

Article

# Genetic Improvement of Wood Properties in *Pinus kesiya* Royle ex Gordon for Sawn Timber Production in Malawi

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**Abstract:** Accurate prediction of genetic potential and response to selection in breeding requires knowledge of genetic parameters for important selection traits. In this study, we estimated genetic parameters for wood properties in Khasi pine (*Pinus kesiya* Royle ex Gordon) grown in Malawi. Data on wood properties and growth traits were collected from six families of *Pinus kesiya* at the age of 30. The results show that wood density had a higher genetic control ( $h^2 = 0.595 \pm 0.055$ ) than wood stiffness ( $h^2 = 0.559 \pm 0.038$ ) and wood strength ( $h^2 = 0.542 \pm 0.091$ ). The genetic correlation among wood quality traits was significantly moderate ( $0.464 \pm 0.061$ ) to high ( $0.735 \pm 0.025$ ). The predicted genetic response indicated that selection for wood density at 10% selection intensity would increase stiffness and strength by 12.6% and 8.85%, respectively. The genetic correlations between growth and wood quality traits were moderately unfavourable. However, sufficient variation exists within the breeding population to select individuals with both good growth rate and high wood quality traits. It is therefore suggested that all trees with both diameter at breast height (DBH) greater than 32.0 cm and density greater than 0.593 g/cm<sup>3</sup> must be selected in order to increase the efficiency of the breeding programme. However, in the long term, it is recommended that the best selection strategy would be to develop a multiple-trait selection index. The selection index should be developed using optimal index weights for the advanced *Pinus kesiya* breeding programme in Malawi.

**Keywords:** *Pinus kesiya*; wood properties; heritability; genetic correlation; correlated response

## 1. Introduction

Khasi pine (*Pinus kesiya* Royle ex Gordon) is a tree that can grow up to 45 m in height and over 100 cm in diameter [1]. It is naturally distributed in the Himalayan region of Asia, which includes: Burma, China, India, Laos, Philippines, Thailand, Tibet, and Vietnam. The species has a large ecological adaptability and growing performance and can be found in a variety of different locations from 300 to 2700 m above the sea level [2]. The most efficient way to meet the increasing global wood demand is to establish plantations with genetically improved seeds. The relative fast growth and wide geographical distribution of the species led to the establishment of a breeding programme in Malawi in the 1970s with seed sources from South Africa and Zimbabwe [3]. The timber of this species is easily sawn and suitable for paneling, cabinet work, joinery, poles and general construction [2,4].

Modulus of elasticity (MoE) and Modulus of Rupture (MoR) are important traits associated with structural quality. MoE is an indication of wood stiffness while MoR is an indication of wood strength [5]. These traits must be considered as composite traits that depend on physical, chemical and

anatomical properties of wood. According to reports from different researchers [6,7], wood density is the most important trait controlling wood stiffness and strength. It has a strong positive correlation with both tensile and compression strength [8]. Therefore, improved wood density trait is expected to meet a wide range of demands and potential for future utilization. Current studies [9–13] have indicated that wood density, with high heritability and large economic gain from selection, is an ideal selection criterion for tree breeding programmes because of its strong effect on wood quality. Heritability of wood density is generally found to be higher than those of growth traits in forest trees. Published heritability of density in pines varies from 0.40–0.85, compared to the usual range of 0.15 to 0.25 for many growth traits [9,14]. This indicates that genetic manipulation of wood density can result in good gains.

The main limitation to the effective breeding programme of *Pinus kesiya* in Malawi has been lack of genetic parameter information on wood properties. The information helps to guide decisions on the most appropriate breeding strategy and to monitor genetic progress. Most of the genetic variation studies in Malawi have focused on growth traits [2]. However, faster growth is generally negatively correlated with important wood quality traits [15,16]. Therefore, there is a need to include wood quality traits in tree selection programmes to ensure future wood supplies have the appropriate mechanical properties for structural applications and other end uses.

In this paper, genetic parameters for wood quality traits, namely wood density, stiffness and strength, were estimated. Genetic parameters for growth traits (DBH, height and volume) were also estimated to provide an indication of the genetic control and relationship between wood properties and growth traits. The objectives in this study were to: (1) estimate heritability and genetic gains in wood density, stiffness and strength; (2) determine the genetic control in wood properties along the radial direction and stem height; (3) estimate genetic correlations among the wood properties; (4) determine the genetic correlation between wood properties and growth traits; and (5) estimate the correlated responses for the target traits. These parameters are important to estimate the direct and indirect responses from selection and to guide the establishment and refinement of the *Pinus kesiya* breeding programme in Malawi.

## 2. Materials and Methods

### 2.1. Study Area and Genetic Materials

The study was undertaken using an open pollinated *Pinus kesiya* orchard located in Chongoni Forest Plantation in Dedza, Malawi. It is situated about 85 km southeast of the capital, Lilongwe, and lies on latitudes 14°10' S and 14°21' S and longitudes 34°09' E and 34°17' E. The orchard was established in a ferruginous soil in 1984 with an 18-family seed source from Zimbabwe. Ten tree plots laid out in a completely randomized design in four replicates were planted at a spacing of 2.75 m × 2.75 m. All the silvicultural treatments were performed on the instruction of the breeder. In May 2014, six families were chosen based on straightness. A total of ninety trees (15 trees from each family) with no major defects were randomly selected for the study.

### 2.2. Growth Data

The sample trees were measured for diameter at breast height (DBH) (1.3 m above the ground level) using a caliper, and total height was measured using a vertex with a transponder. Stem volume (Vol, cm<sup>3</sup>) was calculated as a function of diameter at breast height (DBH, cm) and total height (HGT, m) was calculated according to the following equation [17]:

$$\text{Vol} = 3.6128 \times 10^{-5} \times [\text{DBH}]^2 \times \text{HGT} \quad (1)$$

The average height, diameter at breast height and volume of the trees expressed with standard deviations were 25.9 ± 2.8 m, 32.0 ± 3.9 cm and 0.989 ± 0.319 cm<sup>3</sup>, respectively.

### 2.3. Wood Sample Processing and Measurement

Wood sample processing and measurement was conducted as outlined by Missanjo and Matsumura [18]. Briefly, a total of 1080 wood specimens, measuring 20 mm × 20 mm × 320 mm, were collected from innerwood, middlewood and outerwood at 1.3 m, 3.3 m, 5.3 m and 7.3 m tree height. The specimens were conditioned to 12% moisture content in the laboratory by oven-drying at 105 °C to constant weight. Wood density was calculated as dry mass divided by dry volume, where volume was obtained by the displacement method. The samples were then subjected to bending test using an Instron Tester over a span length of 300 mm. The estimated mean wood density, Modulus of Elasticity (MoE) and Modulus of Rupture (MoR) with standard deviations were  $0.593 \pm 0.033$  g/cm<sup>3</sup>,  $13.5 \pm 2.3$  GPa and  $114 \pm 19$  MPa, respectively.

### 2.4. Statistical Analysis

Data on wood properties (Wood density, MoE and MoR) and growth (DBH, height and volume) were tested for normality and homogeneity with Kolmogorov-Smirnov D and normal probability plot tests in SAS software version 9.1.3 [19]. In a few marginal cases, a graphic residual analysis was also performed; however, no data transformation was deemed necessary. Variance components and covariances were estimated using Mixed procedure and PROC VARCOMP in SAS. Data on wood properties (density, MoE and MoR) were subjected to the following linear mixed model:

$$Y_{ijkl} = \mu + H_i + R_j + F_k + T_l(F_k) + (HR)_{ij} + (HF)_{ik} + (RF)_{jk} + HT(F_k)_{il} + RT(F_k)_{jl} + (HRF)_{ijk} + e_{ijl(k)} \quad (2)$$

where:  $Y_{ijkl}$  is the observation in the  $ijkl^{\text{th}}$  tree;  $\mu$  is the overall mean;  $H_i$  and  $R_j$  are fixed effects of stem height and stem radial position, respectively;  $F_k$  is the random effect of family;  $T_l(F_k)$  is the tree-within-family effect;  $(HR)_{ij}$  is the interaction between stem height and stem radial position effect;  $(RF)_{jk}$  is the interaction between stem radial position and family effect;  $HT(F_k)_{il}$  is the interaction between stem height and tree-within-family effect;  $RT(F_k)_{jl}$  is the interaction between stem radial position and tree-within-family effect;  $(HRF)_{ijk}$  is the interaction between stem height, stem radial position and family effect; and  $e_{ijl(k)}$  is the random error term.

A  $X^2$  test was performed on the difference in the  $-2$  residual log likelihood of the model to select the best model. All the interactions between parameters were removed from the analysis because their contribution to the total variance was negligible. Furthermore, the variance component for these terms could not be estimated or was otherwise insignificant. Equation (2) was therefore reduced to:

$$Y_{ijkl} = \mu + H_i + R_j + F_k + T_l(F_k) + e_{ijl(k)} \quad (3)$$

Growth data were subjected to a linear mixed model with replicate as a fixed factor and family as a random effect factor.

Family mean heritability and individual heritability were calculated using Equations (4) and (5), respectively [20]:

$$h_a^2 = \frac{\sigma_f^2}{\sigma_f^2 + \frac{\sigma_e^2}{bn}} \quad (4)$$

$$h_w^2 = \frac{3\sigma_f^2}{\sigma_e^2} \quad (5)$$

where  $h_a^2$  and  $h_w^2$  are heritability among and within families, respectively;  $\sigma_f^2$  is family variance;  $\sigma_e^2$  is residual error variance;  $b$  is number of positions in the stem height where specimens were collected per tree for specimen-level analysis, while for tree-level analysis, it is the number of replicates; and  $n$  is the number of positions in the radial direction where specimens were collected per log for specimen-level analysis, while for tree-level analysis, it is the number of trees per replicate. The within-family heritability estimate was one third due to the mixed mating that is expected in *Pinus* species [13], rather than one quarter as is appropriate for true half-sibs [20]. Standard errors of heritabilities were estimated by the Delta method and PROC IML in SAS.

Genetic correlations ( $r_A$ ) between traits were estimated using the following formula [20]:

$$r_A = \frac{COV_a(x,y)}{\sqrt{\sigma_{ax}^2 \cdot \sigma_{ay}^2}} \quad (6)$$

where the numerator is the additive genetic covariance between traits  $X$  and  $Y$ ;  $\sigma_{ax}^2$  and  $\sigma_{ay}^2$  are the additive variance components for traits  $X$  and  $Y$ , respectively. Standard errors associated with genetic correlation were calculated using the following equation [20]:

$$SE(r_A) = \frac{1-r_A^2}{\sqrt{2}} \cdot \sqrt{\frac{SE(h_x^2) \cdot SE(h_y^2)}{h_x^2 \cdot h_y^2}} \quad (7)$$

where  $r_A$  is the genetic correlation between the traits;  $h_x^2$  and  $h_y^2$  are heritability for traits  $X$  and  $Y$ , respectively;  $SE(h_x^2)$  and  $SE(h_y^2)$  are standard errors for heritability traits  $X$  and  $Y$ , respectively. Residual correlations ( $r_E$ ) between traits were calculated using the same formula as for genetic correlation. However, residual variance components were used. Phenotypic correlations were calculated as Pearson product moment correlations ( $r_P$ ) using the CORR procedure in SAS.

In most tree breeding programmes, stem wood quality (stiffness and strength) and volume are the most important breeding objective traits [21]. Therefore, genetic gains and correlated response were calculated to improve these three traits (MoE, MoR and Volume) by direct selection and indirect selection using correlated traits. Genetic gains ( $G_x$ ) and correlated response ( $CR_x$ ), expressed in percentage, were calculated using the following formulas [20]:

$$G_x = i \cdot h_x^2 \cdot CV_{px} \quad (8)$$

$$CR_x = i \cdot h_x \cdot h_y \cdot r_A \cdot CV_{px} \quad (9)$$

where  $i$  is the selection intensity;  $h_x^2$  is the heritability of the objective trait;  $r_A$  is the genetic correlation between the traits;  $h_x$  and  $h_y$  are square roots of the heritability for the objective and selected traits, respectively;  $CV_{px}$  is the coefficient of phenotypic variance for the objective trait, expressed as:

$$CV_{px} = \frac{\sigma_{px}}{\mu} \times 100 \quad (10)$$

where  $\sigma_{px}$  is the phenotypic standard deviation for the objective trait;  $\mu$  is the phenotypic mean value of the objective trait.

### 3. Results and Discussion

#### 3.1. Heritability and Genetic Gains

Heritability and genetic gains for wood properties were relatively higher than those for growth traits, except the genetic gain for volume among the family (Table 1). Heritability for wood properties among the family indicated high genetic control, while heritability for growth traits indicated moderate genetic control. This suggests that there is a substantial degree of genetic control and strong potential gains in wood properties compared with growth traits. Therefore, important genetic progress can be achieved using a combined selection from among and within the families. Wood density had higher heritability and genetic gain, indicating that this trait is easier to select, and higher genetic gains can be obtained by direct selection of this trait.

Heritability is an important parameter for economical and biological success of plantation forestry, monitoring genetic progress and developing breeding strategies [20,21]. High heritability for MoE ( $h^2 = 0.559 \pm 0.038$ ) observed in this study is very encouraging. High MoE increases the recovery rate of structural and appearance-grade products, which resulted in a higher economic return [21]. The present results are consistent with those in the literature [22]. On the other hand, the present findings are

higher than those observed by other researchers [23] working with Turkish pine (*Pinus brutia* Ten.). This confirms the promising genetic control of the traits as well as the high potential of the population for selection in the present study.

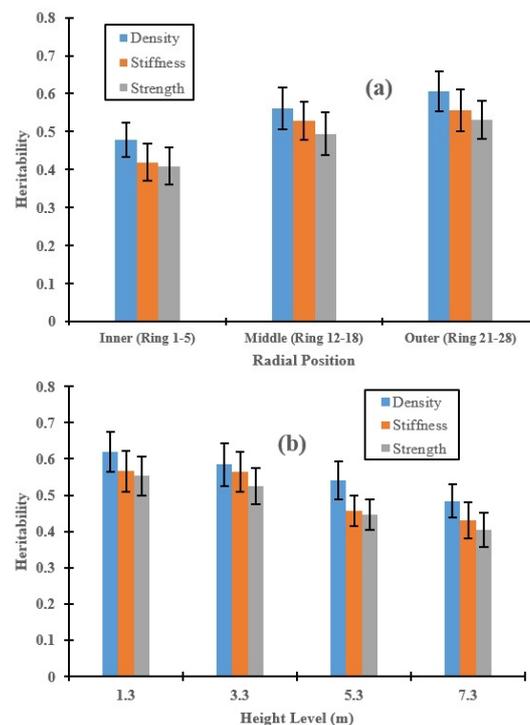
**Table 1.** Heritability ( $h^2$ ) and genetic gains ( $G_s$ ) for wood properties and growth traits.

Traits	Among Families		Within Families	
	$h^2$ (s.e.)	$G_s$ (%)	$h^2$ (s.e.)	$G_s$ (%)
Wood Properties				
Density (g/cm <sup>3</sup> )	0.595 (0.055)	22.6	0.367 (0.100)	13.2
MoE (GPa)	0.559 (0.038)	16.7	0.317 (0.095)	9.01
MoR (MPa)	0.542 (0.091)	15.8	0.295 (0.092)	8.20
Growth Traits				
Total height (m)	0.469 (0.048)	7.11	0.177 (0.078)	2.42
DBH (cm)	0.400 (0.042)	6.05	0.133 (0.073)	1.63
Volume (cm <sup>3</sup> )	0.483 (0.053)	19.4	0.187 (0.079)	7.55

Note: MoE = modulus of Elasticity; MoR = modulus of rupture; DBH = diameter at breast height; s.e. = standard error, Genetic gains ( $G_s$ ) at 10% selection intensity (i.e.,  $i = 1.76$ ).

### 3.2. Genetic Control of Wood Properties along the Radial Direction and Stem Height

Trends in heritability from pith to bark and along the stem height were also investigated for wood density, MoE and MoR (Figure 1). The results show that the heritability for wood density, MoE and MoR increased from pith to bark and decreased from the butt upwards. This suggests that efficiency of selection based on the outer wood for wood density, MoE and MoR would generally be higher than selection based on inner wood. The heritability ranged from  $0.409 \pm 0.048$  (MoR) to  $0.606 \pm 0.052$  (wood density) along the radial direction and  $0.619 \pm 0.055$  (wood density) to  $0.405 \pm 0.047$  (MoR) along the stem height. This indicates that the traits (wood density, MoE and MoR) are under moderate to high genetic control along the radial direction and stem height. Therefore, genetic progress can be achieved through indirect selection of these wood properties (wood density, MoE and MoR). The present results are consistent with the findings of other researchers [24–27] in different species.



**Figure 1.** Radial (a) and axial (b) genetic control of wood density, stiffness and strength.

The increase in heritability for wood density from pith to bark is not surprising since genes may change with age [28]. Phenotypic variances for wood density decrease with age [27], hence strong genetic control for wood density increases from pith to bark. However, the present results are in conflict with those reported by other researchers [29–32] for different species. Hodge and Purnell [29] and Nicholls et al. [30] reported a decrease in heritability of wood density from pith to bark in slash pine (*Pinus elliottii* Engelm.) and radiata pine (*Pinus radiata* D. Don), while other researchers [31,32] found an increase in heritability followed by a decrease from pith to bark of wood density in maritime pine (*Pinus pinaster* Aiton) and *Pinus radiata*.

The reason behind these difference in results may be that the estimates of genetic parameters in the previous studies could have been affected by different factors such as site conditions, genetic material, experimental and measurement procedures for wood density and other factors [27,33,34]. For example, in measurement procedures, wood density in *Pinus pinaster* [31] was measured using ring-by-ring measurements, while in the present study, wood density was the mean of rings 1–5 for inner wood, rings 12–18 for middle wood and rings 21–28 for outer wood.

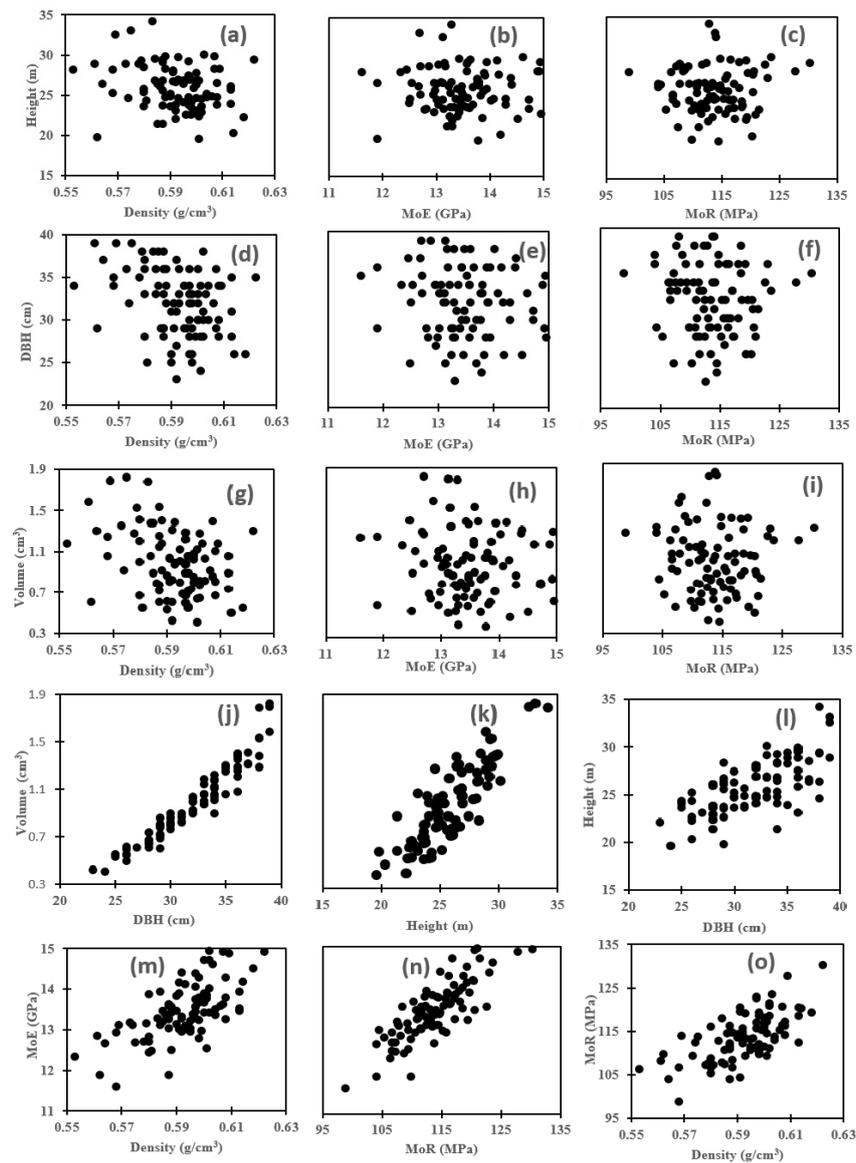
### 3.3. Genetic Correlation among Wood Properties

The genetic correlations are summarized in Table 2. High positive genetic correlation was observed between wood density and MoE ( $r_A = 0.735 \pm 0.025$ ). Strength showed a positive moderate genetic correlation with wood density ( $r_A = 0.539 \pm 0.060$ ) and stiffness ( $r_A = 0.464 \pm 0.061$ ). The corresponding phenotypic relationships are plotted in Figure 2 and summarized in Table 2. The phenotypic correlations among the wood properties were highly significant ( $p < 0.001$ ) and ranged from  $r_p = 0.790 \pm 0.019$  (wood density and MoE) to  $r_p = 0.818 \pm 0.018$  (MoR and MoE). However, the residual correlations ranged from weak ( $r_E = 0.213 \pm 0.053$ ; wood density and MoE) to moderate ( $r_E = 0.521 \pm 0.061$ ; wood density and MoR) (Table 2).

**Table 2.** Phenotypic, genetic and residual correlations between and among growth traits and wood properties.

Traits	Correlation (Standard Error)		
	Phenotypic	Genetic	Residual
<b>Between Growth Traits and Wood Properties</b>			
Height vs. Density	−0.248 (0.010) *	−0.386 (0.057)	−0.052 (0.006)
Height vs. MoE	−0.013 (0.001) <sup>ns</sup>	−0.309 (0.056)	−0.036 (0.002)
Height vs. MoR	0.041 (0.003) <sup>ns</sup>	−0.366 (0.082)	−0.019 (0.009)
DBH vs. Density	−0.338 (0.011) *	−0.496 (0.049)	−0.097 (0.004)
DBH vs. MoE	−0.112 (0.006) <sup>ns</sup>	−0.473 (0.046)	−0.298 (0.083)
DBH vs. MoR	−0.093 (0.004) <sup>ns</sup>	−0.468 (0.071)	−0.149 (0.089)
Volume vs. Density	−0.358 (0.010) *	−0.458 (0.052)	−0.290 (0.061)
Volume vs. MoE	0.099 (0.002) <sup>ns</sup>	−0.399 (0.051)	−0.224 (0.058)
Volume vs. MoR	−0.056 (0.005) <sup>ns</sup>	−0.488 (0.071)	−0.272 (0.086)
<b>Among Growth Traits</b>			
Height vs. DBH	0.688 (0.077) **	0.935 (0.009)	0.545 (0.052)
Height vs. Volume	0.850 (0.056) **	0.684 (0.040)	0.550 (0.052)
DBH vs. Volume	0.955 (0.031) **	0.987 (0.002)	0.921 (0.011)
<b>Among Wood Properties</b>			
Density vs. MoE	0.790 (0.019) **	0.735 (0.025)	0.213 (0.053)
Density vs. MoR	0.793 (0.019) **	0.539 (0.060)	0.521 (0.061)
MoE vs. MoR	0.818 (0.018) **	0.464 (0.061)	0.475 (0.060)

Note: DBH = diameter at breast height, MoE = modulus of elasticity; MoR = modulus of rupture; Standard errors are given in parenthesis. \*\* correlation estimates significantly different from zero ( $p < 0.001$ ); \* correlation estimates significantly different from zero ( $p < 0.05$ ); <sup>ns</sup> = correlation estimates not significantly different from zero ( $p > 0.05$ ).



**Figure 2.** Phenotypic relationship between growth traits and wood properties (a–i); among growth traits (j–l); and among wood properties (m–o).

The phenotypic correlation between traits is a complex of genetic and non-genetic factors. The decomposition of phenotypic correlation into genetic and other correlations is essential to improve understanding of the relationships among the traits [35]. The genetic correlation between wood density and stiffness was very strong in the present study, but their corresponding residual correlations were weak. This implies that the phenotypic relationship between wood density and stiffness mainly depends on the genetic relationship.

Genetic correlations are useful to make inferences about indirect responses of one trait from the selection of others. Wood density is of particular importance because it can have strong impact on wood stiffness and strength [36]. The present study found that the genetic correlations between wood density and mechanical properties (MoE and MoR) were favourable. Therefore, selection based solely on wood density, which is easily measurable, could result in improvements in both wood stiffness and strength. Similar favourable genetic correlations among wood properties (wood density, stiffness and strength) have been reported in previous studies [9,37,38].

Wood density and microfibril angle (MFA) are both regarded as important factors for the prediction of stiffness [21]. However, in the present study, only density was considered. This is because MFA affects both density and stiffness [21]. The genetic correlation between density and stiffness was favourable in the present study, suggesting that the genetic correlation between MFA and stiffness is also likely to be favourable. Thus, wood with high stiffness has high density and small MFA [36]. However, further research may be required to confirm the correlation between MFA and stiffness.

### 3.4. Genetic Correlation between Wood Properties and Growth Traits

Genetic and phenotypic correlations between wood properties (wood density, MoE and MoR) and growth traits (DBH, height and volume) are summarized in Table 2. Weak negative phenotypic correlations between most wood properties and growth traits were observed. Most of the phenotypic correlations between growth traits and wood properties were non-significant with the exception of wood density. The genetic correlations between wood properties and growth traits were unfavourable. The negative correlation between wood properties and growth traits could be due to genetic and environmental causes [21]. The adverse genetic correlations between wood properties and growth traits ranged from  $r_A = -0.309 \pm 0.056$  (height and MoE) to  $r_A = -0.496 \pm 0.049$  (height and wood density). Such unfavourable genetic correlations between wood properties and growth traits were reported in many other conifers [21,39]. On the other hand, other researchers [35] reported a positive genetic correlation between wood properties and growth traits in Japanese larch (*Larix kaempferi* Lamb. Carrière). Based on the present results and previous reports, the genetic correlations between wood properties and growth traits depend on species.

Stiffness is usually a breeding objective trait to increase recovery rate for sawn timber [21], and the adverse genetic correlations between growth traits and stiffness indicate proper index weights should be estimated in future studies [40].

### 3.5. Correlated Response

Correlated response is often used as a measure of the increase or decrease in performance after indirect selection [21]. A summary of the results on correlated responses for three breeding objective traits (MoE, MoR and volume) are presented in Table 3. Correlated responses were assessed under a standardized scenario ( $i = 1.76$  in Equation (9)), which means that about 10% of individuals are retained during selection). The results indicate that selection for wood density had a major impact on wood stiffness and strength. Thus, selection for wood density would increase stiffness and strength by 12.6% and 8.85%, respectively, and decrease volume by 9.78%.

**Table 3.** Correlated genetic responses for three breeding target traits with 10% selection intensity.

Selection Traits	Correlated Response (%) for Target Traits		
	MoE	MoR	Volume
Wood properties			
Density	12.6	8.85	−9.78
MoE	16.7 *	7.43	−8.30
MoR	7.62	15.8 *	−9.96
Growth traits			
DBH	−6.68	−6.32	17.3
Height	−4.74	−5.37	13.0
Volume	−6.18	−7.23	19.4 *

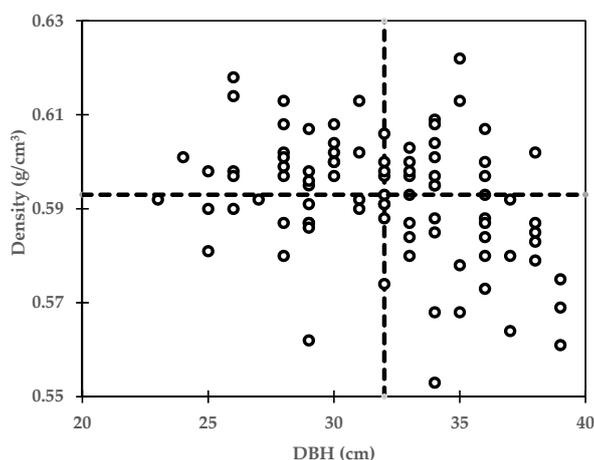
Note: DBH = diameter at breast height, MoE = modulus of elasticity; MoR = modulus of rupture; \* = Genetic gain.

Generally, selection for growth traits (DBH, height) generated a positive correlated response for volume. On the other hand, selection for wood property traits generated negative correlated response for volume. Similarly, selection for growth traits (DBH, height and volume) generated negative correlated response for stiffness and strength. For example, selection for DBH alone would decrease

stiffness and strength by 6.68% and 6.32%, respectively. The negative correlated responses between growth traits and wood quality traits were reported in other pine species [21,39]. Such negative correlated response between growth and wood quality traits indicate the need for a multiple-trait selection index.

### 3.6. Implication of Tree Improvement of *Pinus kesiya* in Malawi

The adverse genetic correlations between wood properties and growth traits were moderate. This suggests that there may be some genotypes with both high growth performance and high wood density, stiffness and strength. Therefore, the adverse genetic correlation between wood properties and growth traits may not entirely prohibit the improvements of both wood quality and growth traits [41]. In the short term, it is possible to achieve significant gains in both density and DBH by selecting families or individuals from the top right quadrant (individuals with both high wood density and DBH) (Figure 3). Therefore, all trees with both DBH greater than 32.0 cm and density greater than 0.593 g/cm<sup>3</sup> must be selected in order to increase the efficiency of the breeding programme. This will result in simultaneous increases in wood stiffness, strength and volume. On the other hand, a long-term strategy would require a larger sample data set to develop a multiple-trait selection index. It is recommended that a multiple-trait selection index should be developed using optimal index weights for the advanced breeding programme of *Pinus kesiya* in Malawi.



**Figure 3.** Selection strategy using individuals with both high density and DBH. Dotted lines are current family means for density and DBH acting as a base (control).

## 4. Conclusions

The study has revealed that wood density has a higher genetic control than mechanical properties (MoE and MoR) and growth traits (DBH, height and volume). The genetic correlation and correlated response among wood properties and growth traits were favourable. Selection for wood density would have a major impact on wood stiffness and strength. On the other hand, the genetic correlation and correlated response between growth and wood quality traits were moderately unfavourable. However, sufficient variation exists within the breeding population to select individuals with both good growth rate and high wood quality traits. It is therefore suggested that all trees with both DBH greater than 32.0 cm and density greater than 0.593 g/cm<sup>3</sup> must be selected in order to increase the efficiency of the breeding programme. However, in the long term, it is recommended that the best selection strategy would be to develop a multiple-trait selection index. The selection index should be developed using optimal index weights for the advanced *Pinus kesiya* breeding programme in Malawi.

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**Author Contributions:** E.M. and J.M. conceived and designed the experiments; E.M. performed the experiments, analyzed the data and wrote the paper; J.M. contributed substantially to the interpretation of the results and to writing the paper.

**Conflicts of Interest:** The authors declare no conflict of interest.

## Abbreviations

The following abbreviations are used in this manuscript:

DBH	Diameter at breast height
HGT	Total tree height
MFA	Microfibril angle
MoE	Modulus of Elasticity
MoR	Modulus of Rupture
PROC	Procedure
SAS	Statistical Analysis System

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