

## Research Article

# Estimation of Genetic and Phenotypic Parameters for Growth Traits in a Clonal Seed Orchard of *Pinus kesiya* in Malawi

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Genetic and phenotypic parameters for height, diameter at breast height (dbh), and volume were estimated for *Pinus kesiya* Royle ex Gordon clonal seed orchard in Malawi using an ASReml program, fitting an individual tree model. The data were from 88 clones assessed at 18, 23, 30, 35, and 40 years of age. Heritability estimates for height, dbh, and volume were moderate to high ranging from 0.19 to 0.54, from 0.14 to 0.53, and from 0.20 to 0.59, respectively, suggesting a strong genetic control of the traits at the individual level, among families, and within families. The genetic and phenotypic correlations between the growth traits were significantly high and ranged from 0.69 to 0.97 and from 0.60 to 0.95, respectively. This suggests the possibility of indirect selection in trait with direct selection in another trait. The predicted genetic gains showed that the optimal rotational age of the *Pinus kesiya* clonal seed orchard is 30 years; therefore, it is recommended to establish a new *Pinus kesiya* clonal seed orchard. However, selective harvest of clones with high breeding values in the old seed orchard should be considered so that the best parents in the old orchard can continue to contribute until the new orchard is well established.

## 1. Introduction

*Pinus kesiya* Royle ex Gordon occurs naturally in Himalaya region (Asian): Burma, China, India, Laos, Philippines, Thailand, Tibet, and Vietnam [1]. This species particularly grows well at altitudes from 600 to 1800 m above sea level [2]. The trees can reach heights of 30–35 or 45 m tall with straight, cylindrical trunk [3]. *Pinus kesiya* is a major exotic plantation species in Malawi and other Southern African countries. Its success as an exotic is due to its fast growth rate and wide adaptability. With the increasing demand for wood products globally [4], maximizing wood production on available land resources is of major importance. The high growth rate of *Pinus kesiya*, the variation evident in natural stands and plantations in Malawi, and the need to improve timber quality and production led to the establishment of a breeding programme in Malawi in the 1970s [5]. The breeding programme included phenotypic mass selection in *Pinus kesiya* stands and use of the material for seed production in clonal seed orchards.

Seed orchards are plantations created for production of genetically improved seeds to create commercial forest

crops [6]. The genetic quality of the seeds depends on the genetic superiority of the plus trees, their relationships, their combination ability, and the rate of pollen contamination, among other factors [7]. The major constraint to the efficient breeding of *Pinus kesiya* in Malawi has been the lack of genetic parameter information to guide decisions on the most appropriate breeding strategy and, more generally, to monitor genetic progress.

Genetic parameters estimates available for *Pinus kesiya* are mainly from studies in Brazil. Heritability estimates for diameter at breast height (dbh) and height from these studies were high [1]. There appear to be no estimates of genetic parameters for height and dbh in *Pinus kesiya* grown in Malawi, which is an issue of concern as fast growing tree crops are likely to exhibit different genetic parameters than slower ones [8]. According to Díaz et al. [9], genetic parameters may differ among regions. This lack of genetic parameter estimates for these economically important traits has potentially adverse consequences for realizing genetic progress in *Pinus kesiya* in Malawi.

TABLE 1: Characteristics of the data sets.

Age (years)	Trait	Mean	SD	CV%	Number of trees
18	Height (m)	12.9	1.23	9.2	1869
	dbh (cm)	24.4	2.01	8.6	1869
	Volume (m <sup>3</sup> )	0.283	0.09	23.5	1869
23	Height (m)	22.5	1.95	8.6	1840
	dbh (cm)	28.2	3.26	7.3	1840
	Volume (m <sup>3</sup> )	0.659	0.15	22.4	1840
30	Height (m)	26.4	1.93	8.9	1743
	dbh (cm)	36.7	2.41	7.5	1743
	Volume (m <sup>3</sup> )	1.298	0.34	20.2	1743
35	Height (m)	28.3	1.56	9.1	1731
	dbh (cm)	37.1	2.53	8.0	1731
	Volume (m <sup>3</sup> )	1.409	0.67	21.8	1731
40	Height (m)	28.5	1.62	8.4	1619
	dbh (cm)	37.4	2.49	7.8	1619
	Volume (m <sup>3</sup> )	1.463	0.69	23.4	1619

SD is the standard deviation; CV is the coefficients of variation.

Many models have been proposed for estimation of genetic parameters of quantitative traits in sort of mixed mating system. The model proposed by [10] is the most complete because it considers use of unbalanced data and allows more accurate prediction of genetic values. The optimum estimation/prediction procedure of genetic values is Reml/Blup, that is, the estimation of the components of variance by restricted maximum likelihood (Reml) and the prediction of genetic values by the best linear unbiased prediction (Blup).

The aim of the study was to estimate genetic parameters: variance components, heritability, genetic and phenotypic correlations, and genetic gains for height, dbh, and volume traits for *Pinus kesiya* clonal seed orchard in Malawi using Reml and prediction of additive genetic and genotypic values by Blup.

## 2. Materials and Methods

**2.1. Study Site.** The study was conducted in Malawi located in Southern Africa in the tropical savannah region at Mapale, Dedza (14°21' S, 34°19' E, and 1690 m above sea level). Mapale receives from 1200 mm to 1800 mm rainfall per annum, with annual temperature ranging from 7°C to 25°C. It is situated about 85 km southeast of the capital Lilongwe.

**2.2. Plant Material and Seed Orchard.** The study was carried out with 88 clones of *Pinus kesiya* seed orchard, which was established in 1972. The clones were selected phenotypically for growth from plantations in Kenya, Malawi, Zambia, and Zimbabwe. The seed orchard was established in a 10 × 10 triple lattice, five trees per plot, and planted following a randomized complete block design in four replications. The trees were planted at a space of 6 × 6 m. At the ages of 18, 23, 30, 35, and 40 years after planting, data were collected for the following traits: total height (distance along the axis of the stem of the

tree from the ground to the uppermost point), dbh, and true volume. Total height was measured using a Suunto clinometer with standard, while dbh was measured at 1.3 m above the ground for each standing tree using a calliper. Tree volume was calculated from the tree dbh and height using a tree volume function [5].

**2.3. Statistical Analysis.** Data obtained were subjected to Kolmogorov-Smirnov D and normal probability plot tests using Statistical Analysis of Systems software version 9.1.3 [11]. This was done in order to check the normality of the data. The characteristics of the data sets for the traits analysed are given in Table 1. Estimation of variance components, heritability, predicted breeding values (EBVs), genetic and phenotypic correlations, and genetic gains was undertaken with the statistical software ASReml [12] using the following individual tree model:

$$Y = Xb + Za + Wc + e, \quad (1)$$

where  $Y$  is vector observation;  $b$ ,  $a$ ,  $c$ , and  $e$  are the data vectors of fixed effects (block means), of additive genetic effects (random), of plot effects (random common environment effects of the plots), and of the random errors, respectively;  $X$ ,  $Z$ , and  $W$  are known matrices of incidences, formed by the values 0 and 1 which associate the incognita  $b$ ,  $a$ , and  $c$ , respectively, with the data vector  $Y$ . Approximate standard errors of statistics were obtained by Taylor expansion within the ASReml programme.

## 3. Results and Discussion

The overall means, standard deviation, and coefficient of variation for height, dbh, and volume and the number of trees at each age are shown in Table 1. The coefficient of variation at all ages was relatively low for height and dbh, ranging from 8.4% to 9.2% and from 7.3% to 8.6%, respectively,

TABLE 2: Variance components and heritability (standard errors) for individual height, dbh and volume traits at different ages.

Age (years)	Trait	$\sigma_A^2$	$\sigma_p^2$	$\sigma_e^2$	$\sigma_w^2$	$h^2$ (s.e)	$G_s$ (%)
18	Height (h)	174	14	81	269	0.48 (0.01)	13.5
	dbh	258	45	324	627	0.26 (0.01)	15.7
	Volume	22	2	11	35	0.46 (0.01)	18.9
23	Height (h)	179	12	80	265	0.50 (0.02)	18.5
	dbh	267	44	311	614	0.28 (0.03)	21.1
	Volume	23	2	11	35	0.48 (0.04)	23.4
30	Height (h)	180	12	80	264	0.50 (0.02)	19.7
	dbh	275	43	309	610	0.29 (0.02)	22.3
	Volume	24	2	11	34	0.51 (0.03)	24.5
35	Height (h)	118	13	71	265	0.34 (0.03)	13.3
	dbh	191	36	323	624	0.19 (0.02)	15.8
	Volume	16	2	10	33	0.36 (0.03)	17.6
40	Height (h)	65	10	70	255	0.19 (0.02)	10.6
	dbh	147	35	320	621	0.15 (0.01)	11.2
	Volume	9	2	10	32	0.20 (0.03)	11.9

$\sigma_A^2$ : additive genetic variance,  $\sigma_p^2$ : genetic variance among families,  $\sigma_w^2$ : genetic variance within families,  $\sigma_e^2$ : residual variance,  $h^2$ : heritability,  $G_s$ : genetic gain.

TABLE 3: Variance components and heritability (standard errors) among families for height, dbh and volume traits at different ages.

Age (years)	Trait	$\sigma_A^2$	$\sigma_p^2$	$\sigma_e^2$	$\sigma_w^2$	$h^2$ (s.e)	$G_s$ (%)
18	Height (h)	130	25	174	329	0.51 (0.01)	11.2
	dbh	200	31	207	438	0.51 (0.01)	12.5
	Volume	19	2	8	29	0.59 (0.01)	14.8
23	Height (h)	135	26	168	320	0.53 (0.03)	14.3
	dbh	206	32	200	431	0.53 (0.04)	16.4
	Volume	20	2	8	28	0.59 (0.04)	17.6
30	Height (h)	137	27	166	318	0.54 (0.05)	15.6
	dbh	210	32	200	429	0.53 (0.06)	16.8
	Volume	21	2	8	27	0.59 (0.04)	17.9
35	Height (h)	123	21	185	349	0.45 (0.03)	11.9
	dbh	195	23	216	444	0.43 (0.02)	12.1
	Volume	13	2	15	39	0.47 (0.05)	12.6
40	Height (h)	114	16	241	385	0.33 (0.02)	10.1
	dbh	172	19	299	492	0.32 (0.04)	10.9
	Volume	11	2	24	42	0.38 (0.05)	11.3

$\sigma_A^2$ : additive genetic variance,  $\sigma_p^2$ : genetic variance among families,  $\sigma_w^2$ : genetic variance within families,  $\sigma_e^2$ : residual variance,  $h^2$ : heritability,  $G_s$ : genetic gain.

indicating that reliable estimates can be obtained from the variance analyses. The coefficient of variation for volume was moderate, ranging from 20.2% to 23.5%. Higher CV value for volume is expected, when comparing to height and dbh parameters, as volume is estimated from these two variables, combining the experimental errors of both of them [13].

**3.1. Variance Components and Heritability Estimates.** Variance components and heritability values are given in Tables 2, 3, and 4. The results indicate that additive variances for all traits in all the three levels (individual, among families and within families) peaked at 18 years and continued to increase with age up to 23 years and almost remained constant up to 30 years of age and then decreased with age. A similar

trend for heritability was also observed. All heritabilities were relatively high, suggesting a strong genetic control of the traits at the individual level, among families, and within families. These results suggest that important genetic progress can be achieved using a simple individual selection in the orchard or a combined selection among and within families. The values observed in this study at the age of 18 years are in agreement with those reported by [1]. However, they are higher than those reported by [14] working with *Pinus caribaea hondurensis* from Isla de Guanaja, confirming the promising genetic control of the traits as well as the high potential of the population for selection.

This study and that of [15] differ in the age of maximum heritability; the estimates were maximum at the same mean

TABLE 4: Variance components and heritability (standard errors) within families for height, dbh and volume traits at different ages.

Age (years)	Trait	$\sigma_A^2$	$\sigma_p^2$	$\sigma_e^2$	$\sigma_w^2$	$h^2$ (s.e)	$G_s$ (%)
18	Height (h)	156	12	113	281	0.51 (0.01)	17.8
	dbh	184	48	385	617	0.22 (0.01)	18.5
	Volume	21	4	15	40	0.43 (0.01)	22.7
23	Height (h)	158	10	102	278	0.53 (0.03)	24.6
	dbh	196	36	376	614	0.26 (0.03)	26.7
	Volume	22	4	14	39	0.46 (0.04)	28.9
30	Height (h)	159	10	99	276	0.54 (0.05)	24.9
	dbh	210	32	371	610	0.29 (0.04)	28.3
	Volume	22	4	13	38	0.47 (0.04)	29.6
35	Height (h)	140	17	108	298	0.41 (0.04)	20.7
	dbh	180	53	380	658	0.19 (0.03)	21.4
	Volume	20	6	15	41	0.33 (0.03)	23.2
40	Height (h)	117	23	113	301	0.31 (0.03)	11.2
	dbh	175	79	381	681	0.14 (0.05)	11.6
	Volume	16	7	16	45	0.20 (0.03)	12.5

$\sigma_A^2$ : additive genetic variance,  $\sigma_p^2$ : genetic variance among families,  $\sigma_w^2$ : genetic variance within families,  $\sigma_e^2$ : residual variance,  $h^2$ : heritability,  $G_s$ : genetic gain.

TABLE 5: Genetic (below diagonal) and phenotypic (above diagonal) correlations and their standard errors in parenthesis for height, dbh and volume traits at different ages.

Age (years)	Trait	Height (h)	dbh	Volume
18	Height (h)		0.68 (0.05)	0.74 (0.04)
	dbh	0.79 (0.04)		0.95 (0.01)
	Volume	0.86 (0.03)	0.97 (0.01)	
23	Height (h)		0.67 (0.05)	0.72 (0.04)
	dbh	0.76 (0.05)		0.93 (0.02)
	Volume	0.85 (0.04)	0.95 (0.01)	
30	Height (h)		0.65 (0.05)	0.69 (0.05)
	dbh	0.75 (0.05)		0.92 (0.02)
	Volume	0.82 (0.03)	0.94 (0.01)	
35	Height (h)		0.62 (0.06)	0.68 (0.05)
	dbh	0.71 (0.06)		0.91 (0.02)
	Volume	0.81 (0.04)	0.92 (0.02)	
40	Height (h)		0.60 (0.05)	0.63 (0.07)
	dbh	0.69 (0.07)		0.90 (0.03)
	Volume	0.78 (0.05)	0.91 (0.03)	

height, suggesting a possible link between mean height and heritability estimate. This is consistent with findings of [16]. The change in heritability in long rotation crops such as trees is not surprising since genes involved in growth may change with age [17], and these changes may be related to different growth phases [18]. In animals, this change in heritability with age was also attributed to the fact that the trait may change genetically with age [19] and is probably related to different growth phases as reported for trees. These growth phases might be due to changing influences of maternal effects in animals and to a lesser extent in trees and to nursery or competition effects in trees. Changes in heritability with age here may also be attributed to management practices.

**3.2. Genetic and Phenotypic Correlations.** The genetic and phenotypic correlations for height, dbh, and volume are given in Table 5. Age-age genetic and phenotypic correlations between traits were high, ranging from 0.69 to 0.97 and from 0.60 to 0.95, respectively. As the age interval increased, genetic and phenotypic correlations for all traits decreased. Genetic correlations were generally higher than phenotypic correlations. This suggests the possibility of indirect selection in trait with direct selection in another trait. As previously discussed, volume was the indicative trait for selection, but this trait was associated with a high experimental error. Thus, as dbh and volume presented very high genetic and phenotypic correlations (0.97 and 0.95, resp.) and dbh is an easily

measurable trait, the selection can be based on this specific trait, resulting in indirect gains in volume. This means that selection of plus trees, aiming to maximise the genetic gains in volume, must be based on the dbh because of the high additive genetic correlation and low standard deviation between dbh trait and volume. These results are in agreement with those in the literature [13–15].

**3.3. Genetic Gains.** Estimates of genetic gains for selection of 50% of families and 50% of trees within families for height, dbh, and volume for *Pinus kesiya* at different ages are given in Tables 2, 3, and 4. The genetic gains were high for all studied traits. These results suggest that the growth improvement through individual selection in the orchard or a combined selection among and within families is possible. The results show that the genetic gains increased with an increased age up to the age of 30 years and decreased with an increased age after the age of 30 years for all the traits. This indicates that the rotational age of the *Pinus kesiya* clonal seed orchard is 30 years of age. According to Andersson et al. [20], Eriksson et al. [21], and Prescher [22], genetic gain is one of the important factors to consider when considering optimal active life span of a seed orchard. Prescher [22] explained that as long as the genetic gain is increasing, the seed orchard can produce genetically better reproductive material. Therefore, this paper recommends an establishment of a new *Pinus kesiya* clonal seed orchard. However, selective harvest of clones with high breeding values in the old seed orchard should be considered so that the best parents in the old orchard can continue to contribute until the new orchard is well established.

#### 4. Conclusion

The evaluated *Pinus kesiya* clonal seed orchard presented potential for improvement in view of high heritability estimates for the traits' height, dbh, and volume. The correlation among growth traits was significantly high and the accuracy of the predicted genotypic values was also of high magnitude, confirming the reliability of the genetic gain estimates. The predicted genetic gains showed that the optimal rotational age of the *Pinus kesiya* clonal seed orchard is 30 years of age; therefore, it is recommended to establish a new *Pinus kesiya* clonal seed orchard. However, selective harvest of clones with high breeding values in the old seed orchard should be considered so that the best parents in the old orchard can continue to contribute until the new orchard is well established.

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