessions introduced from the germplasm pool of International Institute of Tropical Agriculture (IITA., 1990) constituted the test materials of the present study. The experiment was laid out in an 8×8 simple lattice design using single row plots of 8 m each. Each row (plot) consisted of 6 plants spaced at 1 m apart. Spacing between rows (plots) was maintained at 1 m. Stem cuttings of 30 cm long (2-4 cm circumference) were prepared from healthy 12 months aged mother plant stocks was used as planting materials and planted in inclined

Table 1: Analysis of variance and mean performance for 17 traits of 64 cassava accessions tested at Jimma Agricultural Research Center, 2012-2013

						Range	
Traits	MS trt	MSE	RE (%)	CV (%)	Mean	Min.	Max.
PL	14.96**	4.55	86.30	15.60	13.66	7.09	22.83
LL	3.25**	1.06	96.04	9.47	10.88	6.42	13.50
HFB	375.78**	30.31	102.90	10.89	50.53	21.50	93.17
NB	0.90**	0.29	99.38	16.68	3.22	1.67	5.50
CW	1118.22**adj	421.24	109.82	17.09	120.05	56.35	175.39
NN	65.03**	28.30	100.61	15.85	33.56	21.34	51.67
SG	35.54**	15.82	101.40	14.82	26.85	16.67	35.34
LW	0.42ns	0.28	100.79	16.24	3.31	2.00	4.34
PH	1562.16**	686.13	100.06	11.86	220.84	150.00	294.08
SR	3.53**adj	1.18	107.41	21.14	5.14	1.45	7.89
LCR	2.86**	0.52	96.07	20.52	3.52	1.00	7.00
WFSR	2.71**	0.21	84.43	16.40	2.81	0.68	6.84
ABY	5.93**	0.48	93.09	17.28	4.00	0.97	9.30
DMC	54.90**	24.40	102.98	12.87	38.37	24.25	47.50
HI	176.78**	27.54	96.71	12.63	41.54	15.60	62.76
HCN	0.03**	0.01	101.01	4.44	1.79	1.38	1.92
Starch	11.42**adj	1.30	118.41	8.68	13.13	6.98	18.69

**, * and nssignificant at (p<0.01) and (p<0.05) and non significant, respectively, Adi: Adjusted mean, Ms trt: Mean square treatments, MSE: Mean square error, RE: Relative efficiency to RCBD, Min: Minimum, Max: Maximum, PL: Petiole length, LL: Leaf length, HFB: Height to first branch, CW: Canopy width, NB: Branch number, NN: Node number, SG: Stem girth, LW: Leaf width, PH: Plant height, SR: Storage root number, LCR: Commercial root number (>20 cm), WFSR: Fresh storage root weight, ABY: Above ground biomass yield, DMC: Root dry matter content; HI: Harvest index, HCN: Hydrogen cyanide

planting method. Cultivation, weeding and other agronomic practices were carried out according to Tongglum *et al.* (2001) recommendation. The accessions used in the study are provided in Appendix and Table 1.

Descriptors of cassava developed by Fukuda *et al.* (2010) were followed for data collection. Among the descriptors 17 quantitative data were used. Measurements of characters were carried out from middle 4 plants in each plot based on the descriptor. The data were collected from petiole length (cm), leaf length (cm), Leaf width (cm), plant height (m), Height to first branch (cm), main stem number, Canopy width (cm), Node number, Stem girth (cm), storage root numbers, length of commercial root number, fresh storage roots weight (kg), Aboveground biomass yield (kg), Harvest index (%), dry matter (%), starch content (%) and HCN content (%).

Storage root dry matter (DMC) (%): It was determined according to (AOAC., 1990) methods with oven dry method. After a tuberous was washed through water from the individual four plants of tuberous, a sizable amount 50 g from each plant of the apical, distal and middle sections of the tuberous were obtained randomly.

Dried starch content (%) was obtained by a modified method of Asaoka *et al.* (1992). A 1000 g of fresh tuberous root was taken from the distal, middle and apical section of washed tubers from each of the middle four plants randomly. The amount of dried starch obtained from 1000 g of fresh cassava tuberous roots was weighted and expressed as a percent of the fresh tuberous roots. Starch content was determined according to the method of Krochmal and Kilbride (1966) as follows:

$$\text{Starch yield (\%)} = \frac{\text{WDS}}{\text{WFSR}} \times 100$$

where, WDS is the weight of dried starch content and WFSR is the weight of fresh storage root weight.

HCN content was determined by the acid titration method according to AOAC (2005). Samples from the distal, middle and apical sections of peeled tubers were used.

Statistical analysis: Collected data were subjected to ANOVA based on simple lattice design using SAS version 9.2 (SAS., 2008). Then, the differences between genotypes mean were compared using LSD (Least significance difference) at 5% probability level. The ANOVA model for simple lattice design is:

$$Y_{ijklm} = \mu + t_i + \beta + \chi_{(k)} + y_l + \pi_m + o_{ijklm}$$

where, Y_{ijklm} is the response of Y trait from the ith genotypes, jth replication, μ is the overall mean effects, t_i is the effects of ith level of treatments, β is the effects of jth level of replication, χ_k is the effects of Kth level of blocks within replications (adjusted for treatments), y_l is the effects of lst level of intra block error, π_m is the effects of the m^{th} randomized complete block error and O_{ijklm} is a random error component.

Genotypic (σ^2g), environmental (σ^2e) and Phenotypic (σ^2p) variance component were computed as Burton and Devane (1953) as follow:

$$\sigma^2 g = \frac{\text{MSg} - \text{MSe}}{r} \quad \sigma^2 e = \text{MSe}$$

where, MSg is the genotypic mean square, MSe is the error mean square and r is replication.

Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were estimated according to the method suggested by Burton and Devane (1953), as:

$$\text{GCV} = \frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$$

$$\text{PCV} = \frac{\sqrt{\sigma^2 P}}{\bar{x}} \times 100$$

where, $\bar{x}$ is the grand mean value of the trait.

According to Deshmukh *et al.* (1986), PCV and GCV value greater than 20% are considered as high, while values less than 10% are considered low and values between 10 and 20% was considered medium.

The broad sense heritability was calculated according to the method suggested by Robinson *et al.* (1949) as:

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

The broad sense heritability estimates was categorized according to the method suggested by Robinson *et al.* (1949), which were categorized as 0-30% low, 30-60% moderate and 60% and above high heritability.

Expected Genetic Advance (GA) with one cycle of selection and expected genetic advance as present of mean was calculated to compare the extent of predicted genetic advance of different traits under selection according to (Shukla *et al.*, 2006) equation as follows:

$$GA = (K)\ (\sigma ph)\ (h^2)$$

where, K is the selection differential which varied with selection intensity (5% intensity was used at which K = 2.06), σp is the phenotypic standard deviation:

$$GAM = \frac{GA}{\bar{x}} \times 100$$

Genetic advance as percent of population mean (GAM) was categorized according to high which are above 20%, moderate 10-20% and low less than 10%.

RESULTS

Analysis of variance (ANOVA): The analysis of variance was observed highly significant differences between cassava accessions for all quantitative traits measured except for leaf width at ($p<0.01$) (Table 1). The results indicated that there is a presence of variability among the accession which can be exploited for selection and hybridization in order to improve the desired traits. This finding was in agreement with finding of Islam *et al.* (2007) for plant height, stem girth, length of leaf lobe (Raji *et al.*, 2007), for HCN, height up to first branching, Ntawuruhunga and Dixon (2010), for storage root number, fresh storage root yield, plant height, petiole length, Cyanogenic potential and starch content (Boakye *et al.*, 2013), for above ground biomass (Manu-Aduening *et al.*, 2013), for canopy spread and total shoot weights and Elias *et al.* (2001), for leaf width. This genetic variability will be important for developing trait-specific cassava populations. This view is in agreement with the view of (Mignouna and Dixon, 1997; Raji *et al.*, 2007) who suggested that genetic variability is important for emphasis on yield and tuber quality (for food, animal feed and industrial purposes).

The range and mean of genotypes for the studied characters also showed Wide ranges of variation a good amount of variability among accessions (Table 1). Relatively high range performance revealed among the shoot traits from height to first branch (21.5-93.17 cm), canopy width (56.35-175.39 cm), node number (21.34-51.67), plant height (150-294.08 cm), harvest index (15.6-62.76%) and above ground biomass yield (0.97-9.3 kg) was observed. The current result was in line with the findings of Ojulong *et al.* (2008) for harvest index and Islam *et al.* (2007) for plant height. Variability among node number and plant height is important for solving the shortage of planting material. This view was supported by Titus *et al.* (2011) that long cuttings with optimum nodes give higher yields than short cuttings, because long cuttings produce more stems and leaves. The variation among canopy development also supports selection for medium to short plant architecture that would be advantageous for higher use efficiency of both native soil nutrients and applied fertilizers (Cadavid *et al.*, 1998).

Among the storage root traits wide range of variation was observed with dry matter content (24.25-47%), fresh storage root weight (0.68-6.84 kg), starch yield (6.98-18.67%), commercial storage root number (>20%) (1-7) length and storage root number (1.45-7.89%). Genetic variations in root traits of plant parts existed in the current finding. Ojulong *et al.* (2008) also noted genetic variation for dry matter in different cassava accessions and Saleh *et al.* (2004), for storage root number and HCN. Furthermore, Fakir *et al.* (2012) also reported genetic variation for dry matter (37.30-45.26%) and starch yield (15.04-24.97%) in fresh weight basis within accessions. Excluding IITA-TMS1011086, IITA-TMSZ010053, TMEB419, IITA-TMS1010085 and IITA-TMS1071378 the studied accessions exhibited relatively high dry matter percentage above 30% (59 accessions) was recorded.

Raji *et al.* (2007) reported ranges between (33.2-39.2%) were considered high dry matter content. High dry matter content is a principle factor of quality used by most farmers and researchers in selecting cassava varieties. Since, high dry matter leads to higher flour production and/or is associated with eating quality or mealiness when the root is consumed after boiling (Kawano *et al.*, 1987), therefore, it is an important character for the acceptance of cassava by consumers. Furthermore, Kawuki *et al.* (2011) suggested that variability among dry matter content within accessions was indicative of important scope for genetic improvement.

Relatively higher fresh storage root weight per plant was recorded from IITA-TMS1920326 (6.84 kg), IITA-TMS1010098 (5.44 kg), IITA-TMS1980505 (5.27 kg), IITA-TMS MM011196 (4.94 kg), IITA-TMS1980510 (4.72 kg), IITA-TMS1010131 (4.49 kg), IITA-TMS192B00061 (4.25 kg), IITA-TMS1000338 (4.2 kg) and IITATMS105-0127 (4.12 kg). Relatively higher starch yield per plant was recorded from accessions of IITA-TMS1011368 (18.69%), TME1 (18.44%), IITA-TMS1010046 (17.48%), IITA-TMS1070952 (17.38%), IITA-TMS1011412 (16.63%), IITA-TMS1070539 (16.61%), IITA-TMS1000338 (16.57%), IITA-TMS 195 0211 (16.46%), IITA-TMS1070299 (16.41%), IITA-TMS1070374 (16.24%) and IITA-TMS 1011371(16.03%). This finding is in agreement with the finding of (Ebah-Djedji *et al.*, 2012). However, the trait was influenced by genetic, environmental and plant maturity (Sriroth *et al.*, 2001; Ebah-Djedji *et al.*, 2012).

Relatively higher fresh storage root weight and starch content was recorded from the accessions introduced from IITA. Interestingly all these accessions were relatively higher in starch content coupled with high dry matter content. This indicated that the introduced cassava accessions prove to be superior to the previously introducing accessions to an ecosystem. Therefore, selection intensity will increase for further yield improvement program. High starch production attributes suitable quality for a particular food and non food applications (Baguma *et al.*, 2008; Jansson *et al.*, 2009).

Accessions based on cyanogenic glucosides content revealed that all the accessions were found to have <5 mg per 100 g fresh weight. According to IITA (1990) and Ekanayake *et al.* (1998) grouping, these accessions were grouped under sweet type or low cyanogenic glucosides potential cultivars. Therefore, these accessions have the desirable quality attributes of humans and animal safe consumption. This view is supported by Fukuda *et al.* (2010) who suggested that low HCN content was desirable for both safe human and animal utilization. Interestingly, these accessions were found to combine high storage root yield, high starch yield and low HCN content. This may result in high opportunity for a breeding program to improve the local available

Table 2: Estimated genetic variance components for 17 cassava traits of 64 accessions tested at JARC, 2012-2013

Traits	σ^2g	σ^2e	σ^2p	PCV (%)	GCV (%)	h^2	GA	GAM (%)
PL	5.21	4.55	9.76	22.86**	16.70*	53.36*	3.43	25.13**
LL	1.10	1.06	2.16	13.49*	9.62	50.81*	1.54	14.12*
HFB	172.74	30.31	203.05	28.20**	26.01**	85.07**	24.97	49.42**
MS	0.31	0.29	0.60	23.96**	17.15*	51.26*	0.81	25.30**
CW	348.49	421.24	769.73	23.11**	15.55*	45.27*	25.88	21.55**
NN	18.37	28.30	46.67	20.36**	12.77*	39.35*	5.54	16.50*
SG	9.86	15.82	25.68	18.87*	11.69*	38.40*	4.01	14.93*
LW	0.07	0.28	0.35	17.87*	7.99	20.00	5.59	7.36
PH	438.02	686.13	1124.15	15.18*	9.48	38.96*	26.91	12.19*
SR	1.18	1.18	2.36	29.86**	21.09**	49.89*	1.58	30.69**
LCR	1.17	0.52	1.69	36.93**	30.73**	69.23**	1.85	52.67**
WFSR	1.25	0.21	1.46	43.00**	39.79**	85.62**	2.13	75.84**
ABY	2.73	0.48	3.21	44.76**	41.27**	85.02**	3.14	78.39**
DMC	15.25	24.40	39.65	16.41*	10.18*	38.46*	4.99	13.00*
HI	74.62	27.54	102.16	24.33**	20.80**	73.04**	15.21	36.61**
HCN	0.01	0.01	0.02	7.90	5.59	50.00*	0.15	8.14
Starch	5.06	1.30	6.36	19.21*	17.13*	79.56**	4.13	31.48**

**, *Signified high and moderate value, respectively, σ^2 g: Genotypic variance, σ^2 p: Phenotypic variance, σ^2 e: Environmental variation, PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation, h^2: Broad sense heritability, GA: Genetic advance, GAM: Genetic advance as present of mean, PL: Petiole length, LL: Leaf length, HFB: Height to first branch, CW: Canopy width, MS: Main stem number, NN: Node number, SG: Stem girth, PH: Plant height, SR: Storage root number, LCR: Commercial root number (>20 cm), WFSR: Fresh storage root weight, ABY: Above ground biomass yield, DMC: Root dry matter content, HI: Harvest index, HCN: Hydrogen cyanide

accessions that have high HCN content and low yield potential. Therefore, the present result implies that there will be a good opportunity for further improvement in quality and yield of cassava.

DISCUSSION

Phenotypic and genotypic coefficient of variation, broad sense heritability and genetic advance as percent of mean for the genotypes was presented in Table 2. The estimated genetic variance in shoot and root traits indicated that PCV was slightly higher than GCV for all the traits studied indicating that there was a minimal influence of environment on the genotypes. This view is in conformity with the view of Manu-Aduening *et al.* (2013). High PCV was recorded for Petiole length (22.86%), height to first branch (28.2%), main stem number (23.96%), canopy width (23.11%), number of node (20.36%), storage root number (29.86%), commercial root number (36.93%), fresh storage root weight (43%), above ground biomass yield (44.76%) and harvest index (24.33%). This finding was in agreement with Aina *et al.* (2009) and Manu-Aduening *et al.* (2013), for above ground biomass yield. Ntui *et al.* (2006), for storage root number, weight of storage root, length of tuber root and main stem number.

High genotypic coefficient of variation was observed among height to first branch (26.01%), storage root number (21.09%), commercial root number (30.73%), fresh storage root weight (39.79%), above ground biomass yield (41.27%) and harvest index (20.8). Comparable results were reported by Akinwale *et al.* (2010) and Ntawuruhunga and Dixon (2010) for storage root number, Manu-Aduening *et al.* (2013) for above ground biomass yield and root weight. Additionally, these traits have shown high heritability and genetic advance as percent of mean. Therefore, selection based on these traits will be important for further breeding plan.

Relatively narrow differences between GCV and PCV was observed for above ground biomass yield, weight of fresh storage yield, height to first branch, storage root number, commercial root number, stem girth, dry matter content, harvest index, HCN and starch yield. This implies that the traits were less sensitive to environmental effects. This view is similar to the view of Yadav (2000) who suggested that small differences indicated the presence of sufficient genetic variability for the traits which may facilitate selection.

The broad sense heritability estimated values ranged from 38.4-85.62%. High heritability was recorded for fresh storage root weight (85.62%), height to first branch (85.07%), above ground biomass yield (85.02%), starch content (79.56), harvest index (73.04%), commercial root number (69.23%). This result indicted that the traits were under genetic control of fewer genes (Mohammadi *et al.*, 2010). Similar results were reported by Ojulong *et al.* (2008) for commercial root number (Manu-Aduening *et al.*, 2013), for above ground biomass yield and root weight and Aina *et al.* (2009) for number of roots. Ojulong *et al.* (2008) have also reported similar results for harvest index and (Adeniji *et al.*, 2011) for starch yield, canopy spread, petiole length, leaf length and height to first branch. These traits also showed high GCV and genetic advance as percent of mean. Combination of high broad sense heritability, GCV and genetic advance as percent of mean will result in higher response to successful selection in improving the trait of interest (Acquaah, 2007).

Genetic advance as percent of mean estimated was ranged between 8.14-78.39%. High genetic advance as percent of population mean was observed for above ground biomass yield (78.39%), weight of fresh storage root (75.84%), length of commercial root number (52.67%), height to first branch (49.42%), harvest index (36.61%), starch content (31.48%) and storage root number (30.69%). This finding was in agreement with Ntui *et al.* (2006) for petiole length, main stem number, number of tuber, weight of tuber and Akinwale *et al.* (2010) for root number, shoot weight and root weight. High values of genetic advance are indicative of additive gene action, whereas low values are indicative of non-additive gene action (Narayanan and Singh, 1993). According to Ashok *et al.* (2000), traits controlled by additive gene action could be improved through mass selection breeding method.

High genetic advance as percent of mean combined with high heritability was observed in height to first branch, commercial root number, weight of fresh storage root, above ground biomass yield harvest index and starch content. Therefore, as stated by Ubi *et al.* (2001), traits that combined high heritability with high genetic advance will be a more reliable index for further breeding programs. Therefore direct selection based on these traits will be important for further improvement program in the study area. Iwo *et al.* (2012) also suggested that direct selection could be effective if the high heritability is coupled with high genetic advance, however, for low GAM values direct selection may not be possible because of the environmental effect.

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Appendix: List of cassava accessions used in the study at JARC, 2012-2013

No.	Accessions	Source	No.	Accessions	Source
1	TMEB419	IITA	33	IITA-TMS1070295	IITA
2	IITA-TMS1011086	IITA	34	IITA-TMS1070337	IITA
3	IITA-TMSZ010053	IITA	35	IITA-TMS1070048	IITA
4	IITA-TMS1000388	IITA	36	IITA-TMS1070374	IITA
5	IITA-TMSMM97JW2	IITA	37	IITA-TMS130572	IITA
6	IITA-TMSMM011196	IITA	38	IITA-TMS1011206	IITA
7	IITA-TMS1980505	IITA	39	IITA-TMS19102324	IITA
8	IITA-TMS1011097	IITA	40	IITA-TMS192B00061	IITA
9	IITA-TMS1010098	IITA	41	IITA-TMS1920110	IITA
10	IITA-TMS1920326	IITA	42	IITA-TMS1011224	IITA
11	IITA-TMS1011797	IITA	43	IITA-TMS1010093	IITA
12	TMEB693	IITA	44	IITA-TMSMM010540	IITA
13	TME1	IITA	45	IITA-TMSMM010622	IITA
14	IITA-TMS1010046	IITA	46	IITA-TMS1011368	IITA
15	IITA-TMS1010085	IITA	47	IITA-TMS1011371	IITA
16	IITA-TMS1980510	IITA	48	IITA-TMS1011412	IITA
17	IITA-TMS1980581	IITA	49	IITA-TMS1050125	IITA
18	IITA-TMS1010131	IITA	50	IITA-TMS1050127	IITA
19	IITA-TMS1000338	IITA	51	IITA-TMS1050998	IITA
20	IITA-TMS1950211	IITA	52	IITA-TMS1051570	IITA
21	IITA-TMS1071393	IITA	53	IITA-TMS1051740	IITA
22	IITA-TMS1063046	IITA	54	IITA-TMS1061365	IITA
23	IITA-TMS1070045	IITA	55	IITA-TMS1061475	IITA
24	IITA-TMS1070094	IITA	56	IITA-TMS1061630	IITA
25	IITA-TMS1070004	IITA	57	IITA-TMS1061635	IITA
26	IITA-TMS1070258	IITA	58	IITA-TMS1070539	IITA
27	IITA-TMS1070126	IITA	59	IITA-TMS1070593	IITA
28	IITA-TMS1071313	IITA	60	IITA-TMS1070824	IITA
29	IITA-TMS1070299	IITA	61	IITA-TMS1070952	IITA
30	IITA-TMS1070134	IITA	62	4472/Nigeria red	IITA
31	IITA-TMS1071378	IITA	63	4472/Nigeria white	IITA
32	IITA-TMS1062630	IITA	64	4572/Nigeria red	IITA

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