# ESTIMATION OF HERITABILITY AND PREDICTED GENOTYPE MEAN FOR SEED YIELD OF CASTOR (*RICINUS COMMUNIS* L.) USING BEST LINEAR UNBIASED PREDICTION (BLUP)

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**Abstract**: Eighty six castor genotypes were evaluated to estimate heritability and predicted genotype mean for seed yield and its component traits. The genotypes were planted at three locations using incomplete block experimental design with three replications. The results revealed significant effects of genotypes for most of the traits evaluated. Significant interactions of genotypes by locations were observed for six traits including 100 seed weight and seed yield. Genotypic coefficient of variation and phenotypic coefficient of variation were high for number of branches per plant and 100 seed weight. Heritability for the studied traits ranged from 0.21 to 0.92. High genetic advance as percentage of mean coupled with high heritability were observed for most of the traits. Thirty six out of eighty six genotypes evaluated presented predicted genotypic seed yield mean above the general mean. These results revealed moderate to high possibility for improvement of five out of ten traits evaluated.

**Keywords**: Badeggi, component traits, genetic advance, Minna, Phenotypic variation.

## Introduction

Castor oil plant (*Ricinus communis* L.) is one of the most versatile oil crops with high socio-economic values around the world [GANA *& al.* 2013]. The crop has been demonstrating its economic potentials by earning notable foreign exchange credits to many countries like India, China and Brazil [OGBEH, 2014]. The castor oil, which is extracted from castor seed, is very critical to many industrial applications because of its unique ability to withstand high and low temperatures, and to form many valuable derivatives; commanding huge amount of demand at the international market [MUTLU & MEIER, 2010; OGUNNIYI, 2006]. Annual world castor production is estimated at 1,314,193 MT, produced on a total area of 1,369,720 hectare with estimated seed yields of 1,200 kg per hectare [FAOSTAT, 2008]. This was produced majorly in India, China and Brazil. In Nigeria, hectarage was estimated at about 6000 ha, and production at about 3000–4000 MT in 2004. The major producers then were Cross River and Ebonyi states [Raw Material Research and Development Council – RMRDC, 2009]. However in 2013, Kogi, Enugu, Oyo and Osun states were identified as some of major castor producers in Nigeria [GANA, 2015].

The castor production in Nigeria is limited majorly by low average yield among the farmers [AMOSUN *& al.* 2013]. The low productivity is associated with many biotic (insects, diseases & weeds) factors, abiotic (drought, low soil fertility, etc.) factors and lack of improved varieties [SALIHU & al. 2014]. Therefore, developing improved varieties is one

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of important measures to curb the castor production constraints in Nigeria. In this respect, estimation of heritability for important agronomic traits is the primary precondition for any improvement programme. Precise estimation of heritable variance component and accurate selection are of great importance in this regard. This can be achieved through the use of optimal estimation/prediction procedures, which will lead to the maximization of genetic gain from selection. For unbalanced data sets (e.g. data from incomplete block design), the optimum estimation and prediction procedure could be achieved by likelihood ratio test and Best Linear Unbiased Prediction (BLUP). For balanced data sets, the estimation of variance components by the least squares method (analysis of variance) produces similar estimates [RESENDE & HIGA, 1994]. In this present study, 86 castor genotypes were evaluated in an incomplete block design across three locations. The objective of the study was to estimate the heritability, genetic advance and predicted genotype means with the purpose of starting a castor breeding programme within the study area.

## Materials and methods

The research was carried out at three sites in Niger State. The state lies in the northern region of Nigeria with savanna vegetation. The state enjoys six month rainfall season (May to October) and six month dry season (November to April). The average rainfall ranges between 865 mm and 1139 mm, and temperature ranges between 24.3 °C and 33.9 °C. The trial sites within the state were Mokwa (Lat. 9°12`N, Long. 5°20`E), NCRI Badeggi (Lat. 9°45`N, Long. 6°07`E) and Minna (Lat. 9°36`50``N, Long. 6°33`25``E).

The planting material used for the present research comprised of 86 castor accessions obtained from National Cereals Research Institute (NCRI), Badeggi, Nigeria. The eighty six castor genotypes were evaluated at three locations mentioned above. The treatments were laid out on an incomplete block design with three replications. The plot size was 3 m by 1.5 m with Inter-row and intra-row spaces of 75 cm by 75 cm. Two seeds per hole were sown and later thinned to one seedling per hole at three to four weeks after planting. Planting at all the locations was done within a week (12–18th of June, 2015). Fractional fertilizer requirement [OGUNLADE, 1993] for individual plant stand was estimated and applied by band placement. Insecticide (Cepermithrin at 100ml/15L) and Fungicide (Mancozeb at 20g/15L) were applied three times before flowering. Morphological data were taken according to standard castor descriptor [INDIA, 2004]. The parameters considered include: Establishment counts (%), days to first spike flowering, days to first spike maturity, branches per plant, spike per plant, plant height at first raceme maturity, seed yield (Kg/Ha) and 100 Seed weight (g). Data were analyzed using random model procedure of Plant Breeding Tools [PBTOOLS 1.3, 2014]. Estimates of heritability and predicted genotype means were derived using the Best Linear Unbiased Prediction (BLUP). The models for testing the significant effects of each variance component are as follow.

**Genotypic effect:**
Model 1: Trait ~ 1 + (1|Treatment) + (1|Trial) + (1|Rep:Trial) + (1|Rep:Block:Trial) + (1|Treatment:Trial)
Model 2: Trait ~ 1 + (1|Trial) + (1|Rep:Trial) + (1|Rep:Block:Trial) + (1|Treatment:Trial)

**Environment effect:**
Model 1: Trait ~ 1 + (1|Treatment) + (1|Trial) + (1|Rep:Trial) + (1|Rep:Block:Trial) + (1|Treatment:Trial)

Model 2: Trait ~ 1 + (1|Treatment) + (1|Rep:Trial) + (1|Rep:Block:Trial) + (1|Treatment:Trial)

**Genotype by Environment Effect:**

Model 1: Trait ~ 1 + (1|Treatment) + (1|Trial) + (1|Rep:Trial) + (1|Rep:Block:Trial) + (1|Treatment:Trial)

Model 2: Trait ~ 1 + (1|Treatment) + (1|Trial) + (1|Rep:Trial) + (1|Rep:Block:Trial)

The magnitude of the effects was determined using ROBERT & RAFTERY (1995) procedure.

Genotypic variance $(\varsigma^2_g) = \varsigma^2_e + r\,\varsigma^2_g l + r\varsigma^2_g$

$G \times L\ (\varsigma^2 ge) = \varsigma^2_e + r\,\varsigma^2_g l$

Phenotypic variance $(\varsigma^2_p) = \varsigma^2_g + \varsigma^2 ge\,/\,m_{h} + \varsigma^2/\,P_h$ [PIEPHO & MÖHRING, 2007] - for incomplete block design)

$$m_h = \frac{n}{\sum\limits_{i=1}^{n} 1/m_i} \qquad\qquad P_h = \frac{n}{\sum\limits_{i=1}^{n} 1/P_i}$$

$H^2 = 1 - \overline{\upsilon}_{BLUP}/2\,\varsigma^2_g$   [PIEPHO & MÖHRING, 2007]

$GA = H^2 \times I \times \varsigma_p$

GAM (%) = {GA/Mean} x 100

$\varsigma^2_p$ = phenotypic variance

$\varsigma^2_g$ = genotypic variance

$\varsigma^2_{ge}$ = GxE variance

$\varsigma^2$ = residual variance

$m_i$ = number of environments for *ith* genotype

$P_i$ = number of plots for *ith* genotype

n = number of genotypes

$\overline{\upsilon}_{BLUP}$ = mean variance of a difference of the BLUP of $g_i$

$H^2$ = broad sense heritability

GA = genetic advance

$\varsigma_p$ = phenotypic standard deviation

$I$ = selection differential (at 5% = 2.06)

GAM = genetic advance as percentage of mean (expected genetic gain)

### Results and discussion

**Significance tests for effects of all sources of variation**

The results of tests for the effects of all the sources of variation are showed in Tab. 1. The tests revealed significant effects of genotypes for all the studied traits except spikes per plant and plant height at raceme maturity. This is an indication for the existence of considerable genetic variability among the genotypes for most of the traits and as such there is ample scope of selection for different quantitative traits for improvement of the crop. The results revealed significant interactions of genotypes by locations for height at first spike flowering, spikes per plant, days to first raceme maturity, 100 seed weight and seed yield, indicating the possibility of exploiting different environments for development of location specific castor varieties from the genotypes. According to ROBERT & RAFTERY (1995) the magnitude of genotypic effects was found to be more in most of the traits ranging from

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very strong effects (BIC2–BIC1 > 10) to strong (BIC2–BIC1; 6-10). The magnitude of GxL effects was only more (very strong) for spikes per plant and seed yield among the ten traits evaluated. The high magnitude of GxL effects indicated the need for considerable multi-environments testing for the ranking of the genotypes for the superior seed yield performance [GOMEZ & GOMEZ, 1984]. Similar GxL interactions in castor were reported by LAURETI (1988).

### Estimates of variance components
Variability in all the studied traits was estimated through phenotypic and genotypic coefficient of variations. According to DESHMUKH & al. (1986), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (GCV) can be partitioned as high (>20%), moderate (10-20%) or low (< 10%). On this basis, moderate to low GCV and PCV were observed for most of the traits studied (Tab. 2). However, high GCV and PCV were recorded for branches per plant and 100 seed weight. In all the traits, PCV was considerably higher than GCV. However, the magnitude of differences was low for all the traits except in spikes per plant where it was moderate. This is an evidence of low influence of environmental factors on the phenotypic expression of genotypes for the traits and as such there is high chance of improving these characters through selection based on the phenotypic data.  These results are in agreement with the reports of ALLAN & al. (2008), RAO & al. (2009) and ZHENG & al. (2010). But the result is in disagreement with the findings of PATEL & JAIMINI (1988) who reported moderate to high coefficient of variation for most of the traits in castor irrespective of the environment.

### Estimates of heritability in broad sense
Heritability of a character may be categorized to be high (> 0.6), moderate (0.3–0.6) and low when it is less than 0.3 [SHIVANNA, 2008]. High heritability was observed for seedling establishment, days to first spike flowering, spike length, branches per plant, days to first raceme maturity and 100 seed weight (Tab. 2). Low heritability was recorded for height at first spike flowering and spikes per plant, while seed yield showed moderate heritability. The high heritability observed for most of the traits suggested that selection for the traits could be easy and their improvement would be fairly possible using selection breeding. This finding is in accordance with the reports of SEVUGAPERUMAL & al. (2000) and GOLAKIA & al. (2007). SHIVANNA (2008) reported high heritability for all these traits in castor in contrary to the present study where low heritability was recorded for height at first spike flowering and spikes per plant.

### Estimates of Expected genetic advance
Heritability value alone does not imply the actual amount of genetic gain in selection programme [SHIVANNA, 2008]. Heritability estimates along with genetic advance gives best prediction of genetic progress in selection. According to DESHMUKH & al. (1986), genetic advance as percentage of mean (GAM) could be classified as low (<10%), moderate (10–20%) and high (>20%). Based on this classification, plant height at first spike flowering, spikes per plant, height at first raceme maturity and days to first raceme maturity recorded low genetic advance as percentage of mean. High GAM was observed for seedling establishment, days to first spike flowering, branches per plant, 100 seed weight and seed yield. The results showed that selecting the top 5% of the genotypes could result in a genetic improvement of 36.84% for seedling establishment, 52.30% for increased number of

branches, 69.92% for 100 seed weight and 11.33% of seed yield per hectare. The low GAM observed in some of the traits implies that there would be no rewarding selection process for the referenced traits in any new population after one cycle of selection. Similar results on genetic advance as percentage of mean in castor were reported by LAKSHMAMMA & al. (2005). SHIVANNA (2008) reported high GAM for plant at first spike flowering, days to 50% flowering, days to maturity, spike length and spikes per plant.

### Mean performances and predicted genotype seed yield mean

The mean performances and predicted genotype seed yield mean of the genotypes evaluated (Tab. 3) showed a range of 40% (in Acc.041) to 93% (Acc.001) seedling establishment with average mean of 72.14%. Highest number of days (111.78 days) to first spike flowering and number of days (134.44 days) to first raceme maturity were recorded in Acc. 045. The least days to maturity (96.62 days) was observed in Acc.005. Plant height at maturity varied between 91.62 cm (Acc.36M1) and 141.77 cm (Acc.099) with average of 113.70 cm. Length of spike ranged from 13.33 cm (Acc. 036M1) to 29.56 cm (Acc.010). Hundred (100) seed weight ranged from 10.74 g (Acc. 005) to 50.36 g (Acc.045) with average of 24.91 g. Average value of 646.04 kg/ha and a range of 334.76 kg/ha (Acc.067) to 1348.84 kg/ha (Acc.001) was observed for Seed yield (kg/ha). SHIVANNA (2008) and GOLAKIA & al. (2007) reported similar mean performance for various traits in castor.

However, among the 86 genotypes evaluated, thirty six genotypes presented predicted genotype yield means above the general mean (Tab. 3). The genotype with the highest predicted genotypic value was Acc.001 while Acc.067 presented the least predicted genotypic value among all the entries. According to SIMEAO & al. (2002), selection of superior genotypes should be based on the predicted mean components. In this respect, the first best five genotypes with high predicted yield means were Acc.001, Acc.036M1, Acc.036, Acc.010 and Acc.045 among all the genotypes evaluated. The lowest genotypic value prediction observed in genotype Acc.067 may be partly due to its high susceptibility to leaf spot fungi infections incidence in the study area. Similar reports on the uses of BLUP for genetic prediction in annual crops were given by CARBONELL & al. (2004) in their work on 18 common bean genotypes and REIS & al. (2005) reported the estimation of variance components, prediction of breeding values of maize genotypes using REML/BLUP procedures.

**Tab. 1.** Effects of all components of variance for ten agronomic traits in castor at three locations

| Parameters | Genotypic Effect | | Environmental Effect | | Genotype X Environ. | |
|---|---|---|---|---|---|---|
| | Model 1 | Model 2 | Model 1 | Model 2 | Model 1 | Model 2 |
| **Establishment (%)** | | | | | | |
| AIC | 7832.20 | 7894.12 | 7832.20 | 7830.20 | 7832.20 | 7830.21 |
| BIC | 7865.53 | 7922.69 | 7865.53 | 7858.77 | 7865.53 | 7858.78 |
| LogLik. | -3909.10 | -3941.06 | -3909.10 | -3909.10 | -3909.10 | -3909.11 |
| Chisq. | 63.92 | | 0.001 | | 0.01 | |
| Df | 1 | | 1 | | 1 | |
| Pr (>Chisq) | 0.00 | | 0.98 | | 0.92 | |
| $BIC_2 - BIC_1$ | 57.16 | | -6.76 | | -6.75 | |
| **Days to Flowering** | | | | | | |
| AIC | 6749.18 | 6833.60 | 6749.18 | 6754.74 | 6749.18 | 6747.31 |
| BIC | 6782.52 | 6862.18 | 6782.52 | 6783.31 | 6782.52 | 6775.88 |
| LogLik. | -3367.59 | -3410.80 | -3367.59 | -3371.37 | -3367.59 | -3367.65 |
| Chisq. | 86.42 | | 7.55 | | 0.12 | |
| Df | 1 | | 1 | | 1 | |
| Pr (>Chisq) | 0.00 | | 0.01 | | 0.73 | |
| $BIC_2 - BIC_1$ | 79.66 | | 0.79 | | -6.64 | |
| **Height at Flowering (cm)** | | | | | | |
| AIC | 7647.90 | 7659.34 | 7647.90 | 7654.52 | 7647.90 | 7659.26 |
| BIC | 7681.24 | 7687.92 | 7681.24 | 7683.09 | 7681.24 | 7687.84 |
| LogLik. | -3816.95 | -3823.67 | -3816.95 | -3821.26 | -3816.95 | -3823.63 |
| Chisq. | 13.44 | | 8.62 | | 13.36 | |
| Df | 1 | | 1 | | 1 | |
| Pr (>Chisq) | 0.00 | | 0.00 | | 0.00 | |
| $BIC_2 - BIC_1$ | 6.68 | | 1.85 | | 6.60 | |

**Spikes per Plant**

| | | | | | | |
|---|---|---|---|---|---|---|
| AIC | 3017.58 | 3016.54 | 3017.58 | 3042.61 | 3017.58 | 3058.38 |
| BIC | 3050.93 | 3045.12 | 3050.93 | 3071.19 | 3050.93 | 3086.97 |
| LogLik. | -1501.79 | -1502.27 | -1501.79 | -1515.30 | -1501.79 | -1523.19 |
| Chisq. | 0.96 | | 27.03 | | 42.80 | |
| Df | 1 | | 1 | | 1 | |
| Pr (>Chisq) | 0.33 | | 0.00 | | 0.00 | |
| $BIC_2 - BIC_1$ | -5.81 | | 20.26 | | 36.04 | |

**Spike Length (cm)**

| | | | | | | |
|---|---|---|---|---|---|---|
| AIC | 5584.31 | 5596.32 | 5584.31 | 5591.28 | 5584.31 | 5582.72 |
| BIC | 5617.65 | 5624.90 | 5617.65 | 5619.87 | 5617.65 | 5611.30 |
| LogLik. | -2785.15 | -2792.16 | -2785.15 | -2789.64 | -2785.15 | -2785.36 |
| Chisq. | 14.02 | | 8.98 | | 0.41 | |
| Df | 1 | | 1 | | 1 | |
| Pr (>Chisq) | 0.00 | | 0.00 | | 0.52 | |
| $BIC_2 - BIC_1$ | 7.25 | | 2.22 | | -6.35 | |

**Branches per Plant**

| | | | | | | |
|---|---|---|---|---|---|---|
| AIC | 3160.82 | 3192.03 | 3160.82 | 3158.82 | 3160.82 | 3158.86 |
| BIC | 3194.15 | 3220.60 | 3194.15 | 3187.39 | 3194.15 | 3187.43 |
| LogLik. | -1573.41 | -1590.02 | -1573.41 | -1573.41 | -1573.41 | -1573.43 |
| Chisq. | 33.22 | | 0.00 | | 0.05 | |
| Df | 1 | | 1 | | 1 | |
| Pr (>Chisq) | 0.00 | | 0.98 | | 0.83 | |
| $BIC_2 - BIC_1$ | 26.45 | | -6.76 | | -6.72 | |

**Height at Maturity (cm)**

| | | | | | | |
|---|---|---|---|---|---|---|
| AIC | 8012.37 | 8014.09 | 8012.37 | 8020.26 | 8012.37 | 8011.48 |
| BIC | 8045.68 | 8042.65 | 8045.68 | 8048.82 | 8045.68 | 8040.04 |
| LogLik. | -3999.19 | -4001.05 | -3999.18 | -4004.13 | -3999.19 | -3999.74 |

| | | | | | | |
|---|---|---|---|---|---|---|
| Chisq. | 3.73 | | 9.89 | | 1.11 | |
| Df | 1 | | 1 | | 1 | |
| Pr (>Chisq) | 0.05 | | 0.00 | | 0.29 | |
| $BIC_2 - BIC_1$ | -3.03 | | 3.14 | | -5.28 | |
| **Days to Maturity** | | | | | | |
| AIC | 6757.06 | 6780.94 | 6757.06 | 6755.71 | 6757.06 | 6762.77 |
| BIC | 6790.37 | 6809.50 | 6790.37 | 6784.26 | 6790.37 | 6791.33 |
| LogLik. | -3371.53 | -3384.47 | -3371.53 | -3371.85 | -3371.53 | -3375.39 |
| Chisq. | 25.88 | | 0.65 | | 7.71 | |
| Df | 1 | | 1 | | 1 | |
| Pr (>Chisq) | 0.00 | | 0.42 | | 0.00 | |
| $BIC_2 - BIC_1$ | 19.13 | | -6.11 | | 0.96 | |
| **Seed Weight (g)** | | | | | | |
| AIC | 6287.97 | 6306.50 | 6287.97 | 6298.86 | 6287.97 | 6306.50 |
| BIC | 6321.28 | 6335.06 | 6321.28 | 6327.42 | 6321.28 | 6331.06 |
| LogLik. | -3136.98 | -3147.25 | -3136.98 | -3143.43 | -3136.98 | -3147.25 |
| Chisq. | 20.54 | | 12.90 | | 20.54 | |
| Df | 1 | | 1 | | 1 | |
| Pr (>Chisq) | 0.00 | | 0.00 | | 0.00 | |
| $BIC_2 - BIC_1$ | 13.78 | | 6.14 | | 9.78 | |
| **Seed Yield (kg/ha)** | | | | | | |
| AIC | 11121.66 | 11125.35 | 11121.66 | 11124.09 | 11121.66 | 11218.89 |
| BIC | 11154.98 | 11154.99 | 11154.98 | 11152.65 | 11154.98 | 11247.45 |
| LogLik. | -5553.83 | -5556.67 | -5553.82 | -5556.05 | -5553.83 | -5603.45 |
| Chisq. | 5.69 | | 4.43 | | 99.23 | |
| Df | 1 | | 1 | | 1 | |
| Pr (>Chisq) | 0.02 | | 0.04 | | 0.00 | |
| $BIC_2 - BIC_1$ | 0.01 | | -2.33 | | 94.47 | |

AIC – Akaike's Information Criterion, BIC – Bayesian Information Criterion, LogLik. – loglikelihood, Df – degree of freedom between the models

**Tab. 2.** Combined mean values, variance components, heritability and genetic advance for all the traits studied

| Parameters | Mean | $\epsilon^2 g$ | $\overline{\upsilon}_{BLUP}$ | $\epsilon^2 gxe$ | $\epsilon^2 P$ | GCV | PCV | H² | GA | GAM |
|---|---|---|---|---|---|---|---|---|---|---|
| ESTAB | 71.35 | 154.23 | 30.85 | 1.66 | 200.99 | 17.41 | 19.87 | 0.90 | 26.28 | 36.84 |
| DF | 69.21 | 51.73 | 9.31 | 1.62 | 64.88 | 10.39 | 11.64 | 0.91 | 15.10 | 21.82 |
| HF | 71.79 | 46.34 | 73.22 | 54.48 | 99.35 | 9.48 | 13.88 | 0.21 | 4.31 | 6.01 |
| SL | 19.03 | 3.5 | 2.17 | 0.82 | 7.37 | 9.83 | 14.27 | 0.69 | 3.86 | 20.28 |
| BPP | 4.98 | 0.37 | 0.13 | 0.02 | 0.59 | 24.43 | 30.96 | 0.82 | 1.30 | 26.11 |
| SPP | 5.92 | 0.06 | 0.10 | 0.51 | 0.39 | 8.30 | 21.11 | 0.21 | 0.27 | 4.56 |
| HM | 113.7 | 28.92 | 29.50 | 24.67 | 99.93 | 4.73 | 8.79 | 0.49 | 10.09 | 8.88 |
| DM | 109.81 | 24.91 | 13.45 | 14.77 | 42.56 | 4.55 | 5.94 | 0.73 | 9.81 | 8.93 |
| SW | 24.91 | 74.28 | 11.89 | 12.74 | 84.47 | 34.60 | 36.90 | 0.92 | 17.42 | 69.92 |
| SY | 646.04 | 2607.67 | 3129.20 | 10224.27 | 7656.79 | 7.90 | 13.55 | 0.40 | 72.10 | 11.33 |

$\epsilon^2 g$ = genotypic variance, $\upsilon_{BLUP}$ = mean variance of a difference of the BLUP of $g_i$, $\epsilon^2 gxe$ = variance due to interaction of genotype and environment, $\epsilon^2 P$ = phenotypic variance, GCV = genotypic coefficient variance, PCV = phenotypic coefficient variance, H² = broad sense heritability, GA = genetic advance, GAM = genetic advance as percentage of mean;

Parameters: ESTAB = Seedling establishment (%), DF = days to flowering, HF = height at first spike flowering (cm), SL = spike length (cm), BPP = branches per plant, SPP = spikes per plant, HM = height at first raceme maturity (cm), DM = days to first raceme maturity, SW = 100 seeds weight, SY = seed yield (kg/ha).

**Tab. 3.** Combined means for ten agronomic traits of castor across three locations

| Genotypes | ESTAB | DF | HF (cm) | SPP | SL (cm) | BPP | HM (cm) | DF | SW (g) | SY (Kg/Ha) | Predicted SY(Kg/Ha) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Acc.001 | 93.44 | 95.67 | 74.76 | 5.12 | 22.33 | 4.66 | 117.57 | 128.44 | 49.89 | 1349.84 | 1083.24 |
| Acc.036M1 | 88.33 | 70.89 | 49.15 | 10.44 | 13.33 | 12.56 | 91.62 | 122.00 | 13.18 | 1191.04 | 936.64 |
| Acc.036 | 81.11 | 73.67 | 79.35 | 5.56 | 28.59 | 7.12 | 130.93 | 106.89 | 20.58 | 918.86 | 829.74 |
| Acc.010 | 74.44 | 66.78 | 63.24 | 4.88 | 29.56 | 3.78 | 107.77 | 105.44 | 11.31 | 995.96 | 762.26 |
| Acc.045 | 79.67 | 111.78 | 77.55 | 3.56 | 20.96 | 4.00 | 120.56 | 134.44 | 50.38 | 985.32 | 760.04 |
| Acc.005 | 85.88 | 58.38 | 40.17 | 7.24 | 26.83 | 6.24 | 104.31 | 96.62 | 10.74 | 971.66 | 755.82 |
| Acc.026 | 83.33 | 69.33 | 59.56 | 4.66 | 18.30 | 3.56 | 102.65 | 112.11 | 23.16 | 688.82 | 751.06 |
| Acc.053 | 80.00 | 64.22 | 84.23 | 7.34 | 18.48 | 5.56 | 137.33 | 101.78 | 25.96 | 941.70 | 734.96 |
| Acc.099 | 82.22 | 70.56 | 103.55 | 6.00 | 22.07 | 5.12 | 141.77 | 118.67 | 26.71 | 884.92 | 725.90 |
| Acc.040 | 77.78 | 73.89 | 84.83 | 4.00 | 16.70 | 3.56 | 118.20 | 114.67 | 42.29 | 844.94 | 711.88 |
| Acc.048 | 81.25 | 67.38 | 69.11 | 5.76 | 16.33 | 4.24 | 112.28 | 108.75 | 15.92 | 840.88 | 709.16 |
| Acc.003 | 82.07 | 63.22 | 60.87 | 6.22 | 19.44 | 5.12 | 118.88 | 104.00 | 15.88 | 609.42 | 704.48 |
| Acc.046 | 60.00 | 76.50 | 63.16 | 6.00 | 17.83 | 4.00 | 100.92 | 115.70 | 16.25 | 811.90 | 700.80 |
| Acc.009 | 76.67 | 76.22 | 80.38 | 3.12 | 16.63 | 3.78 | 117.66 | 115.44 | 44.98 | 995.02 | 696.78 |
| Acc.022 | 56.67 | 72.11 | 62.14 | 6.22 | 20.85 | 5.56 | 97.57 | 114.00 | 15.06 | 593.14 | 695.08 |
| Acc.019 | 81.11 | 70.11 | 72.68 | 5.78 | 20.04 | 4.00 | 120.72 | 108.25 | 15.12 | 799.44 | 685.78 |
| Acc.042 | 60.00 | 74.44 | 75.73 | 4.22 | 18.56 | 4.44 | 99.36 | 109.22 | 32.23 | 741.62 | 676.46 |
| Acc.012 | 66.67 | 68.56 | 56.62 | 6.44 | 17.89 | 5.78 | 101.82 | 110.67 | 12.87 | 642.62 | 676.12 |
| Acc.002 | 88.89 | 77.44 | 83.21 | 5.56 | 20.96 | 4.00 | 115.44 | 114.00 | 27.61 | 721.72 | 669.08 |
| Acc.091 | 76.67 | 65.11 | 65.54 | 7.12 | 18.44 | 5.34 | 103.14 | 104.11 | 28.87 | 717.92 | 668.68 |
| Acc.072 | 75.56 | 65.11 | 72.87 | 7.12 | 19.67 | 5.34 | 118.34 | 109.33 | 20.17 | 715.98 | 666.64 |
| Acc.016 | 85.56 | 78.00 | 87.58 | 4.44 | 15.89 | 3.34 | 117.92 | 115.78 | 42.80 | 514.36 | 664.24 |

| Acc.006 | 70.00 | 66.89 | 75.58 | 6.66 | 17.74 | 4.88 | 116.31 | 96.78 | 15.65 | 538.88 | 662.86 |
|---------|-------|-------|-------|------|-------|------|--------|--------|-------|---------|--------|
| Acc.044 | 68.89 | 75.89 | 81.81 | 3.78 | 15.63 | 4.00 | 114.12 | 116.50 | 32.65 | 656.12 | 661.40 |
| Acc.027 | 80.00 | 64.89 | 82.20 | 5.78 | 21.37 | 4.22 | 130.76 | 109.67 | 24.07 | 562.74 | 660.44 |
| Acc.097 | 86.25 | 60.62 | 80.30 | 6.00 | 18.25 | 4.24 | 116.79 | 104.88 | 25.62 | 682.64 | 659.12 |
| Acc.103 | 65.56 | 71.67 | 57.65 | 5.56 | 16.44 | 4.00 | 94.57 | 107.56 | 12.20 | 682.06 | 656.92 |
| Acc.073 | 70.44 | 69.89 | 74.07 | 7.56 | 18.67 | 5.12 | 111.24 | 113.11 | 20.00 | 676.66 | 654.96 |
| Acc.061 | 84.44 | 71.22 | 71.81 | 5.12 | 20.18 | 4.88 | 104.36 | 103.89 | 19.09 | 677.46 | 654.76 |
| Acc.062 | 87.78 | 68.33 | 77.96 | 6.00 | 19.96 | 5.78 | 124.66 | 104.11 | 21.14 | 666.02 | 651.98 |
| Acc.047 | 70.33 | 74.44 | 74.04 | 5.34 | 20.78 | 4.22 | 106.72 | 111.33 | 14.28 | 665.44 | 650.16 |
| Acc.051 | 46.25 | 62.25 | 52.87 | 4.00 | 13.50 | 4.00 | 89.66 | 101.25 | 26.05 | 681.90 | 649.44 |
| Acc.100 | 62.22 | 63.75 | 66.52 | 6.66 | 16.85 | 4.88 | 102.24 | 105.62 | 25.46 | 656.68 | 648.62 |
| Acc.095 | 82.00 | 61.50 | 61.34 | 6.80 | 20.23 | 6.00 | 101.23 | 104.60 | 24.50 | 658.10 | 647.82 |
| Acc.070 | 83.00 | 64.20 | 69.80 | 5.60 | 18.97 | 4.80 | 116.02 | 103.60 | 17.32 | 699.22 | 647.10 |
| Acc.035 | 54.44 | 77.44 | 80.40 | 3.34 | 20.37 | 4.00 | 125.98 | 117.67 | 28.30 | 1002.88 | 646.58 |
| Acc.039 | 75.00 | 75.33 | 72.26 | 4.44 | 18.37 | 4.44 | 111.46 | 117.22 | 15.83 | 642.40 | 643.06 |
| Acc.015 | 62.22 | 69.89 | 82.43 | 4.00 | 16.26 | 4.00 | 123.64 | 110.67 | 46.14 | 706.54 | 642.56 |
| Acc.031 | 42.50 | 70.00 | 56.80 | 4.00 | 16.00 | 4.66 | 112.83 | 108.83 | 14.34 | 559.30 | 642.48 |
| Acc.056 | 81.11 | 68.33 | 82.62 | 8.66 | 21.67 | 8.44 | 126.44 | 110.56 | 26.84 | 633.74 | 640.50 |
| Acc.096 | 81.11 | 54.78 | 62.13 | 7.34 | 19.19 | 6.22 | 108.01 | 101.78 | 27.20 | 631.76 | 639.88 |
| Acc.050 | 57.78 | 77.33 | 61.71 | 4.88 | 22.00 | 4.66 | 101.56 | 108.89 | 15.24 | 619.66 | 634.70 |
| Acc.089 | 85.56 | 66.11 | 71.14 | 6.00 | 15.89 | 4.88 | 109.56 | 106.44 | 26.10 | 612.14 | 631.82 |
| Acc.004 | 86.67 | 66.67 | 62.51 | 6.00 | 20.41 | 3.78 | 106.79 | 108.78 | 15.03 | 971.44 | 631.00 |
| Acc.018 | 84.44 | 72.78 | 75.87 | 6.00 | 19.59 | 3.78 | 111.68 | 109.67 | 22.16 | 718.32 | 629.04 |
| Acc.033 | 28.33 | 72.78 | 61.88 | 6.00 | 23.78 | 4.44 | 102.88 | 114.56 | 25.04 | 542.10 | 628.92 |
| Acc.093 | 71.11 | 56.78 | 64.55 | 5.78 | 20.18 | 6.22 | 121.23 | 100.67 | 32.54 | 597.86 | 627.96 |
| Acc.063 | 70.00 | 71.57 | 67.37 | 5.14 | 18.86 | 4.58 | 110.00 | 107.86 | 20.07 | 608.84 | 627.92 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Acc.024 | 82.22 | 75.56 | 82.25 | 4.66 | 15.30 | 4.22 | 120.93 | 114.89 | 31.83 | 961.16 | 625.54 |
| Acc.057 | 80.00 | 57.73 | 93.67 | 8.72 | 19.67 | 4.90 | 131.81 | 100.09 | 22.23 | 565.32 | 623.08 |
| Acc.098 | 58.89 | 67.22 | 66.26 | 6.00 | 17.30 | 4.22 | 109.72 | 110.00 | 23.50 | 583.24 | 622.36 |
| Acc.090 | 54.44 | 69.22 | 83.52 | 7.34 | 19.85 | 6.22 | 114.42 | 109.11 | 29.87 | 565.08 | 620.14 |
| Acc.054 | 77.78 | 70.22 | 73.58 | 5.12 | 21.69 | 4.66 | 124.58 | 110.33 | 31.59 | 569.38 | 620.00 |
| Acc.064 | 87.78 | 66.89 | 74.93 | 6.88 | 15.85 | 5.34 | 108.78 | 112.89 | 25.61 | 566.98 | 618.70 |
| Acc.081 | 80.00 | 75.33 | 84.84 | 5.78 | 19.37 | 5.12 | 124.04 | 114.67 | 25.12 | 565.60 | 616.78 |
| Acc.028 | 81.11 | 72.89 | 67.35 | 6.22 | 18.70 | 5.12 | 110.63 | 117.89 | 23.64 | 531.44 | 616.12 |
| Acc.032 | 78.38 | 79.11 | 69.52 | 4.00 | 17.93 | 4.44 | 104.22 | 116.67 | 34.07 | 597.26 | 613.42 |
| Acc.007 | 74.44 | 63.56 | 66.19 | 5.78 | 18.22 | 3.78 | 113.73 | 110.44 | 30.00 | 541.34 | 608.76 |
| Acc.034 | 70.00 | 70.00 | 72.23 | 6.00 | 21.52 | 4.22 | 112.31 | 110.89 | 17.58 | 654.30 | 608.72 |
| Acc.008 | 73.33 | 73.89 | 67.99 | 4.88 | 16.26 | 4.66 | 120.12 | 107.56 | 29.38 | 797.60 | 608.34 |
| Acc.043 | 38.89 | 80.00 | 69.56 | 3.78 | 18.63 | 3.56 | 102.26 | 120.22 | 48.24 | 536.60 | 606.14 |
| Acc.041 | 40.44 | 74.22 | 78.89 | 5.56 | 19.04 | 5.12 | 110.50 | 112.78 | 38.64 | 533.94 | 605.24 |
| Acc.029 | 85.56 | 71.22 | 58.47 | 6.44 | 19.07 | 4.44 | 107.01 | 111.22 | 14.12 | 646.96 | 604.76 |
| Acc.066 | 56.67 | 67.00 | 74.20 | 6.88 | 19.15 | 5.78 | 116.91 | 99.56 | 23.49 | 526.10 | 604.32 |
| Acc.065 | 69.90 | 66.38 | 78.25 | 8.00 | 21.83 | 5.24 | 126.65 | 107.00 | 18.89 | 505.86 | 604.00 |
| Acc.087 | 79.78 | 66.00 | 73.17 | 6.00 | 15.30 | 5.56 | 112.89 | 103.67 | 32.85 | 519.58 | 601.38 |
| Acc.017 | 52.22 | 71.44 | 62.31 | 5.56 | 18.30 | 5.78 | 109.07 | 122.89 | 17.81 | 601.08 | 600.26 |
| Acc.080 | 76.67 | 69.78 | 68.56 | 6.44 | 20.81 | 5.12 | 122.60 | 109.11 | 25.45 | 516.30 | 599.68 |
| Acc.077 | 62.00 | 68.80 | 79.10 | 6.00 | 21.17 | 4.80 | 119.63 | 110.30 | 19.21 | 511.12 | 592.44 |
| Acc.068 | 83.33 | 64.22 | 77.16 | 5.56 | 17.00 | 4.66 | 126.12 | 101.89 | 23.18 | 496.28 | 592.14 |
| Acc.052 | 66.67 | 60.00 | 67.11 | 7.12 | 17.85 | 4.66 | 107.23 | 101.67 | 23.09 | 489.64 | 591.28 |
| Acc.102 | 55.56 | 75.00 | 62.82 | 5.34 | 18.11 | 4.44 | 97.69 | 115.62 | 14.57 | 488.46 | 590.50 |
| Acc.058 | 68.00 | 64.30 | 69.91 | 5.60 | 17.63 | 4.60 | 114.30 | 106.50 | 16.10 | 455.36 | 582.30 |
| Acc.094 | 70.56 | 65.00 | 64.80 | 6.00 | 16.70 | 4.66 | 104.06 | 109.11 | 30.04 | 450.42 | 577.68 |

| | ESTB | DF | HF | BPP | SPP | SL | CPS | HM | SW | SY | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Acc.085 | 66.67 | 71.00 | 85.79 | 5.78 | 19.30 | 4.66 | 130.53 | 120.33 | 25.60 | 450.54 | 577.08 |
| Acc.060 | 78.89 | 66.44 | 82.55 | 5.34 | 19.15 | 5.34 | 120.62 | 111.22 | 25.68 | 442.70 | 575.30 |
| Acc.071 | 73.33 | 79.11 | 73.23 | 4.44 | 18.93 | 4.00 | 108.71 | 123.78 | 16.88 | 443.70 | 574.16 |
| Acc.075 | 82.22 | 66.56 | 73.57 | 5.56 | 19.81 | 4.66 | 115.91 | 109.44 | 24.85 | 441.60 | 571.72 |
| Acc.088 | 80.00 | 57.44 | 63.83 | 9.12 | 17.52 | 5.78 | 108.98 | 104.11 | 27.01 | 423.82 | 568.06 |
| Acc.059 | 75.00 | 58.00 | 70.60 | 6.76 | 16.38 | 6.24 | 112.31 | 105.88 | 37.00 | 430.26 | 567.26 |
| Acc.076 | 83.33 | 59.11 | 114.78 | 6.66 | 19.00 | 4.66 | 137.71 | 105.11 | 17.34 | 414.30 | 567.14 |
| Acc.055 | 73.33 | 69.11 | 67.06 | 6.00 | 19.56 | 4.88 | 118.87 | 110.22 | 25.06 | 412.52 | 565.40 |
| Acc.069 | 66.67 | 61.44 | 65.04 | 6.44 | 15.52 | 4.66 | 108.04 | 109.00 | 17.11 | 397.58 | 560.16 |
| Acc.101 | 62.00 | 65.30 | 78.13 | 6.60 | 28.57 | 5.20 | 110.63 | 106.70 | 25.25 | 367.30 | 553.66 |
| Acc.083 | 83.33 | 74.67 | 76.93 | 6.88 | 17.56 | 5.34 | 135.58 | 113.22 | 26.84 | 363.92 | 548.20 |
| Acc.067 | 72.00 | 64.75 | 65.74 | 6.76 | 17.92 | 5.50 | 112.62 | 107.38 | 35.95 | 334.76 | 540.76 |
| **Pooled** | **72.14** | **69.21** | **71.79** | | **19.04** | | **113.70** | **109.81** | **24.91** | | | |
| **Mean** | | | | **5.92** | | **4.98** | | | | **645.66** | **646.04** |

ESTB – Seedling Establishment (%); DF – Days to first spike flowering; HF – Height at Flowering (cm); DM – Days to First Spike Maturity; HM – Height at Maturity (cm); BPP – Branches per Plant; SPP – Spikes per Plant; SL – Spike Length (cm); CPS – Capsules per Spike; SW – 100 Seed Weight (g); SY – Seed Yield (kg/ha)

## Conclusions

The results of the study demonstrated moderate to high possibilities for improvement of five out of ten traits evaluated. This information is very critical for commencement of a castor breeding programme in the study area with the evaluated genotypes. It could be concluded that the genotypes evaluated presented potentials for generating superior population in an improvement programme. The use of BLUP provided higher selection accuracy and so permits the identification of potential genotypes for improvement exercise. According to the results, the first best two genotypes (Acc.001 and Acc.036M1) could be recommended for cultivation in the study area. Beside this direct selection for cultivation under short-term breeding plan, the genotypes with predicted values above the general mean could be used to initiate hybridization scheme and/or used to develop potential base breeding populations for medium and long term breeding programme.

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