



Original Research Paper

Genetic diversity of *Terminalia tomentosa* from Achanakmar Amarkantak Biosphere Reserve (Chhattisgarh)

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Abstract

The aim of this study was to assess the genetic diversity within populations of *Terminalia tomentosa* found in the Achanakmar Amarkantak Biosphere Reserve in Chhattisgarh, utilizing genetic analysis techniques. Nine (09) genotypes of *T. tomentosa* were sampled from the three sub-populations of Achanakmar Amarkantak Biosphere Reserve of Chhattisgarh, their growth, physiological and biochemical characteristics were meticulously analyzed to quantify genetic diversity. The results reveal that distinct variations exist across these genotypes in terms of their growth and physiological traits, as well as their biochemical profiles, suggesting a notable level of genetic polymorphism within the reserve. Across all traits, the difference between Phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV) is minimal and environmental coefficient of variation (ECV) values remain very low (ranged from 0.19 to 0.99). Biochemical traits exhibit significantly higher GCV and PCV compared to growth traits. All recorded traits show high heritability, exceeding 74% which determined the genetic architecture of these populations and underscore the potential for selective breeding. The results on the above three genetic variations, estimates broad sense heritability (h^2) and genetic advance (GA) derived from these analyses provide a clear picture on the population structure and genetic differentiation among the sampled individuals. The results of this study can be instrumental in devising effective conservation strategies and sustainable management practices for *T. tomentosa* within the Achanakmar Amarkantak Biosphere Reserve, emphasizing the importance of preserving this valuable genetic resource.

Keywords: *Terminalia tomentosa*, Genetic Diversity, Biosphere Reserve, Conservation.

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1. Introduction

Terminalia tomentosa is a premier timber species and a dominant associate in the tropical deciduous forests of the Indian subcontinent (Chaturvedi *et al.*, 2011). It is highly valued for its exceptionally hard and durable wood, which is utilized for heavy construction, furniture, tool handles, and specialized underwater purposes (Gautam *et al.*, 2024). Beyond timber, the species is an indispensable primary food plant for the tropical Tasar silkworm (Mandal *et al.*, 2024). It is a vital livelihood activity for tribal communities in Central India, particularly in states like Chhattisgarh and Odisha, where thousands of families depend on the cultivation of silkworms on *T. tomentosa* and *T. arjuna* trees (Mazumdar *et al.*, 2023). Additionally, the bark and fruits of the species are used in traditional medicine to treat ailments such as diarrhea and have industrial applications in the tanning and dyeing sectors (Meriga *et al.*, 2017).

The Achanakmar Amarkantak Biosphere Reserve, a UNESCO-recognized World Heritage site since 2012, spans the Deccan Peninsula bio-geographic zone across Chhattisgarh and Madhya Pradesh, located between 21°15' to 22°58'N latitude and 81°25' to 82°05'E longitude (Fig.1.1), the reserve encompasses diverse forest types, ranging from Northern Tropical Moist Deciduous to Southern Dry Mixed Deciduous forests (Kumar *et al.*, 2017). In these ecosystems, *Shorea robusta* is often the dominant species, with *T. tomentosa* serving as a major overstorey associate (Thakur *et al.*, 2019). The reserve is a critical biodiversity hub, supporting a wide array of flora and providing essential ecosystem services, including soil and water conservation and biomass production (Darro *et al.*, 2020).

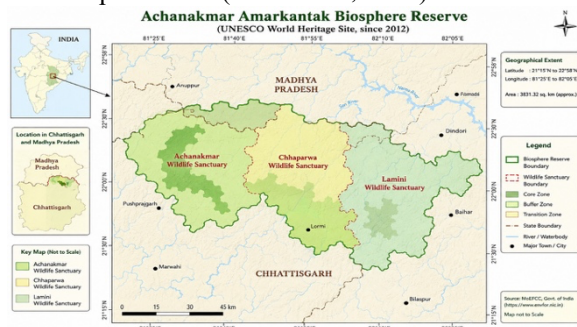


Fig.1.1. Selected site of Achanakmar Amarkantak Biosphere Reserve (AABR), Chhattisgarh

Genetic diversity is the cornerstone of biological variation, enabling forest tree populations to adapt to environmental stressors, climate change, and pathogens (Pither *et al.*, 2003). In the context of Central Indian forests, understanding the genetic structure of dominant species like *T. tomentosa* is essential for the selection of superior germplasm—often referred to as "Candidate Plus Trees"—which

forms the basis of forest improvement and productivity enhancement programs (Ankita *et al.*, 2022). Morphological and biochemical markers have been successfully employed across the *Terminalia* genus to evaluate genetic variation and species relationships (Michotey, 2016; Sharma & Shrivastava, 2016; Warriar *et al.*, 2019). Characterizing this diversity is a prerequisite for the sustainable management and long-term conservation of the species' genetic resources (Nantongo *et al.*, 2022).

Despite the high ecological and economic significance of *T. tomentosa* in Chhattisgarh, systematic research on its genetic variability within the Achanakmar Amarkantak Biosphere Reserve (AABR) remains limited (Kanna *et al.*, 2024). Previous studies in the AABR have primarily focused on floristic composition, regeneration patterns, and litterfall dynamics, but have not extensively explored the molecular-level genetic diversity of *T. tomentosa* populations (Raj, 2018; Singh *et al.*, 2023). Addressing this gap, the present investigation evaluates the genetic estimates of *T. tomentosa* genotypes collected from diverse locations within the AABR. By analyzing a range of growth, physiological and biochemical traits; including plant height, girth at breast height and biochemical markers, this study seeks to identify elite individuals for future hybridization and forest management initiatives.

2. Methodology

2.1. Selection of Genotypes

A total of nine genotypes of *Terminalia* were meticulously selected and collected from various locations within the Achanakmar Amarkantak Biosphere Reserve in Chhattisgarh, ensuring a representative sample for genetic analysis (Table 2.1). The accessions were sourced from three primary sub-populations within the reserve viz; Achanakmar, Chhapparwa, and Lamini (Fig.1.1). The sampled genotypes span a significant altitudinal range, starting from 1,079 meters at the Achanakmar site and reaching up to 1,866 meters at the Lamini site.

Table-2.1. Accessions (Genotypes) of *Terminalia* from Achanakmar Amarkantak Biosphere Reserve (AABR) Chhattisgarh

S. No	Source	Accession ID	Latitude	Longitude	Altitude (m)
01	Achanakmar	TT-A1	22°18'57"	81°57'46"	1079

02	Achana kmar (AABR)	TT- A2	22°20' 14''	81°56' 02''	1134
03	Achana kmar (AABR)	TT- A3	22°23' 49''	81°52' 42''	1515
04	Achana kmar (AABR)	TT- C4	22°24' 21''	81°52' 00''	1481
05	Chhapa rwa (AABR)	TT- C5	22°26' 47''	81°45' 46''	1346
06	Chhapa rwa (AABR)	TT- C6	22°27' 16''	81°45' 18''	1336
07	Lamini (AABR)	TT-L7	22°30' 50''	81°39' 57''	1748
08	Lamini (AABR)	TT-L8	22°31' 04''	81°40' 29''	1597
09	Lamini (AABR)	TT-L9	22°36' 04''	81°46' 44''	1866

2.2. Growth and Physiological Traits

The comprehensive assessment of these growth and physiological traits, detailed in (Table 2.2), offers insights into the phenotypic variability and adaptive mechanisms of *T. tomentosa* across its diverse habitats within the AABR. The different growth and physiological traits recorded for each selected genotype include; tree height, tree basal diameter, tree basal area, tree volume, leaf length, leaf width and leaf area. These measurements were taken on field during the study by adopting standard procedures.

Table-2.2. Growth and Physiological Traits of selected *Terminalia* genotypes from Achanakmar Amarkantak Biosphere Reserve (AABR) Chhattisgarh

Ge not ype	Tree Heig ht (m)	Basal Diam eter (cm)	Basa l Area (cm ²)	Vo lu me (m ³)	Leaf Len gth (cm)	Leaf Wid th (cm)	Lea f Are a (cm ²)
TT- A1	13.2	37.8	59.3	7.8	16.0	6.2	88.3
TT- A2	14.5	42.1	66.1	9.6	15.7	7.3	102.0

TT- A3	12.9	35.3	55.4	7.1	15.2	7.5	101.5
TT- C4	12.2	33.2	52.1	6.4	12.3	5.7	62.4
TT- C5	11.8	31.9	50.1	5.9	11.8	5.9	62.0
TT- C6	11.7	30.5	47.9	5.6	12.0	5.7	60.9
TT- L7	9.5	28.2	44.3	4.2	9.5	6.5	55.0
TT- L8	8.7	27.6	43.3	3.8	10.2	5.4	48.6
TT- L9	10.5	29.5	46.3	4.9	9.0	6.9	55.3

2.3. Biochemical Traits

Further characterization involved the quantification of biochemical attributes, which reflect the metabolic and adaptive capabilities of these genotypes within their specific ecological niches. In this study the different biochemical traits recorded for each selected genotype include; chlorophyll a, chlorophyll b, total chlorophyll, and soluble protein content. The chlorophyll was extracted using 80% acetone from fresh leaf samples and then quantified spectrophotometrically at wavelength of 663 nm and 645 nm respectively (Khan *et al.*, 2022). The soluble protein content was determined by homogenizing 0.5g of fresh leaf tissue in a pre-chilled pestle and mortar with 10 mL of 0.1 M phosphate buffer (pH 7.0). The resulting homogenate was then centrifuged, and the supernatant was used for protein estimation (Lowry, 1951).

2.4. Genetic Estimates

The genetic estimates were calculated on the basis of growth, physiological and biochemical traits for understanding the genetic architecture and diversity of the *T. tomentosa* in sub-populations within the AABR. The computed genetic parameters in the present study include; genotypic coefficient of variation, phenotypic coefficient of variation, environmental coefficient of variation, broad sense heritability (h^2), and genetic advance for all measured traits. These genetic parameters were calculated by employing established statistical formulae and methodologies of (Baenziger *et al.*, 2004; Pliura *et al.*, 2007 and Yoshida *et al.*, 2007) which allowed for a robust assessment of the genetic and environmental contributions to phenotypic variation.

3. Results

The growth and physiological traits of selected *T. tomentosa* genotypes from three sub-populations of Achanakmar Amarkantak Biosphere Reserve in Chhattisgarh summarized in (Table 3.1). The traits recorded include tree height, basal diameter, basal area, volume, and leaf dimensions. These parameters collectively offer insights into the morphological

variations and overall vigor of the sampled genotypes. The genotypes exhibit significant variation in growth metrics. The height of selected genotypes ranges from a minimum of 8.7 m to a maximum of 14.5 m. Genotype TT-A2 recorded the highest basal diameter (42.1 cm) and basal area (66.1 cm²), while TT-L8 showed the lowest values in these categories (27.6 cm and 43.3 cm², respectively). The tree volume varies between 3.8m³ and 9.6m³. Leaf traits, which are critical for assessing the physiological health and photosynthetic capacity of the trees, also show diversity. The largest leaf area was observed in genotype TT-A2 (102.0 cm²), closely followed by TT-A3 (101.5 cm²). The smallest leaf area was recorded for TT-L8 at 48.6 cm². Leaf length ranges from 9.0 cm to 16.0 cm, while leaf width varies between 5.4 cm and 7.5 cm. Overall, the genotypes from the Achanakmar site (TT-A1, TT-A2, TT-A3) generally show superior growth and leaf development compared to those from the Lamini site (TT-L7, TT-L8, TT-L9).

The biochemical traits of these selected genotypes, providing critical data on parameters such as chlorophyll content, and soluble protein concentrations, which are indicative of photosynthetic efficiency and stress tolerance. Specifically, chlorophyll_a content spans from 0.65 to 0.81 mg/g, chlorophyll_b from 0.23 to 0.37 mg/g, and total chlorophyll from 0.89 to 1.37 mg/g, indicating varied photosynthetic capacities among the accessions. The concentration of chlorophyll_a ranges from 0.65 mg/g in genotype TT-L9 to 0.81 mg/g in TT-A2. Chlorophyll b levels are highest in TT-A2 (0.37 mg/g) and lowest in TT-L7 (0.23 mg/g). Genotype TT-A1 recorded the highest total chlorophyll content at 1.37 mg/g, while the lowest value of 0.89 mg/g was observed in TT-L9. The Chlorophyll a/b Ratio reflects the balance between the two pigment types, ranges from 2.18 to 2.95. Protein content is another key biochemical marker recorded in the table. The genotypes show a range of protein concentrations, from a minimum of 17.9 mg/g in TT-L8 to a maximum of 25.6 mg/g in TT-A2. Consistent with the growth trends observed in previous tables, genotypes from the Achanakmar site (TT-A1, TT-A2, TT-A3) generally possess higher biochemical values for both chlorophyll and protein compared to those from the Lamini site (TT-L7, TT-L8, TT-L9).

Table-3.1. Biochemical Traits of selected *T. tomentosa* genotypes from Achanakmar Amarkantak Biosphere Reserve (AABR) Chhattisgarh

Geno type	Chloro phyll _a (mg/g)	Chloro phyll _b (mg/g)	Chl _a /Chl _b	Total Chlorophyll	Prot ein (mg)
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				(mg/g)	/g)
TT-A1	0.78	0.32	2.43	1.37	23.78
TT-A2	0.81	0.37	2.18	1.18	25.6
TT-A3	0.79	0.36	2.19	1.15	24.6
TT-C4	0.74	0.30	2.46	1.04	20.2
TT-C5	0.75	0.31	2.41	1.06	20.9
TT-C6	0.76	0.29	2.62	1.05	21.7
TT-L7	0.68	0.23	2.95	0.91	18.4
TT-L8	0.67	0.24	2.79	0.91	17.9
TT-L9	0.65	0.24	2.70	0.89	18.0

Table 3.2 displays the Pearson's coefficient of correlation between various growth and biochemical traits for the selected *T. tomentosa* genotypes. The results indicate strong relationships between physical growth parameters and physiological markers. There is a highly significant positive correlation among the primary growth parameters such as tree height and volume where Tree height shows an extremely strong positive correlation with tree volume ($r = 0.974$), basal diameter and area, where these traits are perfectly correlated ($r = 1.000$) and also show a very high correlation with volume ($r = 0.993$), leaf dimensions, where leaf length is strongly associated with tree height ($r = 0.890$) and basal diameter ($r = 0.911$) respectively observed.

Table-3.2. Pearson's coefficient of correlation among different traits of *T. tomentosa*

Traits	Tree height	Basal diameter	Basal area	Volume	Leaf length	Leaf width	Leaf area	Chlorophyll a	Chlorophyll b	Chlorophyll a/b	Protein
Tree height	1										
Basal diameter	0.974	1									
Basal area	1.000	1.000	1								
Volume	0.993	0.993	0.993	1							
Leaf length	0.890	0.911	0.911	0.974	1						
Leaf width	0.911	0.974	0.974	0.993	0.974	1					
Leaf area	0.974	0.974	0.974	0.993	0.974	0.974	1				
Chlorophyll a								1			
Chlorophyll b								0.911	1		
Chlorophyll a/b								0.974	0.974	1	
Protein											1

[illegible]

correlated with tree height ($r = -0.906$), total chlorophyll ($r = -0.719$), and protein concentration ($r = -0.883$). These results suggest that as growth metrics like height and volume increase, there is a corresponding increase in chlorophyll and protein levels, while the chlorophyll a/b ratio tends to decrease.

Table 3.3 represents the genetic estimates for various growth, physiological, and biochemical traits of *T. tomentosa* genotypes, providing insights into their heritability and potential for genetic improvement. The table compares the Phenotypic Coefficient of Variation, Genotypic Coefficient of Variation, and Environmental Coefficient of Variation. Across all traits, the difference between

Table-3.3. Genetic estimates of *T. tomentosa* genotypes from Achanakmar Biosphere Reserve (AABR) Chhattisgarh

Traits	Phenotypic Coefficient of Variation	Genotypic Coefficient of Variation	Environmental Coefficient of Variation	Broad Sense Heritability (%)	Genetic Advance (%)
Tree Height (m)	3.87	2.88	0.99	74.419	4.21
Basal Diameter (cm)	4.16	3.21	0.95	77.163	7.89
Growth Traits					
Basal Area (cm ²)	3.94	2.98	0.96	75.635	5.28
Volume (m ³)	5.29	4.87	0.42	92.060	11.02
Physiological Traits					
Leaf Length (cm)	2.87	2.54	0.33	88.502	4.56

its	Leaf Width (cm)	3.19	2.91	0.28	91.223	5.28
	Leaf Area (cm ²)	4.07	3.74	0.33	91.892	8.09
	Chlorophyll a (mg/g)	21.00	20.81	0.19	99.095	24.05
	Chlorophyll b (mg/g)	27.24	27.05	0.19	99.302	35.48
Biochemical Traits	Chlorophyll a/b ratio	24.69	24.21	0.48	98.056	29.91
	Total Chlorophyll (mg/g)	25.19	24.78	0.41	98.372	31.17
	Protein (mg/g)	31.78	31.15	0.63	98.018	56.81

PCV and GCV is minimal, and ECV values remain very low (ranging from 0.19 to 0.99). This suggests that the observed variations are primarily due to genetic factors rather than environmental impact. Biochemical traits exhibit significantly higher GCV and PCV compared to growth traits. For instance, protein concentration shows a GCV of 31.15%, while tree height has a GCV of only 2.88%. The relationship between heritability and genetic advance helps determine the effectiveness of selection for these traits. All recorded traits show high heritability, exceeding 74%. The highest heritability values are found in biochemical traits, such as Chlorophyll b (99.302%) and Chlorophyll a (99.095%), as well as tree volume (92.060%). There is a wide range in GA values. Biochemical traits show the highest potential for improvement through selection, with Protein (56.81%), Chlorophyll b (35.48%), and Total Chlorophyll (31.17%) recording the highest GA values. The combination of high broad-sense heritability and high genetic advance for biochemical

traits suggests that these characteristics are likely governed by additive gene action. Consequently, selection based on these biochemical markers would be highly effective for the genetic improvement of this species. In contrast, while growth traits like tree height and basal diameter show high heritability, their lower genetic advance (4.21% and 7.89% respectively) indicates that they may be under the influence of non-additive gene action, making direct selection less efficient for these specific parameters compared to biochemical traits.

Discussion

The present study explores the genetic diversity and population structure of *Terminalia tomentosa*, a valuable timber species, within the Achanakmar Amarkantak Biosphere Reserve, Chhattisgarh, utilizing morphological and biochemical traits. This comprehensive analysis aims to elucidate the extent of genetic variation present within three sub-populations of these Reserve of Chhattisgarh, which is crucial for conservation strategies and sustainable utilization of the species. Previous research has similarly highlighted the importance of understanding genetic diversity in forest tree species to inform effective conservation and breeding programs (Holliday *et al.*, 2017). The findings of this study, therefore, provide a critical foundation for developing targeted strategies for the preservation and genetic enhancement of *T. tomentosa* in this ecologically significant region. Specifically, the observed high broad-sense heritability coupled with high genetic advance in biochemical traits indicates that these characteristics are predominantly under additive gene action, thereby amenable to direct selection for genetic improvement (Sadia *et al.*, 2021). The minimal difference between phenotypic and genotypic coefficients of variation further supports that these traits are largely under genetic control, with environmental factors playing a negligible role (Bordoloi *et al.*, 2024). This high heritability suggests that selection based on these biochemical markers could be highly effective for genetic improvement programs, aligning with prior research emphasizing the importance of variability studies and heritability assessments for enhancing tree breeding outcomes (Madhusudhana *et al.*, 2012). Study on *Terminalia bellerica* found significant genetic variability and high broad-sense heritability for growth and physiological traits, indicating strong genetic control and potential for effective selection strategies (Singh *et al.*, 2026). Similarly, in a study on *Terminalia arjuna*, Random Amplified Polymorphic DNA markers were successfully employed to assess genetic diversity, revealing significant polymorphism among accessions and supporting the utility of molecular markers in diversity analyses within the Achanakmar

Amarkantak Biosphere Reserve (Lefevre *et al.*, 2016). Similar studies were conducted on genetic diversity of forest tree species which further corroborates the observed variations in biochemical attributes. This extensive genetic diversity observed within *T. tomentosa*, particularly in biochemical traits, underscores the species' adaptive potential and provides a rich genetic pool for targeted breeding initiatives aimed at enhancing resilience and productivity in varying environmental conditions. This robust genetic variation also implies a significant capacity for the species to adapt to future environmental challenges, reinforcing the need for its continued conservation and careful management within the AABR. Further analysis of the genetic estimates confirms that while growth traits like tree height and basal diameter show high heritability, their lower genetic advance suggests that they are influenced by non-additive gene action, making direct selection less efficient for these specific parameters compared to biochemical traits. This distinction highlights the importance of employing different breeding strategies tailored to the genetic architecture of individual traits for optimizing genetic gain in *T. tomentosa*. Moreover, the phenotypic coefficient of variation consistently surpassed the genotypic coefficient of variation across all studied traits, further corroborating the influence of environmental factors on trait expression, albeit to a lesser extent for biochemical traits. This discrepancy indicates that environmental conditions contribute to the observed variability, even though the genetic component remains substantial (Das *et al.*, 2020).

4. Conclusion

The study of genetic diversity are crucial for understanding the evolutionary potential and conservation status of forest tree species. The present study utilizes both morphological and biochemical traits to assess the genetic variation within *T. tomentosa* populations in the Achanakmar Amarkantak Biosphere Reserve, providing a comprehensive insight into the species' genetic makeup and informing effective conservation strategies. The results of this study reveal that the *T. tomentosa* populations within the AABR exhibit significant genetic diversity, particularly in biochemical traits, which possess high heritability and genetic advance, making them ideal targets for genetic improvement programs. The presence of genetic variability among selected genotypes, as evidenced by significant differences in phenotypic and genotypic coefficients across various traits, underscores the species' adaptive potential and provides a rich genetic pool for targeted breeding initiatives aimed at enhancing resilience and productivity in varying environmental conditions.

The results of this study can be used to guide conservation efforts and breeding programs for *T. tomentosa*, particularly in identifying and utilizing genotypes with superior biochemical profiles for enhanced economic and ecological benefits.

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