



International Journal of Research in Agronomy

E-ISSN: 2618-0618
P-ISSN: 2618-060X
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NAAS Rating (2026): 5.20
www.agronomyjournals.com
2026; 9(7): 1637-1643
Received: 11-05-2026
Accepted: 15-06-2026

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Screening Teak (*Tectona grandis* L.f.) clones for variation and resistance to *Loranthus* infestation at the Manchikere clonal seed orchard, Karnataka, India

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DOI: <https://www.doi.org/10.33545/2618060X.2026.v9.i7u.6174>

Abstract

Loranthus (*Dendrophthoe falcata* var. *pubescens*) is a destructive aerial hemiparasitic plant that adversely affects the growth, vigour and productivity of teak (*Tectona grandis* L.f.) plantations and clonal seed orchards. Identification of resistant genotypes is essential for developing sustainable management strategies and improving the genetic quality of planting material. The present study was conducted in the Manchikere Clonal Seed Orchard, Karnataka, India, to evaluate clonal variation in *Loranthus* infestation and identify resistant teak clones. A total of 525 ramets representing 24 teak clones were assessed during September 2024–September 2025 using the weighted infestation scoring system proposed by Gunaga *et al.* (2011). Clones were classified into resistant, tolerant, susceptible and highly susceptible categories based on the orchard mean and standard deviation of weighted infestation scores. Significant clonal variation was observed, with infestation ranging from 0 to 40.0% and weighted infestation scores varying from 0.0 to 60.0. One clone (MySA1) was identified as resistant, two clones (MySS2 and MyHaV1) as tolerant, nineteen clones as susceptible and two clones (MyHuT₆ and MyHuT₇) as highly susceptible. Significant differences were also observed among forest ranges ($P = 0.02$) and geographical regions ($P = 0.003$). Clones originating from the Southern region recorded the highest mean weighted infestation score (40.98 ± 13.16), whereas those from the Central region exhibited the lowest (14.93 ± 12.70). The results demonstrate substantial genetic variation in host response to *Loranthus* infestation and highlight the resistant clone MySA1 and the tolerant clones MySS2 and MyHaV1 as valuable genetic resources for resistance breeding, clonal selection and the establishment of healthier teak clonal seed orchards.

Keywords: *Tectona grandis*, *Dendrophthoe falcata*, clonal seed orchard, host resistance, genetic variation, mistletoe infestation

Introduction

Teak (*Tectona grandis* L.f.) is one of the most valuable tropical hardwood species in the world owing to its excellent timber quality, dimensional stability, natural durability and high economic value (Tewari, 1992) ^[9]. The species is naturally distributed in India, Myanmar, Thailand and Laos, but has been extensively introduced into tropical regions across Asia, Africa and Latin America because of its superior wood properties and adaptability to diverse environmental conditions (Tewari, 1992) ^[9]. The increasing global demand for quality teak timber has accelerated the establishment of plantations, creating a need for genetically superior planting material capable of sustaining high productivity, superior wood quality and enhanced adaptability.

Tree improvement programmes in teak have increasingly focused on the selection and deployment of elite genotypes through clonal forestry to maximize plantation productivity and genetic gain. Clonal seed orchards (CSOs) play a pivotal role in these programmes by producing genetically improved seed from selected parent trees while conserving superior genetic resources for future breeding (Gunaga *et al.*, 2011) ^[2]. Evaluation of clonal performance under field conditions enables the identification of superior genotypes with desirable growth, reproductive potential and adaptability, thereby improving the efficiency of breeding and seed production programmes (Gunaga *et al.*, 2011) ^[2].

Despite considerable progress in teak genetic improvement, the productivity of clonal seed orchards is frequently constrained by insect pests and parasitic plants that adversely affect tree growth, health and seed production (Gunaga *et al.*, 2011)^[2]. Among these biotic constraints, mistletoes belonging to the family Loranthaceae are recognized as one of the most destructive aerial hemiparasitic plants in tropical forests and plantations (Watson, 2001)^[10]. These parasites establish haustorial connections with host branches to extract water and mineral nutrients while retaining their own photosynthetic capability, while their seeds are primarily dispersed by birds, facilitating rapid colonization of susceptible host trees within plantations and seed orchards (Watson, 2001)^[10].

In teak, *Loranthus* infestation diverts water and nutrients from infected branches, resulting in branch dieback, reduced crown development, poor reproductive performance and progressive decline in tree vigour (Gunaga *et al.*, 2011; Watson, 2001)^[2, 10]. Infestation has been reported to reduce diameter increment by (37–42%), highlighting its substantial economic impact on plantation productivity (Ghosh *et al.*, 1983)^[1]. Surveys conducted in teak plantations of Dandeli Province, Karnataka, recorded *Loranthus* infestation ranging from (10.88 to 23.35%) across different age classes of plantations (Hanumantha *et al.*, 2010)^[3]. Similarly, a survey conducted in a 42-year-old teak clonal seed orchard at Waghai, Gujarat, revealed that (21.76%) (47 of 216) ramets were infested, whereas (78.24%) remained healthy, and only one clone was completely free from *Loranthus* infestation, demonstrating considerable inter-clonal variation in susceptibility (Singh *et al.*, 2017)^[8].

Evidence accumulated over the past decade indicates that susceptibility to *Loranthus* varies considerably among teak clones, suggesting that host genotype plays a major role in determining infestation levels (Gunaga *et al.*, 2011)^[2]. In Karnataka, Gunaga *et al.* (2011)^[2] reported significant clonal variation in *Loranthus* infestation and identified clones exhibiting comparatively lower infestation, although no clone exhibited complete resistance. Likewise, Singh *et al.* (2017)^[8] identified one resistant clone and several tolerant and susceptible clones in a teak clonal seed orchard in Gujarat. More recently, Muttaqin *et al.* (2025)^[7] demonstrated that differences in morphological traits among teak clones were associated with variation in mistletoe infestation, indicating that resistance-related characteristics can be incorporated as additional selection criteria in teak breeding programmes.

Although previous studies have confirmed the existence of clonal variation in *Loranthus* susceptibility, information remains limited for several established teak clonal seed orchards in southern India. Furthermore, long-term evaluations of mature seed orchards are essential because infestation intensity may vary with orchard age, environmental conditions and host–parasite interactions. Identification of resistant or tolerant clones would therefore contribute not only to improved orchard management but also to the development of genetically superior planting material for sustainable teak improvement programmes.

Therefore, the present study was undertaken to assess the extent of clonal variation in *Loranthus* infestation among teak genotypes maintained in the Manchikere Clonal Seed Orchard, Karnataka. The study also aimed to identify comparatively resistant and tolerant clones that could be utilized in future breeding programmes and integrated management strategies for enhancing the productivity and sustainability of teak clonal seed orchards.

Materials and Methods

Study Area

The investigation was conducted in the Manchikere Clonal Seed

Orchard (CSO) located in the Manchikere Forest Range of Yellapur Forest Division, Uttara Kannada District, Karnataka, India (14°51'34.1" N, 74°50'41.0" E). The orchard was established by the Karnataka Forest Department in 1980 for the production of genetically improved teak seed through clonal forestry. The plantation occupies approximately 4 ha and was established at a spacing of 8 × 8 m using grafted ramets of phenotypically superior teak trees selected from different forest divisions of Karnataka. The orchard represents diverse geographical origins, making it suitable for evaluating clonal variation in susceptibility to *Loranthus* infestation.

Experimental Material

The study was conducted using 24 teak clones maintained in the Manchikere Clonal Seed Orchard. These clones were originally selected from phenotypically superior trees representing different forest divisions of Karnataka and were established as grafted ramets in the orchard. The experimental material comprised 13 clones from the Haliyal Forest Division (Northern region), four clones from the Shivamogga Forest Division (Central region), six clones from the Hunsur Forest Division (Southern region), and one clone from the Mysore Forest Division (Southern region). Thus, the orchard represented three major geographical regions of Karnataka, providing an appropriate genetic base for evaluating clonal variation in *Loranthus* infestation. The clone identity, forest range, forest division and geographical origin of each genotype are presented in Table 1.

Assessment of *Loranthus* Infestation

Field assessment of *Loranthus* infestation was carried out through systematic visual inspection of all teak clones and their respective ramets maintained in the Manchikere Clonal Seed Orchard from September 2024 to September 2025. Each ramet was carefully examined from the lower branches to the upper crown for the presence of *Loranthus* (*Dendrophthoe falcata* var. *pubescens*). The number of mistletoe clumps attached to each ramet was recorded by direct counting. Based on the observed number of *Loranthus* clumps, every ramet was assigned an infestation score to quantify the severity of parasitism. The recorded data were subsequently pooled at the clonal level to compare infestation intensity among clones and to identify resistant, tolerant, susceptible and highly susceptible genotypes.

Infestation Scoring System

The severity of *Loranthus* infestation was assessed using the weighted scoring system described by Gunaga *et al.* (2011)^[2]. Each ramet was classified into one of six infestation categories according to the number of mistletoe clumps observed.

Category	Description	Score
H	Healthy tree (no <i>Loranthus</i> infestation)	0
A	One mistletoe clump	1
B	Two mistletoe clumps	2
C	Three mistletoe clumps	3
D	Four mistletoe clumps	4
E	More than five mistletoe clumps	5

The weighted infestation score for each clone was calculated by multiplying the number of ramets in each category by the corresponding score and summing the values across all categories. This weighted score represented the overall infestation intensity of each genotype.

Classification of Clone Resistance

The weighted mean infestation score was computed for each

clone, and the overall orchard mean ($\bar{x}$) and standard deviation (SD) of the weighted scores were calculated. Based on the procedure described by Gunaga *et al.* (2011) [2] and subsequently adopted by Singh *et al.* (2017) [8], the clones were classified into four reaction categories as follows:

Reaction	Criterion
Resistant (R)	No ramets infested (Weighted score = 0)
Tolerant (T)	Clonal mean < (Orchard mean - 1 SD)
Susceptible (S)	(Orchard mean - 1 SD) $\leq$ Clonal mean $\leq$ (Orchard mean + 1 SD)
Highly Susceptible (HS)	Clonal mean > (Orchard mean + 1 SD)

This classification was used to categorize the evaluated clones according to their relative resistance or susceptibility to *Loranthus* infestation and to identify promising genotypes for future breeding and clonal seed orchard management.

Statistical Analysis

The infestation data recorded for individual ramets were compiled and analysed using Microsoft Excel. The weighted infestation score for each clone was calculated following the procedure described by Gunaga *et al.* (2011) [2]. Based on the weighted scores, the orchard mean and standard deviation were computed, and the clones were classified into Resistant, Tolerant, Susceptible and Highly Susceptible categories. One-way analysis of variance (ANOVA) was performed to determine significant differences in weighted infestation scores among clones, clonal source (forest range) and geographical regions. Homogeneity of variances was assessed using Bartlett's test prior to ANOVA.

Results and Discussion

Clonal variation in *Loranthus* infestation

A total of 525 ramets representing 24 teak clones were evaluated for *Loranthus* infestation in the Manchikere Clonal Seed Orchard. Considerable clonal variation was observed in the incidence of *Loranthus* among the evaluated clones (Table 2). The proportion of healthy ramets varied from (60.0%) in MyHuT₆ to (100.0%) in MySA1, whereas total infestation ranged from 0 to 40.0%. The weighted infestation scores also exhibited wide variation, ranging from 0.0 in MySA1 to 60.0 in MyHuT₆ (Table 3). Based on the weighted infestation score, one clone (MySA1) was classified as resistant, two clones (MySS2 and MyHaV1) as tolerant, nineteen clones as susceptible, and two clones (MyHuT₆ and MyHuT₇) as highly susceptible, indicating substantial genetic variation in the response of teak clones to *Loranthus* infestation.

The present findings are in close agreement with those of Gunaga *et al.* (2011) [2], who reported marked clonal variation in *Loranthus* infestation among 24 teak clones in the Karka Clonal Seed Orchard. In their study, 142 out of 625 ramets (22.72%) were infested with *Loranthus*, while clone-wise infestation ranged from (3.8%) in MySS1 to (48.1%) in MyHaV2. Similarly, the weighted infestation score varied from 3.8 to 85.2, reflecting substantial differences in susceptibility among clones. The present investigation recorded a comparable pattern of variation, although the maximum infestation (40.0%) and weighted infestation score (60.0) were lower than those reported by Gunaga *et al.* (2011) [2]. The occurrence of clones with no infestation together with highly infested clones in both studies clearly demonstrates that susceptibility to *Loranthus* is strongly influenced by genotype.

Comparable levels of *Loranthus* infestation have also been reported under plantation conditions in Karnataka. Hanumantha *et al.* (2010) [3] observed infestation ranging from (10.88 to

23.35%) in teak plantations of different age classes. In the present study, infestation among individual clones ranged from (0 to 40.0%). While several clones exhibited infestation levels within the range reported by Hanumantha *et al.* (2010) [3], clones such as MyHuT₆ (40.0%) showed substantially higher infestation, indicating pronounced clonal differences in susceptibility under clonal seed orchard conditions.

The present observations are further supported by Singh *et al.* (2017) [8], who evaluated 216 ramets representing 18 teak clones in the Waghai Clonal Seed Orchard, Gujarat, and reported that 47 ramets (21.76%) were infested, whereas 169 ramets (78.24%) remained healthy. Their study also identified one resistant, one tolerant, eleven susceptible and five highly susceptible clones, confirming considerable genetic variability in resistance to *Loranthus*. Although the proportion of susceptibility classes differed slightly from the present investigation, both studies consistently demonstrate that the response of teak to *Loranthus* infestation is largely genotype dependent.

The observed clonal variation may be attributed to inherent differences in host characteristics that influence parasite establishment and development. Successful establishment of *Loranthus* depends not only on seed dispersal by birds but also on the ability of the parasite to penetrate host tissues and establish functional haustoria connections. Variations in bark characteristics, branch architecture, canopy structure and physiological traits among teak clones may therefore influence parasite establishment and survival. A similar explanation was proposed by Gunaga *et al.* (2011), who suggested that biochemical and anatomical characteristics of the host may contribute to differential resistance against *Loranthus*.

From a tree improvement perspective, the identification of MySA1 as a resistant clone and MySS2 and MyHaV1 as tolerant clones provides valuable genetic resources for future breeding and clonal seed orchard programmes. Conversely, highly susceptible clones such as MyHuT₆ and MyHuT₇ should be subjected to regular monitoring and timely removal of *Loranthus* to minimize parasite spread and maintain orchard productivity.

Variation in *Loranthus* infestation among forest ranges

Significant variation in *Loranthus* infestation was observed among teak clones originating from different forest ranges (Table 4). The mean weighted infestation score varied from 9.50 ± 0.00 in clones from Sacrebyle forest range to 43.15 ± 12.84 in clones from Thithimathi forest range. Clones from Virnoli (33.83 ± 2.84), Kulagi (31.60 ± 8.66) and Barchi (30.28 ± 5.19) also recorded relatively higher infestation, whereas those from Arasakre (14.30 ± 20.22), Gundvamoli (20.33 ± 3.22), Bhadravati (21.60 ± 0.00) and Kakanakote (27.30 ± 0.00) exhibited comparatively lower infestation. Analysis of variance indicated significant differences among forest ranges ($P = 0.02$), suggesting that the source forest range significantly influenced the level of *Loranthus* infestation.

The present findings are comparable with those of Gunaga *et al.* (2011), who also reported significant variation in *Loranthus* infestation among teak clones originating from different forest ranges of Karnataka. In their study, the mean weighted infestation score ranged from 5.90 in Sacrebyle to 60.73 in Gundvamoli, representing a difference of 54.83 units between the least and most susceptible forest ranges. In the present investigation, the corresponding values ranged from 9.50 ± 0.00 in Sacrebyle to 43.15 ± 12.84 in Thithimathi, a difference of 33.65 units. Compared with Gunaga *et al.* (2011), the minimum infestation score in the present study was higher (9.50 vs. 5.90), whereas the maximum score was lower (43.15 vs. 60.73), indicating a

narrower range of variation among forest ranges. Nevertheless, both studies consistently demonstrated significant differences in *Loranthus* infestation among forest ranges, confirming that the forest range of origin has a strong influence on host susceptibility. The lower mean weighted infestation recorded in Sacrebyle (9.50 ± 0.00) and Arasakre (14.30 ± 20.22), compared with the relatively higher values observed in Thithimathi (43.15 ± 12.84), Virnoli (33.83 ± 2.84) and Kulagi (31.60 ± 8.66), suggests substantial variation among forest ranges in their response to *Loranthus* infestation. Such differences may be attributed to genetic variation among the selected plus trees, influencing bark characteristics, canopy architecture, branch morphology and host defence mechanisms that affect parasite establishment. The consistent occurrence of significant variation among forest ranges in both the present investigation ($P = 0.02$) and the study of Gunaga *et al.* (2011) ^[2] highlights the importance of considering the forest range of origin while selecting superior clones for breeding programmes and clonal seed orchard establishment.

Variation in *Loranthus* infestation among geographical regions

Significant differences in *Loranthus* infestation were observed among teak clones originating from different geographical regions of Karnataka (Table 5). The mean weighted infestation score was highest in clones originating from the Southern region (40.98 ± 13.16), followed by the Northern region (24.90 ± 18.24), whereas clones from the Central region recorded the lowest infestation (14.93 ± 12.70). Analysis of variance indicated that the differences among geographical regions were statistically significant ($P = 0.003$), suggesting that the geographical origin of the clones significantly influenced their susceptibility to *Loranthus* infestation.

A similar regional trend was reported by Gunaga *et al.* (2011) ^[2], who compared *Loranthus* infestation among teak clones originating from different geographical regions of Karnataka. The authors reported mean weighted infestation scores of 43.20 for the Southern region, 35.88 for the Northern region, and 29.88 for the Central region, with the Southern region exhibiting the highest infestation. The present investigation showed the same overall pattern, with Southern-origin clones recording the greatest infestation (40.98), followed by Northern (24.90) and Central (14.93) clones. Although the absolute infestation scores differed between the two studies, both consistently identified the Southern region as the most susceptible source of teak clones.

The lower infestation observed in Central-region clones compared with those from the Southern region suggests that geographical origin may influence host resistance through differences in the genetic composition of source populations. The nearly 2.7-fold higher weighted infestation score recorded in Southern-origin clones (40.98) compared with Central-origin clones (14.93) indicates substantial regional variation in susceptibility. Similar regional variation reported by Gunaga *et al.* (2011) ^[2] further supports the existence of geographical differences in resistance to *Loranthus* among teak populations in Karnataka.

The observed regional differences may reflect long-term adaptation of teak populations to their native environments, resulting in variation in morphological and physiological characteristics that influence parasite establishment. Differences in canopy architecture, branch characteristics, bark properties and

host defence mechanisms among geographical populations may affect the successful establishment and development of *Loranthus*. From a breeding perspective, the relatively lower infestation observed in Central-region clones indicates that these populations may provide useful genetic material for selecting *Loranthus*-resistant planting stock, whereas highly susceptible Southern-origin clones require careful monitoring and management when incorporated into clonal seed orchards.

Classification of resistant and susceptible teak clones

The classification of teak clones based on weighted *Loranthus* infestation scores revealed clear differences in their response to the parasite (Table 6). Of the 24 clones evaluated, one clone (MySA1) was classified as resistant, two clones (MySS2 and MyHaV1) as tolerant, nineteen clones as susceptible, and two clones (MyHuT₆ and MyHuT₇) as highly susceptible. The resistant clone remained free from *Loranthus* infestation throughout the assessment period, whereas the highly susceptible clones recorded the highest weighted infestation scores, indicating a wide range of host responses within the clonal seed orchard.

A comparable classification pattern was reported by Gunaga *et al.* (2011) ^[2] in the Karka Clonal Seed Orchard, where screening of 24 teak clones identified one resistant clone, one tolerant clone, nineteen susceptible clones and three highly susceptible clones based on weighted infestation scores. Likewise, Singh *et al.* (2017) ^[8] classified 18 teak clones into one resistant, one tolerant, eleven susceptible and five highly susceptible categories. The close agreement among these independent studies, conducted under different agro-climatic conditions, demonstrates that resistance to *Loranthus* is consistently expressed in only a small proportion of teak clones, while the majority remain susceptible to varying degrees.

Although the proportion of resistant and highly susceptible clones differed slightly among studies, the overall trend remained remarkably consistent. The present investigation identified (8.3%) of the evaluated clones (2 of 24) as resistant or tolerant, whereas (91.7%) were classified as susceptible or highly susceptible. Similarly, Gunaga *et al.* (2011) ^[2] reported (8.3%) resistant or tolerant clones (2 of 24) and (91.7%) susceptible or highly susceptible clones, while Singh *et al.* (2017) ^[8] reported (11.1%) resistant or tolerant clones (2 of 18) and (88.9%) susceptible or highly susceptible clones. These findings indicate that natural resistance to *Loranthus* is relatively uncommon in teak germplasm and highlight the importance of systematic screening programmes for identifying resistant planting material. The occurrence of resistant and tolerant clones within the present population suggests that sufficient genetic variability exists for improving *Loranthus* resistance through selection and clonal propagation. Resistant clones such as MySA1 can serve as potential candidates for future breeding programmes and for establishing healthier clonal seed orchards, thereby reducing economic losses associated with mistletoe infestation. Conversely, highly susceptible clones such as MyHuT₆ and MyHuT₇ require regular monitoring and timely removal of *Loranthus* to minimize parasite spread and maintain orchard productivity. The consistent identification of resistant and susceptible clones across the present investigation and earlier studies emphasizes that resistance screening should form an integral component of teak improvement programmes.

Table 1: Clonal I.D., Clonal number and Forest range of the Teak clones considered for the study

Clone number	Clone I. D	Forest Range	Forest Division	Geographical zone
1	MyHaD ₁	Barchi	Haliyal	Northern
2	MyHaD ₂	Barchi	Haliyal	Northern
3	MyHaD ₃	Barchi	Haliyal	Northern
4	MyHaD ₄	Barchi	Haliyal	Northern
5	MyHaV ₁	Gundvamoli	Haliyal	Northern
7	MyHaV ₃	Gundvamoli	Haliyal	Northern
8	MyHaV ₄	Gundvamoli	Haliyal	Northern
9	MyHaV ₅	Virnoli	Haliyal	Northern
10	MyHaV ₆	Virnoli	Haliyal	Northern
11	MyHaV ₇	Virnoli	Haliyal	Northern
13	MySA ₁	Arasakre	Shimoga	Central
14	MySA ₂	Arasakre	Shimoga	Central
16	MySS ₂	Sacrebyle	Shimoga	Central
17	MyHuT ₁	Thithimathi	Hunsur	Southern
18	MyHuT ₂	Thithimathi	Hunsur	Southern
19	MyHuT ₃	Thithimathi	Hunsur	Southern
22	MyHuT ₆	Thithimathi	Hunsur	Southern
23	MyHuT ₇	Thithimathi	Hunsur	Southern
24	MyHuT ₈	Thithimathi	Hunsur	Southern
31	MyBL ₁	Bhadravati	Shimoga	Central
32	MyHaK ₁	Kulagi	Haliyal	Northern
33	MyHaK ₂	Kulagi	Haliyal	Northern
34	MyHaK ₃	Kulagi	Haliyal	Northern
37	MyMK ₃	Kakanakote	Mysore	Southern

Table 2: Variation among Teak Clones of Manchikere CSO for *Loranthus* infestation in percent infestation

Clone I. D	Total no. of ramets	Percent in different infestation category						
		Healthy	A	B	C	D	E	TI
MyHaD ₁	31	74.2	19.4	6.5	0.0	0	0.0	25.8
MyHaD ₂	33	69.7	21.2	9.1	0.0	0	0.0	30.3
MyHaD ₃	33	78.8	18.2	0	3.0	0	0.0	21.2
MyHaD ₄	50	78	18	2	0.0	2	0.0	22
MyHaV ₁	18	88.9	5.6	5.6	0.0	0	0.0	11.1
MyHaV ₃	19	84.2	10.5	5.3	0.0	0	0.0	15.8
MyHaV ₄	13	84.6	7.7	7.7	0.0	0	0.0	15.4
MyHaV ₅	16	81.3	12.5	0	6.3	0	0.0	18.7
MyHaV ₆	19	73.7	21.1	0	5.3	0	0.0	26.3
MyHaV ₇	15	66.7	33.3	0	0.0	0	0.0	33.3
MySA ₁	13	100	0	0	0.0	0	0.0	0
MySA ₂	21	81	14.3	0	4.8	0	0.0	19
MySS ₂	21	90.5	9.5	0	0.0	0	0.0	9.5
MyHuT ₁	14	78.6	14.3	7.1	0.0	0	0.0	21.4
MyHuT ₂	20	80	15	0	0.0	5	0.0	20
MyHuT ₃	10	70	20	10	0.0	0	0.0	30
MyHuT ₆	10	60	20	20	0.0	0	0.0	40
MyHuT ₇	19	73.7	15.8	0	5.3	0	5.3	26.3
MyHuT ₈	8	75	12.5	12.5	0.0	0	0.0	25
MyBL ₁	23	82.6	13	4.3	0.0	0	0.0	17.4
MyHaK ₁	41	75.6	14.6	7.3	2.4	0	0.0	24.4
MyHaK ₂	37	83.8	10.8	5.4	0.0	0	0.0	16.2
MyHaK ₃	30	70	26.7	0	3.3	0	0.0	30
MyMK ₃	11	72.7	27.3	0	0.0	0	0.0	27.3

Note*: The values are the percent ramets in different infestation categories

Table 3: Variation among Teak clones for *Loranthus* infestation based on weighted score

Clone I. D	Total no. of ramets	Weighted score					
		A	B	C	D	E	TI
MyHaD ₁	31	19.4	13	0	0	0	32.4
MyHaD ₂	33	21.2	18.2	0	0	0	39.4
MyHaD ₃	33	18.2	0	9.1	0	0	27.3
MyHaD ₄	50	18	4	0	8	0	30
MyHaV ₁	18	5.6	11.2	0	0	0	16.8
MyHaV ₃	19	10.5	10.6	0	0	0	21.1
MyHaV ₄	13	7.7	15.4	0	0	0	23.1
MyHaV ₅	16	12.5	0	18.8	0	0	31.3
MyHaV ₆	19	21.1	0	15.8	0	0	36.9
MyHaV ₇	15	33.3	0	0	0	0	33.3
MySA ₁	13	0	0	0	0	0	0
MySA ₂	21	14.3	0	14.3	0	0	28.6
MySS ₂	21	9.5	0	0	0	0	9.5
MyHuT ₁	14	14.3	14.2	0	0	0	28.5
MyHuT ₂	20	15	0	0	20	0	35
MyHuT ₃	10	20	20	0	0	0	40
MyHuT ₆	10	20	40	0	0	0	60
MyHuT ₇	19	15.8	0	15.8	0	26.3	57.9
MyHuT ₈	8	12.5	25	0	0	0	37.5
MyBL ₁	23	13	8.6	0	0	0	21.6
MyHaK ₁	41	14.6	14.6	7.3	0	0	36.5
MyHaK ₂	37	10.8	10.8	0	0	0	21.6
MyHaK ₃	30	26.7	0	10	0	0	36.7
MyMK ₃	11	27.3	0	0	0	0	27.3

Note*: Weighted score = % ramets X no. of *Loranthus* in that category

Table 4: Variation in *Loranthus* infestation among teak clones derived from different forest ranges based on weighted infestation score.

Forest Range	No. of. Ramets	<i>Loranthus</i> infestation
		Weighted score Mean $\pm$ SD
Barchi	147	30.28 $\pm$ 5.19
Gundvamoli	50	20.33 $\pm$ 3.22
Virnoli	50	33.83 $\pm$ 2.84
Arasake	34	14.30 $\pm$ 20.22
Sacrebyle	21	9.50 $\pm$ 0.00
Thithimathi	81	43.15 $\pm$ 12.84
Kulagi	108	31.60 $\pm$ 8.66
Kakanakote	11	27.30 $\pm$ 0.00
Bhadravati	23	21.60 $\pm$ 0.00
Mean		30.51
SEm ($\pm$)		2.17
F-ratio		0.724
P-level		0.02
C.V(%)		33.13

Values in the parenthesis are arc-sine transformations

Bartlett's test for the homogeneity of variances:
a. Total Weighted Score: Chi-square = 8.504 (d.f. 5) NS

Table 5: Variation in *Loranthus* infestation among teak clones sourced from different geographical zones

Geographical zones.	No. of. Ramets	<i>Loranthus</i> infestation
		Weighted score Mean $\pm$ SD
North	355	29.72 $\pm$ 7.18
Central	78	14.93 $\pm$ 12.70
South	92	40.98 $\pm$ 13.16
Mean		30.51
SEm ($\pm$)		2.14
F-ratio		7.322
P-level		0.003
C.V(%)		34.74

Bartlett's test for the homogeneity of variances:
a. Total Weighted Score: Chi-square = 3.331 (d.f. 2) NS

Table 6: Tolerant, Susceptible and highly susceptible clones of teak and their infestation status (weighted score)

Resistant	
MySA ₁	0
Tolerant Clones	
MySS ₂	9.5
MyHaV ₁	16.8
Susceptible Clones	
MyHaV ₃	21.1
MyBL ₁	21.6
MyHaK ₂	21.6
MyHaV ₄	23.1
MyHaD ₃	27.3
MyMK ₃	27.3
MyHuT ₁	28.5
MySA ₂	28.6
MyHaD ₄	30.0
MyHaV ₅	31.3
MyHaD ₁	32.4
MyHaV ₇	33.3
MyHuT ₂	35.0
MyHaK ₁	36.5
MyHaK ₃	36.7
MyHaV ₆	36.9
MyHuT ₈	37.5
MyHaD ₂	39.4
MyHuT ₃	40.0
Highly susceptible clones	
MyHuT ₇	57.9
MyHuT ₆	60.0

Conclusion

The present investigation demonstrated substantial clonal variation in *Loranthus* infestation among 24 teak clones evaluated in the Manchikere Clonal Seed Orchard. The infestation ranged from (0 to 40.0%), with weighted infestation scores varying from 0.0 to 60.0, indicating marked differences in susceptibility among clones. Based on the weighted infestation score, MySA₁ was identified as a resistant clone, based on the weighted infestation

score, MySA1 was identified as the resistant clone, MySS2 and MyHaV1 as tolerant clones, and MyHuT₆ and MyHuT₇ as highly susceptible clones.

Significant differences in infestation were also observed among forest ranges and geographical regions. Clones originating from the Southern region recorded the highest mean weighted infestation score (40.98 ± 13.16), whereas those from the Central region exhibited the lowest (14.93 ± 12.70), suggesting that the geographical origin of the planting material influences susceptibility to *Loranthus*.

The present findings are consistent with earlier reports by Gunaga *et al.* (2011) ^[2] and Singh *et al.* (2017) ^[8], which also demonstrated considerable genetic variation in resistance to *Loranthus* among teak clones. The identification of resistant and tolerant clones across independent studies indicates that resistance is a heritable and exploitable trait that can be incorporated into teak improvement programmes.

The resistant clone MySA1 and the tolerant clones MySS2 and MyHaV1 represent valuable genetic resources for clonal propagation, breeding and the establishment of healthier clonal seed orchards. Conversely, highly susceptible clones should be subjected to regular surveillance and timely removal of *Loranthus* to reduce parasite spread and maintain orchard productivity. Incorporating resistance screening into routine evaluation programmes will contribute to the development of productive and sustainable teak plantations.

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