

Article

Multiple Trait Selection Index for Simultaneous Improvement of Wood Properties and Growth Traits in *Pinus kesiya* Royle ex Gordon in Malawi

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Abstract: Tree breeders face the problem of negative correlations between wood properties and growth traits. It is necessary to overcome this difficulty in order to obtain promising genotypes. The selection index is one of the helpful tools in this process, because it allows multiple features of interest to be selected. In this study, a multiple trait selection index for Khasi pine (*Pinus kesiya* Royle ex Gordon) grown in Malawi was developed. Data on wood properties and growth traits were collected from six families of *P. kesiya* at the age of 30 years. The breeding objective was defined in terms of wood stiffness, wood strength and volume. Selection traits included in the index were wood stiffness (MoE), wood strength (MoR), volume (Vol.), wood density (WD), and diameter at breast height (DBH). The index was termed as $I_T = -80.36 \text{ MoE} - 14.60 \text{ MoR} + 132.07 \text{ Vol.} + 4858.09 \text{ WD} - 7.56 \text{ DBH}$. The accuracy of the index was 98.8% and the correlation between the index and the aggregate breeding objective was 0.994. A genetic gain of 16.7% for volume, 14.8% for wood stiffness and 13.2% for wood strength would be expected from a standardized 10% selection intensity. Therefore, application of the developed selection index is necessary in order to increase the efficiency of the *Pinus kesiya* breeding programme in Malawi.

Keywords: *Pinus kesiya*; selection index; wood properties; growth traits; breeding objective

1. Introduction

Breeding programmes are designed to identify superior genotypes for different traits of economic interest. This is based on the performance information of individual trees or families for dissemination of their genes in the population [1,2]. However, one of the major difficulties faced by tree breeders is the negative correlation between wood properties and growth traits. It is necessary to overcome this difficulty to obtain promising genotypes. Literature shows that the selection index is one of the helpful tools in this process, because it allows multiple features of interest to be selected simultaneously [2,3].

Selection indexes have frequently been used for selection in recurrent selection programmes for various plant species [3–6]. These indexes have been robust in their application. Although the theory of selection indexes was introduced into plant breeding more than 70 years ago [7] and is highly developed in various forms, its application in the forest tree breeding sector is still not very extensive. Possible explanations for this are (i) the complexity of the forest production system; (ii) difficulties in determining the relationship between wood properties and final product quantity and quality; and (iii) uncertainty about the future use of trees due to long rotational age [8]. Furthermore, the optimal

selection index may not be extensively used due to difficulties in the derivation of relative economic values as well as the scarcity of information on the relationships among the traits [1].

Khasi pine (*Pinus kesiya* Royle ex Gordon) is one of the major exotic plantation tree species grown in Malawi. It is mainly used for sawn timber production. Its morphology, uses and application in Malawi have been well explained by other researchers [9,10]. The breeding programme for this species in Malawi started in early 1970s with the aim of improving growth characteristics and tree stem form [10]. The selection of the second generation trees and evaluation of the wood properties of the first generation plus-tree clones are currently being undertaken [9].

Genetic parameters and genetic correlations among traits are essential in the establishment and refinement of tree breeding programmes [11–13]. Missanjo and Matsumura [9] identified high heritabilities in the wood properties (0.542 to 0.595) (density, stiffness and strength) and growth traits (0.400 to 0.483) (volume, height and diameter) of *Pinus kesiya* in Malawi. This indicates that it is possible to improve these traits through selection. On the other hand, Missanjo and Matsumura [9] reported an adverse genetic correlation (−0.309 to −0.496) between the wood properties and growth traits of *Pinus kesiya*. This shows that selection for wood properties would result in a decrease in growth traits and vice versa. Such a negatively correlated response between wood properties and growth traits, indicates the need of a multiple-trait selection index.

The objective of this study was to investigate the potential of simultaneous genetic improvement of wood properties and growth traits through a multiple-trait selection index and also to estimate the genetic gains from various selection intensities. The selection index would help to guide the establishment and refinement of the *Pinus kesiya* breeding programme in Malawi.

2. Materials and Methods

2.1. Study Area, Genetic Materials and Assessment

The study used an open pollinated progeny trial of *P. kesiya* at 30 years of age that was established in a ferruginous soil in Chongoni Forest Plantation in Dedza, Malawi, in 1984. It is located 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 progeny trial comprised 18 families with seed source from Zimbabwe. The test stand was established using ten-tree plots laid out in a completely randomized design in four replicates. The initial planting density was 1320 stems/ha, and all the silvicultural treatments were done on the instruction of the breeder [14].

In May 2014, six families were chosen based on straightness. A sample of 15 trees from each family (a total of ninety trees) with no major defects were randomly selected for the study. The mean height, diameter at breast height (DBH), and volume of the trees expressed with standard deviations during sampling were 25.9 ± 2.8 m, 32.0 ± 3.9 cm and 0.989 ± 0.319 cm³, respectively. Wood sample processing and measurement was conducted as outlined by Missanjo and Matsumura [10]. Briefly, a total of 1080 wood specimens, measured 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 of the stem height. The estimated mean wood density, Modulus of Elasticity (MoE) and Modulus of Rupture (MoR) with standard deviations were 0.593 ± 0.033 g/cm³, 13.5 ± 2.3 GPa and 114 ± 19 MPa, respectively.

2.2. Statistical Analysis

Genetic parameters that were used in the construction of the selection index were those obtained in our previous study [9] (Table 1). The genetic parameters for the wood quality traits (density, MoE and MoR) were estimated using a linear mixed model with stem height, stem radial position and replicate as fixed effects, and family as a random effect. However, replicate was removed from the analysis because its contribution to the total variance was negligible. On the other hand, genetic parameters for growth traits (DBH and volume) were estimated using a linear mixed model with replicate as a fixed factor and family as a random effect factor. The statistical analysis was done using

SAS Mixed procedure and PROC VARCOMP in SAS software version 9.1.3 (SAS Institute Inc., Cary, NC, USA) [15].

Table 1. Heritability (bold and diagonal), genetic correlations (above diagonal), phenotypic correlations (below diagonal), means, phenotypic standard deviation (σ_p), genetic standard deviation (σ_A), economic weights (a) and estimated breeding values (EBV) used to construct the selection index.

Traits	Density (g/cm ³)	MoE (GPa)	MoR (MPa)	DBH (cm)	Volume (cm ³)
Density	0.595 (0.055)	0.735 (0.025)	0.539 (0.060)	−0.496 (0.049)	−0.458 (0.052)
MoE	0.790 (0.019) **	0.559 (0.038)	0.464 (0.061)	−0.473 (0.046)	−0.399 (0.051)
MoR	0.793 (0.019) **	0.818 (0.018) **	0.542 (0.091)	−0.468 (0.071)	−0.488 (0.071)
DBH	−0.338 (0.011) *	−0.112 (0.006) ^{ns}	−0.093 (0.004) ^{ns}	0.400 (0.042)	0.987 (0.002)
Volume	−0.358 (0.010) *	0.099 (0.002) ^{ns}	−0.056 (0.005) ^{ns}	0.955 (0.031) **	0.483 (0.053)
Means	0.593 (0.001)	13.5 (0.1)	114 (1)	32.0 (0.4)	0.989 (0.034)
σ_p	0.128	2.28	18.8	2.75	0.225
σ_A	0.085	1.41	11.3	1.13	0.109
a	0.020	0.449	3.79	1.07	0.033
EBV		3.69	6.95		3.76

MoE = modulus of elasticity; MoR = modulus of rupture; DBH = diameter at breast height; values in parenthesis are standard errors; ** correlation estimates significantly different from zero ($p < 0.001$); * correlation estimates significantly different from zero ($p < 0.05$); ^{ns} correlation estimates not significantly different from zero ($p > 0.05$).

The selection index was constructed using the following equation given in matrix expression according to Lee [16]:

$$Pb = Ga \quad (1)$$

where P is the phenotypic variances (cov.) matrix; G is the genetic variances (cov.) matrix; a is the economic weights column vector; and b is the weighting factors column vector. In this study, the economic weights were not in monetary values, but were the mean annual increment (MAI) of the studied traits for a rotation period of 30 years. The economic weights of the studied traits are presented in Table 1. The objective traits were MoE, MoR and volume, while the other traits included in the construction of the index were wood density and DBH.

The selection index weights were then calculated as:

$$b = P^{-1}Ga \quad (2)$$

The accuracy of the selection index, which is defined as the function of the correlation (r_{HI}) between the index and the aggregate genotype (breeding objective variance) [17] was calculated as:

$$r_{HI}^2 = \frac{\sigma_I^2}{\sigma_H^2} \quad (3)$$

where σ_I^2 and σ_H^2 are the variances of the index and the aggregate genotype, respectively. These variances were calculated using the following equations according to Lee [16]:

$$\sigma_I^2 = b'Ga \quad (4)$$

$$\sigma_H^2 = a'Ga \quad (5)$$

where $b' = (b_1, b_2 \dots b_n)$ is the vector of selection index weight values and $a' = (a_1, a_2 \dots a_n)$ is the vector of economic weight values.

The expected genetic change (ΔG) and the standard deviation (σ) for each trait after one generation of selection on the indexes were estimated by solving the following equations [18]:

$$\Delta G = \frac{b'Gi}{\sigma_I} \quad (6)$$

$$\sigma = \sqrt{\frac{\sum(x - \mu)^2}{n - 1}} \quad (7)$$

where i is the selection intensity, σ_I is the standard deviation of the index, b' and G are as explained earlier, x is individual observations, μ is the overall mean, and n is the number of observations. Genetic gain is often referred to as the amount of increase in performance that is achieved through artificial genetic improvement programmes. This is usually used to refer to the increase after one generation has passed [2]. Data obtained on expected genetic change was subjected to one-way analysis of variance (ANOVA) using SAS software version 9.1.3 [15]. Differences between means were separated using Fischer's least significant difference (LSD) at 0.05 level.

3. Results and Discussion

3.1. Selection Index

The selection indexes constructed are presented in Table 2. Three selection indexes (I_1 , I_2 and I_T) were constructed according to three strategies with the aim to improve the objective traits (MoE, MoR and volume). The first strategy was indirect selection, which involved selecting the density and DBH. The second strategy was direct selection, while the third strategy was the combination of indirect and direct selection. Wood density and DBH were selected because they are positively genetically correlated with mechanical properties (MoE, MoR) and volume, respectively.

Table 2. Index weights (b -values), index variance (σ_I^2) and index accuracy (r_{HI}^2) to improve wood quality and growth traits in *Pinus kesiya*.

lection Index	Selection Traits	b -Values	σ_I^2	$r_{HI}^2(\%)$
I_1	WD	20.93	19.79	70.4
	DBH	0.2306		
I_2	MoE	44.63	22.32	79.4
	MoR	−2.790		
	Vol	−243.5		
I_T	MoE	−80.36	27.75	98.8
	MoR	−14.60		
	Vol	132.07		
	WD	4858.09		
	DBH	−7.56		

MoE = modulus of elasticity; MoR = modulus of rupture; DBH = diameter at breast height; WD = wood density; Vol. = volume.

The comparisons of the three selection indexes indicate that the selection index, I_T , which incorporated MoE, MoR, density, DBH and volume is the most efficient ($r_{HI}^2 = 98.8\%$) compared to I_2 ($r_{HI}^2 = 79.4\%$) and I_1 ($r_{HI}^2 = 70.4\%$). This means that the selection index, I_T , is recommended for improving the objective traits (MoE, MoR and volume) in *Pinus kesiya* in Malawi. Thus, individual trees can be ranked according to their index values and selection based on these rankings.

The results revealed that omitting density and DBH as selection traits reduced the index accuracy by 19.4%. It is also clear from the results that the index not including MoE, MoR and volume as selection traits, showed a reduction in index accuracy of 28.4%. As in many other studies [4,16,19–21],

the present study suggests that the accuracy of the index is influenced by which traits are included in the index.

3.2. Expected Genetic Gain

A summary of the results on expected genetic gains after one generation for the traits studied under different selection indexes is presented in Table 3. The expected genetic gains were assessed under a standardized scenario ($i = 1.76$ in Equation (6), which means that about 10% of individuals are retained during selection). The results show that when the accuracy of the index increased, the expected genetic gains for all incorporated traits significantly increased. For instance, when the accuracy of the index increased from 70.4% for I_1 to 79.4% for I_2 , the mean expected genetic gain for all the traits increased from 5.73% to 8.75%. MoR had the largest expected genetic gain increase (2.59% to 8.55%). Similarly, when the accuracy of the index increased from 79.4% for I_2 , to 98.8% for I_T , the mean expected genetic gain for all the traits increased from 8.75% to 13.68%. Volume had the largest expected genetic gain increase (9.37% to 16.7%).

Table 3. Expected genetic gains per generation when using indexes to improve wood quality and growth traits in *Pinus kesiya* with 10% selection intensity ($i = 1.76$).

Traits	Expected Genetic Gain (%) under Different Selection Indexes		
	I_1	I_2	I_T
MoE	5.93 (1.30) ^c	10.4 (1.5) ^b	14.8 (1.5) ^a
MoR	2.59 (0.11) ^c	8.55 (1.11) ^b	13.2 (1.4) ^a
Vol	7.46 (0.78) ^c	9.37 (1.03) ^b	16.7 (2.2) ^a
WD	9.72 (1.05) ^c	12.1 (1.1) ^b	18.5 (2.7) ^a
DBH	2.96 (0.13) ^c	3.34 (0.16) ^b	5.21 (1.02) ^a

MoE = modulus of elasticity; MoR = modulus of rupture; DBH = diameter at breast height; WD = wood density; Vol. = volume; values in parenthesis are standard deviations. Mean values followed by different superscripts within a row significantly differ ($p < 0.001$)

The present findings indicate that the rates of genetic gain would be affected by the accuracy of the selection index. Thus, increasing the accuracy of the selection index results in increasing the expected genetic gain. The present findings are in agreement to those in the literature [4,21]. Zhang et al. [21] reported that when the selection accuracy increased, a corresponding increase was also noticed in genetic gain for a breeding programme of tea-tree (*Melaleuca alternifolia* (Maiden and Betcher) Cheel) in Australia. Similarly, Sanhueza et al. [4] observed an increase in expected genetic gain when the accuracy of the index increased for a breeding programme of Tasmanian blue gum (*Eucalyptus globulus* Labill.) in Chile. In contrast, Lee [16] and Park et al. [20] reported a constant expected genetic gain for the objective traits when the selection accuracy increased for breeding programmes of Sitka spruce (*Picea sitchensis* (Bong.) Carr.) in Scotland and Jack pine (*Pinus banksiana* Lamb.) in Canada, respectively. The differences in the results could be attributed to the genotype of the species [21].

Other factors such as heritability, selection intensity and generation interval between parents and progeny could also affect genetic gain [16]. Hong et al. [11] investigated the performance of Scots pine under single trait selection and found that a large increase of genetic gain could be achieved for the high heritable traits. In contrast, the present study revealed that a larger genetic gain increase was achieved for the trait with moderate heritability (volume, in our case) under multi-trait selection. This is likely due to the high emphasis on the simultaneous improvement of wood quality and growth traits in the present study.

The number of families used in the present study is limited (six families); further studies incorporating all the eighteen families may be required to confirm the present findings. However, the selection index, I_T , constructed, is reliable because of its high accuracy. Therefore, application of

the developed selection index, I_T , is necessary in order to increase the efficiency of the *Pinus kesiya* breeding programme in Malawi.

4. Conclusions

The study has revealed that there is potential for simultaneous genetic improvement of the wood properties (density, MoE, MoR) and growth traits (DBH, volume) of *Pinus kesiya* in Malawi through a multiple-trait selection index. The selection index developed showed high accuracy. High expected genetic gains of the traits incorporated in the index were also obtained. The expected genetic gains increased with an increase of selection accuracy. Therefore, application of the developed selection index is necessary in order to increase the efficiency of the *Pinus kesiya* breeding programme in Malawi.

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

Abbreviations

The following abbreviations are used in this manuscript:

DBH	Diameter at breast height
LSD	Least significant difference
MAI	Mean Annual Increment
MoE	Modulus of Elasticity
MoR	Modulus of Rupture
PROC	Procedure
SAS	Statistical Analysis System
Vol.	Volume
WD	Wood density

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