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Original Article

Assessment of Genetic Diversity of Promising Castor Bean (*Ricinus communis* L.) Genotypes in Nigeria

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Abstract

Castor oil plant (*Ricinus communis* L.) is an important oil crop with little research attention in Nigeria. In the present research, extent of genetic diversity among 20 Nigerian castor genotypes was determined using morphological descriptors and molecular markers. The genotypes were laid out on a randomized complete block design with three replicated plots. Molecular genotyping of the genotypes was carried out using genomic Simple Sequence Repeats (SSR). The genotypes revealed high divergence in seed colour, seed shape, seed mottle, seed caruncle and seed sizes. Seedling establishment varied from 70.18% (in Acc. 006) to 93.25% (Acc. 001) with average mean of 81.53%. Raceme length ranged from 15.90 cm to 29.54 cm with population mean of 20.80 cm. The highest seed yield (1222.98 kg/ha) was recorded in Acc. 001 and the least (611.46 kg/ha) was observed in Acc. 006. Seed oil content varied between 32.15% in Acc. 042 and 54.03% in Acc. 006. Agglomerative cluster dendrogram constructed from morphological data showed random distribution of the genotypes into three cluster groups irrespective of the sources/collection points. The genetic diversity based on SSR Marker Analysis revealed high average expected heterozygosity (0.74), Polymorphic information content (0.68), Nei's gene diversity index (0.72) and Shannon's Information index (1.43). The dendrogram constructed from molecular data grouped the twenty genotypes into three groups at coefficient of 0.34. From these findings, it showed that the twenty genotypes evaluated are divergent in nature and they could serve as good genetic material for castor breeding in Nigeria.

Keywords: agglomerative; castor oil plant; molecular markers; morphological descriptors

Introduction

Castor (*Ricinus communis* L.) is a flowering plant in the family Euphorbiaceae (Spurge) and subfamily Acalyphoideae. *Ricinus* is a monotypic genus that belongs to a subtribe *Ricininae* (Weiss, 2000). The origin of castor is obscure because of its extensive distribution in earliest times and the speed/ease at which it establishes itself as a native plant. While some researchers suggested that castor might have originated from Asian, most authors agreed that it is a native to Africa (Anjani, 2012).

Castor is one of neglected crops with high economic values around the globe. The crop has been demonstrating its economic potentials, contributing notable foreign exchange credits to economy of many countries, including India, Brazil and China (Salihu *et al.*, 2014). Castor has been recognized as an ideal crop which has potential to generate thousands of jobs for African youths and women (Gana *et al.*, 2013). In Nigeria, it presently serves as an alternative source of income to resource-poor farmers across the country, earning them about N 35, 000 per 100 kg on season and N 50, 000 per 100 kg off season at local markets (Amosun *et al.*, 2013). Also, being a hardy and low nutrient

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demanding crop, it helps in reclaiming marginalized farm land (Gana *et al*., 2013). The oil, which is extracted from castor seed, is very critical to many industrial applications because of its ability to form many important derivatives (Ogunniyi, 2006).

Despite the huge economic benefits of castor, its genetic improvement in Nigeria has not been receiving much attention due to lack of organized germplasm. Unlike other important oilseed crops (like oil palm and soybean) castor germplasm is still poorly characterized in many of the repository centres (Sayama *et al*., 2011). In fact, the crop (castor) had long been ignored until in the late 2000s, when a study on genetic divergence in its germplasm was first documented (Allan *et al*., 2008). In this research, some selected promising castor genotypes from Nigerian germplasm were characterized using phenotypic and molecular markers. This is to improve the germplasm usefulness and present more organized genetic resources to Nigerian Castor Breeding Programme.

Materials and Methods

Evaluation of 20 castor genotypes for morphological characters

The plant genetic materials used for this research were obtained from castor research programme of National Cereals Research Institute (NCRI), Nigeria. The genetic materials comprised of twenty (20) genotypes, including 12 genotypes from Nigeria, five (5) from Brazil, one (1) from Turkey, Panama and South Africa. The genotypes were evaluated at Badeggi - Nigeria (Lat. 9° 45' N, long. 6° 07' E) between June and December, 2016. The treatments were laid out on a randomized complete block design with three replicated plots. The plot size was 3 m by 3 m with inter-row and intra-row spaces of 75 cm by 75 cm. Two seeds per hole were planted and later thinned to one seedling per stand at four weeks after planting. Fertilizer (N, P, K) requirement for individual plant stand was estimated and applied by band placement (Ogunlade, 1993). Standard agronomic practices for castor were followed. Qualitative and quantitative data were taken from 20 plant samples per plot, using Standard Castor Descriptors (India, 2004).

Molecular genotyping of 20 castor genotypes using SSR markers

Total genomic DNA of the accessions was extracted from leaves of 30 - 35 days old plant samples, using a modified cetyltrimethyl ammonium bromide (CTAB) method (Dellaporta *et al*., 1983). About 1 g of the leaf samples of the selected 20 promising accessions were grounded to fine powder and used for the DNA extraction, using 2.0 ml extraction tubes. 700 µl of 2 x CTAB buffer (Pre-warmed - 55 °C), 1.3 µl of mercaptoethanol and a pinch of polyvinyl-pyrrolidone (PVP) were added to the sample tubes. The samples were then incubated at 65 °C for one hour and vortexed intermittently within the period. Five hundred microliters (500 µl) of chloroform/isomyalcohol (24:1) was added to the samples and mixed for 5 minutes. The samples were then centrifuged at 14,000 rpm for 5 minutes. After centrifuge, the liquid phase (Supernatant) was removed and transferred into a 1.5 µl tube. Five hundred microliters (500 µl) ice cold isopropanol was added to the extract and incubated in -20 °C for about 30 minutes to 60 minutes, and then centrifuged for 2 minutes at 14,000 rpm. The upper liquid layer was carefully removed, 100 µl of 70 % ethanol was added to the tube and then spun for 2 minutes at 14,000 rpm. This step was repeated two times and the DNA pellet obtained was dried at room temperature for the ethanol to evaporate. 100 µl of 1% TE-buffer and 2 µl RNase was added to preserve the DNA and remove the RNA respectively.

The DNA was quantified using NANODROP Spectrophotometer (Thermo Scientific, 2000/2000 c) and diluted to 25 ng/µl for Polymorphic Chain Reaction (PCR) analysis. After DNA quantification, samples from three diverse accessions were screened over 10 genomic SSR primers for generation of informative characters and five distinct polymorphic primers were selected to screen the 20 accessions. The SSR primers' sequences used were retrieved from www .intechopen.com and http:// www. amjbot .org/ doi:10.3732/ajb.1000395. The primers and their sequences are presented in Table 1.

Polymerase chain reaction (PCR) was performed in a 10 µL volume containing 1x *Taq* buffer with $(NH_4)_2SO_4$, 40 ng DNA, 2.5 µM forward and reverse primers, 20 mM $MgCl_2$, 200 µM each dNTP, 1 unit *Taq* DNA polymerase. The PCR programme used included the initial denaturation at 94 °C for 3 minutes followed by denaturation at 94 °C for 1 minute, annealing at 40 °C for 2 minutes and extension at 72 °C for 2 minutes, and these steps were repeated for 45 cycles with a final extension at 72 °C for 5 minutes and hold at 4 °C. The PCR reaction was carried out using Applied Biosystem PCR machine. The PCR bands were determined using 1.8% agarose gels. Ethidium bromide stained gels were visualized and documented using gel documentation system. The analysis was carried out at Bioscience Centre of International Institute for Tropical Agriculture, Ibadan, Nigeria.

Data analysis

The quantitative parameters were subjected to analysis of variance to test for significance of the differences among the entries. Agglomerative cluster analysis was carried out, using both quantitative and qualitative (scores) data. Number of clusters was determined using Rule of Thumb. Being a mixed variables and also nonparental-progeny data, Gower Cluster Distance and Complete Linkage Clustering Method were applied. The statistical package, Statistical Tools for Agricultural Research (STAR 2.1.0), was used to analyze the data.

A 50 based-pair (bp) DNA ladder added in the first load of the gel was used to score the bands in each gel. The bands scored were only those that had more than 50 bp in length and reproducible. The scoring of the visual bands was done according to the size of the DNA ladder bands as defined in the ladder. Genetic parameter, including number of observed and expected alleles, and Shannon's Information index were estimated according to Ahmad *et al.* (2015). Polymorphic information content (PIC) value and expected heterozygosity for each of the SSR markers were estimated using the PIC calculator (http://www.liv.ac.uk/~kempsj/pic.html). Cluster analysis was performed to investigate the structure of the collections, using NTSYS-pc 2.10 software (Rohlf, 2002).

Table 1. List of simple sequence repeat (SSR) primers used for the genetic diversity study

Primer	Sequence 5' - 3'		Temp (°C)	SSR motif
	Forward	Reverse		
RC645-V30156.92	CTTGAGGGTCGTAGGAGCAG	GGTAGCAACTCTCTTTCTTCGC	59.8	(AT)
RC151- V29842.130	TTGTGTCCATACCAACATCG	GGATAGGAGCATCAAGAAGGTT	58.3	(AT)
RC034-GF102174	TCGGTTAAGGGTATGGGTTG	CACACTTCATTTCGCAGACC	60	(GT)
RC504-V30056.29	GCAAGCTCGTTTATATGCTCAA	ATCCAACACCGACACTCCA	59.7	(AAT)
RC338-V29828.6	GCCCTACTTCTAACCATGTGC	GTGGTCCTTATGCAACCCAT	59.2	(AT)
RC436-V29763.7	AGTGTTTGCTTGATGGGTTGA	TGCAGGCTTTCCAAATCG	60.7	(AT)
RC594-V30156.41	TGTGAAAAGGGAGTTCGGAG	ATTGCGGGTAAAACTGAAGC	59.7	(AT) (TA)
RC650-V30156.97	ATAATTCCAGGGGCAAAATC	CAAATGGCACCCAATAAGAA	58.2	(AT)
RC410-V29745.2	TCTCTATCGCCACATCACCA	ATTTGATACCACCACCGCTC	60.0	(TA)
RC584-V30156.31	GCCTTGTTCCTTCTAAAATTCG	GAGGGAGAGCTGTTGTTGGT	59.3	(AT) (GT)

Results

The genotypes revealed high divergence in seed color, seed shape, seed mottle, seed caruncle and seed sizes (Table 2). Exotic genotypes comprised of 2 large-seeded (diameter > 15 mm) castor types, 2 medium-seeded types (diameter, 9 mm - 15 mm) and 4 small-seeded (diameter < 9 mm) ones. The locals include 4 large seeded and 8 small seeded types. Seed color varied from white through brown to black color among the genotypes (Fig. 1).

The mean values and mean squares for the 11 traits among 20 castor genotypes evaluated are presented in Tables 3. There were significant differences for all the studied traits among the entries. Seedling establishment varied from 70.18% (in Acc. 006) to 93.25% (Acc. 001) with average mean of 81.53%. Raceme length ranged from 15.90 cm to 29.54 cm with population mean of 20.80 cm. Days to maturity varied between 96.78 days and 134.44 days. The highest seed yield (1,222.98 kg/ha) was recorded in Acc. 001 and the least (611.46 kg/ha) was observed in Acc. 006. Seed oil content among the entries varied between 32.15% in Acc. 042 and 54.03 % in Acc. 006.

Agglomerative cluster dendrogram constructed from morphological data of the 20 genotypes evaluated is presented in Fig. 2. The cluster groups were three with random distribution of the genotypes irrespective of the sources/collection points. The cophenetic correlation coefficient was 0.774. Cluster 3 was the largest group with 14 cluster members. Cluster 1 and Cluster 2 had 4 and 2 cluster members respectively. Cluster group 1 and 2 had group average seed yield performance of 883.36 kg/ha and 962.85 kg/ha respectively (Table 4). Members of cluster 2 recorded the highest group average number of racemes per plant (9.78), longest raceme length (27.56 cm) and highest seed oil content (49.25%). The least seed yielding group was cluster group 3 with average group seed yield of 730.42 kg/ha, less than population mean.

The estimates of genetic diversity parameters among the five SSR markers used are presented in Table 5. A total sum of 27 alleles with mean of 5.40 was observed among the markers. Number of effective alleles among the markers ranged from 3.18 to 4.65 with a mean of 3.66. Among the markers, RC 594-V 30156.41 (SSR Marker) recorded the highest values for expected heterozygosity (0.805), Polymorphic information content (0.761), Nei's gene diversity index (0.785) and Shannon's Information index (1.752) and the least values for these diversity parameters were observed in marker RC 584-V 30156.31.

The cluster analysis grouped the twenty genotypes into three clusters at coefficient of 0.34 (Fig. 3). The group II had the highest cluster members (14) followed by group I with six (5) cluster members. The cluster group III had least (unit) cluster member. The local and exotic genotypes were grouped randomly irrespective of their sources or places of collection. In cluster group I, the genotype Acc. 005, Acc. 045 and Acc. 026 which are locals were grouped together with genotype Acc. 001 and Acc. 036 M that are exotic collections. Likewise, in cluster group II, exotic genotypes Acc. 003, Acc. 053, Acc. 002, Acc. 072 and Acc. 036 were grouped together with other nine local genotypes.

Discussion

From the result, the genotypes showed significant differences among themselves for all the traits studied. This is an indication that there is adequate variability for the traits studied and as such there is ample scope of selection for their improvement. Golakia *et al.* (2015) also documented adequate variability for most of characters in castor, including seed yield per plant. This result is also in concurrence with the report of Rao *et al.* (2009)

The result of the cluster analysis revealed divergence among the studied genotypes. This gives information on possible parental combinations to get useful recombinants. The high yielding groups (cluster I and II) are the potential parents for development of useful segregating generations for increased seed yield. The random distribution of the genotypes into various clusters irrespective of the geographical sources revealed no geographic influence, suggesting other forces such as natural and artificial selection, and genetic drift for variability observed. High genetic variability in segregating populations can only be generated by crossing genetically diverse individuals. It has been long theoretically demonstrated that the higher the divergence between the genotypes, the higher will be the heterosis (Shivanna, 2008).

Table 2. Seed physical characteristics of 20 promising castor genotypes at NCRI Badeggi, Nigeria

NCRI accessions' number	Source	Type of germplasm	Seed shape	Seed colour	Seed mottle	Caruncle	Seed size
ACC. 001	Brazil	Exotic	Square	Black	Less conspicuous	Conspicuous	Large
ACC. 002	Brazil	Exotic	Oval	Dark Chocolate	Conspicuous	Conspicuous	Small
ACC. 003	Brazil	Exotic	Oval	Dark Chocolate	Conspicuous	Less conspicuous	Small
ACC. 005	Nigeria	Local	Oval	Brown	Less conspicuous	Less conspicuous	Small
ACC. 006	Nigeria	Local	Oval	Brown	Less conspicuous	Less conspicuous	Small
ACC. 009	Nigeria	Local	Square	White	Conspicuous	Conspicuous	Large
ACC. 010	Nigeria	Local	Oval	Dark Chocolate	Less conspicuous	Conspicuous	Small
ACC. 012	Nigeria	Local	Elongated	Brown	Less conspicuous	Less conspicuous	Small
ACC. 016	Nigeria	Local	Square	White	Conspicuous	Conspicuous	Large
ACC. 019	Nigeria	Local	Elongated	Brown	Less conspicuous	Conspicuous	Small
ACC. 022	Nigeria	Local	Oval	Dark Chocolate	Less conspicuous	Conspicuous	Small
ACC. 026	Nigeria	Local	Oval	Brown	Less conspicuous	Conspicuous	Small
ACC. 036	Brazil	Exotic	Oval	Dark-chocolate	Conspicuous	Less conspicuous	Small
ACC. 036 M	Brazil	Exotic	Elongated	Dark-chocolate	Conspicuous	Conspicuous	Medium
ACC. 042	Nigeria	Local	Oval	Brownish Red	Conspicuous	Less conspicuous	Small
ACC. 045	Nigeria	Local	Square	White	Less conspicuous	Less conspicuous	Large
ACC. 048	Nigeria	Local	Square	Brownish Red	Conspicuous	Conspicuous	Large
ACC. 053	Turkey	Exotic	Oval	Dark Chocolate	Less conspicuous	Less conspicuous	Medium
ACC. 072	Panama	Exotic	Oval	Brown	Conspicuous	Less conspicuous	Small
ACC. 091	S. Africa	Exotic	Oval	Dark Chocolate	Conspicuous	Less conspicuous	Large

Table 3. Mean performances of 20 castor genotypes for 11 agronomic traits at Badeggi-Nigeria

Accessions	ESTAB	DF	HF	BPP	RL	RPP	HM	DM	SW	SY	SOC
Acc. 001	93.25	95.67	74.76	7.45	25.32	7.61	117.57	128.44	49.89	1222.98	47.25
Acc. 002	88.77	77.44	83.21	5.56	20.96	5.36	115.44	114.00	27.61	700.53	35.61
Acc. 003	82.06	63.22	60.87	6.22	19.44	5.15	118.88	104.00	15.88	664.30	34.49
Acc. 005	85.81	58.38	40.17	7.24	26.82	7.20	104.31	98.62	10.74	859.15	48.20
Acc. 006	70.18	66.89	75.58	6.66	17.75	6.53	116.31	96.78	15.65	611.46	54.03
Acc. 009	76.75	76.22	80.38	3.13	16.64	3.85	117.66	115.44	44.98	842.34	38.45
Acc. 010	74.55	66.78	63.24	4.88	29.54	4.82	107.77	105.44	11.31	873.63	51.23
Acc. 012	86.59	68.56	56.62	6.44	17.90	6.76	101.82	110.67	12.87	666.58	37.38
Acc. 016	85.50	78.00	87.58	4.44	15.90	5.69	117.92	115.78	42.80	600.56	33.61
Acc. 019	81.12	70.11	72.68	5.78	20.04	5.03	120.72	108.25	15.12	745.02	35.33
Acc. 022	76.75	72.11	62.14	6.22	20.85	5.58	97.57	114.00	15.06	652.20	34.70
Acc. 026	83.30	69.33	59.56	4.66	18.31	6.55	102.65	112.11	23.16	723.65	36.04
Acc. 036	81.12	73.67	79.35	5.56	26.91	8.70	130.93	106.89	20.58	869.10	35.46
Acc. 036M	91.50	70.89	49.15	10.43	28.31	12.36	91.62	122.00	13.18	1066.54	50.30
Acc. 042	80.02	74.44	75.73	4.22	18.57	4.49	99.36	109.22	32.23	713.38	32.15
Acc. 045	79.70	111.78	77.55	3.56	20.96	4.07	120.56	134.44	50.38	867.57	45.94
Acc. 048	81.25	67.38	69.11	5.76	16.34	4.30	112.28	108.75	15.92	775.55	33.91
Acc. 053	80.02	64.22	84.23	7.34	18.49	5.90	137.33	101.78	25.96	835.21	33.93
Acc. 072	75.66	65.11	72.87	7.12	19.67	5.36	118.34	109.33	20.17	696.68	33.56
Acc. 091	76.75	65.11	65.54	7.12	18.45	6.76	103.14	104.11	28.87	698.55	35.57
Mean	81.53	72.77	69.52	5.99	20.86	6.10	112.61	111.00	24.62	784.25	39.36
SEM	1.30	2.69	2.74	0.37	0.93	0.43	2.56	2.08	2.91	34.32	1.59
CV	7.12	16.50	17.65	27.52	20.02	31.67	10.16	8.37	52.92	19.57	18.05
Mean Sq.	104.54**	469.87**	446.46**	8.17**	52.58**	11.94**	351.12**	249.45**	507.06**	66426.43**	173.61**
HSD	4.00	3.67	5.13	1.00	2.06	1.89	8.28	5.61	2.22	183.58	10.73

Table 4. Membership performance summary of 20 castor genotypes in three cluster groups

Parameters		Cluster I	Cluster II	Cluster III
Seedling establishment (%)	Min	76.75	85.81	70.18
	Max	93.25	91.50	88.77
	Mean	83.80	88.66	79.87
Days to 50% flowering	Min	76.22	58.38	63.22
	Max	111.78	70.89	77.44
	Mean	90.42	64.64	68.88
Height at 50% flowering (cm)	Min	74.76	40.17	56.62
	Max	87.58	49.15	84.23
	Mean	80.07	44.66	70.05
Number of branches per plant	Min	3.13	7.24	4.22
	Max	7.45	10.43	7.34
	Mean	4.65	8.84	5.97
Raceme length (cm)	Min	15.90	26.82	16.34
	Max	25.32	28.31	29.54
	Mean	19.71	27.56	20.23
Number of racemes per plant	Min	3.85	7.20	4.30
	Max	7.61	12.36	8.70
	Mean	5.31	9.78	5.81
Height at maturity of first raceme	Min	117.57	91.62	97.57
	Max	120.56	104.31	137.33
	Mean	118.43	97.97	113.04
Days to maturity of first raceme	Min	115.44	98.62	96.78
	Max	134.44	122.00	114.00
	Mean	123.53	110.31	107.52
Seed weight (g)	Min	42.80	10.74	11.31
	Max	50.38	13.18	32.23
	Mean	47.01	11.96	20.03
Seed yield (kg/ha)	Min	600.56	859.15	611.46
	Max	1222.98	1066.54	873.63
	Mean	883.36	962.85	730.42
Seed oil content (%)	Min	33.61	48.20	32.15
	Max	47.25	50.30	54.03
	Mean	41.31	49.25	37.38
Number of member		4	2	14
Cluster members		Acc. 009, Acc. 016, Acc. 001, Acc. 045	Acc. 005, Acc. 036 M	Acc. 003, Acc. 010, Acc. 002, Acc. 042, Acc. 072, Acc. 091, Acc. 006, Acc. 036, Acc. 053, Acc. 048, Acc. 019, Acc. 022, Acc. 012, Acc. 026

Cophenetic Correlation Coefficient = 0.774

Table 5. Genetic diversity parameters among 5 SSR markers for 20 promising accessions selected from Nigerian castor germplasm

SSR Markers	No	Ne	Ho	He	PIC	Nei	I
RC-151V29842.130	4.00	3.31	0.79	0.72	0.65	0.70	1.30
RC594-V30156.41	8.00	4.65	0.95	0.81	0.76	0.79	1.75
RC436-V29763.7	4.00	3.78	1.00	0.76	0.69	0.74	1.36
RC584- V30156.31	4.00	3.18	0.38	0.71	0.63	0.69	1.24
RC034-GF102174	7.00	3.38	0.85	0.72	0.66	0.70	1.49
Mean	5.40	3.66	0.79	0.74	0.68	0.72	1.43
St. Dev	1.95	0.60	0.25	0.04	0.03	0.04	0.21

Note: No = observed number of allele, Ne = expected number of allele, Ho = observed heterozygosity, He = expected heterozygosity, PIC = Polymorphic information content, Nei = Nei's index, I = Shannon's Information index

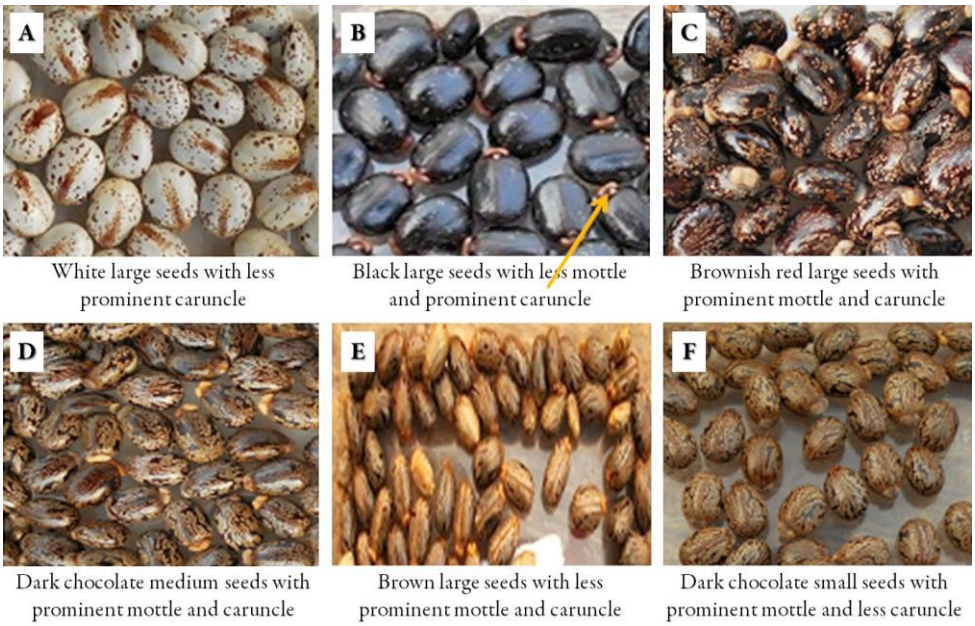

Fig. 1. Different seed physical characteristics among the castor genotypes evaluated
Note: A - Seeds of Acc. 045, B - Acc. 001, C - Acc. 048, D - Acc. 036 M, E - Acc. 012 and F - Acc. 036

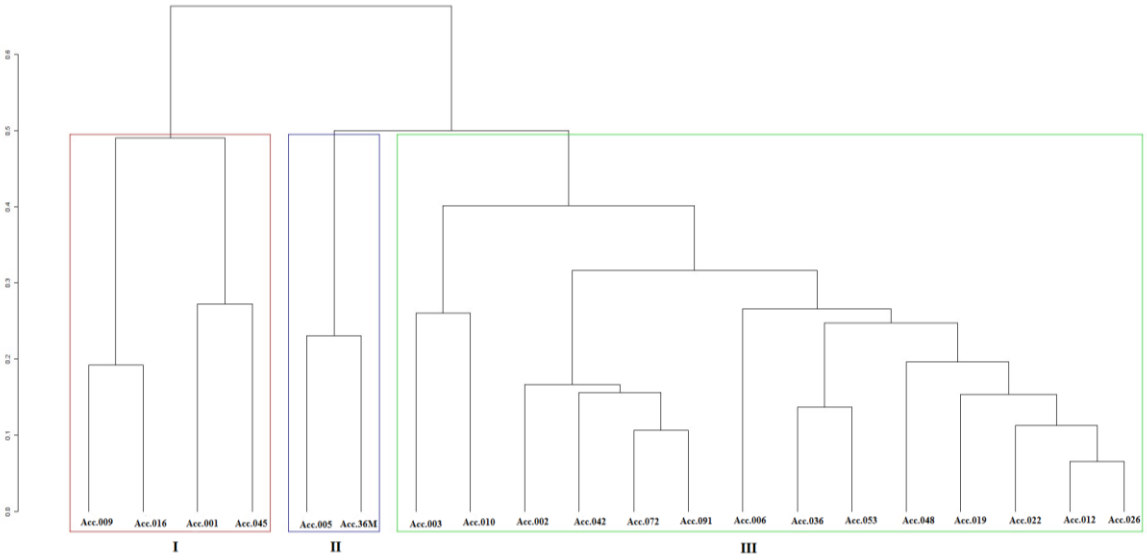

Fig. 2. Agglomerative cluster dendrogram constructed from morphological data of 20 Nigerian castor genotypes

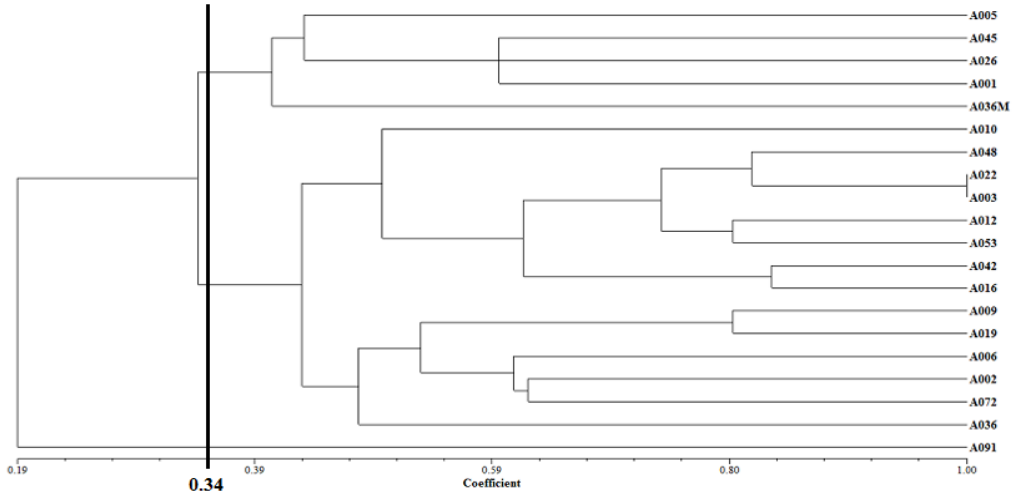

Fig. 3. UPGMA dendrogram constructed from molecular data (SSR Marker Analysis) of 20 Nigerian castor genotypes

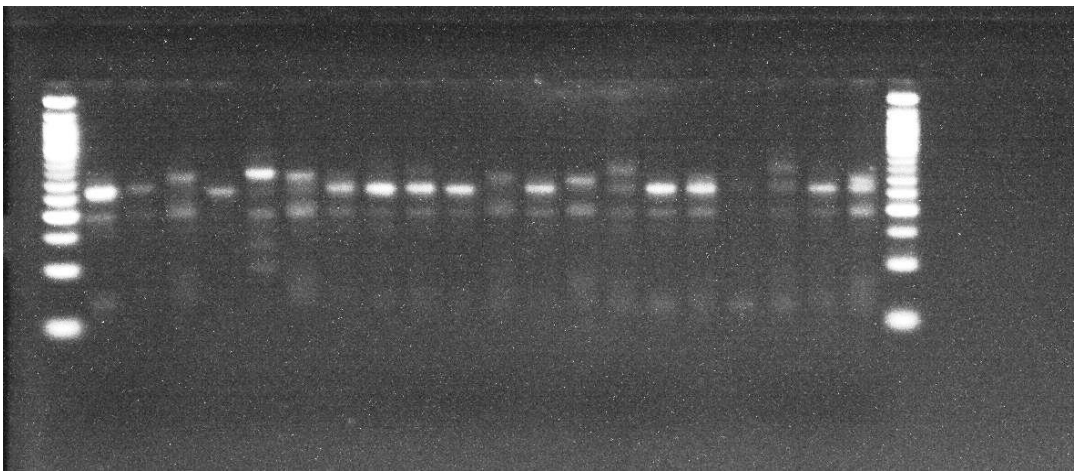

Fig. 4. Polymorphic band for SSR markers (A - RC594-V30156.41) among 20 castor genotype

The absence of correlation between genetic diversity and geographic diversity is in accordance with the reports of Costa *et al.* (2006) and Zheng *et al.* (2010). Besides being useful in hybridization programme, the potential groups could be selected for further yield trials in multiple locations; an attempt towards development of varieties by selection.

The result of molecular genotyping revealed that the markers used have high discriminating power for the entries. The average number of effective alleles (3.66) documented in the present study is similar to those reported by Qiu *et al.* (2010) and Seo *et al.* (2011) but lower than 5.5 described by Quintero *et al.* (2013). The high average PIC values (0.68) observed is an evidence of the effectiveness of the markers. A marker is informative (effective) if its PIC values is higher than 0.5 (Ahmad *et al.*, 2015). High PIC was also reported by Quintero *et al.* (2013). However, this is in contrary with the conclusions of Allan *et al.* (2008) and Seo *et al.* (2011) who recorded PIC mean of 0.403 and 0.260 respectively in castor. The mean of expected heterozygosity (0.74), Nei's gene diversity index (0.72) and Shannon's information index (1.43) were high, indicating adequate genetic diversity among the genotypes evaluated. The genetic diversity parameters reported in the current study were higher than those reported in previous study (Allan *et al.*, 2008; Seo *et al.*, 2011; Rukhsar *et al.*, 2017). This may be due to utilization of different markers and the germplasm assessed in the studies. The resolution of the relationships among the genotypes through the dendogram revealed high genetic diversity among the genotypes. Also similar to the result of morphological data, the local genotypes and the exotic ones were distributed randomly among the cluster groups. The clustering pattern and random distribution of the genotypes showed no evidence of geographic influence on the diversity observed and thus suggesting other forces such as natural and artificial selection, and genetic drift as contributory factors to the observed diversity among the studied genotypes. The genetic diversity and non-geographical correlations observed among the genotypes are similar to the findings of Allan *et al.* (2008), Milani *et al.* (2009) and Foster *et al.* (2010). In a case, rather than the present outcomes, some level of geologically organized clusters was seen among 8 genotypes examined by Qiu *et al.* (2010). Though, few sample sizes which could affect the result was acknowledged by the investigators.

Conclusions

In the present study, high genetic diversity among the genotypes studied and no geographical correlation to the diversity were observed. The PIC estimated for the SSR primers were relatively high. From these findings, it is showed that the twenty genotypes are divergent in nature and they could serve as good genetic material for castor breeding in Nigeria.

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Conflict of Interest

The authors declare that there are no conflicts of interest related to this article.

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