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Genetic variability, genetic gain and relationships of yield and yield components in castor (*Ricinus communis* L.)

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ABSTRACT

Thirty (30) castor accessions were evaluated in 3 locations in 2011 and 5 locations in 2012 wet seasons in the Nigerian savannas. Data were collected for yield and the yield components: Peduncle length (PL), Number of nodes to the first raceme (NFR), Number of capsules in the first raceme (Noc), Number of secondary branching (NSB), Number of spikes/plant and Plant height at harvest (H@H). Analysis of the data showed that the GCV was low for all the yield components but moderate for yield. The PCV was also low for PL, NFR and height, while it was moderate for NOC, NOSB, No.S/p and Yield. Amongst the yield components height at harvest had the highest difference between GCV and PCV (RD=71.4%) while all the others were also high except No.S/p (RD=36%). These indicate that the observed variations for the traits were mostly due to environment factors. Moderate broad sense heritability coupled with moderate Genetic gain (GA) were observed for NOSB, No.S/p and Yield indicating that these traits are mainly controlled by additive type of genes and that direct selection for these traits could be effective. However, moderate heritability coupled with low GA was observed for PL. Thus this character is controlled by non-additive genes (dominance and epistasis). Low heritability with low GA observed in height and NFR indicates environmental control on the expression of these traits. Location by traits biplot revealed that NOC, NFR, Height at harvest, PL and yield had stronger association. The Trait Association by Environment (TAE) biplot grouped the eight environments into three distinct groups: the first group consisted of three environments, Kadawa, Talata mafara and Bakura in the Sudano-sahelian savanna, the second group consisted of Samaru2012 in the northern guinea savanna and Minjibir of the sudan savanna, the third group consisted of Geshere and Samaru kataf in the southern guinea savanna and Samaru2011 of the northern guinea. The first group sites were characterized by strong positive associations of NFR vs. No.S/p, NFR vs. NOC and height vs. yield. This implied that accessions with higher number of nodes to first racemes had higher yield at these sites. The second group were characterized by strong positive associations of NOC vs. Yield, height at harvest vs. yield. Therefore, at these locations, taller genotypes and those with more number of capsules in first raceme tended to give higher yields. The third group were characterised by strong positive associations for NFR vs. NOSB and NOC vs. Yield implying that genotypes with higher NFR, NOC and NOSB tended to have higher yields in these sites.

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KEYWORDS

Castor;
GCV;
PCV;
Genetic gain;
Biplot.

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INTRODUCTION

Castor plant (*Ricinus communis* L.) is a monotypic species in the spurge family (Euphorbiaceae) with $2n = 20$ chromosomes. It is an important non-edible oilseed crop. The seeds of castor bean contain more than 45% oil and its oil is rich (80 to 90%) in an unusual hydroxyl fatty acid, ricinoleic acid^[10]. Castor bean is considered to be native to tropical Africa^[18,22], but it is cultivated in many tropical and subtropical regions of the world^[7]. It is well adapted to Nigeria climatic conditions and thus widely grown as ornamentals^[17] in all the states in Nigeria especially in the mid-west and eastern part of country. Castor oil is a critical raw material for the industrial chemical markets for the production of soaps, lubricants, hydraulic and brake fluids, paints, dyes, coatings, inks, cold resistant plastics, waxes and polishes, nylon, pharmaceuticals and perfumes^[17] and biodiesel. These have increased the demands for high yielding varieties for efficient provision of feedstock. However, breeding for improved yield has been limited by a low genetic variability for productivity traits^[9]. To increase the genetic yield potential, the maximum utilization of the desirable characters for synthesizing of any ideal genotypes is essential. As yield is the main object of a breeder, it is important to know the relationship between various characters that have direct and indirect effect on yield. The degree of relationship or association of these characters with yield will also be required. This would aid in suggesting efficient breeding strategies for improving the yield potential via its components^[4]. Hence, there is need to estimate the amount of genetic variability, heritability and genetic advance over mean for yield and yield components and to estimate the relationships among the traits. To achieve this, performance trials have to be conducted in multiple environments due to the presence of Genotype by Environment interaction (GE). This is because yield and its components are quantitative traits that are not under simple genetic control. To effectively estimate the location by traits and traits association by environment, the use of biplot will be employed. The biplot is a scatter plot that approximates and graphically displays relationships among the genotypes (G), environments (E) and Traits as well as the underlying interactions between them to be visualized simultaneously^[20,21].

MATERIALS AND METHODS

Thirty (30) castor accessions were evaluated in 3 locations in 2011 and 5 locations in 2012 wet seasons in Nigerian savannas. The locations in 2011 were Samaru (N11°11.297'; E007°37.078'; 2206ft) in the northern guinea savanna, Samaru kataf (N09°45.764' E008°22.630' 2834ft) in the southern guinea savanna and Bakura (N12°41.110' E005°53.208' 951ft) in the sahel savanna. In 2012 the locations were Samaru again, Geshere (N10°07.701'; E008°28.432'; 2425ft) in the southern guinea savanna, Kadawa (N11.659' E8°45') sudan savanna, Minjibir (N12°08.466'; E008°40.331'; 1401ft) and Talata Mafara (N12°34.651'; E006°00.418'; 996ft) both in the sahel savanna. All the trials were established in Two-row plots of 5m long, intra-row spacing of 0.5m and inter-row spacing of 0.75m. The evaluation was done in randomised complete block design with three replications. Two seeds were planted per hill in each trial. Inorganic fertilizer at the rate of 20kg/ha N, 20kg/ha P₂O₅ and 20kg/ha K₂O was applied in a single dose (NPK 15:15:15) applied 30 days after planting. The experiments were kept weed-free by chemical weed control and manual weeding. Data were collected on 10 individuals in each plot for yield and the yield components: Peduncle length (PL), Number of nodes to the first raceme (NFR), Number of capsules in the first raceme (Noc), Number of secondary branching (NSB), Number of spikes/plant and Plant height at harvest (H@H).

Statistical analysis

Phenotypic variance (σ_p^2), genotypic variance (σ_g^2), environmental variance (σ_e^2) and genotype by environment interaction variance (σ_{ge}^2) were determined according to^[15] as described in Hallauer, *et. al.*^[18] reviews (see TABLE 1).

Genotypic and phenotypic co-efficient of variation was calculated according to Burton and Devane (1953):

$$\text{GCV} = \sigma_g \times 100 / \text{grand mean}; \text{PCV} = \sigma_p \times 100 / \text{grand mean}.$$

RD %: Relative difference between PCV% and GCV% = [100 (PCV-GCV)] / PCV (Nechifor, *et al.* 2011)

Broad sense heritability (h_b^2) was estimated as suggested in Hallauer *et. al.*^[8]:

$$h_b^2 = \sigma_g^2 / (\sigma_g^2 + (\sigma^2/re) + (\sigma_{ge}^2/e))$$

The genetic advance (GA) was calculated according to Allard^[2]:

$$GA = h^2_b \times \Delta S \times \sigma_p,$$

The genetic covariate by environment biplot and the Trait Association by Environment (TAE) biplot were also estimated according to Yan and Tinker^[20] using GGE biplot Version 5.4^[21].

TABLE 1: Form of Expected Mean Square for Analysis of variance of inbred lines/accessions repeated over environments

SOV	df	MS	E(MS)
Environments (E)	e-1		
Replications/E	e(r-1)		
Inbred lines	n-1	M3	$\sigma^2 + r\sigma_{ge}^2 + re\sigma_g^2$
E × inbred lines	(e-1)(n-1)	M2	$\sigma^2 + r\sigma_{ge}^2$
Pooled error	e(r-1)(n-1)	M1	σ^2

e, r, and n refer to the number of environments, replications within environments, accessions/genotypes. (Source: Hallauer et. al, 2010)

RESULTS AND DISCUSSIONS

Means, Variance components, Heritability and Genetic gain

TABLE 2 presents the variations of means for the germplasm accessions, environments and their interactions for yield and its components. There were significant difference of means among all the sources of variations (SOV) for all the measured traits. The results in table 3 shows the range and mean values of the measured traits across eight environments, estimates of genotypic and phenotypic variances, genotypic and phenotypic coefficients of variations, broad sense heritability and genetic advance for the traits. Based on the

classification of GCV and PCV by Sivasubramanian and Menon^[16], the GCV was low for all the yield components but moderate for yield. The PCV was also low for PL, NFR and height, while it was moderate for NOC, NOSB, No.S/p and Yield. Thus to judge the extent of genetic variation in these traits the RD which is the estimate of GCV in relation to the respective PCV was estimated. Amongst the yield components height at harvest had the highest difference between GCV and PCV (RD=71.4%) while all the others were also high except No.S/p (RD=36%). These indicate that the observed variations for the traits were mostly due to environment factors. However, the environment played a little role on the expression of No.S/p. According to Robinson et. al.^[14] heritability percentage of 0-30% is low, 30-60% moderate, and 60% and above high. Thus, results in table 3 showed that the broad sense heritability was low for NFR, NOC and height while it was moderate for PL, NOSB, No.S/p and Yield. Meanwhile, according to Johnson et. al.^[11] effectiveness of selection depends not only on heritability but also on genetic advance (GA). Thus, moderate heritability coupled with moderate GA were observed for NOSB, No.S/p and Yield indicating that these traits are mainly controlled by additive type of genes and that direct selection for these traits could be effective. However, moderate heritability coupled with low GA was observed for PL. Thus this character is controlled by non-additive genes (dominance and epistasis). Low heritability with low GA observed in height and NFR indicates environmental control on the expression of these traits. These results agreed with those of Uguru and Abuka^[17], Patel et. al.^[13] and Adeyanju et. al.^[1].

TABLE 2: Mean squares from Analysis of variance of 30 castor accessions evaluated over 8 environments across the Savanna agro-ecologies of Nigeria.

SOV	df	PL	NFR	NOC	NOSB	No.S/p	H@H (m)	Yield (Kg/ha)
Environments (E)	7	170.34**	665.73**	25187.3**	190.87**	77.35**	44.97**	825996.25**
Replications/E	16	2.12**	7.47	623.28**	18.63**	14.80**	1.09**	80881.43
accessions	29	2.9**	16.37**	807.82**	7.25**	11.94**	0.14**	124996.76**
E × accessions	203	1.99**	13.60**	581.32**	4.86**	7.12**	0.15**	82025.84*
Pooled error	461	25.99	6.76	266.31	2.01	4.36	0.07	66500.52

*significant at 0.05, **significant at 0.01

The covariate by environment biplot

The covariate by environment biplot in Figure 1 represent the MET data of 2011 and 2012 trials of the thirty castor accessions tested across 8 locations. Num-

bers of capsules in first raceme (NOC), NFR, Height at harvest, peduncle length and yield have stronger association as indicated by the shorter vectors and the acute angles among them. This finding agreed with

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Goodarzi *et. al.*^[6], The Genotypes with higher NOSB tended to have higher yields in the guinea savanna environments while those with higher peduncle length, height at harvest, NOC and NFR gave higher yields at the sudano-sahelian savanna. Thus, Figure 1 suggests possible indirect selection strategies when direct selection for yield is not possible. Higher number of secondary

branching (NOSB) accession should be selected for Geshere, Samaru kataf and Samaru of the guinea savanna, whereas varieties with longer peduncle length, taller height and higher number of capsules should be selected for Bakura, Talata mafara, and kadawa of the sudano-sahelian savanna to maximize yield in these environments.

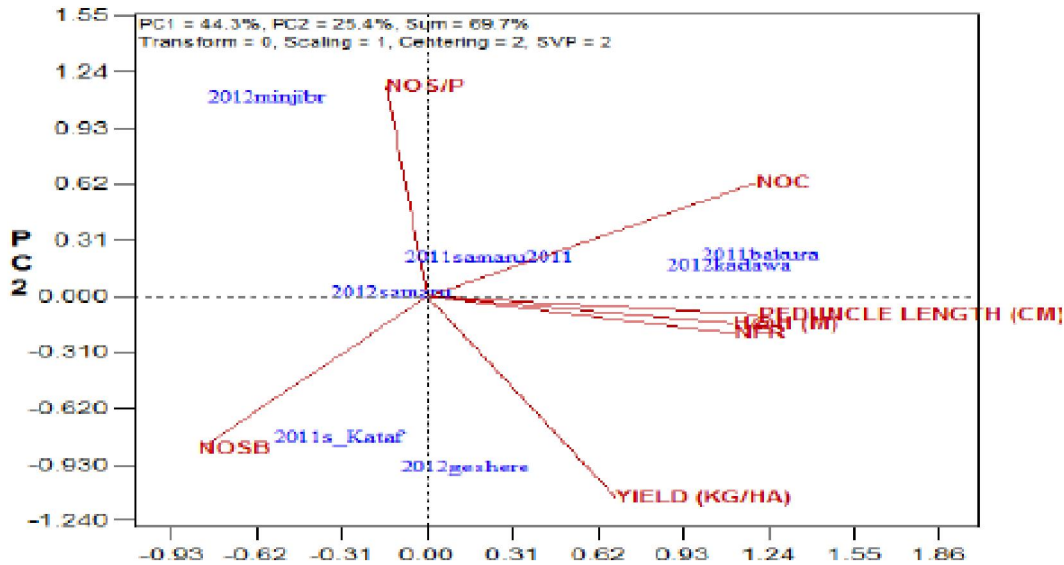


Figure 1: A genetic covariate by environment biplot of 30 Castor accessions based on 2011 and 2012 Multi-Environment Trials data

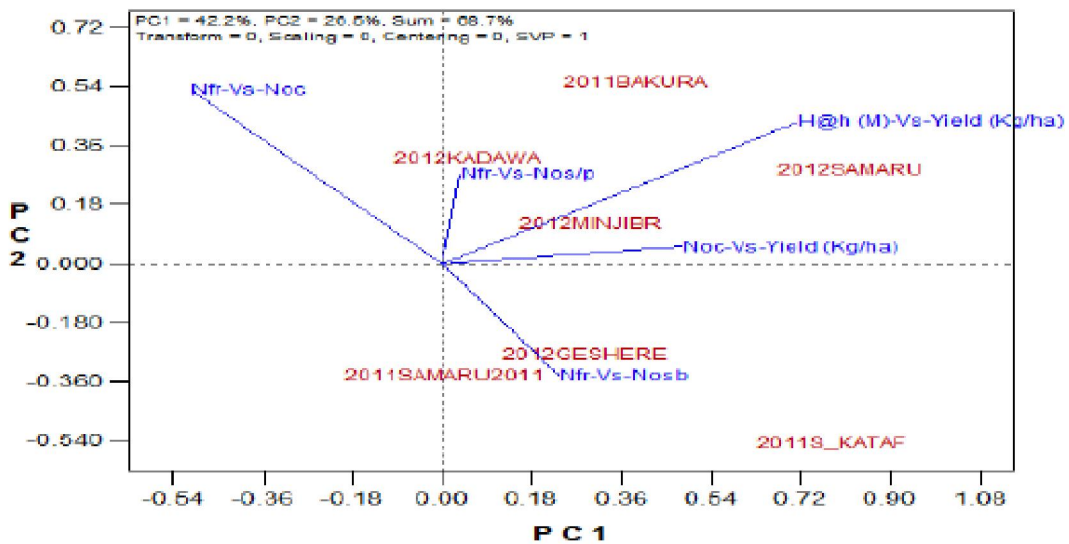


Figure 2 : A trait association by environment biplot of 30 castor accessions based on 2011 and 2012 Multi-Environment Trials data.

Trait association by environment (TAE) biplot

Trait Association by Environment (TAE) biplot using GGEbiplot is shown in Figure 2. The following can be seen from this biplot: (1) The eight environments fell into three distinct groups: the first group consisted of three environments, Kadawa, Talata mafara and Bakura

in the Sudano-sahelian savanna, the second group consisted of Samaru2012 in the northern guinea savanna and Minjibir of the sudan savanna (due the high water lodging experienced at Minjibir in 2012 wet season as result of the changing climate), the third group consisted of Geshere and Samaru kataf in the southern guinea

savanna and Samaru2011 of the northern guinea. (2) The first group sites were characterized by strong positive associations of NFR vs. No.S/p, NFR vs. NOC and height vs. yield. This implied that accessions with higher number of nodes to first racemes had higher yield at these sites. (3) The second group were characterized by strong positive associations of NOC vs. Yield,

height at harvest vs. yield. Therefore, at these locations, taller genotypes and those with more number of capsules in first raceme tended to give yield. (4) The third group were characterised by strong positive associations for NFR vs. NOSB and NOC vs. Yield implying that genotypes with higher NFR, NOC and NOSB tend to have higher yields in these sites.

TABLE 3 : Range, mean, Standard error of mean (SE), genotypic (σ^2_g) and phenotypic (σ^2_p) variances, genotypic and phenotypic coefficient of variations (GCV and PCV), relative difference (RD), broad sense heritability (h^2_b) and genetic gain (GA) for yield and yield components of 30 castor accessions evaluated across 8 environments in 2011 and 2012 in the Savanna ecologies of Nigeria.

‡Traits	Range	Mean	SE	σ^2_g	σ^2_p	GCV (%)	PCV (%)	RD(%)	h^2_b (%)	GA
PL	5-50	21.16	0.33	0.04	0.12	0.92	1.64	43.98	31.38	22.47
NFR	4-27	12.08	0.15	0.12	0.68	2.81	6.84	58.92	16.94	28.78
Noc	3-184	35.95	0.94	9.44	33.66	8.55	16.14	47.03	28.04	335.12
NOSB	1-17	4.62	0.09	0.10	0.30	6.83	11.90	42.61	32.98	37.21
Nos/p	1-16	5.17	0.09	0.20	0.50	8.67	13.64	36.44	40.40	58.85
H@H (m)	0.46-3.9	1.73	0.03	0.001	0.007	1.36	4.76	71.43	8.140	1.40
Yield (Kg/ha)	110.44-2186.43	405.72	10.63	1790.46	5208.20	10.43	17.79	41.37	34.38	5110.78

‡Peduncle length (PL), Number of nodes to the first raceme (NFR), Number of capsules in the first raceme (Noc), Number of secondary branching (NSB), Number of spikes/plant and Plant height at harvest (H@H).

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