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Selection of ideal castor genotypes for production of food condiment (*Ogiri*) in Nigeria

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ABSTRACT INFO	ABSTRACT
Research Paper	Castor (<i>Ricinus communis</i> L.), besides being cultivated for its oil, its seed is used to prepare a food condiment (<i>Ogiri</i>). <i>Ogiri</i> is a highly proteinous fermented food condiment
	step-wise selection was carried out for ideal genotypes that could be cultivated for the condiment in Nigeria. The trial was conducted based on the basic protocol for varietal release and registration in Nigeria. The trials were carried out on replicated plots from 2014 through 2019, using Randomised Complete Block Design. Selections were made from seventeen (17) large seeded castors based on yield performances, reaction to pests, nutrient contents, yield stability and farmers' preference. Results showed that only eight, out of the 17 genotypes initially evaluated, performed above the norm in all the traits
Received: 28 Jan 2022	considered at the on-station assessments. The eight genotypes had appreciable seed yield (726.96 kg/ha to 1481.01 kg/ha), adequate seed oil content (29.11% to 39.60%),
Accepted: 03 Sep 2022	good nutrient contents, and tolerance to major insect pests and disease. Based on the stability assessment, two genotypes (Acc001 and Acc045) were identified as the most ideal for farmers' participatory selection. The two genotypes recorded higher seed yields and stability across the locations. The on-farm performance appraisal revealed high farmers' preference for the genotype Acc001 because of its higher yield and market value. The genotype Acc001 could be recommended for registration and release in Nigeria.
	<i>Key words:</i> Castor condiment, Farmers' preference, On-farm performance appraisal, On-station trials, Stability assessment, Varietal registration.

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INTRODUCTION

Castor (Ricinus communis L.) is a flowering plant in the family Euphorbiaceae (Spurge) and subfamily Acalyphoideae. It is a monotypic genus (Ricinus) that belongs to a sub-tribe Ricininae (Weiss, 2000). The origin of castor is obscure because of its extensive distribution in the earliest times and the speed/ease at which it establishes itself as a native plant. While some researchers believed that castor originated from Asia, most authors agreed that it is native to Africa (Anjani, 2012). Castor is one of neglected oilseed crops recently regaining popularity due to its economic value around the world (Ogunniyi, 2006; Gana et al., 2013). The castor seed contains oil which is used for many industrial applications (Salihu et al., 2014). The castor production contributes notable foreign exchange credits to economy of many countries, including India, Brazil and China (Ibeagha and Onwualu, 2015). India, being the major producer of castor in the world (accounting for 85% of production), earns foreign exchange to the tune of nearly € 92 million through the export of castor oil, cake and seed (Manjunatha et al., 2019a). However, out of about 1,512,761.80 metric tons of the world castor production, Nigeria contributes only about 0.26% to the production and the country local consumption rate of castor oil and its derivatives has been estimated at about 300,000 tons per year (RMRDC, 2009; Salihu et al., 2014; Ibeagha and Onwualu, 2015; AgriWatch, 2015). Castor has a wide-range of variability for characteristics such as seed size (Wiess, 2000). The small seeded castor is commonly chosen if the interest is on the seed oil while the large seeded ones are preferred if the interest is on the product derived from seed endosperm (Salihu et al., 2015). In Nigeria and some other parts of West Africa, the large seeded castors are used to produce 'Ogiri' - a local condiment (Gana, 2015). The small seeded castor seeds are not used for the condiment due to the drudgery involved in the removal of the seed coat and low endosperm yield. Ogiri from castor seeds is an historical condiment in Nigeria prepared through fermentation. During the fermentation, the water soluble toxic compounds (Ricin) in the endosperm dissolve into the water, leaving unharmed endosperm for consumption (Odunfa and Oyeyiola, 1985). The condiment is a highly proteinous fermented food supplement traditionally consume by about 20% of the Nigerian population (Okeke et al., 2009). The castor condiment has been reported to have 5.70 and 2.57 times higher protein content than pumpkin and snail respectively (Okeke et al., 2009). The condiment, besides providing supplementary protein, has been reported to have health benefits of improving the eye vision and digestion (Okeke et al., 2009). Because of the high protein content, the castor meal has been extensively considered as an alternative source of protein for animal feeds. The residual meal, after detoxification by boiling, could be used as protein supplement in preparation of broiler finishing diets without any harmful effects (Ani and Okorie, 2009). Also, the meal (autoclaved) could be used in place of soybean in sheep rations. Organic fertilizer produced from castor meal was reported to have advantage of high nitrogen content, fast mineralization and antinematode effects (Lima et al., 2011). The high potential yield and unique fatty acid composition of castor oil present a unique opportunity to expand industrial vegetable oil production in Africa, including Nigeria. Castor is not consumed by ruminant animals, thus it is herders-farmers friendly.

In Nigeria and some parts of Africa, castor is found growing in wild and in some cases it is cultivated as a cash crop with little or no management practice (Salihu et al., 2014). Castor is not a food crop; it therefore, serves as an alternative source of vegetable oil to subdue the conflicting demand between oil for food and oil for the industries. Despite the huge economic benefits of castor, its productions in Africa have been limited by a number of factors; prominent among them are lack of improved varieties and little research attention across the continent. The potential of Nigeria to exploit castor production can be harnessed with the ideal climate for its commercial production across the country. However, unlike other oil crops, castor improvement programme in Nigeria has not been receiving much attention, resulting in lack of ideal varieties for its production demand (Amosun et al., 2013). Low yield is a major limitation of production in Nigeria (Gana, 2015). Against average yield of 1,200–3,000 kg/ha obtainable in other countries like India, China and Brazil; the average yield among farmers in Nigeria ranges between 300 kg/ha and 600 kg/ha (Amosun et al., 2013). Another major limitation in the country is poor and unorganized castor market (Salihu et al., 2015). The major off take of castor seed in Nigeria presently are the local condiment producers and some cottage oil industries; thus, farmers have preference for the large seeded castor because of the available market. Therefore, the objectives of this research were to (i) evaluate the performance of the large seeded castor for yield potential, pest/disease reactions and agronomic performance, (ii) to identify and release a baseline castor variety for the production of food condiment (Ogiri) in Nigeria. The objectives

were achieved based on the basic protocol for varietal release and registration in Nigeria (NACGRAB, 2016).

MATERIALS AND METHODS

The genetic materials evaluated in this work were obtained from the Castor Research Programme of the National Cereals Research Institute (NCRI) Badeggi, Nigeria. The materials were evaluated from 2014 through 2019. Selections were made from seventeen (17) large seeded castor genotypes during the study. Widely cultivated large seeded farmers' cultivar (Large Ogba Okah) was considered as checks, as there was no standard check at the time of evaluation. This was to ensure optimum selection accuracy for farmers' acceptability. Yield trials (On-station, multi-location and on-farm) were carried out on the genotypes for the selection of ideal genotypes for a major production demand (*Ogiri*) in the country.

On-station yield assessment

At the on-station, the seventeen (17) large seeded genotypes were evaluated at the National Cereals Research Institute (NCRI) Badeggi Nigeria during 2014 and 2015 rainy seasons. The trials were arranged in Randomised Complete Block Design (RCBD) with three replications. Plot size of 5×3 m and plant spacing of 1.00 m by 0.75 m were used. Two seeds were sown and later thinned to one stand per hill. Fertilizers at 60:30:30 kg/ha of N:P:K respectively were applied. Weeding was carried out at 3, 7 and 11 weeks after planting.

Assessment of reactions to major pests

On-field observations on major disease (Cercospora leaf spot) and insect pests (Leaf worms - Spodoptera spp.; Shoot and Capsule Borers - Conogethes (Dichocrosis) punctiferalis) were made on the 17 genotypes at two locations (Badeggi and Ibadan) during 2014 and 2015 raining seasons. The protocol for this study is the same as reported in the on-station trial above. Records on leaf spot diseases and insect damage incidence (%) due to leaf miner, sucking insects and capsule borers were taken. The scoring of the diseased plants was done using a 1 - 5 scale as described by Mamza (2008). The percentage of insect damage incidence was taken on the leaves, inflorescences and capsules two times before harvest maturity following the procedure of Kataria and Kumar (2012). Observations were made on 10 plant samples in each plot, amounting to 30 plant samples per genotype. The disease observations were made at flowering and maturity.

Proximate analysis of the condiment (Ogiri)

The fermentation of castor seeds into the condiment

(*Ogiri*) was carried out according to Ojimelukwe et al. (2011). The seeds were sorted to remove chaff and unwanted materials. The sorted seeds were boiled for 5 hours and then dehulled. The endosperms were wrapped in jute bag and boiled for 3 hours to soften. Then, it was left to ferment at the prevailing ambient temperature (32-35 °C) for 5 days. At the end of the fermentation period, the seeds were ground into a paste and packaged after the unique aroma of *Ogiri* developed. The *Ogiri* was then stored in a refrigerator at 5 °C for chemical analysis. The proximate analysis of the samples for moisture, total ash, crude fibre and fat was carried out in triplicates using methods described by Onwuka (2005). Both the seeds and *Ogiri* were analyzed.

Yield performances and stability of the selects

Based on performance, eight (8) large seeded genotypes (including the check), from the on-station trials, were evaluated at eight (8) locations in 2016 and 2017 raining seasons. The trials were arranged in a Randomised Complete Block Design (RCBD) with three replications. The genotypes were evaluated on plot size of $5m \times 6m$ with a plant spacing of 1.00 m by 0.75 m. Two seeds were sown and later thinned to one stand per hill. Fertilizer at 60:30:30 kg/ha of N:P:K, respectively, was applied. Weeding was carried out at 3, 7 and 11 weeks after planting. The locations used were NCRI Badeggi (9° 45' 0" N, 6° 07' 0" E), Federal University of Technology (FUT) Minna (9° 36' 50" N, 6° 33' 25" E), Federal College of Agriculture Zuru, NCRI Mokwa Station (9° 12' 0" N, 5° 20' 0" E), NCRI Bacita Station (9° 5' 0" N, 4° 57' 0" E), NCRI Riyom Station (9° 38' 0" N, 8° 46' 0" E), NCRI Ibadan (8°0'0" N, 3°10′60″ E) and Amakama (5.4704° N, 7.4841° E).

Farmers' participatory selection activity

Based on the performance in the multi-locational trials, two high yielding genotypes (Acc.001 and Acc.045) were evaluated at farmers' fields alongside farmers' cultivars, during 2019 raining season. The on-farm trials were conducted on the farmers' fields in Kogi, Niger and Kwara States of Nigeria. A total of ten farmers from different villages were used across the states. The two castor genotypes were evaluated at farmers' fields in Bacita and Marafa, Kwara State (8.9669° N, 4.3874° E); Ndwanguwa and Chimbi in Niger State (9.9309° N, 5.5983° E); Agbeji, Ajenejo, Ajogu, Out, Imale in Kogi State (7.7337° N, 6.6906° E). The trials were coordinated in collaboration with the staff of Agricultural Development Projects (ADP) in the selected states. Farmers were interviewed on their perception about the attributes of the new varieties, in comparison to their cultivars.

Data collection and analysis

Data were collected on days to flowering (DF), days to maturity (DM), height at maturity (HM), number of spikes per plant (SPP), spike length (SL), 100 seed weight (SW), seed yield (SY) and percentage seed oil content (SOC - as described by Abayeh et al., 1998). Records were also taken on the genotypes reactions to pest/diseases, and quality of the Ogiri and seeds. The morphological parameters were taken according to a castor descriptor (India, 2004). Data generated were subjected to analysis of variance for testing of significant differences among the entries. Genotype ranking scores (RS) for selection at the onstation evaluation was done using modified method described by Akçura et al. (2011). The method was modified by ranking in descending order to direction of the trait advantage. That is genotype with shorter days to maturity was ranked with the highest numeral instead of lowest numeral; therefore, the performance/ selection was determined by the magnitude of the total ranked scores. Also, the result of the individual trial was considered as a unit rank score and thus the score pool sum was estimated as the sum rank score (Rank Score+Standard deviation) for the selection. Yield Performances and Stability Analysis (GGE Biplot) for the multi-locational data was done following the procedure of a statistical package PBTools 1.3 version.

RESULTS AND DISCUSSION

On-station selection of superior genotypes

The results of on-station trials revealed significant differences among the genotypes for seven morphological traits considered except days to maturity (Table 1). There was a significant effect of year variation on the seed yield (SY), plant height (PH), spikes per plant (SPP) and spike length (SL) (Table 1). The seed yield ranged from 399.73 kg to 1481.01 kg. The days to maturity (DM) varied between 104.00 and 124.50 days. Hundred seed weight (100 SW) ranged from 39.23 g to 57.23 g. The seed oil content (SOC) among the genotypes was between 29.11% and 40.11%. The total ranking score was between 36 and 108 with an average mean (Norm) of 72. Among the genotypes, only seven scored above the norm (72). The wide range of variability among the entries gives room for selection among them. This gave opportunity for selection of superior genotypes for multi-locational yield trials. Several authors have reported significant variations among castor germplasm (Popova and Moshkin, 1986; Rao et al., 2009; Alhaji et al., 2019). Seed yield range similar to the finding reported here has also been reported in several studies by many authors.

In India average seed yield ranged between 371 kg/ ha and 1864 kg/ha across different environments and agronomic conditions was reported by Basappa (2007). Silva *et al.* (2009) reported average yield of 1600 kg/ ha in state of Parana in Brazil. However, average seed yield of castor ranges between 1,000 kg/ha and 3,000 kg/ha could be achieved depending on variety, crop management practices and climatic conditions (Maroyi, 2007; Swapan *et al.*, 2021). Abimiku *et al.* (2012) reported seed yield between 127 kg/ha and 601 among nine castor accession evaluated at two locations in Nigeria.

Reactions to major pests

The result of reactions to disease (Cercospora leaf spot) is presented in Table 2. There was a significant difference in reactions to the disease among the genotypes at the two locations. The reaction was also affected by the locations as well as year variations at the locations. The pool means for the two locations ranged between 1.32 and 2.87. The total ranked scores showed that only eight out of the seventeen genotypes evaluated recorded scores lower than the norm (18) for reaction to leaf spot disease. Reaction to prevailing diseases in a target region is an integral part of criteria for varietal nomination. This is normally on field reactions under normal farmers' production practices. In Nigeria, the most prevailing disease in the target region of production was *Cercospora* leaf spot (Gana et al., 2014). Damage to castor leaves caused reduction in seed yield and any 1m² loss of leaf area resulted in production loss of 37.83 g and 24.4 g seed yield and seed oil yield per hectare, respectively (Lakshmi et al., 2010). Yield loss of 80% to 100% has been attributed to fungal disease in India (Anjani et al., 2004). Variations in reaction to disease among castor varieties and lines have also been reported in several studies (Holliday, 1980; Sussel et al., 2009; Chagas et al., 2010; Soares, 2012). The results reported here are different from the findings of Salihu et al. (2019) who reported a range between 1.43 and 4.17 scores with average score of 2.89 for leaf spot disease among 86 castor genotypes. The dissimilarity might have arisen from the differences in the number of genotypes considered in the two studies. Similar to the scores reported here was the finding of Mamza et al. (2008) who studied fungal leaf blight incidence and severity on castor seedling at different stages.

Tables 3, 4 and 5 show the results of insect pest incidence on leaves, inflorescence and capsules, respectively. A similar trend of significant differences for the sources of variations was observed for the incidences on the three parts of the crop. Significant

)])))]])	• •)	100 SW)	SOC)
Intries	SY (Kg/ha)	Score	DM	Score	HM (cm)	Score	SPP	Score	LS (cm)	Score	(g)	Score	(%)	Sc
.cc001	1481.01	17	107.29	14	224.66	4	7.74	17	30.59	17	52.12	12	37.24	1
.cc014	427.05	ω	107.50	13	172.00	13	3.11	4	20.57	ω	42.98	ω	31.56	4
.cc015	515.00	7	121.50	ω	235.00	ω	3.01	ω	19.00	<u>د</u>	53.76	13	29.67	N
.cc016	457.47	4	109.00	1	187.00	12	2.50	-	26.00	1	53.78	14	30.91	ω
vcc020	776.59	11	124.50	-	146.50	17	2.50	2	23.00	4	55.34	15	39.12	12
.cc024	726.96	10	105.00	16	268.50	2	3.50	СI	23.00	о	47.80	4	29.11	-
vcc040	788.51	12	108.00	12	206.50	8	3.76	10	24.76	8	57.23	17	40.09	16
vcc041	554.63	9	118.50	4	206.50	9	3.57	œ	23.00	Ωı	55.82	16	34.12	7
vcc042	519.59	ω	112.00	7	216.00	ი	4.44	12	28.00	12	49.22	7	35.82	10
vcc043	502.46	თ	111.00	∞	197.50	11	3.56	7	29.51	15	50.57	10	33.01	ი
.cc044	399.73	-	104.00	17	218.00	Сı	3.65	9	24.76	9	39.23	-	39.56	14 4
vcc045	919.05	14	115.96	Сı	169.39	14	5.97	15	30.47	16	50.01	9	39.60	ე
.cc046	496.70	GI	106.00	15	208.00	7	3.55	о	24.50	7	49.99	8	40.11	17
vcc048	1182.38	16	109.00	10	151.50	16	7.12	16	25.50	10	51.00	11	31.81	J
vcc049	420.39	Ν	113.00	ი	206.50	10	3.78	11	20.50	Ν	42.31	2	39.19	⊒
cc050	812.93	13	110.00	9	167.50	15	5.87	14	28.11	13	49.09	0	34.45	œ
ocal Check	941.77	15	123.46	2	272.95	-	4.57	13	28.31	14	48.45	σ	35.4	9
irand Mean	718.95		112.69		202.59		4.25		25.27		50.88		35.28	
IS Year (Y)	342900.68*		749.03		24932.66*		6.44*		122.96*		360.19		478.70	
IS Block within	24684.91		421.72		2388.63		0.77		9.74		76.02		85.75	
IS Genotype (G)) 642310.62**		706.05		19199.30*	*	15.17**		227.36**		210.51**		154.78**	
IS G×Y	16863.41		208.43		1635.16		0.81*		22.37		32.87		26.93	
			649.09		960.92		0.31		11.01		30.53		40 <u>98</u>	

spike, 100SW: Weight of 100 seeds, SOC: Seed oil content.

0		l	Badeggi				Ibadan		Pool	Total
Genotypes	2016	2017	Combined	Ranking score	2016	2017	Combined	Ranking score	mean	score
Acc.014	2.20	2.15	2.18	6	1.84	1.86	1.85	11	2.01	17
Acc.048	1.36	1.24	1.30	16	1.39	1.31	1.35	16	1.32	32
Acc.049	2.31	2.21	2.26	4	2.50	2.36	2.43	4	2.34	8
Acc.050	1.14	1.00	1.07	17	2.05	1.86	1.96	8	1.51	25
Acc001	1.62	1.65	1.64	13	1.84	1.85	1.85	12	1.74	25
Acc015	2.29	2.01	2.15	7	2.79	2.52	2.65	1	2.40	8
Acc016	1.59	1.45	1.52	14	2.20	2.07	2.13	5	1.83	19
Acc020	1.47	1.42	1.45	15	1.98	1.83	1.90	10	1.68	25
Acc024	2.34	2.23	2.29	3	1.62	1.59	1.60	15	1.95	18
Acc040	1.81	1.74	1.77	10	2.07	1.91	1.99	6	1.88	16
Acc041	2.12	1.98	2.05	9	1.14	1.01	1.08	17	1.56	26
Acc042	3.27	3.12	3.19	1	2.56	2.53	2.54	2	2.87	3
Acc043	2.66	2.60	2.63	2	1.75	1.76	1.75	14	2.19	16
Acc044	2.22	1.99	2.10	8	2.06	1.92	1.99	7	2.05	15
Acc045	1.82	1.67	1.75	11	1.82	1.82	1.82	13	1.78	24
Acc046	2.29	2.14	2.22	5	2.50	2.41	2.45	3	2.33	8
Local Check	1.71	1.64	1.68	12	1.96	1.88	1.92	9	1.80	21
Mean	2.01	1.90	1.95		2.00	1.91	1.96		1.96	18
MS Location (L)									0.11	
MS Block within	3.7	1.98	5.47		0.65	1.55	1.87		3.72	
MS Year (Y)			3.48**				2.18**		5.62**	
MS Genotype (G)	8.32**	7.89**	16.08**		5.41**	4.76**	10.06**		17.51**	
MS Y×G			0.08				0.11		0.1	
MS L×Y									0.11	
MS L×G									8.61**	
MS L×Y×G									0.1	
MS Error	0.22	0.1	0.13		0.1	0.24	0.17		0.15	

Table 2. Scores for *Cercospora* leaf spot disease on the 17 castor genotypes evaluated at Badeggi and Ibadan across two seasons.

Note: MS: Mean square, *: Significance at 0.05, **: Significance at 0.01.

effects of genotypes and genotype by year interaction at the two locations were observed for the insect pest incidence in the three parts. The pooled mean for the insect pest incidence on the leaves varied between 11.71% and 34.30% with an average of 18.57% (Table 3). For the inflorescence, the pooled mean varied between 6.74% and 18.88% (Table 4). A range between 5.45% and 16.71% was observed for the incidence of capsule borer (Table 5). Castor suffers from insect pest infestation which could set limitation to the castor production in some areas. Therefore, in addition to the major breeding objective, any potential variety must be screened for its reaction to the major insect pests in the target area of production. Several insect pests have been reported as being economically important in castor field. Insects that infest castor crop are more than 100, but only a few major pests are responsible for the crop losses (Kolte, 1995). Semilooper (Achaea *janata*), castor shoot borer (*Conogethes punctiferalis*), capsule borer (Dichocrosis punctiferalis), tobacco

caterpillar (Spodoptera litura), red hairy caterpillar (Amsacta spp.), and leaf miner (Liriomyza trifolii) have been reported as being important in India (Basappa, 2007; Anjani et al., 2010). Soares et al. (2001), and Ribeiro and Costa (2008) reported stink bug (Nezara viridula), leaf hopper (Empoasca spp.), defoliators including armyworm (Spodoptera frugiperda), A. janata, and black cutworm (Agrotis ipsilon), and the mites Tetranychus urticae and Tetranychus ludeni as the major pests of castor in Brazil. In Nigeria, leaf worms (Spodoptera spp.), and capsule and shoot borers were identified as major insect-pests of castor (Gana et al., 2014). The observed variation in reaction to the insect-pests among genotypes in the present study is in concurrence with that reported by Puneet et al. (2020) in a study on twelve castor genotypes screened against major insect-pests in South-West Haryana. Puneet et al. (2020) reported mean damage incidence between 5.23% and 14.43% for soot and capsule borer infestation among the twelve genotypes studied.

		Bade	ggi			Iba	dan		Pool	Total
Genotypes	2016	2017	Mean	Rank score	2016	2017	Mean	Rank score	mean	Score
Acc001	12.07	13.66	12.86	16	12.98	11.81	12.94	14	12.90	30
Acc014	35.15	32.55	33.85	2	34.08	31.15	32.62	2	33.23	4
Acc015	37.74	34.01	35.87	1	33.63	31.84	32.73	1	34.30	2
Acc016	29.53	28.45	28.99	3	25.77	25.33	25.55	3	27.27	6
Acc020	13.65	13.95	13.80	12	13.38	12.41	12.90	15	13.35	27
Acc024	13.19	11.06	12.12	17	12.17	10.42	11.30	17	11.71	34
Acc040	16.74	17.80	17.27	8	15.11	16.52	15.82	9	16.54	17
Acc041	16.24	19.77	18.01	6	16.10	18.65	17.37	6	17.69	12
Acc042	16.21	16.63	16.42	10	14.78	16.53	15.66	10	16.04	20
Acc043	28.37	18.94	23.66	4	24.91	16.86	20.89	5	22.27	9
Acc044	21.65	23.13	22.39	5	20.82	21.05	20.94	4	21.66	9
Acc045	13.60	13.23	13.42	15	12.97	12.22	12.59	16	13.01	31
Acc046	15.20	19.08	17.14	9	13.41	18.25	15.83	8	16.49	17
Acc048	12.55	14.93	13.74	14	12.90	13.08	12.99	13	13.37	27
Acc049	16.92	18.03	17.48	7	14.60	17.80	16.20	7	16.84	14
Acc050	16.32	16.03	16.17	11	13.42	16.17	14.80	11	15.48	22
Local Check	13.73	13.80	13.77	13	13.78	13.03	13.41	12	13.59	25
Mean	19.34	19.12	19.23		17.84	17.81	17.91		18.57	18
MS Location (L)									6.86	
MS Block within	31.14	5.74	18.44		32.11	28.38	30.25		56.38	
MS Genotypes (G)) 200.80**	136.18**	322.42**		161.50**	122.03**	270.89**		590.96**	
MS Year			1.27				1.03		1.96	
MS G×Y			14.56**				12.64**		4.28*	
MS L×G									25.58**	
MS L×Y									1.54	
MS L×G×Y									2.92	
MS Error	1.51	0.81	1.16		3.69	2.57	3.13		2.20	

Table 3. Percentage damage incidence of leaf worms on the leaves of the 17 Castor genotypes evaluated at two locations across two seasons.

Capsule infestation of 15.50% and 40% incidence of leaf miner were reported by Manjunatha (2019b). Losses in castor due to insect-pests are estimated to be in the tune of 35-50 percent (Kolte, 1995).

Nutritional composition of the condiment (Ogiri)

The results of the proximate analysis for the local condiment (*Ogiri*) and the seed are presented in Tables 6 and 7, respectively. Significant differences were observed among the genotypes for the proximate indices of both seeds and condiment produced from the seeds. No effect of location and $G \times L$ interaction was observed for the indices in both samples. For the condiment, average protein content ranged from 12.49 to 20.61 percent (Table 6). Average value ranges of 17.26 to 24.58, 1.20 to 1.96 and 15.16 to 29.43 were observed for fats, fibre and carbohydrates (CHO) respectively among the genotypes (Table 6). Total rank scores for the indices showed that 10 out of the 17 genotypes recorded scores higher than the average (Table 6). On average, a range between 12.39 and 25.40 percent

65

proteins was recorded in the seeds of the genotypes (Table 7). The total rank scores for the proximate indices (seeds) revealed that only six genotypes recorded scores above the average score (Table 7). This finding shows adequate variation and the possibility of genetic manipulation to enhance nutrient contents of the genotypes evaluated. Similar proximate indices to the present study have been reported by earlier researchers. Crude protein of 13.88 to 17.90% and crude fat of 48.76 to 57.00% from fermented castor seeds were reported by Ojimelukwe et al. (2011). Carbohydrate content between 15% and 30% was recorded from Ogiri fermented for different periods (Ojimelukwe et al., 2011). Under the prevailing nutritional insecurity, fermented foods (main dishes & condiments) have been identified as essential components of the diet in many African countries, including Nigeria (Steinkraus, 1996). Besides its characteristic flavor and taste in traditional soups and sauces, castor condiment (Ogiri) contributes to protein and essential fatty acid intake in West Africa (Oke and Umoh, 1998). The condiment has 5.70 and

•		Ba	adeggi			II	badan		Pool	Total
Genotypes	2016	2017	Combined	Ranking score	2016	2017	Combined	Ranking score	mean	score
Acc001	9.45	11.52	10.49	12	12.07	8.97	10.52	12	10.50	24
Acc014	18.38	20.06	19.22	1	17.23	19.86	18.55	1	18.88	2
Acc015	18.77	14.38	16.58	3	18.43	13.97	16.20	3	16.39	6
Acc016	19.42	17.52	18.47	2	18.76	16.10	17.43	2	17.95	4
Acc020	12.33	10.34	11.34	10	11.60	9.53	10.57	11	10.95	21
Acc024	10.98	7.05	9.02	16	10.50	6.83	8.67	16	8.84	32
Acc040	10.62	8.28	9.45	14	10.70	7.93	9.32	14	9.38	28
Acc041	13.99	16.91	15.45	6	13.65	16.54	15.10	5	15.27	11
Acc042	14.63	12.82	13.73	9	14.76	13.14	13.95	8	13.84	17
Acc043	13.24	18.05	15.65	5	12.89	16.66	14.78	6	15.21	11
Acc044	14.98	14.49	14.74	8	13.77	13.60	13.69	9	14.21	17
Acc045	10.34	8.43	9.39	15	10.10	8.04	9.07	15	9.23	30
Acc046	11.85	17.66	14.76	7	11.64	17.44	14.54	7	14.65	14
Acc048	7.14	6.37	6.76	17	7.18	6.27	6.73	17	6.74	34
Acc049	14.96	16.93	15.95	4	14.85	16.32	15.59	4	15.77	8
Acc050	11.54	9.10	10.32	13	10.33	8.92	9.63	13	9.97	26
Local Check	10.07	11.28	10.68	11	9.76	11.40	10.58	10	10.63	21
Mean	13.10	12.89	13.00		12.6	12.44	12.52		12.76	18
MS Location (L)									10.69	
MS Block within	10.73	7.6	9.16		11.49	2.01	6.75		15.95	
MS Genotypes (G)) 35.82**	58.53**	* 81.75**		34.66**	[•] 54.51*'	76.93**		158.26**	
MS Year			4.07				6.51		2.31	
MS G×Y			12.60**				21.25*		4.61	
MS L×G									240.61**	
MS L×Y									2.64	
MS L×G×Y									3.69	
MS Error	6.65	5.59	4.21		6.16	7.17	10.16		9.32	

Table 4. Percentage damage incidence of shoot borers on the inflorescence of the 17 castor genotypes evaluated at two locations across two seasons.

2.57 times higher protein content than pumpkin and snail, respectively (Okeke *et al.*, 2009).

Table 8 shows the selection indices for ideal candidates for multi-environment trials. The pooled total ranking scores for the parameters considered revealed that eight out of the seventeen genotypes performed averagely across the traits. The genotypes selected (Acc001, Acc020, Acc024, Acc040, Acc045, Acc048, Acc050 and Local Check) had sum scores ranged between 275.78 and 370.71 against the average 275.21. The selected genotypes had appreciable seed yields ranging between 726.96 kg/ha recorded by Acc024 and 1481.01 kg/ha by Acc001 (Table 1), adequate seed oil content between 29.11% and 39.60% (Table 1), good protein content (Tables 6 and 7) and tolerance to major insect pests and disease (Tables 2, 3, 4 and 5).

Yield performance and stability of the selects

Tables 9 and 10 present the results of the multilocational trials. The ANOVA for individual location revealed significant effects of genotypes (G), Year (Y) and genotype by year interaction (GY) for seed yields in four locations (Badeggi, Mokwa, Ibadan, Zuru) (Table 9). A significant contribution of genotypes to the variation in seed yield was registered in all the locations (Table 9). Also, the pooled ANOVA showed that there were significant differences in the seed yield and all other traits considered among the genotypes (Table 10). Significant effects of environments as well as genotype by environment were observed for seed yield, height at maturity, spike per plant and seed oil content (Table 10). Pooled means showed that the genotype Acc001 recorded the highest average seed yield of 1263.53 kg/ ha while the least mean was recorded by the local check (i.e popular farmers' accession – not standard check) (Table 10). The least days to first raceme maturity was observed in genotype Acc040 and the highest seed oil content was recorded in genotype Acc020 (Table 10). The significant effects of locations as well as G×L interactions observed for the seed yield, height at maturity, number of racemes and seed oil content have

		Ba	adeggi			I	badan		Pool	Total
Genotypes	2016	2017	Combined	Ranking score	2016	2017	Combined	Ranking score	mean	score
Acc001	7.19	8.63	7.91	15	8.66	9.24	8.95	13	8.43	28
Acc014	16.26	14.89	15.58	3	16.22	14.84	15.53	2	15.56	5
Acc015	20.03	14.83	17.43	1	18.36	13.6	15.98	1	16.71	2
Acc016	14.5	11.43	12.97	5	12.98	10.18	11.58	5	12.28	10
Acc020	7.19	10.21	8.70	11	6.66	9.09	7.88	14	8.29	25
Acc024	5.95	5.23	5.59	17	5.69	4.94	5.32	17	5.45	34
Acc040	8.40	4.48	6.44	16	7.87	4.15	6.01	16	6.23	32
Acc041	12.6	10.77	11.69	6	11.39	10.13	10.76	7	11.23	13
Acc042	9.55	12.7	11.13	7	8.92	12.68	10.80	6	10.97	13
Acc043	13.32	13.49	13.41	4	11.95	12.48	12.22	4	12.81	8
Acc044	11.53	9.86	10.70	8	10.58	8.73	9.66	9	10.18	17
Acc045	9.04	8.83	8.94	10	8.47	8.15	8.31	12	8.63	22
Acc046	17.11	14.47	15.79	2	15.67	13.82	14.75	3	15.27	5
Acc048	7.38	9.62	8.50	12	7.32	9.53	8.43	11	8.46	23
Acc049	8.66	12.05	10.36	9	8.10	11.68	9.89	8	10.13	17
Acc050	9.44	6.72	8.08	13	8.55	6.67	7.61	15	7.85	28
Local Check	7.63	8.32	7.98	14	10.38	7.62	9.00	10	8.49	24
Mean	10.93	10.27	10.6		10.16	9.68	9.92		10.26	18
MS Location (L)									16.76	
MS Block within	5.19	5.03	5.11		11.4	8.13	4.77		9.59	
MS Genotypes (G) 49.99**	32.24**	* 72.52**		41.96*	* 30.43*	* 63.67**		1350.63**	
MS Year			11.21				5.96		3.475	
MS G×Y			9.72*				18.72*		5.81	
MS L×G									180.31**	
MS L×Y									0.4	
MS L×G×Y									5.994	
MS Error	4.22	3.85	4.03		10.02	7.31	8.78		7.484	

Table 5. Percentage damage incidence of capsule borers on the capsules of the 17 castor genotypes evaluated at two locations across two growing seasons.

also been reported by Solanki and Joshi (2003), Kumari et al. (2003), Patel and Pathak (2006), Aher et al. (2015) in their works on castor. Dave et al. (2017) reported significant influences of environments (E), genotypes (G) and genotype×environment interaction (GEI) on oil yield among 56 genotypes of castor evaluated.

According to the GGE Biplots, a total of 84.3% (61.1%+23.3%) variation was attributed to the Principal Component Axis 1 and 2 (Figures 1, 2, 3, 4) revealing the adequacy of the axes to explain substantial part of the variation observed. The GGE Biplots revealed that the eight locations could be grouped into two clusters with Badeggi (E3), Ibadan (E4), Amakama (E1) and Zuru (E8) in a cluster while Bacita (E2), Riyon (E7), Mokwa (E5) and Minna (E6) in another cluster (Figure 1). Ibadan and Mokwa locations showed the highest discriminating ability among the locations in the two clusters, respectively. This is evident from their longest vectors in each of the two mega environments. In the environmental cluster one, the locations are

highly correlated as angles between each pair of the locations are less than 90° (Acute angle). In terms of representativeness, Zuru (E8) with least angle to the average environmental axis (AEA) in Figure 2 is the most representative of other locations in its environmental cluster; however, it is the second less discriminating in the group. Bacita is the most representative in its group and also second highest discriminating location (Figure 2). The locations with high correlations could be merged and the representative location could be selected for future trials; if the correlations persist over years for several experiments.

The high contribution to variation within the PCA1 and PCA2 observed in the present study was also reported by Sakhare *et al.* (2018) who carried out GGE Bi-plot analysis in castor (*Riccinus communis* L.) for Vidarbha region of Maharashtra state.

In Figures 3 and 4, performance and stability of the genotypes are presented. The vertical axis represents the average yield.

Constrans		Moist	ure			A	sh			Protei	ns		Total
Genotypes	В	I	Mean	RS	В	I	Mean	RS	В	I	Mean	RS	RS
Acc001	31.19	28.8	29.99	11	1.98	2.04	2.01	5	21.15	20.06	20.61	17	
Acc014	25.88	25.27	25.58	4	3.88	3.92	3.90	16	17.38	18.28	17.83	12	
Acc015	29.87	26.98	28.43	9	2.43	2.43	2.43	6	17.08	15.90	16.49	8	
Acc016	36.44	35.58	36.01	16	3.2	3.20	3.20	14	14.54	14.78	14.66	4	
Acc020	27.42	25.14	26.28	6	1.99	2.02	2.01	4	19.15	18.99	19.07	15	
Acc024	28.24	25.24	26.74	7	1.83	1.80	1.82	2	20.10	19.49	19.79	16	
Acc040	28.96	28.78	28.87	10	1.37	1.28	1.33	1	19.67	18.20	18.94	14	
Acc041	37.70	37.56	37.63	17	3.93	3.79	3.86	15	15.87	14.10	14.99	5	
Acc042	28.64	27.62	28.13	8	2.94	2.93	2.93	11	16.87	16.71	16.79	10	
Acc043	31.48	31.38	31.43	13	3.09	2.94	3.02	12	14.88	13.74	14.31	3	
Acc044	26.74	25.58	26.16	5	2.04	1.75	1.89	3	19.15	17.17	18.16	13	
Acc045	32.86	31.65	32.26	14	2.62	2.57	2.59	7	13.07	11.90	12.49	1	
Acc046	35.34	31 17	33 26	15	2 64	2.58	2 61	9	17 40	15.90	16 65	9	
Acc048	23.36	20.02	21.69	2	3 19	3.01	3 10	13	18 65	16.22	17 44	11	
Acc049	22 15	19.82	20.99	1	4 67	4 46	4 57	17	13 55	12 11	12.83	2	
Acc050	25.61	23.08	20.00	3	2.64	2 57	2.61	8	16.00	14 27	15.00	6	
Local Check	31 48	28.89	30.19	12	2.04	2.54	2.67	10	16.63	14.48	15.56	7	
Mean	29.61	27.85	28.73	12	2 77	2 70	2.73	10	17 14	16.02	16.58		
MS Locations (L)	20.01	21.00	78 76		2.11	2.70	0.15		17.14	10.02	32 17		
MS Block within	77 47	56.03	75 75		0 16	0.1	0.13		16 4 1	19 92	18 16		
MS Genotypes (G)	157 36**	167 95**	123 06**		2 15**	2.06**	4 19**		36 09**	38 17**	33 04**		
MS GxI	107.00	107.50	12 25		2.10	2.00	0.02		00.00	00.17	11 22		
MS Error	42 38	34 52	43.45		0.21	0.04	0.02		10.86	12.08	10.47		
	42.00	-	10.10		0.21		0.01		10.00	12.00	10.47		
		Fats	S			- Fi	bre			CHC)		Tatal
Genotypes													
Genotypes	В	1	Mean	RS	В	I	Mean	RS	В	1	Mean	RS	RS
Genotypes	B 20.60	l 20.39	Mean 20.50	RS 11	B 1.90	l 1.81	Mean 1.86	RS 15	B 21.69	I 21.47	Mean 21.58	RS 6	RS 61
Genotypes Acc001 Acc014	B 20.60 21.92	l 20.39 21.26	Mean 20.50 21.59	RS 11 13	B 1.90 1.52	l 1.81 1.48	Mean 1.86 1.50	RS 15 7	B 21.69 18.78	I 21.47 18.22	Mean 21.58 18.50	RS 6 3	61 65
Genotypes Acc001 Acc014 Acc015	B 20.60 21.92 18.60	l 20.39 21.26 17.82	Mean 20.50 21.59 18.21	RS 11 13 4	B 1.90 1.52 1.53	l 1.81 1.48 1.41	Mean 1.86 1.50 1.47	RS 15 7 6	B 21.69 18.78 22.25	I 21.47 18.22 21.32	Mean 21.58 18.50 21.79	RS 6 3 8	61 65 41
Genotypes Acc001 Acc014 Acc015 Acc016	B 20.60 21.92 18.60 18.73	l 20.39 21.26 17.82 18.79	Mean 20.50 21.59 18.21 18.76	RS 11 13 4 5	B 1.90 1.52 1.53 1.34	l 1.81 1.48 1.41 1.33	Mean 1.86 1.50 1.47 1.34	RS 15 7 6 3	B 21.69 18.78 22.25 19.07	I 21.47 18.22 21.32 19.13	Mean 21.58 18.50 21.79 19.10	RS 6 3 8 5	61 65 41 33
Genotypes Acc001 Acc014 Acc015 Acc016 Acc020	B 20.60 21.92 18.60 18.73 19.32	I 20.39 21.26 17.82 18.79 18.25	Mean 20.50 21.59 18.21 18.76 18.79	RS 11 13 4 5 6	B 1.90 1.52 1.53 1.34 1.54	I 1.81 1.48 1.41 1.33 1.50	Mean 1.86 1.50 1.47 1.34 1.52	RS 15 7 6 3 8	B 21.69 18.78 22.25 19.07 26.83	I 21.47 18.22 21.32 19.13 25.35	Mean 21.58 18.50 21.79 19.10 26.09	RS 6 3 8 5 15	61 65 41 33 60
Acc001 Acc014 Acc015 Acc016 Acc020 Acc024	B 20.60 21.92 18.60 18.73 19.32 22.28	I 20.39 21.26 17.82 18.79 18.25 23.57	Mean 20.50 21.59 18.21 18.76 18.79 22.93	RS 11 13 4 5 6 16	B 1.90 1.52 1.53 1.34 1.54 1.94	I 1.81 1.48 1.41 1.33 1.50 1.98	Mean 1.86 1.50 1.47 1.34 1.52 1.96	RS 15 7 6 3 8 17	B 21.69 18.78 22.25 19.07 26.83 24.11	I 21.47 18.22 21.32 19.13 25.35 25.51	Mean 21.58 18.50 21.79 19.10 26.09 24.81	RS 6 3 8 5 15 11	61 65 41 33 60 73
Genotypes Acc001 Acc014 Acc015 Acc016 Acc020 Acc024 Acc040	B 20.60 21.92 18.60 18.73 19.32 22.28 23.53	l 20.39 21.26 17.82 18.79 18.25 23.57 21.54	Mean 20.50 21.59 18.21 18.76 18.79 22.93 22.54	RS 11 13 4 5 6 16 14	B 1.90 1.52 1.53 1.34 1.54 1.94 1.37	I 1.81 1.48 1.41 1.33 1.50 1.98 1.21	Mean 1.86 1.50 1.47 1.34 1.52 1.96 1.29	RS 15 7 6 3 8 17 2	B 21.69 18.78 22.25 19.07 26.83 24.11 23.68	I 21.47 18.22 21.32 19.13 25.35 25.51 21.68	Mean 21.58 18.50 21.79 19.10 26.09 24.81 22.68	RS 6 3 8 5 15 11 9	61 65 41 33 60 73 48
Genotypes Acc001 Acc014 Acc015 Acc016 Acc020 Acc020 Acc024 Acc040 Acc041	B 20.60 21.92 18.60 18.73 19.32 22.28 23.53 18.33	I 20.39 21.26 17.82 18.79 18.25 23.57 21.54 16.78	Mean 20.50 21.59 18.21 18.76 18.79 22.93 22.54 17.56	RS 11 13 4 5 6 16 14 2	B 1.90 1.52 1.53 1.34 1.54 1.94 1.37 1.48	I 1.81 1.48 1.41 1.33 1.50 1.98 1.21 1.31	Mean 1.86 1.50 1.47 1.34 1.52 1.96 1.29 1.40	RS 15 7 6 3 8 17 2 5	B 21.69 18.78 22.25 19.07 26.83 24.11 23.68 18.85	I 21.47 18.22 21.32 19.13 25.35 25.51 21.68 17.26	Mean 21.58 18.50 21.79 19.10 26.09 24.81 22.68 18.06	RS 6 3 8 5 15 11 9 2	61 65 41 33 60 73 48 30
Genotypes Acc001 Acc014 Acc015 Acc016 Acc020 Acc020 Acc024 Acc040 Acc041 Acc042	B 20.60 21.92 18.60 18.73 19.32 22.28 23.53 18.33 18.70	I 20.39 21.26 17.82 18.79 18.25 23.57 21.54 16.78 19.14	Mean 20.50 21.59 18.21 18.76 18.79 22.93 22.54 17.56 18.92	RS 11 13 4 5 6 16 14 2 7	B 1.90 1.52 1.53 1.34 1.54 1.94 1.37 1.48 1.66	I 1.81 1.48 1.41 1.33 1.50 1.98 1.21 1.31 1.63	Mean 1.86 1.50 1.47 1.34 1.52 1.96 1.29 1.40 1.65	RS 15 7 6 3 8 17 2 5 14	B 21.69 18.78 22.25 19.07 26.83 24.11 23.68 18.85 25.12	I 21.47 18.22 21.32 19.13 25.35 25.51 21.68 17.26 25.71	Mean 21.58 18.50 21.79 19.10 26.09 24.81 22.68 18.06 25.42	RS 6 3 8 5 15 11 9 2 12	61 65 41 33 60 73 48 30 64
Genotypes Acc001 Acc014 Acc015 Acc016 Acc020 Acc020 Acc024 Acc040 Acc041 Acc042 Acc043	B 20.60 21.92 18.60 18.73 19.32 22.28 23.53 18.33 18.70 24.63	I 20.39 21.26 17.82 18.79 18.25 23.57 21.54 16.78 19.14 24.52	Mean 20.50 21.59 18.21 18.76 18.79 22.93 22.54 17.56 18.92 24.58	RS 11 13 4 5 6 16 14 2 7 17	B 1.90 1.52 1.53 1.34 1.54 1.94 1.37 1.48 1.66 1.38	I 1.81 1.48 1.41 1.33 1.50 1.98 1.21 1.31 1.63 1.33	Mean 1.86 1.50 1.47 1.34 1.52 1.96 1.29 1.40 1.65 1.36	RS 15 7 6 3 8 17 2 5 14 4	B 21.69 18.78 22.25 19.07 26.83 24.11 23.68 18.85 25.12 15.19	I 21.47 18.22 21.32 19.13 25.35 25.51 21.68 17.26 25.71 15.12	Mean 21.58 18.50 21.79 19.10 26.09 24.81 22.68 18.06 25.42 15.16	RS 6 3 5 15 11 9 2 12 1	61 65 41 33 60 73 48 30 64 42
Genotypes Acc001 Acc014 Acc015 Acc016 Acc020 Acc020 Acc024 Acc040 Acc041 Acc042 Acc043 Acc044	B 20.60 21.92 18.60 18.73 19.32 22.28 23.53 18.33 18.70 24.63 20.22	I 20.39 21.26 17.82 18.79 18.25 23.57 21.54 16.78 19.14 24.52 18.57	Mean 20.50 21.59 18.21 18.76 18.79 22.93 22.54 17.56 18.92 24.58 19.40	RS 11 13 4 5 6 16 14 2 7 17 9	B 1.90 1.52 1.53 1.34 1.54 1.94 1.37 1.48 1.66 1.38 1.66	I 1.81 1.48 1.41 1.33 1.50 1.98 1.21 1.31 1.63 1.33 1.47	Mean 1.86 1.50 1.47 1.34 1.52 1.96 1.29 1.40 1.65 1.36 1.57	RS 15 7 6 3 8 17 2 5 14 4 11	B 21.69 18.78 22.25 19.07 26.83 24.11 23.68 18.85 25.12 15.19 22.70	I 21.47 18.22 21.32 19.13 25.35 25.51 21.68 17.26 25.71 15.12 20.83	Mean 21.58 18.50 21.79 19.10 26.09 24.81 22.68 18.06 25.42 15.16 21.77	RS 6 3 5 15 11 9 2 12 1 7	61 65 41 33 60 73 48 30 64 42 56
Genotypes Acc001 Acc014 Acc015 Acc016 Acc020 Acc020 Acc024 Acc040 Acc041 Acc042 Acc043 Acc044 Acc045	B 20.60 21.92 18.60 18.73 19.32 22.28 23.53 18.33 18.70 24.63 20.22 19.71	I 20.39 21.26 17.82 18.79 18.25 23.57 21.54 16.78 19.14 24.52 18.57 18.44	Mean 20.50 21.59 18.21 18.76 18.79 22.93 22.54 17.56 18.92 24.58 19.40 19.08	RS 11 13 4 5 6 16 14 2 7 17 9 8	B 1.90 1.52 1.53 1.34 1.54 1.94 1.37 1.48 1.66 1.38 1.66 1.62	I 1.81 1.48 1.41 1.33 1.50 1.98 1.21 1.31 1.63 1.33 1.47 1.46	Mean 1.86 1.50 1.47 1.34 1.52 1.96 1.29 1.40 1.65 1.36 1.57 1.54	RS 15 7 6 3 8 17 2 5 14 4 11 9	B 21.69 18.78 22.25 19.07 26.83 24.11 23.68 18.85 25.12 15.19 22.70 26.34	I 21.47 18.22 21.32 19.13 25.35 25.51 21.68 17.26 25.71 15.12 20.83 24.64	Mean 21.58 18.50 21.79 19.10 26.09 24.81 22.68 18.06 25.42 15.16 21.77 25.49	RS 6 3 5 15 11 9 2 12 1 7 13	61 65 41 33 60 73 48 30 64 42 56 42
Genotypes Acc001 Acc014 Acc015 Acc016 Acc020 Acc024 Acc024 Acc040 Acc041 Acc042 Acc043 Acc043 Acc044 Acc045 Acc046	B 20.60 21.92 18.60 18.73 19.32 22.28 23.53 18.33 18.70 24.63 20.22 19.71 17.86	I 20.39 21.26 17.82 18.79 18.25 23.57 21.54 16.78 19.14 24.52 18.57 18.44 16.66	Mean 20.50 21.59 18.21 18.76 18.79 22.93 22.54 17.56 18.92 24.58 19.40 19.08 17.26	RS 11 13 4 5 6 16 14 2 7 17 9 8 1	B 1.90 1.52 1.53 1.34 1.54 1.94 1.37 1.48 1.66 1.38 1.66 1.62 1.62	I 1.81 1.48 1.41 1.33 1.50 1.98 1.21 1.31 1.63 1.33 1.47 1.46 1.47	Mean 1.86 1.50 1.47 1.34 1.52 1.96 1.29 1.40 1.65 1.36 1.57 1.54 1.55	RS 15 7 6 3 8 17 2 5 14 4 11 9 10	B 21.69 18.78 22.25 19.07 26.83 24.11 23.68 18.85 25.12 15.19 22.70 26.34 19.20	I 21.47 18.22 21.32 19.13 25.35 25.51 21.68 17.26 25.71 15.12 20.83 24.64 17.91	Mean 21.58 18.50 21.79 19.10 26.09 24.81 22.68 18.06 25.42 15.16 21.77 25.49 18.56	RS 6 3 5 15 11 9 2 12 1 7 13 4	61 65 41 33 60 73 48 30 64 42 56 42 36
Genotypes Acc001 Acc014 Acc015 Acc016 Acc020 Acc020 Acc024 Acc040 Acc041 Acc042 Acc042 Acc043 Acc043 Acc044 Acc045 Acc046 Acc048	B 20.60 21.92 18.60 18.73 19.32 22.28 23.53 18.33 18.70 24.63 20.22 19.71 17.86 20.72	I 20.39 21.26 17.82 18.79 18.25 23.57 21.54 16.78 19.14 24.52 18.57 18.44 16.66 18.58	Mean 20.50 21.59 18.21 18.76 18.79 22.93 22.54 17.56 18.92 24.58 19.40 19.08 17.26 19.65	RS 11 13 4 5 6 16 14 2 7 17 9 8 1 10	B 1.90 1.52 1.53 1.34 1.54 1.94 1.37 1.48 1.66 1.38 1.66 1.62 1.62 1.62	I 1.81 1.48 1.41 1.33 1.50 1.98 1.21 1.31 1.63 1.33 1.47 1.46 1.47 1.49	Mean 1.86 1.50 1.47 1.34 1.52 1.96 1.29 1.40 1.65 1.36 1.57 1.54 1.55 1.61	RS 15 7 6 3 8 17 2 5 14 4 11 9 10 13	B 21.69 18.78 22.25 19.07 26.83 24.11 23.68 18.85 25.12 15.19 22.70 26.34 19.20 31.03	I 21.47 18.22 21.32 19.13 25.35 25.51 21.68 17.26 25.71 15.12 20.83 24.64 17.91 27.83	Mean 21.58 18.50 21.79 19.10 26.09 24.81 22.68 18.06 25.42 15.16 21.77 25.49 18.56 29.43	RS 6 3 5 15 11 9 2 12 1 7 13 4 17	61 65 41 33 60 73 48 30 64 42 56 42 36 80
Genotypes Acc001 Acc014 Acc015 Acc016 Acc020 Acc020 Acc024 Acc040 Acc041 Acc042 Acc042 Acc043 Acc043 Acc044 Acc045 Acc046 Acc048 Acc049	B 20.60 21.92 18.60 18.73 19.32 22.28 23.53 18.33 18.70 24.63 20.22 19.71 17.86 20.72 19.04	I 20.39 21.26 17.82 18.79 18.25 23.57 21.54 16.78 19.14 24.52 18.57 18.44 16.66 18.58 17.36	Mean 20.50 21.59 18.21 18.76 18.79 22.93 22.54 17.56 18.92 24.58 19.40 19.08 17.26 19.65 18.20	RS 11 13 4 5 6 16 14 2 7 17 9 8 1 10 3	B 1.90 1.52 1.53 1.34 1.54 1.94 1.37 1.48 1.66 1.38 1.66 1.62 1.62 1.62 1.73 1.27	I 1.81 1.48 1.41 1.33 1.50 1.98 1.21 1.31 1.63 1.33 1.47 1.46 1.47 1.49 1.12	Mean 1.86 1.50 1.47 1.34 1.52 1.96 1.29 1.40 1.65 1.36 1.57 1.54 1.55 1.61 1.20	RS 15 7 6 3 8 17 2 5 14 4 11 9 10 13 1	B 21.69 18.78 22.25 19.07 26.83 24.11 23.68 18.85 25.12 15.19 22.70 26.34 19.20 31.03 28.43	I 21.47 18.22 21.32 19.13 25.35 25.51 21.68 17.26 25.71 15.12 20.83 24.64 17.91 27.83 25.93	Mean 21.58 18.50 21.79 19.10 26.09 24.81 22.68 18.06 25.42 15.16 21.77 25.49 18.56 29.43 27.18	RS 6 3 5 15 11 9 2 12 1 7 13 4 17 16	61 65 41 33 60 73 48 30 64 42 56 42 36 80 56
Genotypes Acc001 Acc014 Acc015 Acc016 Acc020 Acc024 Acc040 Acc041 Acc042 Acc042 Acc043 Acc043 Acc044 Acc045 Acc046 Acc049 Acc050	B 20.60 21.92 18.60 18.73 19.32 22.28 23.53 18.33 18.70 24.63 20.22 19.71 17.86 20.72 19.04 23.22	I 20.39 21.26 17.82 18.79 18.25 23.57 21.54 16.78 19.14 24.52 18.57 18.44 16.66 18.58 17.36 22.39	Mean 20.50 21.59 18.21 18.76 18.79 22.93 22.54 17.56 18.92 24.58 19.40 19.08 17.26 19.65 18.20 22.81	RS 11 13 4 5 6 16 14 2 7 17 9 8 1 10 3 15	B 1.90 1.52 1.53 1.34 1.54 1.94 1.37 1.48 1.66 1.38 1.66 1.62 1.62 1.62 1.73 1.27 1.89	I 1.81 1.48 1.41 1.33 1.50 1.98 1.21 1.31 1.63 1.33 1.47 1.46 1.47 1.49 1.12 1.88	Mean 1.86 1.50 1.47 1.34 1.52 1.96 1.29 1.40 1.65 1.36 1.57 1.54 1.55 1.61 1.20 1.89	RS 15 7 6 3 8 17 2 5 14 4 11 9 10 13 1 16	B 21.69 18.78 22.25 19.07 26.83 24.11 23.68 18.85 25.12 15.19 22.70 26.34 19.20 31.03 28.43 26.53	I 21.47 18.22 21.32 19.13 25.35 25.51 21.68 17.26 25.71 15.12 20.83 24.64 17.91 27.83 25.93 25.59	Mean 21.58 18.50 21.79 19.10 26.09 24.81 22.68 18.06 25.42 15.16 21.77 25.49 18.56 29.43 27.18 26.06	RS 6 3 5 15 11 9 2 12 1 7 13 4 17 16 14	61 65 41 33 60 73 48 30 64 42 56 42 36 80 56 74
Genotypes Acc001 Acc014 Acc015 Acc016 Acc020 Acc024 Acc040 Acc040 Acc041 Acc042 Acc043 Acc043 Acc044 Acc045 Acc046 Acc048 Acc049 Acc050 Local Check	B 20.60 21.92 18.60 18.73 19.32 22.28 23.53 18.33 18.70 24.63 20.22 19.71 17.86 20.72 19.04 23.22 21.40	I 20.39 21.26 17.82 18.79 18.25 23.57 21.54 16.78 19.14 24.52 18.57 18.44 16.66 18.58 17.36 22.39 20.64	Mean 20.50 21.59 18.21 18.76 18.79 22.93 22.54 17.56 18.92 24.58 19.40 19.08 17.26 19.65 18.20 22.81 21.02	RS 11 13 4 5 6 16 14 2 7 17 9 8 1 10 3 15 12	B 1.90 1.52 1.53 1.34 1.54 1.94 1.37 1.48 1.66 1.38 1.66 1.62 1.62 1.62 1.73 1.27 1.89 1.62	I 1.81 1.48 1.41 1.33 1.50 1.98 1.21 1.31 1.63 1.33 1.47 1.46 1.47 1.49 1.12 1.88 1.51	Mean 1.86 1.50 1.47 1.34 1.52 1.96 1.29 1.40 1.65 1.36 1.57 1.54 1.55 1.61 1.20 1.89 1.57	RS 15 7 6 3 8 17 2 5 14 4 11 9 10 13 1 16 12	B 21.69 18.78 22.25 19.07 26.83 24.11 23.68 18.85 25.12 15.19 22.70 26.34 19.20 31.03 28.43 26.53 24.44	I 21.47 18.22 21.32 19.13 25.35 25.51 21.68 17.26 25.71 15.12 20.83 24.64 17.91 27.83 25.93 25.59 23.57	Mean 21.58 18.50 21.79 19.10 26.09 24.81 22.68 18.06 25.42 15.16 21.77 25.49 18.56 29.43 27.18 26.06 24.02	RS 6 3 5 15 11 9 2 12 1 7 13 4 17 16 14 10	61 65 41 33 60 73 48 30 64 42 56 42 36 80 56 74 57
Genotypes Acc001 Acc014 Acc015 Acc016 Acc020 Acc024 Acc040 Acc041 Acc042 Acc043 Acc043 Acc044 Acc045 Acc046 Acc048 Acc049 Acc050 Local Check Mean	B 20.60 21.92 18.60 18.73 19.32 22.28 23.53 18.33 18.70 24.63 20.22 19.71 17.86 20.72 19.04 23.22 21.40 20.52	I 20.39 21.26 17.82 18.79 18.25 23.57 21.54 16.78 19.14 24.52 18.57 18.44 16.66 18.58 17.36 22.39 20.64 19.69	Mean 20.50 21.59 18.21 18.76 18.79 22.93 22.54 17.56 18.92 24.58 19.40 19.08 17.26 19.65 18.20 22.81 21.02 20.10	RS 11 13 4 5 6 16 14 2 7 17 9 8 1 10 3 15 12	B 1.90 1.52 1.53 1.34 1.54 1.94 1.37 1.48 1.66 1.38 1.66 1.62 1.62 1.73 1.27 1.89 1.62 1.59	I 1.81 1.48 1.41 1.33 1.50 1.98 1.21 1.31 1.63 1.33 1.47 1.46 1.47 1.49 1.12 1.88 1.51 1.49	Mean 1.86 1.50 1.47 1.34 1.52 1.96 1.29 1.40 1.65 1.36 1.57 1.54 1.55 1.61 1.20 1.89 1.57 1.54	RS 15 7 6 3 8 17 2 5 14 4 11 9 10 13 1 16 12	B 21.69 18.78 22.25 19.07 26.83 24.11 23.68 18.85 25.12 15.19 22.70 26.34 19.20 31.03 28.43 26.53 24.44 23.19	I 21.47 18.22 21.32 19.13 25.35 25.51 21.68 17.26 25.71 15.12 20.83 24.64 17.91 27.83 25.93 25.59 23.57 22.18	Mean 21.58 18.50 21.79 19.10 26.09 24.81 22.68 18.06 25.42 15.16 21.77 25.49 18.56 29.43 27.18 26.06 24.02 22.69	RS 6 3 5 15 11 9 2 12 1 7 13 4 17 16 14 10	fold RS 61 65 41 33 60 73 48 30 64 42 56 42 36 80 56 74 57 54
Genotypes Acc001 Acc014 Acc015 Acc016 Acc020 Acc024 Acc040 Acc041 Acc042 Acc043 Acc044 Acc044 Acc045 Acc046 Acc048 Acc048 Acc049 Acc050 Local Check Mean MS Locations (L)	B 20.60 21.92 18.60 18.73 19.32 22.28 23.53 18.33 18.70 24.63 20.22 19.71 17.86 20.72 19.04 23.22 21.40 20.52	I 20.39 21.26 17.82 18.79 18.25 23.57 21.54 16.78 19.14 24.52 18.57 18.44 16.66 18.58 17.36 22.39 20.64 19.69	Mean 20.50 21.59 18.21 18.76 18.79 22.93 22.54 17.56 18.92 24.58 19.40 19.08 17.26 19.65 18.20 22.81 21.02 20.10 17.53	RS 11 13 4 5 6 16 14 2 7 17 9 8 1 10 3 15 12	B 1.90 1.52 1.53 1.34 1.54 1.94 1.37 1.48 1.66 1.38 1.66 1.62 1.62 1.73 1.27 1.89 1.62 1.59	I 1.81 1.48 1.41 1.33 1.50 1.98 1.21 1.31 1.63 1.33 1.47 1.46 1.47 1.49 1.12 1.88 1.51 1.49	Mean 1.86 1.50 1.47 1.34 1.52 1.96 1.29 1.40 1.65 1.36 1.57 1.54 1.55 1.61 1.20 1.89 1.57 1.54 0.24	RS 15 7 6 3 8 17 2 5 14 4 11 9 10 13 1 16 12	B 21.69 18.78 22.25 19.07 26.83 24.11 23.68 18.85 25.12 15.19 22.70 26.34 19.20 31.03 28.43 26.53 24.44 23.19	I 21.47 18.22 21.32 19.13 25.35 25.51 21.68 17.26 25.71 15.12 20.83 24.64 17.91 27.83 25.93 25.59 23.57 22.18	Mean 21.58 18.50 21.79 19.10 26.09 24.81 22.68 18.06 25.42 15.16 21.77 25.49 18.56 29.43 27.18 26.06 24.02 22.69 26.04	RS 6 3 5 15 11 9 2 12 1 7 13 4 17 16 14 10	61 65 41 33 60 73 48 30 64 42 56 42 36 80 56 74 57 54
Genotypes Acc001 Acc014 Acc015 Acc016 Acc020 Acc020 Acc024 Acc040 Acc041 Acc042 Acc043 Acc043 Acc044 Acc045 Acc046 Acc048 Acc048 Acc049 Acc050 Local Check Mean MS Locations (L) MS Block within	B 20.60 21.92 18.60 18.73 19.32 22.28 23.53 18.33 18.70 24.63 20.22 19.71 17.86 20.72 19.04 23.22 21.40 20.52 20.71	I 20.39 21.26 17.82 18.79 18.25 23.57 21.54 16.78 19.14 24.52 18.57 18.44 16.66 18.58 17.36 22.39 20.64 19.69	Mean 20.50 21.59 18.21 18.76 18.79 22.93 22.54 17.56 18.92 24.58 19.40 19.08 17.26 19.65 18.20 22.81 21.02 20.10 17.53 17.98	RS 11 13 4 5 6 16 14 2 7 17 9 8 1 10 3 15 12	B 1.90 1.52 1.53 1.34 1.54 1.94 1.37 1.48 1.66 1.38 1.66 1.62 1.62 1.62 1.73 1.27 1.89 1.62 1.59 0.13	I 1.81 1.48 1.41 1.33 1.50 1.98 1.21 1.31 1.63 1.33 1.47 1.46 1.47 1.49 1.12 1.88 1.51 1.49 0.16	Mean 1.86 1.50 1.47 1.34 1.52 1.96 1.29 1.40 1.65 1.36 1.57 1.54 1.55 1.61 1.20 1.89 1.57 1.54 0.24 0.14	RS 15 7 6 3 8 17 2 5 14 4 11 9 10 13 1 16 12	B 21.69 18.78 22.25 19.07 26.83 24.11 23.68 18.85 25.12 15.19 22.70 26.34 19.20 31.03 28.43 26.53 24.44 23.19 25.16	I 21.47 18.22 21.32 19.13 25.35 25.51 21.68 17.26 25.71 15.12 20.83 24.64 17.91 27.83 25.93 25.59 23.57 22.18 17.4	Mean 21.58 18.50 21.79 19.10 26.09 24.81 22.68 18.06 25.42 15.16 21.77 25.49 18.56 29.43 27.18 26.06 24.02 22.69 26.04 21.28	RS 6 3 5 15 11 9 2 12 1 7 13 4 17 16 14 10	fold RS 61 65 41 33 60 73 48 30 64 42 56 74 57 54
Genotypes Acc001 Acc014 Acc015 Acc016 Acc020 Acc020 Acc024 Acc040 Acc041 Acc042 Acc043 Acc043 Acc044 Acc045 Acc046 Acc048 Acc048 Acc049 Acc050 Local Check Mean MS Locations (L) MS Block within MS Genotypes (G)	B 20.60 21.92 18.60 18.73 19.32 22.28 23.53 18.33 18.70 24.63 20.22 19.71 17.86 20.72 19.04 23.22 21.40 20.52 20.71 35.28**	I 20.39 21.26 17.82 18.79 18.25 23.57 21.54 16.78 19.14 24.52 18.57 18.44 16.66 18.58 17.36 22.39 20.64 19.69 15.24 46.27**	Mean 20.50 21.59 18.21 18.76 18.79 22.93 22.54 17.56 18.92 24.58 19.40 19.08 17.26 19.65 18.20 22.81 21.02 20.10 17.53 17.98 37.32**	RS 11 13 4 5 6 16 14 2 7 17 9 8 1 10 3 15 12	B 1.90 1.52 1.53 1.34 1.54 1.94 1.37 1.48 1.66 1.38 1.66 1.62 1.62 1.73 1.27 1.89 1.62 1.59 0.13 0.72**	I 1.81 1.48 1.41 1.33 1.50 1.98 1.21 1.31 1.63 1.33 1.47 1.46 1.47 1.49 1.12 1.88 1.51 1.49 0.16 1.15**	Mean 1.86 1.50 1.47 1.34 1.52 1.96 1.29 1.40 1.65 1.36 1.57 1.54 1.55 1.61 1.20 1.89 1.57 1.54 0.24 0.14 2.26**	RS 15 7 6 3 8 17 2 5 14 4 11 9 10 13 1 16 12	B 21.69 18.78 22.25 19.07 26.83 24.11 23.68 18.85 25.12 15.19 22.70 26.34 19.20 31.03 28.43 26.53 24.44 23.19 25.16 50.28***	I 21.47 18.22 21.32 19.13 25.35 25.51 21.68 17.26 25.71 15.12 20.83 24.64 17.91 27.83 25.93 25.59 23.57 22.18 17.4 41.19**	Mean 21.58 18.50 21.79 19.10 26.09 24.81 22.68 18.06 25.42 15.16 21.77 25.49 18.56 29.43 27.18 26.06 24.02 22.69 26.04 21.28 89.49**	RS 6 3 5 15 11 9 2 12 1 7 13 4 17 16 14 10	fold RS 61 65 41 33 60 73 48 30 64 42 56 74 57 54
Genotypes Acc001 Acc014 Acc015 Acc016 Acc020 Acc024 Acc040 Acc041 Acc042 Acc043 Acc044 Acc045 Acc044 Acc045 Acc046 Acc048 Acc049 Acc050 Local Check Mean MS Locations (L) MS Block within MS Genotypes (G)	B 20.60 21.92 18.60 18.73 19.32 22.28 23.53 18.33 18.70 24.63 20.22 19.71 17.86 20.72 19.04 23.22 21.40 20.52 20.71 35.28**	I 20.39 21.26 17.82 18.79 18.25 23.57 21.54 16.78 19.14 24.52 18.57 18.44 16.66 18.58 17.36 22.39 20.64 19.69 15.24 46.27**	Mean 20.50 21.59 18.21 18.76 18.79 22.93 22.54 17.56 18.92 24.58 19.40 19.08 17.26 19.65 18.20 22.81 21.02 20.10 17.53 17.98 37.32*** 10.23	RS 11 13 4 5 6 16 14 2 7 17 9 8 1 10 3 15 12	B 1.90 1.52 1.53 1.34 1.54 1.94 1.37 1.48 1.66 1.38 1.66 1.62 1.62 1.62 1.73 1.27 1.89 1.62 1.59 0.13 0.72**	I 1.81 1.48 1.41 1.33 1.50 1.98 1.21 1.31 1.63 1.33 1.47 1.46 1.47 1.49 1.12 1.88 1.51 1.49 0.16 1.15**	Mean 1.86 1.50 1.47 1.34 1.52 1.96 1.29 1.40 1.65 1.36 1.57 1.54 1.55 1.61 1.20 1.89 1.57 1.54 0.24 0.14 2.26** 0.11	RS 15 7 6 3 8 17 2 5 14 4 11 9 10 13 1 16 12	B 21.69 18.78 22.25 19.07 26.83 24.11 23.68 18.85 25.12 15.19 22.70 26.34 19.20 31.03 28.43 26.53 24.44 23.19 25.16 50.28***	I 21.47 18.22 21.32 19.13 25.35 25.51 21.68 17.26 25.71 15.12 20.83 24.64 17.91 27.83 25.93 25.59 23.57 22.18 17.4 41.19**	Mean 21.58 18.50 21.79 19.10 26.09 24.81 22.68 18.06 25.42 15.16 21.77 25.49 18.56 29.43 27.18 26.06 24.02 22.69 26.04 21.28 89.49** 21.97	RS 6 3 5 15 11 9 2 12 1 7 13 4 17 16 14 10	fold RS 61 65 41 33 60 73 48 30 64 42 56 74 57 54
Genotypes Acc001 Acc014 Acc015 Acc016 Acc020 Acc024 Acc040 Acc041 Acc042 Acc043 Acc044 Acc045 Acc045 Acc046 Acc048 Acc048 Acc049 Acc050 Local Check Mean MS Locations (L) MS Block within MS Genotypes (G) MS G×L MS Error	B 20.60 21.92 18.60 18.73 19.32 22.28 23.53 18.33 18.70 24.63 20.22 19.71 17.86 20.72 19.04 23.22 21.40 20.52 20.71 35.28** 11.33	I 20.39 21.26 17.82 18.79 18.25 23.57 21.54 16.78 19.14 24.52 18.57 18.44 16.66 18.58 17.36 22.39 20.64 19.69 15.24 46.27** 11.65	Mean 20.50 21.59 18.21 18.76 18.79 22.93 22.54 17.56 18.92 24.58 19.40 19.08 17.26 19.65 18.20 22.81 21.02 20.10 17.53 17.98 37.32** 10.23 12.99	RS 11 13 4 5 6 16 14 2 7 17 9 8 1 10 3 15 12	B 1.90 1.52 1.53 1.34 1.54 1.94 1.37 1.48 1.66 1.62 1.62 1.73 1.27 1.89 1.62 1.59 0.13 0.72** 0.07	I 1.81 1.48 1.41 1.33 1.50 1.98 1.21 1.31 1.63 1.33 1.47 1.46 1.47 1.49 1.12 1.88 1.51 1.49 0.16 1.15** 0.17	Mean 1.86 1.50 1.47 1.34 1.52 1.96 1.29 1.40 1.65 1.36 1.57 1.54 1.55 1.61 1.20 1.89 1.57 1.54 0.24 0.14 2.26** 0.11 0.12	RS 15 7 6 3 8 17 2 5 14 4 11 9 10 13 1 16 12	B 21.69 18.78 22.25 19.07 26.83 24.11 23.68 18.85 25.12 15.19 22.70 26.34 19.20 31.03 28.43 26.53 24.44 23.19 25.16 50.28** 12.7	I 21.47 18.22 21.32 19.13 25.35 25.51 21.68 17.26 25.71 15.12 20.83 24.64 17.91 27.83 25.93 25.59 23.57 22.18 17.4 41.19** 13.41	Mean 21.58 18.50 21.79 19.10 26.09 24.81 22.68 18.06 25.42 15.16 21.77 25.49 18.56 29.43 27.18 26.06 24.02 22.69 26.04 21.28 89.49** 21.97 22.55	RS 6 3 5 15 11 9 2 12 1 7 13 4 17 16 14 10	fold RS 61 65 41 33 60 73 48 30 64 42 56 74 57 54

Table 6. Nutritional compositions of local condiment (Ogiri) of the 17 castor genotypes evaluated at two locations.

Note: B: Badeggi location, I: Ibadan location, RS: Ranking score.

O		Moistu	ure			A	sh			Proteii	าร		Total
Genotypes	В	I	Mean	RS	В	I	Mean	RS	В	I	Mean	RS	RS
Acc001	2.78	2.62	2.70	13	3.30	3.10	3.20	7	24.76	24.60	24.68	16	
Acc014	2.40	2.13	2.27	16	3.21	3.14	3.18	6	21.46	21.42	21.44	14	
Acc015	2.96	2.95	2.96	5	3.73	3.84	3.79	10	20.35	18.82	19.59	13	
Acc016	3.01	2.79	2.90	6	4.45	4.41	4.43	13	14.26	14.19	14.23	4	
Acc020	3.02	2.77	2.90	7	2.09	2.10	2.10	3	19.50	18.78	19.14	12	
Acc024	2.44	2.37	2.41	15	1.61	1.62	1.62	1	25.95	24.84	25.40	17	
Acc040	2.98	2.68	2.83	8	4.08	3.79	3.94	11	18.04	17.74	17.89	8	
Acc041	2.94	2.69	2.82	10	6.48	6.57	6.53	17	17.91	17.39	17.65	7	
Acc042	3.15	3.04	3.10	3	3.62	3.35	3.49	8	14.77	13.93	14.35	5	
Acc043	2.93	2.73	2.83	9	2.67	2.64	2.66	4	24.37	24.54	24.46	15	
Acc044	4.05	3.85	3.95	1	5.83	5.73	5.78	15	14.18	13.34	13.76	3	
Acc045	2.66	2.40	2.53	14	5.94	5.97	5.96	16	12.56	12.22	12.39	1	
Acc046	2.89	2.54	2.72	12	4.62	4.49	4.56	14	13.38	12.38	12.88	2	
Acc048	3.24	3.12	3.18	2	4.10	3.93	4.02	12	19.21	18.60	18.91	11	
Acc049	2.07	1.93	2.00	17	3.06	2.95	3.01	5	18.81	18.50	18.66	9	
Acc050	3 17	2 75	2.96	4	2 13	2.06	2 10	2	18.91	18 60	18 76	10	
Local Check	2.95	2.65	2.80		3 76	3 76	3 76	9	17.37	16.62	17 00	6	
Mean	2.92	2 71	2.81	••	3.8	3.73	3 77	•	18.58	18.03	18.3	<u> </u>	
MS Locations (L)	2.02	1 17	2.01		0.0	0.13	0.77		10.00	7 54	10.0		
MS Block within	0.06	0.12	0.84		0 16	0.10	0 14		5 73	3.01	4 37		
MS Genotypes (G)	0.00	0.12	1.05**		5 65**	6 76**	11 30**		48 19**	50 09**	97 99**		
MS GxI	0.00	0.77	0.02		0.00	0.70	0.02		40.10	00.00	2.89		
MS Error	0 12	0 10	0.31		0 15	0.21	0.02		7.38	12 87	10.81		
	0	Fate			0110	Fi	bre			СНС			
Genotypes		186	3			11	bie			one			Total
	В	I	Mean	RS	В	I	Mean	RS	В	I	Mean	RS	кə
Acc001	32.90	30.95	31.93	3	2.71	2.55	2.63	17	28.24	26.57	27.41	16	72
Acc014	47.90	42.40	45.15	11	1.69	1.66	1.68	11	16.26	14.39	15.33	2	60
Acc015	30.17	30.10	30.14	1	2.17	2.24	2.21	16	42.71	42.61	42.66	17	62
Acc016	46.18	42.76	44.47	10	1.39	1.38	1.39	6	19.42	17.98	18.70	7	46
Acc020	39.52	36.15	37.84	5	1.72	1.73	1.73	12	23.95	21.90	22.93	14	53
Acc024	38.28	37.13	37.71	4	1.30	1.30	1.30	5	22.24	21.57	21.91	12	54
Acc040	46.71	41.94	44.33	9	1.56	1.45	1.51	7	22.06	19.80	20.93	11	54
Acc041	47.68	43.60	45.64	12	1.76	1.78	1.77	13	18.42	16.84	17.63	6	65
Acc042	51.83	49.98	50.91	15	1.22	1.13	1.18	1	17.46	16.84	17.15	5	37
Acc043	32.57	30.26	31.42	2	1.87	1.85	1.86	15	28.12	26.13	27.13	15	60
Acc044	58.08	55.23	56.66	17	1.57	1.54	1.56	10	14.38	13.68	14.03	1	47
Acc045	49.26	44.58	46.92	13	1.29	1.30	1.30	4	20.18	18.26	19.22	9	57
Acc046	50.82	44.68	47.75	14	1.53	1.49	1.51	8	17.96	15.79	16.88	4	54
Acc048	42.14	40.61	41.38	6	1.32	1.27	1.30	3	22.51	21.69	22.10	13	47
Acc049	45.55	42.66	44.11	8	1.26	1.21	1.24	2	21.32	19.97	20.65	10	51
Acc050	58.75	51.10	54.93	16	1.84	1.79	1.82	14	17.13	14.89	16.01	3	49
Local Check	45.66	41.00	43.33	7	1.55	1.55	1.55	9	20.22	18.16	19.19	8	50
Mean	44.94	41.48	43.21		1.63	1.6	1.62		21.92	20.42	21.17		54
MS Locations (L)		30.19				0.26				57.39			
MS Block within	37.52	84.47	21		0.03	0.04	0.03		49.67	27.79	38.73		
MS Genotypes (G)	203.24**	149.38**	346.88**		0.43**	0.37**	0.77**		128.91**	139.47**	267.70**		
MS G×L			5.76				0.04				20.68		
MS Error	66.46	45.51	15.99		0.07	0.03	0.02		31.57	16.2	23.9		

Table 7. Nutritional compositions of the seeds of the 17 castor genotypes evaluated at two locations.

Note: B: Badeggi location, I: Ibadan location, RS: Ranking score.

Genotypes	Agronomic traits	Percentage disease incidence	Percentage insect damage on leaves	Percentage insect damage on inflorescence	Percentage insect damage on capsule	Proximate of <i>Ogiri</i>	Proximate of seed	**Sum rank score	Remarks
Acc001	108	17	30	24	28	61	72	370.71	Selected*
Acc014	57	32	4	2	5	65	60	251.49	
Acc015	36	8	2	6	2	41	62	179.06	
Acc016	61	25	6	4	10	33	46	205.05	
Acc020	63	25	27	21	25	60	53	291.21	Selected*
Acc024	57	8	34	32	34	73	54	311.69	Selected*
Acc040	95	19	17	28	32	48	54	318.18	Selected*
Acc041	61	25	12	11	13	30	65	238.31	
Acc042	70	18	20	17	13	64	37	261.00	
Acc043	73	16	9	11	8	42	60	243.97	
Acc044	71	26	9	17	17	56	47	264.66	
Acc045	94	3	31	30	22	42	57	305.95	Selected*
Acc046	76	16	17	14	5	36	54	241.80	
Acc048	101	15	27	34	23	80	47	356.70	Selected*
Acc049	55	24	14	8	17	56	51	244.47	
Acc050	85	8	22	26	28	74	49	318.54	Selected*
Local Check	61	21	25	21	24	57	50	275.78	Selected*
Norm								275.21	

Table 8. Selection of ideal candidates for multi-environment trials based on the total ranking scores in the parameters considered.



Figure 1. GGE Biplot grouping the eight locations into mega environments.

Genotypes are ranked based on their position to high or low PC1 values and their stability is determined by the length of their vectors on the stability axis (Perpendicular line). From Figure 3, the genotype Acc001 (Gen3) was the highest yielding genotype which also showed good stability and falls within the concentric cycle of ideal genotype, representing the most ideal genotype among the entries. Being the most ideal means most responsive genotype to a better environment but with less negative responsive to the worse environment.

Table 9. Mean	values for se	ed yield of e	ight castor gen	otypes evalu:	ated at eight	locations in 20	16 and 2017	growing sea	asons.			
						Locat	lions					
Genotypes		Bacita			Badeggi			Zuru			Amakama	
	2016	2017	Combined	2016	2017	Combined	2016	2017	Combined	2016	2017	Combined
Acc048	1235.92	1286.27	1261.10	980.08	1321.80	1150.94	466.74	695.65	581.20	701.51	695.65	698.58
Acc050	1226.72	1165.02	1195.87	625.72	1187.30	906.51	660.36	877.02	768.69	297.80	877.02	587.41
Acc001	1891.62	1442.28	1666.95	1230.27	1402.61	1316.44	681.92	889.67	785.80	955.08	989.67	972.38
Acc020	786.72	1122.28	954.50	987.61	1364.53	1176.07	415.51	562.46	488.99	778.95	562.46	670.71
Acc024	774.10	1203.73	988.91	1206.15	1088.47	1147.31	317.65	511.04	414.34	806.53	511.04	658.78
Acc040	1162.40	966.16	1064.28	1305.31	1340.17	1322.74	846.05	871.45	858.75	858.42	871.45	864.93
Acc045	1424.80	1455.46	1440.13	1212.00	1395.22	1303.61	767.14	948.90	858.02	788.84	948.90	868.87
Local Check	597.93	919.38	758.65	1251.54	1213.94	1232.74	335.69	591.95	463.82	447.16	591.95	519.55
Grand Mean	1137.53	1195.07	1166.30	1099.83	1289.25	1194.54	561.38	743.52	652.45	629.29	743.52	686.40
MS Year (Y)	'	ı	39738.74	'	'	430555.13**	'	'	398075.42**	ı	•	2099.97
MS Block within	16243.42	17894.13	17068.77	8252.84	33206.85	6328.09	1269.38	15971.01	1724.09	4106.47	2178.82	5671.01
MS Genotype (G) 521035.46**	116535.54**	504345.29**	153367.82**	299127.03**	113216.10**	123547.51**	317287.75**	205874.55**	117845.37**	89926.47**	233958.62**
MS G×Y	'	•	133225.71**	'	'	78626.57**	'	'	7599.43**			611.78
MS Error	13259.77	//15.06	1/98/.41	4780.54	1288.96	3768.63	2192.60	/362.12	1438.92	4862.44	685.23	8712.82
						Locat	ions					
Genotypes		Ibadan			Mokwa			Minna			Riyom	
	2016	2017	Combined	2016	2017	Combined	2016	2017	Combined	2016	2017	Combined
Acc048	899.33	1047.18	973.26	891.30	1196.92	1044.11	724.91	635.00	679.96	921.46	1321.80	1121.63
Acc050	626.12	1220.30	923.21	943.95	1443.86	1193.90	668.93	620.29	644.61	807.44	1187.30	997.37
Acc001	1493.37	1610.50	1551.93	1501.31	1617.42	1559.36	903.92	877.88	890.90	1326.35	1402.61	1364.48
Acc020	1224.79	1354.99	1289.89	321.49	350.78	336.13	762.35	702.07	732.21	389.71	1364.53	877.12
Acc024	1083.76	877.89	980.82	688.35	1142.97	915.66	790.47	712.62	751.54	1008.00	1088.47	1048.24
Acc040	1332.20	1721.64	1526.92	762.69	836.73	799.71	593.98	532.41	563.19	533.72	1340.17	936.94
Acc045	945.40	1264.30	1104.85	772.68	955.41	864.05	756.10	743.92	750.01	1199.37	1395.22	1297.29
Local Check	642.70	857.42	750.06	544.90	851.40	698.15	864.92	838.49	851.70	735.19	1213.94	974.56
Grand Mean	1018.46	1244.28	1131.37	803.33	1049.43	926.38	758.20	707.83	733.02	865.16	1289.25	1077.20
MS Year (Y)	'	'	611933.12*	'	'	726789.81**	'	'	30436.77		•	7972.23
MS Block within	41042.44	7235.53	37124.64	1268.78	537.00	902.89	3495.80	19436.44	11466.12	7688.73	4403.35	11829.87
MS Genotype (G) 257348.24**	116725.03**	476568.26**	355478.98**	467184.96**	777104.14**	29885.15**	39037.18**	67814.72**	301757.52**	38474.85**	616317.26**
MS G×Y	ı	I	79907.01**	ı	ı	45559.81**	ı	ı	1107.60	I		2728.01
MS Error	44577.84	12563.19	2933.41	2593.45	2054.79	2324.12	1843.14	2121.48	11982.31	3365.23	2756.71	5363.67
Note: MS: Mea	n square, *: (Significance a	at 0.05, **: Sigr	nificance at 0	.01.							

Genotypes	Seed yield (kg/ha)	Days to 50% flowering	Day to maturity	Height at maturity (cm)	Spikes per plant	Length of spike (cm)	100 seed weight (g)	Seed Oil Content (%)
Acc.048	938.85	74.78	106.77	159.37	5.30	25.10	45.24	43.54
Acc.050	902.2	62.21	102.18	145.92	4.58	37.36	46.52	36.37
Acc001	1263.53	85.31	109.45	141.12	7.86	19.90	50.50	35.14
Acc020	815.7	80.92	171.37	250.85	4.03	31.68	44.77	51.28
Acc024	863.2	76.54	161.32	149.07	5.20	22.60	42.93	46.35
Acc040	992.18	71.88	98.16	186.70	3.63	19.56	50.15	30.92
Acc045	1060.85	72.28	99.25	240.94	3.17	27.00	48.56	28.88
Local Check	781.16	67.27	143.72	212.41	6.00	26.50	49.07	34.03
Pooled Mean	952.20	73.90	124.03	185.80	4.47	26.21	50.22	38.31
MS Locations (L)	2602095.24**	3.97	8114.95	660.17**	0.84**	382.40	1089.49	1407.31*
MS Block within	15467.50	24.18	29158.25	301.52	0.24	876.81	1615.04	500.44
MS Genotypes (G)	1070249.84**	2568.64**	43138.24*	93365.11**	44.71**	1735.12**	4901.86**	7549.01**
MS Year (Y)	988173.33**	4.26	2299.71	42.68	0.09	231.44	374.24	7.80
MS G×Y	45577.42**	10.58	7519.86	153.21	0.06	240.56	479.75	4.22
MS L×G	274992.73**	13.68	15042.92	1204.17**	5.08**	445.31	1013.41	1594.43**
MS L×Y	179918.27**	7.17	12880.17	26.02	0.08	461.84	1487.32	491.86
MS L×G×Y	43398.35**	23.42	22775.72	282.13*	0.08	689.63	1581	512.24
Pooled Error	9830.41	20.75	19361.13	190.95	0.09	603.98	1431.6	469.11

Table 10. Pooled mean for seed yield and other agronomic traits of Acc001 and other castor genotypes across eight (8) locations in Nigeria, 2016-2017.

Note: MS: Mean square, *: Significance at 0.05, **: Significance at 0.01.



Figure 2. GGE Biplot showing representative and discriminating abilities of the the eight locations.



Figure 3. Mean performance and stability of the 8 castor genotypes evaluated across 8 locations in Nigeria.



Figure 4. The which-won-where view of the GGE biplot showing which genotypes performed best in which environment across different environments.

States	Genotypes	Seed yield (Kg/ha) Mean±SEM	Days to maturity Mean±SEM	100 seed weight (g) Mean±SEM
	Acc001	968.42±49.69	112.75±4.13	51.82±2.97
Kogi	Acc045	661.42±54.86	116.88±5.83	48.93±1.71
	Farmer's cultivar	454.11±32.86	130.16±1.13	52.14±2.00
	Acc001	865.20±39.33	107.27±2.96	50.16±2.61
Kwara	Acc045	498.58±30.45	107.77±6.18	48.02±1.14
	Farmer's cultivar	432.49±31.83	126.10±3.88	48.98±1.42
	Acc001	905.23±61.47	111.15±6.40	49.97±1.52
Niger	Acc045	751.07±32.33	125.95±5.27	49.62±2.29
	Farmer's cultivar	594.16±36.38	128.23±6.53	51.40±2.54

Table 11. Mean performances of the selected genotypes on the farmers' fields.

Genotype Acc045 (Gen7) recorded second highest yield but highest stability, representing an ideal genotype for broad adaptability. Genotype Acc040 (Gen6) also yielded above the average but represents the least stable genotype among the genotype above the average yield. Genotype Acc020 (Gen4) and Acc050 (Gen2) recorded low yield and low stability. The which-won-where biplot for the entries is presented in Figure 4. The winning genotypes are those in the polygon vertex. The genotype Acc001 (Gen3) out yielded others in Amakama (E1), Bacita (E2), Mokwa (E6), Riyon (E7) and Zuru (8). Genotype Acco040 (Gen6) out yielded all others at Badeggi (E3) and Ibadan (E4). The winner in the location "Minna" was genotype Acc050 (Gen2). From the results of the performance and stability assessments, it is logical to recommend both Acc001 and Acc045 for on farm trials in both identified clusters of environments so as to exploit the opportunity of both broad adaptation and specific adaptation to the environments if any.

Farmers' preference appraisals

The on-farm performance appraisal is presented in Tables 11 and 12. The genotypes Acc001 and Acc045, on average, out yielded the farmers' cultivars in the three states and also showed earliness to maturity (Table 11). The seed weights among the genotypes are comparable. The preference criteria revealed the highest preference for genotype Acc001 among the farmers (Table 12). The genotype was mostly accepted by the farmers because of its high yield, seed colour and market value. Since castor is not a major food crop in the country, the yielding ability and marketability of the seed became paramount indices for its acceptability among the farmers. In a study on profitability of castor seed production in a north eastern state of Nigeria, Mohammed et al. (2015) reported that output price in production systems had higher marginal effects **Table 12.** Average farmers' preference criteria for the selected castor genotypes at the on-farm.

Parameters	Acc001	Acc045	Farmer's cultivar
High Yield	3	2	1
Early Maturity	2	2	2
Short Stalk	2	2	2
Shelling	3	3	3
Seed Size	3	3	3
Seed Colour	3	2	2
Market Value	3	2	2
Total Score	19	16	15
Rank	1 st	2 nd	3 rd

3: Excellent, 2: Very Good, 1: Good.

on profit than input costs; therefore, marketability influenced profit more than input costs. Agricultural sector accounts for more than forty percent of the Nigerian Gross Domestic Product (GDP) and has the highest growth rate of 2.4% in 2010 (Central Bank of Nigeria - CBN, 2010). The sector is largely dominated by small-holder farmers which are scarcely affected by reform policies targeted at improving the agricultural sector performance (Mohammed et al., 2015). Meanwhile, under such condition, the feature of individual production is largely subsistence, mainly utilizing poor and traditional methods. Against this background, castor, a harsh-weather tolerant and high valued industrial crop, was promoted in order to augment farm incomes of rural farmers in Nigeria (Amosun et al., 2013). Although none of the past studies on castor has incorporated farmers' preference for seed market value, several studies on castor production and other cash crops have shown that yielding ability and marketability are the most paramount indices to smallholder farmers (Abdulai and Huffman, 1998; Rahman, 2003; Amaza et al., 2007; Hyuha et al., 2007; Mohammed et al., 2015).

CONCLUSION

Seventeen promising large seeded castor genotypes were evaluated in the study. Selections were made from the 17 entries to identify the most ideal genotypes that could be recommended to farmers for profitable cultivation. The selection was based on the yield performances, observation on reactions to major disease and insect pests, nutritional composition of Ogiri and seeds of the genotypes, performances and stability at multi-locational trials, and farmers' preference at the participatory on-farm trials. The results revealed a wide range of variability among the entries to give room for accurate selection. Out of the 17 genotypes evaluated, two genotypes (Acc001 and Acc045) were identified as the most ideal for farmers' participatory selection; however, genotype Acc001 was the most preferred by the majority of the farmers. Therefore, the genotype Acc001 could be recommended for release and registration for the benefit of the farmers.

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Competing interests

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Author's contributions

All authors contributed to the conception, design and execution of the study. Material preparation, data collection and analysis were performed by Bolaji Zuluqurineen SALIHU, Christiana Oreoluwa OKE, Bernard Oddy EHIRIM, Junior Dickson NWOSU, Opeyemi Shaheed KOLAWOLE, Obukohwo Benson APUYOR, Maryam Alfa KABARAINI, Sunkanmi Tokunbo GBADEYAN, Adija Abolore AJADI, Muhammed Sani SALAHU, Oluwagbenga Foluso AJAYE, Obasola Babatunde OLANIYAN and Attairu Muhammed TANIMU. The first draft of the manuscript was written by Bolaji Zuluqurineen SALIHU and all co-authors commented on previous versions of the manuscript. All authors read and approved the final manuscript.

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