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RESEARCH ARTICLE

Selection of Superior Trees, Growth Attributes and Biomass Estimation of *Melia dubia* Genetic Resources

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Abstract

The present study is about *Melia dubia* Cav., a member of the Meliaceae family. *Melia dubia* plantation was raised during January 2010 under the National Agriculture Innovation Project at the Forest College and Research Institute, Mettupalayam, Tamil Nadu. Selection of superior genetic resources was carried out in the year 2016 by the comparison tree method. A total of 46 candidate plus trees (CPT) were identified from the plantation based on morphometric traits *viz.,* tree height, basal diameter, girth at breast height (GBH), texture of bark, bole straightness and pest and disease incidence. Scores were given for each character, and the trees that showed greater performance than the mean were selected. Further screening was done, and thirty superior trees were finally screened for biomass estimation through destructive analysis. The superior trees exhibited good variability in terms of growth attributes. The basal girth of the superior tree ranged from 48 cm (MTPMD 10) to 122 cm (MTPMD 1). The GBH of the superior tree ranged between 44 cm (MTPMD 10, MTPMD 36) and 85 cm (MTPMD 1). Similarly, the height of superior tree ranged between 12 m (MTPMD 7 and MTPMD 8) and 17.5 m (MTPMD 9). Total biomass ranged from 97 kg (MTPMD 30) to 545 kg (MTPMD 1). Stem weight, branch weight and leaf weight also vary between the genetic resources. The regression analysis demonstrated significant positive relationships between growth attributes and fresh biomass of the selected *Melia dubia* genetic resources. Among the growth variables evaluated GBH was the most reliable predictor of biomass accumulation, explaining 91.6% of the variation in total fresh biomass ($R^2 = 0.916$).

Keywords: Biomass estimation, Comparison tree method, Genetic improvement, *Melia dubia*, Superior tree selection

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Introduction

Forest productivity in India is considerably lower than the global average, with a productivity of around 1.0 m^3/ha/year, compared to the worldwide average of 3.0 m^3/ha/year. Despite supporting nearly 17% of the global population, the country's plantations under farm forestry and agroforestry systems continue to exhibit relatively low productivity. A key factor contributing to this situation is the limited availability of high-quality planting material, which restricts the growth potential and overall yield of these plantations (ICFRE, 2012). This is primarily attributed to the fact that plantations are generally raised through seed-based seedlings, which results in wider variability, contributing to uncertain and unproductive yields. This necessitated the establishment of a strong research and development mechanism to identify and develop high-yielding and short-rotation varieties. The objective of selection programme is to obtain significant amounts of genetic gain as quickly and inexpensively as possible, while at the same time maintaining a broad genetic base to ensure future gains. The

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selection and subsequent progeny trial of selected superior trees is a base for genetic improvement.

Melia dubia Cav. is commonly known as 'Malabar neem' and locally called as 'Malai vembu' in Tamil, and is a member of the family Meliaceae. It is distributed in India, Sri Lanka, Malaysia, Bhutan, Burma, Australia and Africa. It is found in Sikkim, Himalayas, North Bengal, Upper Assam, Khasi hills, Hills of Orissa, Deccan plateau and Western Ghats at an altitude of 1500 - 1800 m above MSL in India. It's a multipurpose agroforestry tree used for pulpwood, timber, fuelwood, fodder, plywood and afforestation purposes (Akhilraj and Parthiban, 2020; Akhilraj *et al*., 2023). Due to its superior quality in pulp, paper and plywood manufacturing, this species is now being attracted by many industries. High growth rate, suitability for intercropping, rapid returns and high industrial demands made this species to be chosen by the farmers compared to other industrial plantation species. In ordered to develop a high yielding, short rotational variety there must be a good selection from the existing plantations to screen the superior quality trait. Hence, this study was undertaken to select the superior trees of *Melia dubia* for further breeding programmes.

Materials and Methods

The study was carried out in the existing progeny trial (11.19° N, 76.56° E) present in the Forest College and Research Institute campus, Mettupalayam, Tamil Nadu. The plantation was established in 2010 under the National Agriculture Innovation Project (NAIP). Study site characterized by well drained red sandy loam with a pH of 7.5 and situated at an altitude of 300 MSL. The site receives an average annual rainfall of 922 mm. The mean maximum and minimum temperatures of the location were 32.2^{o}C and 23.2^{o}C, respectively.

Selection of superior trees was carried out by the comparison tree method (Pitcher and Dorn, 1966) in the year 2016. The preliminary reporting of the candidate trees serves the purpose of screening as many trees as possible. After a superior tree candidate is shortlisted, it is scored for traits of interest in relation to several surrounding proximate trees, the "comparison trees". If the candidate tree exceeds the comparison trees by a certain arbitrary amount, it is selected as a candidate plus tree. The characters considered for selection of superior trees are basal girth, GBH, height of the tree, texture of bark, bole straightness and insect-pest incidence. All the observations are recorded for both candidate and comparison trees. The outstanding tree among the comparison trees is selected as the candidate for evaluation.

The basal girth and GBH of each selected tree were measured using a measuring tape, while tree height was determined using a Ravi altimeter. The trees were graded by assigning scores based on visual assessment of parameters such as bark texture, bole straightness, and the incidence of insect pests and diseases. Among the 46 phenotypically superior trees, 30 superior trees were selected and felled for biomass estimation after excluding the border trees. Destructive sampling was used for biomass estimation. The fresh biomass of leaves, stem, and branches was recorded separately using a spring weighing balance and the total fresh biomass of each tree was computed by summing the biomass of all components. Simple linear regression analysis was performed to evaluate the relationship between GBH and fresh biomass of different tree components in the selected *Melia dubia* genetic resources.

Results and Discussion

A total of 46 CPT's were identified from the plantation based on morphometric traits *viz*., tree height, basal diameter, GBH, texture of bark, bole straightness and free from pest and disease through check tree method. Scores were given for each character, and the trees which showed greater performance than the mean were selected.

The plus trees exhibited good variability in terms of growth attributes. The basal girth of the plus tree ranged from 48 cm (MTPMD 10) to 122 cm (MTPMD 1). The GBH of the plus tree ranged between 44 cm (MTPMD 10, MTPMD 36) and 85 cm (MTPMD 1). Similarly, the height of the plus tree ranged between 12 m (MTPMD 7 and MTPMD 8) and 17.5 m (MTPMD 9) (Table 1). Texture of the bark, bole straightness and disease and pest incidence were visually assessed, and scores were given for all the trees. The tree that performed outstandingly among the comparison became the candidate plus tree. This kind of selection system was reported in many hardwood species with success (Zobel and Talbert, 1984), which thus endorses the selection programme deployed in the current investigation.

Table 1: Biometric attributes of superior plus trees of *Melia dubia*

Sampling	Basal girth (cm)	GBH (cm)	Height (m)	Texture of bark	Bole straightness	Disease-pest attack	Assigned Number
PS 1	122	85	14	MR	1	0	MTPMD 1
Mean ± SD	75.62 ± 26.67	59.25 ± 15.93	12.17 ±1.13	-	2.00 ± 0.63	0 ± 0	
PS 2	77.5	61	14	S	1	0	MTPMD 2
Mean ± SD	66.08 ± 10.92	50.75 ± 13.64	13.42 ± 0.58	-	1.67 ± 0.52	0 ± 0	
PS 3	67	54.5	12.5	S	1	0	MTPMD 3
Mean ± SD	55.57 ±7.07	45.50 ± 4.79	11.58 ± 1.39	-	2.17 ±0.75	0 ± 0	
PS 4	70	58	14.5	S	1	0	MTPMD 4
Mean ± SD	58.67 ± 13.11	48.83 ± 10.05	9.83 ± 3.14	-	1.83 ± 0.75	0 ± 0	
PS 5	60	53.5	14	S	1	0	MTPMD 5
Mean ± SD	50.17 ± 8.87	42.33 ± 8.74	11.00 ± 2.19	-	2.67 ± 1.37	0 ± 0	
PS 6	65	55	14.5	S	1	0	MTPMD 6
Mean ± SD	57.17 ± 10.34	47.83 ± 8.66	13.42 ± 1.28	-	2.00 ± 0.63	0 ± 0	
PS 7	66	57	12	S	1	0	MTPMD 7
Mean ± SD	55.58 ± 6.47	48.58 ± 5.70	12.50 ± 1.52	-	2.17 ± 0.75	0 ± 0	
PS 8	61	51	12	S	1	0	MTPMD 8
Mean ± SD	51.67 ± 9.67	45.17 ± 7.70	11.83 ± 1.47	-	2.17 ± 0.75	0 ± 0	
PS 9	58	47	17.5	S	1	0	MTPMD 9
Mean ± SD	51.17 ± 4.83	42.50 ± 2.81	12.25 ± 2.62	-	2.17 ± 0.75	0 ± 0	
PS 10	48	44	14	S	1	0	MTPMD 10
Mean ± SD	51.17 ± 3.76	44.00 ± 2.95	12.17 ± 1.60	-	2.33 ± 0.82	0 ± 0	
PS 11	64	52	14.5	S	1	0	MTPMD 11
Mean ± SD	50.50 ± 8.85	42.08 ± 5.99	11.58 ± 2.01	-	1.83 ± 0.75	0 ± 0	
PS 12	59	49.5	15	S	1	0	MTPMD 12
Mean ± SD	49.50 ± 6.59	41.75 ± 5.98	13.00 ± 1.38	-	2.17 ± 0.75	0 ± 0\	
PS 13	59	51	15.5	S	1	0	MTPMD 13
Mean ± SD	50.83 ± 7.96	44.67 ± 8.07	12.42 ± 1.91	-	2.17 ± 0.75	0 ± 0	
PS 14	58	54	15.5	S	1	0	MTPMD 14
Mean ± SD	51.33 ± 4.46	43.33 ± 5.68	12.42 ± 1.80	-	2.33 ± 0.82	0 ± 0	
PS 15	68	52	15	S	1	0	MTPMD 15
Mean ± SD	58.33 ± 7.45	48.17 ± 3.37	13.25 ± 0.99	-	2.00 ± 0.63	0 ± 0\	
PS 16	60	50	13.5	S	1	0	MTPMD 16
Mean ± SD	57.00 ± 7.01	48.17 ± 2.99	13.17 ± 1.03	-	1.83 ± 0.41	0 ± 0\	
PS 17	68	57	14	S	1	0	MTPMD 17
Mean ± SD	55.17 ± 7.73	46.33 ± 7.12	12.00 ± 1.10	-	2.17 ± 0.75	0 ± 0	
PS 18	56	48	13	S	1	0	MTPMD 18
Mean ± SD	54.50 ± 4.04	45.83 ± 3.54	12.58 ± 0.92	-	2.00 ± 0.63	0 ± 0	
PS 19	58	50	15	S	1	0	MTPMD 19
Mean ± SD	53.67 ± 3.39	47.67 ± 3.61	13.50 ± 0.89	-	2.17 ± 0.75	0 ± 0	
PS 20	56	48	14.5	S	1	0	MTPMD 20
Mean ± SD	53.17 ± 3.66	44.00 ± 4.86	12.75 ± 1.04	-	2.00 ± 0.63	0 ± 0	
PS 21	57	50	14.5	S	1	0	MTPMD 21
Mean ± SD	53.17 ± 5.00	46.50 ± 4.93	12.75 ± 1.17	-	2.17 ± 0.75	0 ± 0	
PS 22	58	48	15	S	1	0	MTPMD 22
Mean ± SD	52.83 ± 3.60	44.00 ± 2.37	13.00 ± 1.14	-	2.00 ± 0.63	0 ± 0	

PS 23	55	49	15.5	S	1	0	MTPMD 23
Mean ± SD	51.67 ± 3.44	43.50 ± 3.99	13.50 ± 1.14	-	2.00 ± 0.63	0 ± 0	
PS 24	58	49	16	S	1	0	MTPMD 24
Mean ± SD	51.00 ± 7.29	44.50 ± 6.72	14.00 ± 1.38	-	2.17 ± 0.75	0 ± 0	
PS 25	61	50.5	15.5	S	1	0	MTPMD 25
Mean ± SD	52.00 ± 6.63	44.08 ± 4.77	12.92 ± 1.32	-	2.17 ± 0.75	0 ± 0	
PS 26	68	54	13	S	1	0	MTPMD 26
Mean ± SD	57.50 ± 5.65	47.17 ± 4.58	12.75 ± 0.61	-	2.17 ± 0.75	0 ± 0	
PS 27	59	48	15	S	1	0	MTPMD 27
Mean ± SD	53.33 ± 4.50	44.42 ± 5.41	12.92 ± 1.28	-	2.00 ± 0.63	0 ± 0	
PS 28	67	50	13.5	S	1	0	MTPMD 28
Mean ± SD	56.83 ± 6.68	47.50 ± 4.76	12.58 ± 0.66	-	2.00 ± 0.63	0 ± 0	
PS 29	59	48	16	S	1	0	MTPMD 29
Mean ± SD	50.67 ± 8.59	43.67 ± 7.61	13.00 ± 2.43	-	2.33 ± 0.82	0 ± 0	
PS 30	58	50	14	S	1	0	MTPMD 30
Mean ± SD	54.67 ± 3.44	47.08 ± 2.80	13.50 ± 0.45	-	2.17 ± 0.75	0 ± 0	
PS 31	58	49	14	S	1	0	MTPMD 31
Mean ± SD	52.33 ± 7.94	43.50 ± 7.82	12.67 ± 1.40	-	2.17 ± 0.75	0 ± 0	
PS 32	57	49	15	S	1	0	MTPMD 32
Mean ± SD	50.33 ± 7.12	42.50 ± 5.01	14.00 ± 0.71	-	2.17 ± 0.75	0 ± 0	
PS 33	57	49	14	S	1	0	MTPMD 33
Mean ± SD	52.33 ± 5.57	44.67 ± 6.47	12.08 ± 1.36	-	2.00 ± 0.63	0 ± 0	
PS 34	65	51	14	S	1	0	MTPMD 34
Mean ± SD	54.83 ± 5.38	43.00 ± 4.47	13.00 ± 0.71	-	2.17 ± 0.75	0 ± 0	
PS 35	**0**56	47	14	S	1	0	MTPMD 35
Mean ± SD	51.50 ± 4.97	42.17 ± 3.76	13.08 ± 0.66	-	2.00 ± 0.63	0 ± 0	
PS 36	52	44	14.5	S	1	0	MTPMD 36
Mean ± SD	49.00 ± 2.53	41.00 ± 1.79	13.00 ± 0.95	-	2.17 ± 0.75	0 ± 0	
PS 37	54	47	14	S	1	0	MTPMD 37
Mean ± SD	52.17 ± 1.47	44.00 ± 2.53	12.83 ± 0.68	-	2.00 ± 0.63	0 ± 0	
PS 38	57	50	13	S	1	0	MTPMD 38
Mean ± SD	50.50 ± 8.36	44.50 ± 8.14	12.58 ± 0.49	-	1.83 ± 0.75	0 ± 0	
PS 39	62	52	13	S	1	0	MTPMD 39
Mean ± SD	48.83 ± 8.35	41.17 ± 7.36	11.67 ± 1.03	-	2.17 ± 0.75	0 ± 0	
PS 40	64	52	13.5	S	1	0	MTPMD 40
Mean ± SD	56.17 ± 6.34	46.83 ± 4.96	12.42 ± 0.92	-	2.17 ± 0.75	0 ± 0	
PS 41	66	53	14	S	1	0	MTPMD 41
Mean ± SD	57.67 ± 6.86	47.67 ± 4.23	12.92 ± 0.80	-	2.00 ± 0.63	0 ± 0	
PS 42	73	65	15	S	1	0	MTPMD 42
Mean ± SD	58.17 ± 14.80	49.17 ± 14.29	12.75 ± 1.17	-	2.17 ± 0.75	0 ± 0	
PS 43	57	51	14	S	1	0	MTPMD 43
Mean ± SD	41.33 ± 10.41	35.50 ± 10.23	10.83 ± 2.71	-	2.00 ± 0.63	0 ± 0	
PS 44	61	55	14	S	1	0	MTPMD 44
Mean ± SD	45.67 ± 12.19	40.17 ± 11.13	11.92 ± 1.43	-	2.17 ± 0.75	0 ± 0	
PS 45	50	42	14	S	1	0	MTPMD 45
Mean ± SD	47.67 ± 1.37	39.67 ± 1.37	12.83 ± 0.68	-	2.00 ± 0.63	0 ± 0	
PS 46	57	48	13	S	1	0	MTPMD 46
Mean ± SD	55.17 ± 10.21	46.83 ± 7.28	12.50 ± 0.77	-	2.00 ± 0.63	0 ± 0	

The identification and selection of candidate plus trees (CPT's) constitute the first and most crucial step in any tree improvement programme, as the genetic quality of the selected trees determines the success of subsequent breeding, propagation and plantation establishment. In the present study, thirty superior *Melia dubia* trees were selected from the surveyed population using the comparison check tree method based on quantitative traits such as tree height, basal girth and girth at breast height, together with qualitative characteristics including bark texture, bole straightness and freedom from insect-pest incidence. The observed variation in these phenotypic traits reflects the existence of considerable genetic variability among the selected trees, providing ample scope for the identification of superior planting material for future genetic improvement programmes.

The comparison check tree method adopted in the present investigation has been successfully employed in the selection of plus trees in several forest tree species. Chauhan *et al*., (2018) selected 20 CPT's were identified in *Melia dubia* based on economically important quantitative and qualitative traits such as tree height, girth at breast height, clear bole height, stem straightness and disease resistance. Variability in growth and phenotypic characters of *Melia dubia* populations has also been reported from the Western Ghats of Kerala, supporting the potential for selection of superior trees for genetic improvement programmes (Binu and Santhoshkumar, 2019). Singh and Majidwani (2016) selected thirty CPT's of *Pongamia pinnata* from different locations of Uttar Pradesh using the comparison tree method for evaluating genetic divergence in pod and seed characteristics for subsequent breeding programmes. Similarly, Gera *et al*., (2016) identified twenty-eight CPT's of *Acacia catechu*, Singh and Mahanta (2013) selected thirty-three plus trees of *Pinus kesiya* and used the point grading method to identify superior phenotypes. Thus, the current selection employed here is in line with the above studies.

Further, screening has been done based on biomass estimation through destructive analysis. The details of finally screened 30 genetic resources along with the biomass estimates are presented in Table 2.

Table 2: Biomass estimation of superior plus trees of *Melia dubia*

Genetic Resource No.	Tree height (m)	Basal girth (cm)	GBH (cm)	Fresh weight (kg)			
				Stem weight	Branch weight	Leaf weight	Total biomass
MTPMD 1	15.44*	112.50*	83.40*	338*	159*	48*	545
MTPMD 2	16.44*	72.50*	60.60*	169*	51*	18*	238
MTPMD 3	15.47*	67.00*	54.70*	168*	49*	22*	239
MTPMD 4	13.44	66.50*	59.20*	157*	20	14*	191
MTPMD 5	14.47*	59.00	52.00	90	37*	1	128
MTPMD 6	15.42*	64.50	56.80*	127*	51*	16*	194
MTPMD 7	14.5*	66.00*	57.00*	120	28	10	158
MTPMD 11	14.76*	63.00	51.00	124*	24	8	156
MTPMD 12	14.16	59.00	49.00	94	16	9	119
MTPMD 13	14.04	57.00	51.00	9518	7	120	
MTPMD 14	14.52*	66.00*	53.00	98	13	11	122
MTPMD 15	14.98*	65.00	50.00	108	8	8	124
MTPMD 17	14.19	67.00*	55.00*	97	16	12*	125
MTPMD 19	13.29	57.00	50.00	85	18	12*	115
MTPMD 21	14.05	56.00	48.00	107	20	9	136
MTPMD 22	14.15	57.00	46.00	83	9	9	101

cont...

Genetic Resource No.	Tree height (m)	Basal girth (cm)	GBH (cm)	Fresh weight (kg) Stem weight	Branch weight	Leaf weight	Total biomass
MTPMD 23	14.82*	67.00*	56.00*	124*	24	18*	166
MTPMD 24	16.46*	57.00	50.00	111	19	8	138
MTPMD 25	13.93	54.00	47.00	78	19	6	103
MTPMD 26	14.68*	59.00	51.00	88	18	8	114
MTPMD 29	12.74	69.00*	50.00	95	17	10	122
MTPMD 30	14.47*	62.00	47.00	82	10	5	97
MTPMD 32	15.23*	58.50	48.50	90	24	2	116
MTPMD 34	13.91	58.00	49.00	101	18	9	128
MTPMD 39	15.52*	64.50	50.00	96	15	10	121
MTPMD 40	13.86	65.00	50.50	90	13	1	104
MTPMD 42	14.08	74.00*	63.00*	214*	65*	33*	312
MTPMD 43	12.15	57.00	48.00	88	36*	5	129
MTPMD 44	11.7	61.00	54.00	98	61*	7	166
MTPMD 46	16.97*	89.50*	71.50*	280*	54*	19*	353
Mean	14.46	65.02	53.74	123.17	31	11.83	166

MTPMD 1 exhibited highest fresh biomass in terms of stem (338 kg), branch (159 kg), leaf (48 kg) and total fresh biomass (545 kg) and the lowest stem fresh weight (78 kg), branch fresh weight (8 kg), leaf fresh wight (1 kg) were recorded in MTPMD 25, MTP MD 15 and MTPMD 5 & 40 respectively. The lowest total fresh biomass (97 kg) was recorded in MTPMD 30.

Simple linear regression analysis revealed significant positive relationships between growth parameters and total fresh biomass (Table 3). Among the variables studied, GBH was the strongest predictor of total fresh biomass, explaining 91.6% of the observed variation (R^2 = 0.916). The fitted regression equation indicates a substantial increase in biomass with increasing GBH. Basal girth also showed a strong positive relationship with biomass (R^2 = 0.854), whereas tree height exhibited a comparatively weak association (R^2 = 0.145). These findings suggest that stem girth measurements, particularly GBH, are more reliable predictors of fresh biomass than tree height in the selected *Melia dubia* genetic resources.

GBH exhibited highly significant positive linear relationships (P<0.001) with stem, branch, leaf and total fresh biomass. Among the biomass components, GBH was the strongest predictor of stem fresh biomass (R^2 = 0.908). Moderate but highly significant relationships were also observed for branch (R^2 = 0.738) and leaf fresh biomass (R^2 = 0.736). These findings demonstrate that GBH is a reliable and practical predictor of fresh biomass and its components in *Melia dubia* genetic resources and can be effectively used for rapid biomass estimation in tree improvement and plantation programmes.

Table 3: Linear regression models relating growth parameters in *Melia dubia* genetic resources

Response variable	Predictor	Regression equation	R^2	F- value	P-value
Total fresh biomass	Tree height	Y= -278.065 + 30.707 H	0.145	4.75	0.038
Total fresh biomass	Basal girth	Y= -328.742 + 7.609 BG	0.854	163.13	<0.001
Total fresh biomass	GBH	Y= -450.929 + 11.480 GBH	0.916	305.55	<0.001
Stem fresh biomass	GBH	Y= –266.556 + 7.252 GBH	0.908	277.47	<0.001
Branch fresh biomass	GBH	Y= –140.345 + 3.188 GBH	0.738	79.04	<0.001
Leaf fresh biomass	GBH	Y= -44.028 + 1.039 GBH	0.736	77.89	<0.001

The superiority of GBH as a predictor of biomass is biologically justified because radial stem growth directly reflects cambial activity and wood formation, which contribute the greatest proportion of aboveground biomass. In contrast, tree height growth tends to stabilize earlier, while stem diameter continues to increase and trees of similar height may differ considerably in stem thickness and wood volume. Consequently, diameter-based variables are expected to provide more accurate estimates of biomass than height alone. Similar observations have been reported in several forestry studies, where diameter at breast height consistently emerged as the principal variable for biomass prediction and allometric model development. Chave *et al*., (2014) emphasized that stem diameter, together with tree height and wood density, forms the basis of robust pan-tropical biomass models, while species-specific studies have also demonstrated that diameter-based equations provide highly reliable biomass estimates.

The strong relationship between GBH and total fresh biomass observed in the present study (Fig. 1) is consistent with previous work on *Melia dubia*. Thakur *et al*., (2021) developed biomass prediction models using destructively sampled trees and reported that regression models incorporating diameter and height produced excellent prediction accuracy, with the best model explaining approximately 96% of the variation in fresh biomass. Although the present study evaluated CPT's and used GBH as the principal predictor, the high coefficient of determination (R^2 = 0.916) obtained confirms that stem girth alone can serve as a practical and reliable predictor of biomass under plantation conditions.

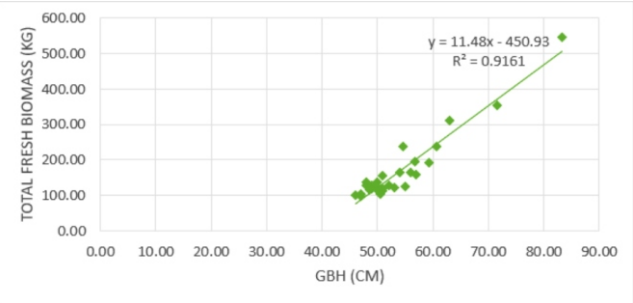


Fig. 1: Regression relationship between GBH and total fresh biomass of *Melia dubia* genetic resources.

The regression models also revealed differences in the predictive accuracy for individual biomass components. GBH explained over 90% of the variation in stem biomass but only about 74% of the variation in branch and leaf biomass. This difference is expected because stem biomass is directly associated with radial growth, whereas branch and leaf biomass are influenced by crown architecture, branching habit, foliage retention, site conditions and seasonal variation. Greater variability in crown characteristics among genetically diverse trees therefore reduces the precision of branch and leaf biomass prediction compared with stem biomass.

The comparatively poor relationship between tree height and total fresh biomass (R^2 = 0.145) further highlights the limitations of using height alone for biomass estimation. Trees with similar heights frequently differed substantially in basal girth and GBH, resulting in considerable differences in biomass accumulation. Therefore, tree height alone cannot adequately represent tree productivity in *Melia dubia*. Similar conclusions have been reported in biomass modelling studies, where diameter-based variables generally outperform height when used independently for predicting aboveground biomass.

Conclusion

The present investigation demonstrated considerable phenotypic variability among *Melia dubia* genetic resources, providing substantial scope for the identification and selection of superior planting material for future tree improvement programmes. Candidate trees were initially identified based on quantitative growth attributes and qualitative stem characteristics using the comparison check tree method, followed by further screening through destructive biomass estimation. The selected genetic resources exhibited considerable variation in stem, branch, leaf and total fresh biomass, indicating differences in productivity among the candidate trees. Among the growth attributes evaluated, GBH emerged as the most reliable predictor of total fresh biomass, accounting for 91.6% of the variation, while basal girth also showed a strong association with biomass. In contrast, tree height alone showed a comparatively weak relationship with total fresh biomass. GBH also exhibited strong and highly significant relationships with individual biomass components, particularly stem biomass. The results establish that GBH can serve as simple, reliable and practical indicators for rapid biomass assessment and preliminary screening of superior *Melia dubia* genetic resources. The identification of high-biomass candidate trees combined with the use of GBH-based biomass prediction provides a useful foundation for selecting superior genotypes for clonal propagation, plantation establishment and subsequent genetic improvement programmes in *Melia dubia* genetic resources.

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