

## Performance of Clones of Different Provenances for Growth and Biomass in a Clonal Orchard of Teak (*Tectona grandis* L. f.), Haliyal, Karnataka

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### ABSTRACT

Teak (*Tectona grandis* L.f.) is one of the most valuable timber yielding tree with predominant distribution in tropical and sub-tropical countries. The present study was conducted in a Teak clonal orchard at Janganamatti, Haliyal Taluk of Uttara Kannada district, Karnataka. The orchard was planted with 2401 saplings (ramets) representing 49 clones collected from diverse provenances and planted at 8×8 m spacing. The study aimed to evaluate clone-wise growth performance, examine provenance effects and biomass estimation under uniform management conditions. Among the individual clones, MYHV5, MYHUT8, MYKB1, MYMK2, MYHUT9 and MYHUT7 demonstrated superior growth, combining higher diameter and height to achieve greater basal area and volume. The correlation analysis indicated strong positive relationships among diameter, basal area and volume ( $r=0.91$ ), highlighting diameter as a reliable trait for early selection in clonal improvement programmes. The provenance effects were also evident, with clones from Thithimathi/Muthagaddo, Tithimathi/Devamachi and Arasali/ Masrur performed better than other clones, whereas those from Kulagi/ Amga showed lower growth, underscoring the importance of matching germplasm with ecological conditions. The estimated total biomass ranged from 15.54 to 53.75 t ha<sup>-1</sup> with an overall mean of 39.79 t ha<sup>-1</sup>, indicating 3.5 fold variation among provenances. The findings provide critical insights for selecting and deploying high-performing teak clones in Karnataka and similar agro-climatic regions, contributing to enhanced productivity and sustainable clonal forestry.

**Keywords :** Teak, Clonal forestry, Genotype, Provenance, Genetic improvement

**T**EAK (*Tectona grandis* L. f.) popularly known as the 'King of Timbers', as the wood possess medium density, excellent dimensional stability, high mechanical strength and strong resistance against physical and biological degradation (Gunaga *et al.*, 2013). Its aesthetic appeal with attractive colour, grain and texture further enhances its global demand. The legacy of teak is well established for its exquisite furniture, crafted during the eighteenth century, signifying its timeless durability (Thulasidas *et al.*, 2008). The Teakwood is known to vary according to its geographical origin, ranging from golden brown

to darker streaked varieties, with Indian teak characterised by straight or wavy grains, oily feel and silica glistening. The wood's exceptional durability is attributed to active extractives in the heartwood such as polyphenols and quinines, which render resistance against termites, fungi and water penetration. These intrinsic properties make teak one of the most valuable and durable timbers in the tropics (Gunaga *et al.*, 2013).

The plantations of *Tectona grandis* are raised in long rotations of 80-100 years to produce longer logs with

high heartwood content and premium quality (Behera *et al.*, 2021). However, due to increasing demand, shorter rotations of 20-30 years are now widely practised in many tropical countries for sawn timber and veneer production. Today, such plantations are supported by superior planting stock and scientific silvicultural practices, to meet the growing timber requirements and provide sustainable livelihood opportunities in the humid and semi-humid tropics (Nayak *et al.*, 2015).

Teak clonal forestry has received considerable attention owing to its potential for enhancing productivity and timber quality in recent decades. The success of clonal plantations worldwide, particularly in Asia, has been facilitated by advances in vegetative propagation techniques that allow mass multiplication of selected superior genotypes (Monteuuis and Goh 1999). Unlike seedlings, which exhibit wide genetic variability, clonal plantations offer greater uniformity in growth, form and wood traits, thereby meeting the market demand for consistent timber quality. The empirical studies have demonstrated that clonal teak plantation achieve two to four fold enhancement in productivity compared to conventional seedling plantations, with MAI values reaching up to 10 m ha<sup>-1</sup> year<sup>-1</sup> under superior clonal material and improved silvicultural management. The clonal forestry is not without limitations. The deployment of a narrow genetic base leads to reduced adaptability and higher vulnerability to pests, diseases and climatic stresses (Kjaer and Foster 1996). Site × genotype interactions are also significant in teak, necessitating multi-location trials and careful evaluation before large-scale deployment (Goh and Monteuuis, 2005). Hence, clonal orchards and clonal trials play a dual role thereby serving as test beds for assessing growth performance of diverse clones under varied conditions and as sources of improved planting material for future plantations (Monteuuis *et al.* 2011).

Although, extensive research have been conducted on Teak growth, timber quality and clonal propagation of teak trees, the knowledge gaps remains elusive. The previous studies have focussed on the

performance of clones under controlled or experimental conditions, with limited long-term assessment of clone-wise growth variation in established plantations across provenances (Chaix *et al.* 2011). Also, the influence of provenance on growth and heartwood formation is recognized yet, the systematic evaluation of clone performance considering multiple growth and productivity parameters is limited for Indian conditions (Gunaga *et al.*, 2013).

Therefore, the present study was undertaken to address these gaps by evaluating the growth performance of teak clones established in a long-term clonal orchard at Haliyal, Karnataka. The study intends to systematically analysing clone-wise growth parameters and comparing performance across provenances. The study aims to provide practical insights for selecting superior clones for commercial plantations and enhancing timber quality.

#### MATERIAL AND METHODS

The present study was conducted in Teak (*Tectona grandis* L. f.) clonal seed orchard at Janganamatti, Haliyal taluk of Uttara Kannada district, Karnataka. The clonal orchard was established in the year 1982 in 15.36 hectare by the Karnataka Forest Department. The site lies within Northern Transitional zone of Karnataka and is classified under moist deciduous forest type. The region experiences 21-36 °C and receives an annual rainfall ranging from 904 mm to 3695 mm. The soil in the region is mainly clayey to lateritic with shallow depth.

The clonal seed orchard consisted of 49 teak clones collected from different provenances of Karnataka as given in Table 2. A total of 2401 ramets (49 ramets per clone), were originally planted and distributed across seven plots in a block planting design at 8 m × 8 m spacing. Each plot contained multiple ramets of all clones.

For statistical analysis, means of plot wise clone means were computed by averaging growth measurements of all surviving ramets of a given clone within each plot. Thus, for each clone, up to seven

plot level mean observations were obtained, resulting in a total of 343 plot wise clone means (49 clones  $\times$  7 plots). In instances where a clone had no surviving or measurable ramets in a particular plot due to long term mortality, such observations were excluded. Consequently, the number of plot wise observations per clone varied from 5 to 7. The plot level clone means were used as experimental units for statistical analysis to avoid pseudo replication arising from individual tree measurement.

The observations pertaining to growth parameters at tree level were recorded for attributes such as diameter at breast height (m) at 1.37 above ground level using caliper and tree height (m) using laser hypsometer. The volume was estimated using locally developed regression model for teak in Karnataka ( $V_t = 0.00120 \times D^{1.91671} \times H^{0.87021}$ ) (Tewari *et al.*, 2013). To assess the inter-relationships among clonal sources (provenances), a hierarchical cluster analysis was performed using Ward's minimum variance method and Euclidean distance as a similarity measure and the results were represented as a dendrogram. The Principal Component Analysis (PCA) was conducted to identify major contributing traits and visualise grouping patterns among provenances.

The above ground biomass for each provenance was estimated from the mean tree volume using a standard wood density value of 0.65 t m<sup>-3</sup>, commonly adopted for teak in peninsular India (Kaul *et al.*, 2011). The below-ground biomass (BGB) was derived as 26 per cent of AGB following the ratio proposed by MacDicken (1997). The total biomass (TB) was obtained as the sum of AGB and BGB. The resulting values were expressed on per hectare basis.

The data were subjected to descriptive statistical analysis to estimate mean, standard deviation and co-efficient of variation. The data were analysed following Completely Randomized Design (CRD), considering plot wise means as experimental units. The Analysis of Variance was carried out to test the significance of variation among clones, provenance and treatments means were compared using Tukey's HSD test at 5 per cent significant level. All the

statistical analysis were performed using R software (version 4.3.2) and results were cross validated to ensure computational accuracy.

## RESULTS AND DISCUSSION

The clone-wise performance of 44 year old clonal seed orchard data revealed significant variation in growth and yield attributes among the 49 evaluated teak clones. The tree height varied from 3.60 (MYSS1) to 7.86 m (MYHV5), while the diameter ranged from 0.23 m (MYSSI and MYHK3) to 0.36 m (MYHV1 and MYHUT9). The basal area extended from 0.040 m<sup>2</sup> (MYHK3) to 0.110 m<sup>2</sup> ((MYHUT9), whereas stem volume ranged from 0.130 m<sup>3</sup> (MYSSI and MYHK3) to 0.490 m<sup>3</sup> (MYHUT9). Based on overall performance, six clones (MYHV5, MYHUT8, MYHUT9, MYHUT7, MYMK2 and MYKB1) were identified as superior, consistently recording higher growth and biomass accumulation (Table 1). The superior performance of these clones may be attributed to better genetic vigour, site adaptability and efficient utilisation of site resources under prevailing environmental conditions (Gunaga *et al.*, 2013).

Although most clones exhibited comparatively lower growth performance, the clone MYVH5 emerged as exception, indicating local origin alone does not necessarily confer superior growth potential and that considerable genetic variability exists within local populations. Interestingly, several superior clones originated from central and southern regions characterised by relatively drier environments. Their enhanced performance at the present site suggests a high degree of adaptive plasticity and favourable genotype-environment interaction. The clustering of clones such as MYVH5, MYHUT8 and MYHUT7 with other high performing clones in multivariate analysis further supports their genetic similarity and consistent growth advantage. Overall, the observed differences among clones under uniform management conditions reflect inherent genetic variability, emphasising the importance of selecting and deploying superior clones to enhance productivity in teak plantations (Gunaga *et al.*, 2013). In contrast,

**TABLE 1**  
**Clone wise growth performance of *Tectona grandis* in the Clonal Orchard in Haliyal taluk**

| Clone | Clone Name | Source                    | N | Height (m)  | Diameter (m) | Basal Area (m <sup>2</sup> ) | Volume (m <sup>3</sup> ) |
|-------|------------|---------------------------|---|-------------|--------------|------------------------------|--------------------------|
| 1     | MYHD1      | Dandeli/ Barchi           | 6 | 5.83 ± 0.91 | 0.26 ± 0.02  | 0.06 ± 0.01                  | 0.21 ± 0.05              |
| 2     | MYHD2      | Dandeli/ Barchi           | 7 | 7.71 ± 0.75 | 0.27 ± 0.01  | 0.06 ± 0.01                  | 0.31 ± 0.05              |
| 3     | MYHD3      | Dandeli/ Barchi           | 7 | 5.43 ± 0.57 | 0.26 ± 0.03  | 0.06 ± 0.01                  | 0.23 ± 0.07              |
| 4     | MYHD4      | Dandeli/ Barchi           | 7 | 5.86 ± 0.40 | 0.27 ± 0.03  | 0.06 ± 0.01                  | 0.25 ± 0.05              |
| 5     | MYHV1      | Virnoli/ Hudsa            | 7 | 6.29 ± 0.84 | 0.36 ± 0.03  | 0.11 ± 0.02                  | 0.48 ± 0.12              |
| 6     | MYHV2      | Virnoli/ Hudsa            | 7 | 7.00 ± 1.02 | 0.29 ± 0.03  | 0.07 ± 0.01                  | 0.34 ± 0.08              |
| 7     | MYHV3      | Virnoli/ Hudsa            | 6 | 5.33 ± 0.92 | 0.27 ± 0.03  | 0.06 ± 0.01                  | 0.24 ± 0.10              |
| 8     | MYHV4      | Virnoli/ Hudsa            | 7 | 5.29 ± 0.68 | 0.34 ± 0.03  | 0.09 ± 0.02                  | 0.32 ± 0.06              |
| 9     | MYHV5      | Virnoli/ Veerampalli      | 7 | 7.86 ± 0.74 | 0.32 ± 0.02  | 0.08 ± 0.01                  | 0.44 ± 0.07              |
| 10    | MYHV6      | Virnoli/ Veerampalli      | 7 | 6.14 ± 0.59 | 0.28 ± 0.03  | 0.07 ± 0.01                  | 0.27 ± 0.06              |
| 11    | MYHV7      | Virnoli/ Veerampalli      | 6 | 6.83 ± 1.01 | 0.30 ± 0.04  | 0.08 ± 0.01                  | 0.36 ± 0.09              |
| 12    | MYS A1     | Arasali/ Masrur           | 7 | 5.57 ± 0.72 | 0.31 ± 0.03  | 0.08 ± 0.02                  | 0.31 ± 0.07              |
| 13    | MYS A2     | Arasali/ Masrur           | 7 | 6.43 ± 0.97 | 0.31 ± 0.05  | 0.08 ± 0.02                  | 0.41 ± 0.13              |
| 14    | MYSS1      | Sacrebailu/ Bommanalli    | 5 | 3.60 ± 0.60 | 0.23 ± 0.04  | 0.05 ± 0.01                  | 0.13 ± 0.05              |
| 15    | MYSS2      | Sacrebailu/ Bommanalli    | 6 | 6.67 ± 0.56 | 0.32 ± 0.02  | 0.08 ± 0.01                  | 0.38 ± 0.10              |
| 16    | MYHUT1     | Tithimathi/ Mallipatna    | 6 | 5.33 ± 0.92 | 0.24 ± 0.04  | 0.05 ± 0.01                  | 0.21 ± 0.06              |
| 17    | MYHUT2     | Tithimathi/ Mallipatna    | 7 | 5.57 ± 0.75 | 0.28 ± 0.03  | 0.07 ± 0.01                  | 0.27 ± 0.07              |
| 18    | MYHUT3     | Tithimathi/ Mallipatna    | 7 | 5.00 ± 0.69 | 0.26 ± 0.02  | 0.05 ± 0.01                  | 0.19 ± 0.05              |
| 19    | MYHUT4     | Tithimathi/ Mallipatna    | 7 | 6.00 ± 0.87 | 0.27 ± 0.03  | 0.06 ± 0.01                  | 0.28 ± 0.08              |
| 20    | MYHUT5     | Tithimathi/ Devamachi     | 7 | 6.29 ± 0.61 | 0.28 ± 0.01  | 0.06 ± 0.01                  | 0.26 ± 0.05              |
| 21    | MYHUT6     | Tithimathi/Devamachi      | 7 | 5.86 ± 0.67 | 0.33 ± 0.04  | 0.09 ± 0.02                  | 0.38 ± 0.10              |
| 22    | MYHUT7     | Tithimathi/Devamachi      | 6 | 6.50 ± 0.85 | 0.32 ± 0.04  | 0.09 ± 0.03                  | 0.43 ± 0.20              |
| 23    | MYHUT8     | Tithimathi/Muthagaddo     | 7 | 7.29 ± 0.71 | 0.33 ± 0.02  | 0.09 ± 0.01                  | 0.42 ± 0.07              |
| 24    | MYHUT9     | Tithimathi/Devamachi      | 5 | 6.20 ± 1.02 | 0.36 ± 0.05  | 0.11 ± 0.02                  | 0.49 ± 0.14              |
| 25    | MYKB1      | Balehonnuru/ Basavanakote | 7 | 6.71 ± 0.47 | 0.34 ± 0.02  | 0.09 ± 0.01                  | 0.41 ± 0.06              |
| 26    | MYKB2      | Balehonnuru/ Basavanakote | 7 | 5.86 ± 0.74 | 0.30 ± 0.03  | 0.07 ± 0.01                  | 0.31 ± 0.07              |
| 27    | MYKB3      | Balehonnuru/ Basavanakote | 7 | 6.00 ± 1.11 | 0.28 ± 0.04  | 0.07 ± 0.01                  | 0.33 ± 0.09              |
| 28    | MYKB4      | Balehonnuru/ Basavanakote | 6 | 6.17 ± 0.48 | 0.28 ± 0.05  | 0.07 ± 0.02                  | 0.30 ± 0.09              |
| 29    | MYKB5      | Balehonnuru/ Basavanakote | 7 | 6.14 ± 1.12 | 0.31 ± 0.04  | 0.08 ± 0.02                  | 0.42 ± 0.15              |
| 30    | MYBL1      | Lakkavalli                | 7 | 5.57 ± 0.84 | 0.31 ± 0.03  | 0.08 ± 0.01                  | 0.33 ± 0.08              |
| 31    | MYHAVB     | Virnoli                   | 7 | 6.14 ± 0.77 | 0.27 ± 0.02  | 0.06 ± 0.01                  | 0.25 ± 0.05              |
| 32    | MYHK1      | Kulagi/Amga               | 6 | 6.33 ± 0.33 | 0.27 ± 0.02  | 0.06 ± 0.01                  | 0.24 ± 0.02              |
| 33    | MYHK2      | Kulagi/Amga               | 5 | 5.80 ± 0.86 | 0.27 ± 0.03  | 0.06 ± 0.01                  | 0.26 ± 0.09              |
| 34    | MYHK3      | Kulagi/Amga               | 5 | 4.40 ± 0.40 | 0.23 ± 0.02  | 0.04 ± 0.01                  | 0.13 ± 0.03              |
| 35    | MYMK1      | Kakanakote/ Bylanakoppa   | 7 | 5.43 ± 0.61 | 0.28 ± 0.03  | 0.06 ± 0.01                  | 0.25 ± 0.07              |
| 36    | MYMK2      | Kakanakote/ Bylanakoppa   | 7 | 6.71 ± 0.81 | 0.32 ± 0.04  | 0.09 ± 0.02                  | 0.43 ± 0.12              |
| 37    | MYMK3      | Kakanakote/ Bylanakoppa   | 7 | 5.86 ± 0.99 | 0.30 ± 0.05  | 0.08 ± 0.02                  | 0.37 ± 0.11              |

Continued....

TABLE 1 Continued....

| Clone | Clone Name | Source                  | N | Height (m)  | Diameter (m) | Basal Area (m <sup>2</sup> ) | Volume (m <sup>3</sup> ) |
|-------|------------|-------------------------|---|-------------|--------------|------------------------------|--------------------------|
| 38    | MYMK4      | Kakanakote/ Bylanakoppa | 7 | 7.00 ± 1.09 | 0.29 ± 0.03  | 0.07 ± 0.01                  | 0.36 ± 0.09              |
| 39    | MYMK5      | Kakanakote/ Bylanakoppa | 6 | 5.83 ± 0.70 | 0.34 ± 0.04  | 0.10 ± 0.03                  | 0.40 ± 0.14              |
| 40    | MYMK6      | Kakanakote/ Bylanakoppa | 5 | 5.80 ± 0.58 | 0.26 ± 0.03  | 0.06 ± 0.01                  | 0.22 ± 0.05              |
| 41    | MYHUN1     | Nagarahole              | 5 | 7.20 ± 0.73 | 0.29 ± 0.02  | 0.07 ± 0.01                  | 0.33 ± 0.09              |
| 42    | MYHUN2     | Nagarahole              | 6 | 7.00 ± 0.58 | 0.31 ± 0.02  | 0.08 ± 0.01                  | 0.37 ± 0.06              |
| 43    | MYHUN3     | Nagarahole              | 7 | 6.14 ± 0.70 | 0.28 ± 0.02  | 0.06 ± 0.01                  | 0.27 ± 0.06              |
| 44    | MYHUN4     | Nagarahole              | 7 | 4.57 ± 0.75 | 0.26 ± 0.02  | 0.06 ± 0.01                  | 0.18 ± 0.06              |
| 45    | MYHUN5     | Nagarahole              | 6 | 5.67 ± 0.84 | 0.32 ± 0.03  | 0.08 ± 0.02                  | 0.33 ± 0.09              |
| 46    | MYKN1      | NR Pura                 | 6 | 6.83 ± 0.79 | 0.28 ± 0.03  | 0.07 ± 0.01                  | 0.33 ± 0.10              |
| 47    | MYCM1      | Muthodi                 | 6 | 4.33 ± 0.42 | 0.26 ± 0.03  | 0.06 ± 0.01                  | 0.18 ± 0.05              |
| 48    | MYCM2      | Muthodi                 | 7 | 6.14 ± 0.91 | 0.27 ± 0.02  | 0.06 ± 0.01                  | 0.27 ± 0.07              |
| 49    | MYCM3      | Muthodi                 | 7 | 6.43 ± 1.09 | 0.31 ± 0.05  | 0.09 ± 0.02                  | 0.42 ± 0.13              |

the clones such as MYSS1, MYHK3 and MYHUN4 exhibited relatively lower growth, possibly due to slower juvenile growth rate, of these clones coupled with higher sensitivity to micro-site variation and poorer crown development. These results suggest that selection and multiplication of superior clones like MYHV5, MYHUT8, MYHUT9, MYHUT7, MYMK2 and MYKB1 could substantially enhance productivity in teak plantations (Table 1).

The comparatively lower coefficient of variation for diameter indicated that radial growth remained relatively stable across clones, whereas height showed moderate variation, suggesting greater influence of site and micro-environmental factors on vertical growth (Pradeep and Murthy, 2023). Basal area exhibited higher variability than diameter, possibly due to differences in stand density, crown form and stem taper among clones. The highest variability was recorded for volume, which is expected since it integrates both height and diameter, thereby amplifying the combined effects of genetic and environmental interactions. Similar trends were also reported in teak improvement trials conducted in Odisha and Kerala, where higher variation was observed for height compared to diameter (Behera *et al.*, 2021 and Thulasidas *et al.*, 2008).

The correlation analysis revealed strong positive associations among all the growth traits (Table 2). The diameter depicted significant correlation with both the basal area ( $r=0.91$ ) and volume ( $r=0.91$ ), indicating that, radial growth contributes substantially to overall productivity in Teak. The height was also positively correlated with basal area ( $r=0.79$ ) and volume ( $r=0.79$ ), although its association with diameter ( $r=0.61$ ) was comparatively moderate. These relationships suggest that the diameter can be effectively used as a reliable proxy trait for predicting both basal area and volume in teak plantations. This is advantageous in operational breeding programmes, because the diameter at breast height

**TABLE 2**  
**Correlation matrix among growth traits of teak clones in the Clonal Orchard of Haliyal taluk**

| Trait 1                      | Trait 2                      | r    |
|------------------------------|------------------------------|------|
| Height (m)                   | Diameter (m)                 | 0.61 |
| Height (m)                   | Basal area (m <sub>c</sub> ) | 0.79 |
| Height (m)                   | Volume (m <sub>l</sub> )     | 0.79 |
| Diameter (m)                 | Basal area (m <sub>c</sub> ) | 0.91 |
| Diameter (m)                 | Volume (m <sub>l</sub> )     | 0.91 |
| Basal area (m <sub>c</sub> ) | Volume (m <sub>l</sub> )     | 0.91 |

(DBH) is simple to measure, less influenced by temporary environmental fluctuations and can serve as an early selection criterion for identifying superior clones (Monteuuis *et al.*, 2011). Since height growth tends to be more environment-sensitive compared to diameter growth, site-specific evaluation should accompany such selection to ensure stability of performance. Similar strong correlations between DBH and volume have been reported from teak clonal trials in different parts of India and Southeast Asia (Nayak *et al.*, 2015 and Saura *et al.*, 2023).

The hierarchical cluster analysis based on mean growth parameters (height, diameter, basal area and volume) grouped sixteen clone sources into distinct similarity clusters (Fig. 1). The dendrogram revealed three major clusters, indicating close genetic and phenotypic proximity among certain provenances. The first cluster mainly comprised sources such as Kakanakote/Bylanakoppa, Balehonnuru Basavanakote and Arasali/Masrur, which recorded comparatively higher mean values for height, diameter and volume, reflecting superior growth performance. The seconds

cluster included moderately performing sources like Virnoli/Veerampalli, Virnoli/Hudsa and Nagarahole, while the third cluster grouped the relatively low-performing provenances such as Muthodi and Sacrebailu/Bommanalli. The clear separation of clusters suggests that the variability among sources is not random but are structured which could be due to genetic differentiation and environmental adaptation of the original seed sources. Similar grouping patterns have also been reported by Thulasidas *et al.* (2008) and Behera *et al.* (2021), who observed distinct clustering of teak provenances in Kerala and Odisha based on growth and wood properties.

The Principal Component Analysis (PCA) was performed using the same growth parameters to further validate the cluster pattern and to visualise the contribution of each trait to provenance differentiation (Fig. 2). The first two principal components (PC and PC<sub>2</sub>) together explained over 82 per cent of total variation, signifying that most of the variability in the dataset was effectively captured by these two axes. PC showed strong positive loadings

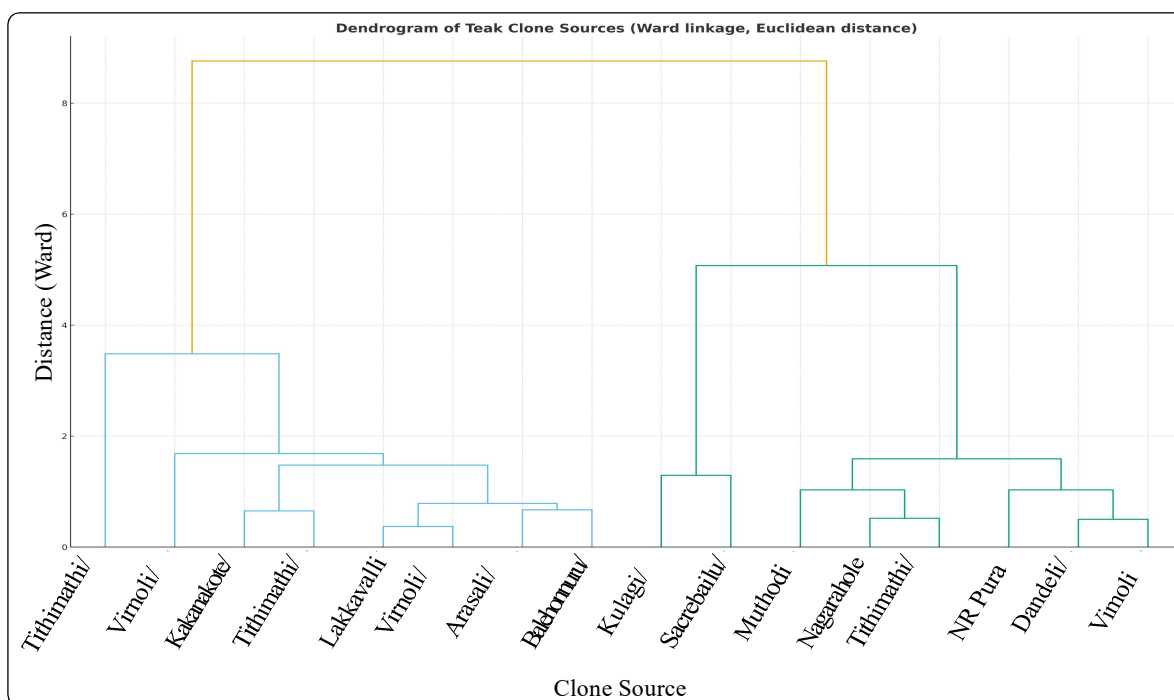


Fig. 1 : Hierarchical clustering of provenances (clonal sources) based on growth attributes in Teak

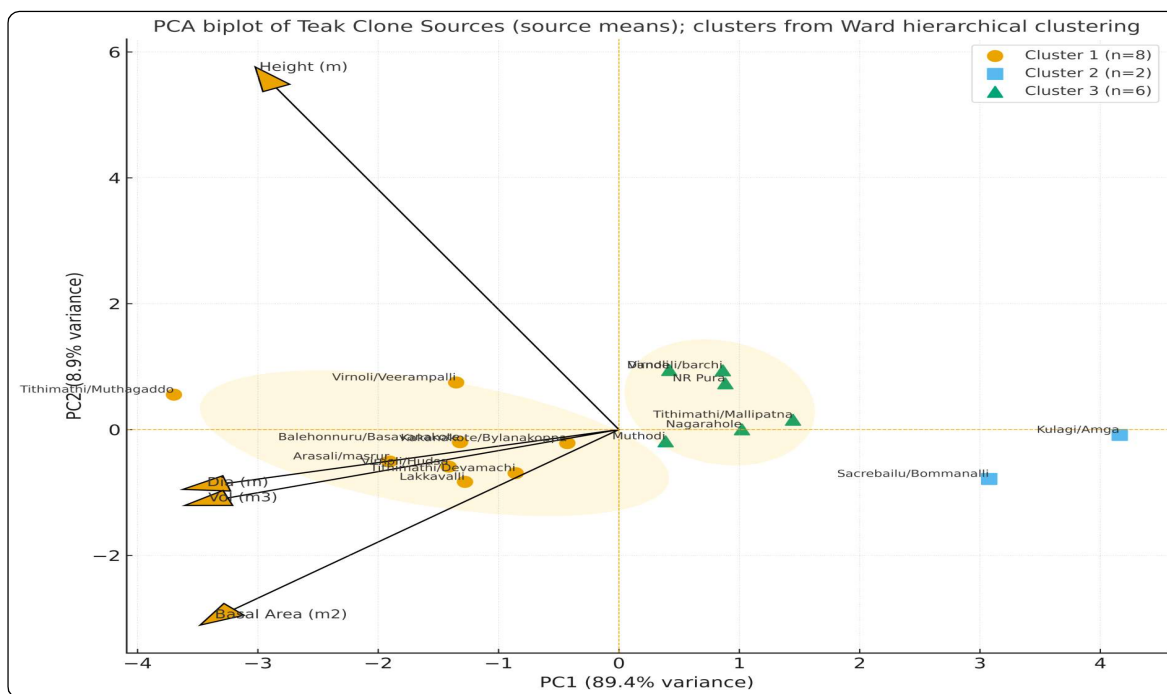


Fig. 2 : Principal Component Analysis biplot showing interrelationships among provenances based on growth traits in teak

for diameter, basal area and volume, indicating that these parameters were the major discriminating traits among clone sources. PC<sub>1</sub> was mainly influenced by height, representing the vertical growth component. The PCA biplot distinctly separated the high-performing provenances (Kakanakote/ Bylanakoppa, Balehonnuru/ Basavakote, Arasali/ Masrur) on the positive side of PC<sub>1</sub>, corresponding to their superior size attributes and total biomass accumulation. In contrast, the low-performing sources such as Muthodi and Sacrebailu/ Bommanalli were located on the opposite side, reflecting their comparatively weak performance across growth traits. The proximity of vectors for diameter, basal area and volume suggested strong positive inter-correlation among these variables, as typically observed in mature teak stands.

The provenance-wise clonal comparison (Table 3) revealed that the clones sourced from Tithimathi/ Muthagadda recorded the highest mean basal area (0.09 m<sup>2</sup>) and volume (0.56 m<sup>3</sup>), closely followed by Tithimathi/Devamachi (0.09 m<sup>2</sup> and 0.52 m<sup>3</sup>) and Arasali/ Masrur (0.08 m<sup>2</sup> and 0.49 m<sup>3</sup>). In contrast,

the lowest performance was observed in clones from Kulagi/Amga (0.05 m<sup>2</sup> and 0.30 m<sup>3</sup>). The superior growth of Tithimathi and Arasali sources may be attributed to their favourable genetic constitution and ecological compatibility with Haliyal, which falls within the moist deciduous belt of the Northern Transitional Zone in Karnataka. The relatively uniform performance among top-ranking sources indicates stable adaptability of these clones under local soil and climatic conditions. Conversely, the lower growth of Kulagi and Mallipatna sources could be associated with their origin from comparatively drier or edaphically constrained sites, where these clones may not express full growth potential under the high-moisture regimes. These results underline the importance of matching site and the source while deploying teak clones for large-scale planting. Similar findings have been reported by Nayak *et al.* (2015) and Behera *et al.* (2021), who observed that the teak provenances from moist zones tend to perform better when tested under humid environments.

The biomass estimates for clone sources revealed

**TABLE 3**  
**Provenance comparison of basal area and volume of teak clones in clonal orchard of Haliyal taluk**

| Clone Source               | N  | Basal area (m <sup>2</sup> ) | Volume (m <sup>3</sup> ) |
|----------------------------|----|------------------------------|--------------------------|
| Tithimathi / Muthagaddo    | 7  | 0.09 <sup>a</sup> ± 0.02     | 0.56 <sup>a</sup> ± 0.24 |
| Tithimathi / Devamachi     | 25 | 0.09 <sup>a</sup> ± 0.03     | 0.52 <sup>a</sup> ± 0.39 |
| Arasali / Masrur           | 14 | 0.08 <sup>a</sup> ± 0.03     | 0.49 <sup>a</sup> ± 0.34 |
| Virnoli / Veerampalli      | 20 | 0.08 <sup>a</sup> ± 0.03     | 0.48 <sup>a</sup> ± 0.24 |
| Balehonnuru / Basavanakote | 34 | 0.08 <sup>a</sup> ± 0.03     | 0.48 <sup>a</sup> ± 0.31 |
| Virnoli / Hudsa            | 27 | 0.08 <sup>a</sup> ± 0.03     | 0.48 <sup>a</sup> ± 0.31 |
| Kakanakote / Bylanakoppa   | 39 | 0.08 <sup>a</sup> ± 0.03     | 0.46 <sup>a</sup> ± 0.33 |
| Lakkavalli                 | 7  | 0.08 <sup>a</sup> ± 0.03     | 0.45 <sup>a</sup> ± 0.27 |
| NR Pura                    | 6  | 0.07 <sup>a</sup> ± 0.04     | 0.44 <sup>a</sup> ± 0.32 |
| Muthodi                    | 20 | 0.07 <sup>a</sup> ± 0.03     | 0.40 <sup>a</sup> ± 0.32 |
| Nagarahole                 | 31 | 0.07 <sup>a</sup> ± 0.02     | 0.40 <sup>a</sup> ± 0.23 |
| Sacrebailu / Bommanalli    | 11 | 0.07 <sup>a</sup> ± 0.03     | 0.36 <sup>a</sup> ± 0.29 |
| Dandeli / Barchi           | 27 | 0.06 <sup>a</sup> ± 0.01     | 0.35 <sup>a</sup> ± 0.19 |
| Virnoli                    | 7  | 0.06 <sup>a</sup> ± 0.02     | 0.34 <sup>a</sup> ± 0.17 |
| Tithimathi / Mallipatna    | 27 | 0.06 <sup>a</sup> ± 0.02     | 0.33 <sup>a</sup> ± 0.22 |
| Kulagi / Amga              | 16 | 0.05 <sup>a</sup> ± 0.02     | 0.30 <sup>a</sup> ± 0.17 |

substantial variation, with above-ground biomass (AGB) ranging from 12.33 t ha<sup>-1</sup> (Sacrebailu/Bommanalli) to 42.66 t ha<sup>-1</sup> (Kakanakote/Bylanakoppa), while below-ground biomass (BGB) varied from 3.21 t ha<sup>-1</sup> to 11.09 t ha<sup>-1</sup> and total biomass (TB) ranged from 15.54 t ha<sup>-1</sup> to 53.75 t ha<sup>-1</sup> (mean AGB 31.58 t ha<sup>-1</sup>; mean BGB 8.21 t ha<sup>-1</sup>; mean TB 39.79 t ha<sup>-1</sup>). The coefficient of variation (34.12 %) was identical across AGB, BGB and TB, indicating that the relative variability is similar in all biomass compartments. The highest-performing provenance (Kakanakote/Bylanakoppa) exhibited roughly 1.35 times the mean AGB, whereas the lowest (Sacrebailu/Bommanalli) recorded only about 0.39 times the mean values (Table 4). Such magnitude of variation suggested clear provenance-wise differences in biomass accumulation. The critical difference at 5 percent (AGB = 13.63 t ha<sup>-1</sup>; BGB = 3.54 t ha<sup>-1</sup>; TB = 17.17 t ha<sup>-1</sup>) indicated that the differences between the extreme sources are statistically meaningful, though

smaller contrasts among mid-range provenances may not be significant. These findings align with Buvanewaran *et al.* (2006) showing provenance or site-specific biomass variation.

The present study revealed substantial genetic and phenotypic variability among the 49 teak (*Tectona grandis* L.f.) clones and their respective provenance sources evaluated under uniform site and management conditions at Janganamatti, Haliyal taluk, Uttara Kannada district of Karnataka. The consistently superior performance of clones such as MYHV5, MYHUT9, MYMK2 MYHUT7, MYHUT8 and MYKB1 and provenance sources like Kakanakote/Bylanakoppa, Balehonnuru/Basavana kote and Arasali/Masrur, reflected high adaptability and genetic vigour under the moist deciduous conditions. The strong positive correlations among diameter, basal area and volume confirmed that diameter at breast height (DBH) serves as a reliable and efficient indicator trait for early selection of

**TABLE 4**  
**Source wise mean aboveground biomass (AGB), belowground biomass (BGB) and total biomass (TB)**  
**of Teak clones in clonal orchard at Haliyal taluk**

| Clone Source               | AGB (t ha <sup>-1</sup> ) | BGB (t ha <sup>-1</sup> ) | TB (t ha <sup>-1</sup> ) |
|----------------------------|---------------------------|---------------------------|--------------------------|
| Kakanakote / Bylanakoppa   | 42.66                     | 11.09                     | 53.75                    |
| Balehonnuru / Basavanakote | 38.42                     | 9.99                      | 48.41                    |
| Arasali / Masrur           | 38.01                     | 9.88                      | 47.89                    |
| Virnoli / Veerampalli      | 36.16                     | 9.4                       | 45.56                    |
| Virnoli / Hudsa            | 33.79                     | 8.79                      | 42.58                    |
| Nagarahole                 | 33.27                     | 8.65                      | 41.92                    |
| NR Pura                    | 32.29                     | 8.4                       | 40.69                    |
| Dandeli / Barchi           | 31.89                     | 8.29                      | 40.18                    |
| Tithimathi / Devamachi     | 30.37                     | 7.9                       | 38.27                    |
| Kakanakote / Bylanakoppa   | 29.88                     | 7.76                      | 37.64                    |
| Balehonnuru / Basavanakote | 29.1                      | 7.57                      | 36.67                    |
| Lakkavalli                 | 25.66                     | 6.67                      | 32.33                    |
| Kulagi / Amga              | 24.85                     | 6.46                      | 31.31                    |
| Tithimathi / Mallipatna    | 24.52                     | 6.38                      | 30.9                     |
| Muthodi                    | 18.19                     | 4.73                      | 22.92                    |
| Sacrebailu / Bommanalli    | 12.33                     | 3.21                      | 15.54                    |
| Mean                       | 31.58                     | 8.21                      | 39.79                    |
| CV (%)                     | 34.12                     | 34.12                     | 34.12                    |
| CD (5%)                    | 13.63                     | 3.54                      | 17.17                    |

superior clones in teak breeding programmes. The multivariate analyses through cluster and principal component approaches substantiated the structured genetic variation among sources, highlighting the dominance of radial growth traits in explaining total variability. The grouping pattern of clones in the dendrogram and PCA biplot reaffirmed the existence of distinct provenance based divergence, which can guide region-specific deployment and hybridisation strategies. The pronounced differences in biomass accumulation across sources, with 3.5 fold variation between extremes, underline the significant potential for enhancing productivity through selection of high-biomass genotypes. These results establish a clear basis for identifying elite teak clones and provenance groups suited to the ecological conditions of the region.

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