Full Length Research Paper

Estimation of heritability and genetic gain in height growth in *Ceiba pentandra*

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Ceiba pentandra (L.) has been selected for plantation establishment in Ghana under the National Forest Plantation Development Programme of Ghana (NFPDP). This has led to a rise in demand for its seedlings for large scale commercial plantation establishments with seed of *C. pentandra* being collected from the wild and used to raise seedlings to meet the demands of the programme. The primary purpose of most of these plantations is timber with height growth as one of the key economic traits. However, there is relatively inefficient information available on the heritability and genetic gain in height growth in *C. pentandra* based on which selection and subsequent breeding could be made. This poses a major challenge to the production of new cultivars for the forestry industry of Ghana. The current study looked at the estimation of narrow sense heritability (h^2) and genetic gain in height growth in *C. pentandra* using 37 accessions from Ghana. Narrow sense heritability was 0.56 and genetic gain in height ranged from -52.82 to 37.30 cm/yr. Twenty-two (22) accessions (59.46%) had mean height increment above the overall mean performance and were recommended for conservation as seed trees. The results were discussed in relation with the conservation of *C. pentandra* genetic resources and the potential of accessions for high genetic gains.

Key words: *Ceiba pentandra*, narrow sense heritability, genetic gain, height growth, stem dieback disease.

INTRODUCTION

Heritability is the measure of the degree to which parents transfer heritable characteristics to their offspring (Jansson, 2005). The differences in the degree of transfer of these characteristics result in variation in genotypes among the offspring. This variation is usually referred to as genetic variance (additive and non-additive variance) and that of the environment as environmental variance (Lavi et al., 1993; Suzuki et al., 1986). Additive genetic variance is responsible for the similarities between relatives and the population in response to selection (Lavi et al., 1993) and mostly transmissible by seed (Wright, 1976). Generally, heritability is useful, among other things, in predicting genetic gain from selection (Paikhomba et al., 2014; Holland et al., 2003) and in

selecting superior phenotypes on the basis of the phenotypic performance of quantitative characters (Vasudeva et al., 2004). In trees, several traits are known to be under genetic influence including growth rate, fibre yield, photosynthetic efficiency and pest resistance (Namkoong et al., 1980). Selection of genotypes based on the phenotypes becomes difficult when heritability is low (Jansson, 2005) whereas genetic gain increases with increase in heritability (Mckeand et al., 2008). Further, characters with high heritability also has high additive effect and respond effectively on phenotypic selection (Lewis et al., 2010). Several methods of estimation of heritability have been proposed, including the use of the variance components from the analysis of variance tables and from parent-offspring regression lines. The later is practice when heritable traits from both parents and offsprings are measured which in most cases is difficult to achieve due to the long regeneration time of forest trees. The use of half-sib, full-sib or clonal tests allow the partitioning of the phenotypic variances into genetic and environmental components using analysis of variance (Jansson, 2005).

Ceiba pentandra (L.) has been selected for plantation establishment in Ghana with the onset of the National Forest Plantation Programme in Ghana (NFPDP) (Ghana Forest Service Division, 2005). The wood is used for making stools in the Ashanti Region of Ghana, domestic utensils, boxes, wooden figures, quivers, drums, dugout canoes, plates, trays and coffins, especially, in the Ada area of Ghana (Burkill, 1985; Irvine, 1961). It is also suitable for wooden sandals, heels, rafts, floats, lifeboats, models, particle board and for papermaking. The seeds are very rich in unsaturated fatty acids such as palmitic, linoleic, oleic, and stearic acids (Burkill, 1985). The fibre, commonly called kapok, is used for stuffing cushions, pillows and mattresses, insulation, as an absorbent material and tinder. The gum is eaten to relieve stomach upset, whereas the leaves and fruits are used as a laxative and infusion from the leaf is used for colic treatment in human and livestock (Irvine, 1961). Therefore, demand its seedlings for large scale commercial plantation establishment has become inevitable. As such, seeds of *C. pentandra* are being collected from the wild and are being to raise seedlings to meet this demand. However, there is relatively inefficient information available on the heritability and genetic gain in height growth in *C. pentandra* base on which selection and subsequent breeding could be made. Also, dieback of *C. pentandra* seedlings and saplings has been observed in both the nursery and plantation (Apetorgbor et al., 2003) and it poses a great threat to large scale commercial establishment of this species and puts high investment in this direction at risk. There is therefore the need for the identification and use of resistant stock. The estimation of genetic parameters, such as prediction of breeding values, is also essential for the selection of genetic resistant genotypes.

Height is a key economic trait in plantation development of this species since growth in height depends on the level of resistance to dieback or recuperative ability after fungal infection. Also, height is a composite trait with different growth components and its variation is under different degrees of inheritance. A better understanding of the genetics of height growth components will result in a better understanding of it and simplifies selection in tree breeding (Rweyongeza et al., 2003).

The rationale of the study was that wild, undomesticated, out-bred forest trees are highly variable and their natural populations retain a wide genetic diversity that helps them resist pests and diseases. The objective of the study was to estimate the level of narrow sense heritability and genetic gain in height growth of C. *pentandra*.

MATERIALS AND METHODS

Study site

The field test was done at Abofour, one of the research plots of the Forestry Research Institute of Ghana of the Council for Scientific and Industrial Research. Abofour is located between latitude 6.15º N and longitude 1.10º W in the Afram Headwaters Forest Reserve. It falls within the Dry Semi-Deciduous Forest Zone with mean annual precipitation in the range of 1250 to 1500 mm (Hall and Swaine, 1981). The reserved was created in 1908 and it is about 123.3 sq-km (47.6 sq-miles). Several factors influenced the choice of this site: It is one of the sites which is most likely to be reforested with the end products of the planting stock that is being assessed and it is neither too dry (compared to the Savanna Zone) nor too wet (compared to the Moist/Wet Evergreen Zones).

Progeny trials

Seeds from 37 half-sib families (open-pollinated trees in which only one parent; the female, is known) were used in this study. The seeds were germinated and screened maintained under shed made from palm branches. The seedlings were transplanted to the field at the age of five months. The design for field testing was done using 30 seedlings per accession in randomized complete block design (RCBD) with three replications each. RCBD was used to control variation in spatial effects in the field so that observed differences are majorly due to true differences between treatments. Ten seedlings were planted in each block in two rows with 5 seedlings per row. The planting distance was 2.5 m × 2.5 m within and between rows. Weed controlled was done by manual weeding at least once every month after planting.

Data collection and analysis

Growth in height was estimated as y_2-y_1, where y_1 and y_2 are height at time of planting and 12 months, respectively. Data were subjected to analysis of variance using Microsoft Excel 2007 at a P-value of 0.05. Mortality data were arc-sine transformed (Snedecor and Cochran, 1980) before subjecting the data to analysis of variance. Standard errors of mean height were also computed to depict the variation about the means. The procedure proposed by Zobel and Talbert (1991) was used to estimate the narrow sense heritability (h^2), selection differential and the genetic gain. This

Table 1. Analysis of variance.

Source of variation	Df	MS	F
Between accessions	f-1	MS_1	MS_1/MS_3
Blocks	r-1	MS_2	
Within accessions	f (r-1)	MS_3	

Table 2. Analysis of variance in height growth.

Source of variation	df	SS	MS	F	P-value	F crit
Between accessions	36	163693.80	4547.05	2.26	0.00	1.58
Blocks	2	27205.45	13602.73	6.77	0.20	8.12
Within accessions	72	144644.50	2008.95			
Total	110	335543.70				

procedure is as described below:

$$h^2 = V_G/V_P \tag{1}$$
$$V_P = V_G+V_E \tag{2}$$

Where, h^2 = Narrow sense heritability, V_G = Variations arising from differences in genetic constitution (between accessions variation), V_P = Variations in phenotypic characters, V_E = Variation due to environment (within accessions variation).

From the analysis of variance table (Table 1),

$$V_G = (MS_1-MS_3)/r \tag{3}$$

Where, MS_1 = Mean square between accessions =

$$V_E + rV_G \tag{4}$$

MS_2 = Mean square of blocks, MS_3 =Mean square among accessions = V_E, r =Number of replications = number of blocks.

The selection differential (S) was estimated as shown below.

$$S = Xs - X\mu \tag{5}$$

Where, S = Selection differential (difference between mean of selected individual and the population mean (Jansson, 2005)), $X\mu$ = Mean of population, Xs   = Mean phenotypic value after selection (sample mean), Genetic gain (G) was estimated as:

$$G = Percentage\ gain\ *h^2 \tag{6}$$

Where, h^2 = Narrow sense heritability.

RESULTS

Mean height increment was significantly different (P < 0.001) among the 37 accessions studied (Table 2). Height increment, selection differential, narrow sense heritability and genetic gain varied among the accessions (Table 3). Narrow sense heritability (h^2) in height growth was 0.56 indicating that 56% or more of the observed variation in height growth was genetically controlled.

Genetic gain varied from 20.89% (DNY 1) above mean performance to as low as -29.58% (TAN 1) below mean performance. Twenty-two accessions (59.46%), out of the 37 accessions screened, had mean height increment above the overall mean height growth of 106.24 cm/yr. The genetic gain in height growth for selecting a particular accession is shown in Table 3.

Estimation of selection differential, narrow sense heritability and genetic gain in individual accessions

From equation 3 above, V_G was estimated as:

$$V_G = MS_1 - MS_3/r$$

From the analysis of variance table (Tables 1 and 2)

MS_1 = 4547.05, MS_3 = 2008.95 and r = 3

$$V_G = (4547.05 - 2008.95)/3 = 846.03$$

From the analysis of variance (Tables 1 and 2)

$$V_E = MS_3/r = 2008.95/3 = 669.65$$

From equation 2, V_P was estimated as:

$$V_P = V_G+V_E = 846.03 + 669.65 = 1515.68$$

From equation 1, h^2 was estimated as:

$$h^2 = V_G/V_P = 846.03 /1515.68 = 0.56$$

Taking accession DNY 1 for instance. From equation 5, selection differential/deviation (S) was estimated as:

$$S = Xs - X\mu$$

Xs = sample mean (mean height increment of accession

Table 3. Height increment and genetic gain in height growth among 37 accessions of *C. pentandra*

Accession	Mean height (cm/yr)	Deviation	Percentage deviation	Percentage gain	Genetic gain	Rank
DNY 1	177.00	70.76	66.61	37.30	20.89	1
KON 8	163.27	57.03	53.68	30.06	16.83	2
AYE 1	157.62	51.38	48.36	27.08	15.16	3
SOF 1	157.39	51.15	48.15	26.96	15.10	4
ODO 6	150.82	44.58	41.96	23.50	13.16	5
SKD 1	148.87	42.63	40.13	22.47	12.58	6
BUF 1	140.73	34.49	32.46	18.18	10.18	7
NKIN 2	138.65	32.41	30.50	17.08	9.56	8
POK 1	131.78	25.54	24.04	13.46	7.54	9
KWA 1	129.61	23.37	22.00	12.32	6.90	10
MAM 1	129.61	23.37	22.00	12.32	6.90	11
KUE 2	127.33	21.09	19.85	11.12	6.23	12
NKA 2	124.92	18.68	17.58	9.84	5.51	13
ABF 1	123.14	16.90	15.91	8.91	4.99	14
ACH 1	118.48	12.24	11.53	6.46	3.62	15
EDW 1	117.79	11.55	10.87	6.09	3.41	16
GYE 1	116.80	10.56	9.94	5.57	3.12	17
NKA 1	115.98	9.74	9.16	5.13	2.87	18
DAN 1	115.30	9.06	8.53	4.78	2.68	19
NKIN 1	113.07	6.83	6.43	3.60	2.02	20
KEC 10	109.59	3.35	3.15	1.76	0.99	21
KUE 1	109.38	3.14	2.96	1.66	0.93	22
ASE 1	104.38	-1.86	-1.75	-0.98	-0.55	23
AYE 2	96.48	-9.76	-9.18	-5.14	-2.88	24
KUE 3	91.47	-14.77	-13.91	-7.79	-4.36	25
KEC 9	88.97	-17.27	-16.26	-9.11	-5.10	26
BAW 10	83.20	-23.04	-21.69	-12.15	-6.80	27
KON 9	82.37	-23.87	-22.47	-12.58	-7.04	28
MSH 1	75.17	-31.07	-29.25	-16.38	-9.17	29
BAW 1	73.49	-32.75	-30.83	-17.26	-9.67	30
MAA 1	59.38	-46.86	-44.11	-24.70	-13.83	31
BAW 4	55.28	-50.96	-47.96	-26.86	-15.04	32
PAW 5	52.09	-54.15	-50.97	-28.54	-15.98	33
KON 13	49.30	-56.94	-53.59	-30.01	-16.81	34
WOA 1	48.92	-57.32	-53.96	-30.22	-16.92	35
BAW 5	47.15	-59.09	-55.62	-31.15	-17.44	36
TAN1	6.03	-100.21	-94.33	-52.82	-29.58	37
Mean	106.24					

DNY 1)

$X\mu$ = population mean (mean height increment of all the 37 accessions)

S = 177.00 -106.24

= 70.76 cm/yr (See Table 3).

$$\text{Percentage deviation} = \frac{\text{Deviation x 100\%}}{\text{Mean}}$$

$$= \frac{70.76 \times 100\%}{106.24}$$

= 66.60%

Percentage gain = percentage deviation x heritability = 66.60 x 0.56
= 37.3 % (Table 3)

Genetic gain = percentage gain x heritability = 37.3 x 0.56

= 20.89

This procedure was repeated for all the accessions. The results produced are as shown in Table 3.

Estimation of selection differentials and genetic gain in the 22 selected accessions (accessions with mean height performance above the overall mean. These are ranked 1 to 22 in Table 3).

$$S = Xs - Xµ.$$

Where, Xs = sample mean (mean height increment of the 22 selected accessions), Xµ = population mean (mean height increment of all the 37 accessions).

$$S = 132.60 - 106.24$$
$$= 26.36 \text{ cm/yr}$$

$$\text{Percentage deviation} = \frac{26.36 \times 100\%}{132.60}$$
$$= 19.88 \%$$

Percentage gain = percentage deviation x heritability = 19.88 x 0.56
$$= 11.13 \%$$

DISCUSSION

The narrow sense heritability estimated was 0.56. Since heritability is a measure of the degree to which parents transfer heritable traits to their offspring (Jansson, 2005; Zobel and Talbert, 1991), the variation in height that is genetically controlled is higher or equal to 56%. This value is similar to results from other studies in forest trees. For instance, heritability values of 0.74 and 0.51 were recorded in the total height growth of two-year old *Khaya anthotheca* and *Khaya ivorensis* respectively (Ofori et al., 2007). McKeand et al. (2008) also reported narrow sense heritability in height growth of Loblolly pine to range from 0 to 0.62 at different planting sites. A positive correlation is known to exist between phenotype and breeding value, increased potential for natural selection and high heritability (Paikhomba et al., 2014; Jansson, 2005). According to Santos et al. (2014), high heritability enables greater dynamism in the breeding program, allowing recombination of the best individuals in a shorter period of time. The high heritability obtained in the current study, therefore, suggests that selection of individuals based on height increment has the potential to retain high productivity in future generation of the species. Heritability estimates are known to be population, trait and test environment specific (Gonçalves et al., 2009; Jansson, 2005). Also, tree characteristics vary in the degree of genetic versus environmental influence and

that genetically inferior trees may appear phenotypically desirable if planted in an unusually favourable micro-environment. Likewise, genetically superior trees may appear phenotypically undesirable due to poor environmental conditions (Frampton, 1996). Hence, the accessions which performed below average could possibly do well if planted in a different test environment and those which performed above the mean could possibly perform poorly if planted in another environment. It is therefore, suggested that this study be repeated in all the ecological zones and the differences in genetic gain be established.

The values of the genetic gain (-29.58 to 20.89 cm/yr) obtained in the study indicate the presence of different levels of resistance to dieback and, hence, a high potential for selection of dieback tolerant individuals. The 22 accessions that had mean height above the mean performance (Table 3) were, therefore, recommended for selection, protection and use as seed trees. Selection is preferred, in a decreasing order, from DNY1 to KUE 1. This followed the recommendations of Namkoong et al. (2000) that only genotypes whose phenotypes approximate the population mean are good for selection while those below should be considered as selection disadvantage. *C. pentandra* is known to have a pan tropical distribution (Lobo et al., 2005) and to be a widespread rainforest tree species (Dick et al., 2007). In Ghana, it is found in all the forest types (Hall and Swaine, 1981). This suggests that the species has a wide environmental adaptability. However, the 44% variability attributable to the growth environment suggests that some environments may be more suitable for the growth of the species than others.

Selection becomes a more effective tool in genetic improvement when all traits of economic importance are evaluated (Silva et al., 2008). Therefore, this study should be repeated and heritability estimated based on other economic traits, such as seed size, seed weight, seed colour, number of seeds per pod, leaf size, leaf length, leaf width, petiole length, petiole colour, degree of spines, stem colour and stem diameter. This will enable the accurate prediction of genetic gain for efficient selection in *C. pentandra* and also enhances its use as a multipurpose species.

Conclusion

At 12 months, there was significant variation in tree heights among accessions across the country and this is important for tree breeders who would like to carry out selection as early as possible. It could be concluded that greater gains in plantation yield of *C. pentandra* could be realized by selecting fast growing accessions. Therefore, based on these results, 22 accessions were selected from a total of 37 accessions to advance their generations. Though the genetic gains estimated in the study were encouraging, higher values could be obtained when

full-sib progenies are used. It is therefore, suggested that a breeding program for *C. pentandra* be initiated to enhance its profitability in the future. This is the first study to demonstrate the existence of variability in narrow sense heritability and genetic gain in *C. pentandra* and it has important practical implications for genetic resource management and tree improvement programs in Ghana. The detection of genetic differences at an early age would therefore be very useful for agroforestry tree improvement programs in Ghana.

Conflict of Interests

The authors have not declared any conflict of interests.

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