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SEEDLING SUSCEPTIBILITY OF DIFFERENT LOBLOLLY PINE FAMILIES TO *LECANOSTICTA ACICOLA* IN BROWN SPOT NEEDLE BLIGHT-INFESTED PLOTS

by
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ABSTRACT

Lecanosticta acicola is a foliar pathogen that threatens loblolly pine plantations by impairing needle function, lowering photosynthesis, and increasing its vulnerability to environmental stresses, sometimes culminating in tree death. Effective control of this disease relies on understanding genetic resistance within pine populations. This study evaluated the susceptibility of seventeen loblolly pine families to *L. acicola* under a natural inoculum exposure in BSNB-infected plots. We quantified inter-family differences in disease severity and explored how the field environments shaped disease symptom expression and identified families with better tolerance and those that were susceptible. Our findings emphasize the genetic and environmental determinants of needle blight resistance and highlight promising genotypes for breeding programs, ultimately supporting the development of more resilient loblolly pine stands.

Keywords: Brown spot needle blight, loblolly pine, *Lecanosticta acicola*

INTRODUCTION

Loblolly pine (*Pinus taeda* L.) is the most widely planted timber species in the southeastern U.S., valued for its rapid growth and versatile wood products (Wakeley, 1970). However, its productivity is increasingly threatened by brown spot needle blight (BSNB), caused by the ascomycete *Lecanosticta acicola*, which has recently expanded its range and severity in commercial and natural stands worldwide (van der Nest et al., 2019). Infected needles exhibit small brown lesions that coalesce, leading to premature defoliation, reduced photosynthetic capacity, and under severe epidemics, stunted growth or mortality (Wakeley, 1970; Huang et al., 1995).

Genetic variation among host families often underpins differences in disease susceptibility and has been harnessed in breeding programs to develop resistant stock. Early work on fusiform rust (*Cronartium quercuum* f. sp. *fusiforme* Peck ex Hedgcock & N. R. Hunt) demonstrated striking family-level differences in infection rates and gall development, with heritability estimates indicating substantial genetic control (Kinloch & Stonecypher, 1969). More recent provenance trials have corroborated these findings, showing that controlled-pollinated and open-pollinated loblolly pine families differ significantly in survival, growth and resistance to fungal pathogens (McKeand et al., 2003; Devkota et al., 2019). Such studies highlight the potential of selecting superior genetic families to mitigate pathogen impacts.

Despite these previous research works, little is known about inter-family variation in susceptibility to *L. acicola* at the seedling stage. Seedlings represent the most vulnerable life stage, when rapid early growth coincides with immature defense systems, and differential survival here can shape stand composition and long-term yield. Therefore, this chapter investigates whether different genetic families of loblolly pine seedlings exhibit varying tolerance to *L.*

acicola. By measuring seedling height, root collar diameter, disease rating, and relative water content in field plots, we aim to (1) quantify family-level differences in BSNB severity, (2) relate physiological traits to disease response, and (3) identify candidate families for incorporation into targeted breeding programs.

MATERIALS and METHODS

Study Location

The study was conducted at Osko Forest, Cullman county. Cullman county is in North-Central Alabama. Its average temperature in summer often reaches the upper 80s °F (about 31-32 °C), and winters commonly drop into the lower 30s °F (around 0-2 °C). Annual rainfall typically ranges from about 50 to 55 inches (1270-1400 mm). Rainfall is relatively well-distributed throughout the year, though slightly heavier in late winter and spring months. Five plots (each having an area of ~2.23 acres) were set up for this experiment. Each plot is comprised of four subplots; a central subplot and three other subplots located on a bearing of 120°, 240°, and 360° from the center (RR25-01: Table 1, Figure 1)

Table 1. *Pinus taeda* families used for the study

Family code	Company
F1	Westervelt
F2	Westervelt
F3	Westervelt
F4	Westervelt
F5	Westervelt
F6	Westervelt
F7	IFCO
F8	IFCO
F9	IFCO
F10	IFCO
F11	IFCO
F12	Aborgen
F13	Aborgen
F14	Aborgen
F15	Aborgen
F16	Aborgen
F17	Aborgen

Seedlings

Bareroot seedlings of seventeen commercially grown loblolly pine families were obtained from Aborgen, Westervelt, and the International Forest Company (IFCO) for this study (Table 1). In January 2024, 2,550 seedlings (150 per family) were planted in 2.4-liter pots (1 trade gallon) with ProMix BX® peat-based potting mix (Premier Tech, Quebec, Canada). Seedlings were kept in a shade-house and watered weekly for 8 weeks to enable them to acclimate to the environment until they were deployed to the plots in March 2024.

Inoculation

The BSNB-infested plots had an adequate amount of infected needles that had fallen off the pine trees. These infected needles served as a natural inoculum source for healthy seedlings. The seedlings were deployed to the field randomly into the plots such that one seedling per family was represented on each subplot (Figure 1), resulting in 4 seedlings per family per plot, for a total of 340 seedlings across the five plots.

Measurements

Root collar diameter (RCD) and height measurements were taken monthly and recorded for all seedlings from March to November using a digital caliper and a meter ruler. Seedling RCD and height trajectories across families and treatments were used to distinguish lines that tolerate infection and maintain near-normal growth from those that simply show low disease and normal growth (Eckhardt et al., 2016; Walkinshaw and Barnett, 1998).

Relative water content (RWC), which measures the degree of water insufficiency or unsaturation in plant tissues was assessed on seedlings by taking fresh fascicles from each seedling in the center subplots of every plot. The fascicles were initially weighed to the nearest 0.01g (W_W) and then soaked in distilled water overnight, reweighed in the morning to obtain turgid weights (W_T), dried at 70 °C to equilibrium, and reweighed (W_D). Fascicle relative water content (RWC_F, %) will be determined by the equation:

$$RWC_F = [(W_W - W_D) / (W_T - W_D)] * 100$$

Figure 1. Seedlings deployed in the field in Osko Forest

Disease rating was assessed based on observation of symptoms such as chlorosis, mortality (necrosis or death of needles), infection (tiny black fruiting bodies of the fungus in dead spots or bands), and needle discoloration (presence of brown, tan, or gray lesions on the needles). These symptoms were matched on a five-point scale 0 to 4 i.e.: 0 - No visible symptom, fully healthy needles; 1 - slight infection, very few needles (< 10% chlorotic or bearing small lesions, no chlorosis); 2 - moderate infection, noticeable chlorotic and discrete brown or tan lesions (10-25% of foliage affected); 3 - severe infection, widespread needle discoloration and necrosis (affecting 25-50% of foliage); 4 - Very severe infection (>50% of needles severely necrotic or dead).

Statistical Analysis

Statistical analysis was performed using R version 4.3.1. The data was first checked for normality after which nonparametric tests were conducted to evaluate differences between measured parameters among families and plots. Mixed effects models were used to assess the relationship between RWC families and by plots. Statistical differences were considered significant at $p < 0.05$.

RESULTS

Assessment of seedling symptomatology after exposure

The healthy seedlings in the field started showing disease symptoms in the month of April, approximately a month after being deployed and this was first noticed on plot 10 in families F1, F3, F10 and F6. However, in the subsequent months throughout the exposure period, disease symptoms were noticed in various plots and seedling families. The mild symptoms observed were small necrotic spots of about 1-3 mm, tan to reddish-brown lesions, usually near the needle tip or along the midrib. A narrow yellow halo usually surrounds each spot, reflecting local toxin activity before full necrosis. Disease rating varied from 0 to 3, with no occurrence of disease rating of 4 recorded.

Table 2. Summary statistics of seedling height development by families

Family	Sample size(n)	Mean (cm)	Standard deviation	Minimum	Maximum
F1	163	44.87	11.45	20.07	66.00
F10	167	44.51	11.84	22.86	73.00
F11	160	44.51	12.14	23.37	72.30
F12	169	47.99	9.376	28.96	65.50
F13	176	47.08	11.13	23.00	69.00
F14	178	44.79	7.59	28.96	59.50
F15	171	44.50	7.51	26.16	64.00
F16	180	45.44	8.53	25.40	60.70
F17	179	44.71	7.82	26.67	64.40
F2	170	52.33	37.17	20.57	50.50
F3	154	49.72	9.80	26.67	73.00
F4	166	48.73	12.53	26.67	80.10
F5	155	45.34	12.04	24.00	80.00
F6	171	55.49	13.93	27.43	46.60
F7	170	44.47	12.19	20.83	69.00
F8	163	46.59	12.30	22.61	69.00
F9	162	52.92	15.57	25.4	56.42

Table 3. Summary statistics of seedling root collar diameter development by families.

Family	Sample size (n)	Mean (mm)	Standard deviation	Minimum	Maximum
F1	163	5.36	1.31	0.48	9.33
F10	167	5.58	1.53	2.39	11.00
F11	160	5.33	1.35	2.38	12.95
F12	169	5.70	1.02	3.53	8.36
F13	176	6.22	1.24	3.76	9.31
F14	178	6.19	1.52	3.54	12.45
F15	171	5.96	1.15	3.91	12.74
F16	180	6.01	1.38	3.46	10.52
F17	179	5.74	1.05	3.99	10.52
F2	170	5.63	1.18	3.00	9.27
F3	154	8.72	1.2	3.17	4.13
F4	166	6.16	1.49	3.09	9.90
F5	155	5.80	1.29	3.00	9.79
F6	171	5.84	1.33	3.40	12.43
F7	170	5.53	1.30	3.11	9.32
F8	163	5.47	1.27	3.01	9.00
F9	162	5.92	1.55	2.98	10.40

Seedling height and RCD variation across genetic families

The analysis revealed significant variation in mean seedling height across the evaluated pine families. Among the 17 families examined (Table 2), family F6 exhibited the highest average height (55.49 cm), followed by F9 (52.92 cm) and F2 (52 cm). In contrast, families F1, F10, F11, F14, F15, and F17 showed comparatively lower mean heights, each ranging between 44.47 cm and 44.87 cm. Despite similarities in their means, the standard deviations indicated differing levels of variability within these groups. Notably, family F3 (49.72 cm) and F4 (48.73 cm) also demonstrated moderate height performance. Minimum and maximum height values are further confirmed substantial within family variability, with family F9 showing a wide range from 25.4 cm to 56.42 cm and F2 from 20.57 cm to 50.50 cm. These findings suggest notable genetic influence on early seedling height, with potential implications for selection strategies focused on initial growth vigor.

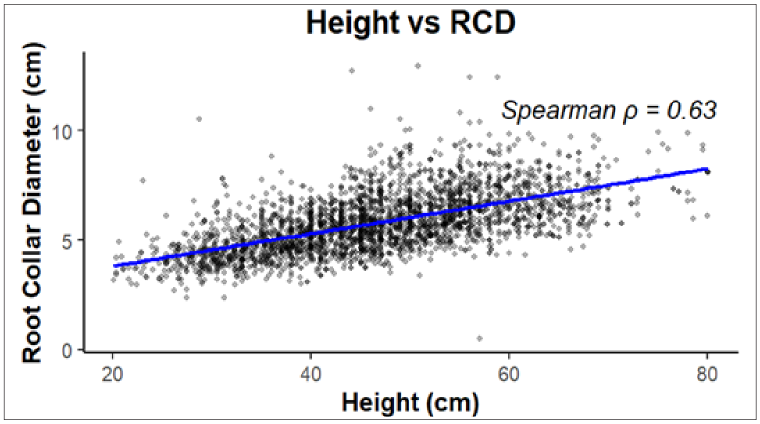

Figure 2. Relationship between height and RCD between pine seedlings across plots

Root collar diameter (RCD) measurements also varied across the evaluated families, indicating differences in stem development among genotypes. Family F3 recorded the highest mean RCD (M = 8.72 mm, SD = 1.30). Families F6 (5.83 mm), F9 (5.90 mm), and F5 (5.80 mm) followed closely in average RCD values. Conversely, families F12 (5.70 mm), F1 (5.37 cm), and F10 (5.59 mm) exhibited comparatively lower RCDs. While most families showed RCD means clustered between 5 mm and 6 mm, a few such as F3 stood out due to their elevated average. These differences point to potential variation in stem robustness and structural development among families at this early stage, which may influence future growth and mechanical stability (Table 3).

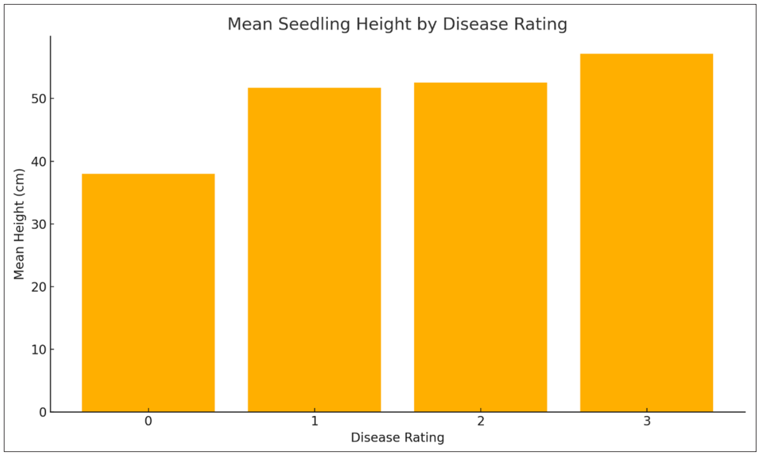

Figure 3. Relationship between height and disease between pine seedlings across plots

Disease severity trends among genetic families

Disease rating trends revealed relatively low average infection severity across families (Table 4), though some differences were observed. Family F11 reported the highest mean disease rating (0.69), followed closely by F10 (0.69) and F1 (0.64), indicating a slightly higher presence of moderate infection symptoms in those families. In contrast, family F13 exhibited the lowest mean disease rating (0.58), suggesting a relatively healthier status or greater resistance to early infection. Across all families, most seedlings scored between 0 and 2, with no consistent occurrence of severe infections (rating = 3). These results suggest a modest but measurable level of disease pressure, with some genetic lines displaying more favorable resistance profiles during early development.

Statistical comparison of seedling performance by families

Non-parametric Kruskal-Wallis tests were conducted to evaluate whether differences in height, RCD, and disease severity among families were statistically significant. Results showed that both height and RCD differed significantly across families ($p < 0.001$), confirming that genetic origin had a measurable effect on seedling growth traits. In contrast, no statistically significant difference was detected among families for disease rating ($p = 0.869$), indicating similar disease response patterns across genetic lines. To identify which families differed, post hoc pairwise comparisons using Dunn's test with Bonferroni correction were conducted for height and RCD (Tables 5 and 6). For height, multiple families showed significant differences, with families F6, F9, and F2 generally outperforming families such as F1, F10, and F15 (adjusted $p < 0.05$). Similar trends were observed in RCD comparisons, where families F13, F14, and F4 demonstrated significantly larger diameters compared to those with lower mean values. These pairwise comparisons reinforced the genetic influence on early seedling vigor and highlighted specific families with superior performance potential.

Variation in seedling performance across plots

Seedling growth and disease response exhibited notable variability across the five experimental plots (Table 7), highlighting the influence of localized environmental or management factors on early development. Plot 10 seedlings demonstrated the highest average seedling height (M = 50.6 cm, SD = 27.5), closely followed by plot 14 (M = 48.8 cm, SD = 12.3) and plot 11 (M = 48.0 cm, SD = 24.1). In contrast, plot 12 seedlings recorded the lowest mean height (M = 43.3 cm, SD = 19.3). This relationship possibly reflects how more open plot 10 is, with an increased seedling exposure to sunlight while plot 12 is unthinned, with tree crowns creating much shade and very low light exposure to the seedlings. Plot 13 seedlings showed an intermediate mean height (M = 45.8 cm), though still notably lower than plot 10 seedlings.

In terms of stem development, plot 14 seedlings had the highest mean RCD at 6.80 mm. More consistent and robust RCD measurements were observed in plot 10 seedlings (M = 6.16 mm, SD = 1.45) and plot 11 seedlings (M = 5.99 mm, SD = 1.35), while plot 12 seedlings again had the lowest mean RCD (M = 5.09 mm, SD = 0.98), indicating its relatively poor performance. Disease severity followed a similar pattern of spatial variability. Plot 14 seedlings exhibited the highest average disease rating (M = 0.762, SD = 0.754), followed closely by plot 13 seedlings (M = 0.731, SD = 0.76), suggesting increased susceptibility or localized disease pressure in these areas. In contrast, plots 11 (M = 0.579, SD = 0.632) and 12 (M = 0.552, SD = 0.656) recorded the lowest average disease scores, indicating comparatively healthier seedlings.

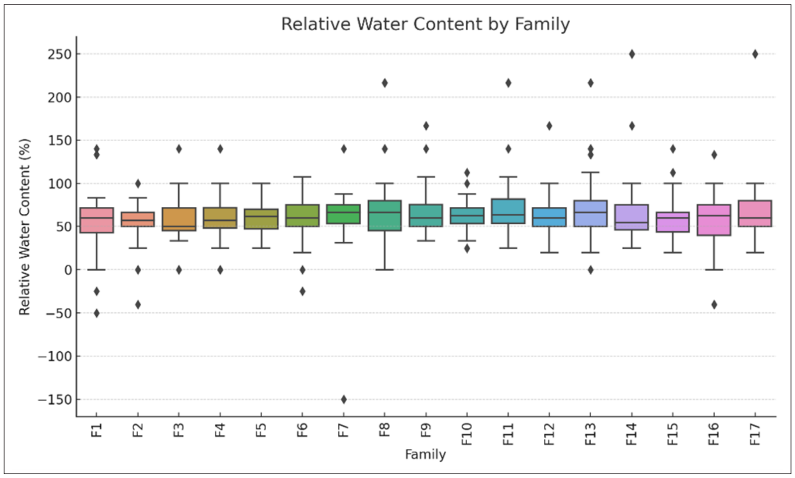

Figure 4A. Box plot showing RWC variation by families.

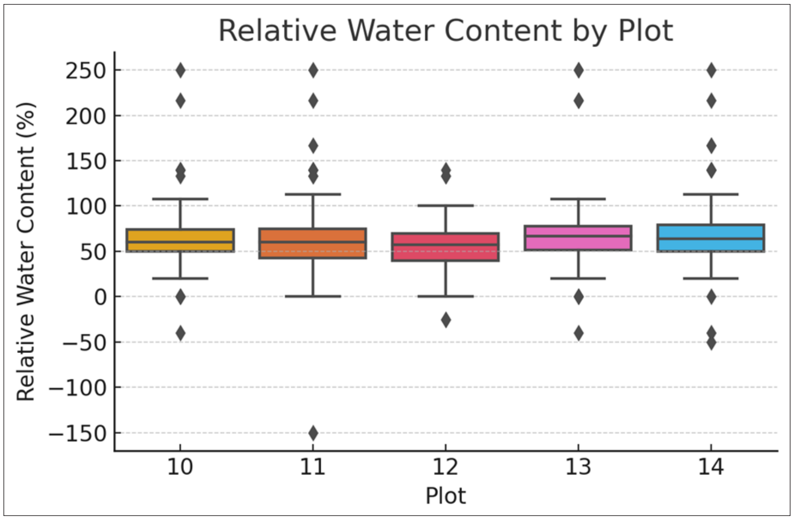

Figure 4B. Box plot showing RWC by plots.

To determine whether these observed differences were statistically significant, Kruskal-Wallis tests were performed for each variable across plots. The results confirmed that plot-level variation in seedling performance was significant for all three traits. Specifically, there was a strong effect of plot on height ($p < 0.001$) and RCD ($p < 0.001$), reinforcing the influence of site-specific factors on early growth. Although variation in disease severity was somewhat less pronounced, it was still statistically significant ($p < 0.001$), suggesting that spatial factors also play a role in disease development.

To further examine these differences, Dunn's post hoc comparisons were conducted using Bonferroni adjustments. For height, plot 12 differed significantly from all other plots ($p < 0.001$), consistently underperforming in terms of seedling growth. Plot 10 also differed significantly from plot 11 ($p = 0.032$), while plot 13 showed statistically lower height compared to both plot 10 and plot 12 ($p < 0.001$). No significant differences were observed between plots 10 and 14 or between plots 11 and 14, suggesting more comparable height performance in those groups. For RCD, plot 12 showed significantly smaller diameters than all other plots ($p < 0.001$). Plot 13 also had lower RCD values compared to plots 10, 11, and 14 ($p < 0.01$). Notably, plots 10, 11 and 14 did not differ significantly from each other, indicating consistent stem development across these locations.

Regarding disease severity, plot 14 showed significantly higher disease ratings compared to plots 11, 12, and 10 (adjusted $p < 0.05$), suggesting localized conditions favorable to disease expression. Plot 13 also differed significantly from plot 12 ($p < 0.001$), and marginally from plot 11 ($p = 0.029$), though differences with other plots were not statistically significant. These findings imply that, while environmental variability affected all measured traits, its influence was most strongly observed in growth-related parameters and to a lesser extent in disease development. Taken together, these results underscore the need to account for spatial heterogeneity when evaluating seedling performance in field studies. Differences in plot-level conditions can have a significant impact not only on growth metrics such as height and stem diameter, but also on disease dynamics, ultimately influencing genetic evaluations and selection outcomes.

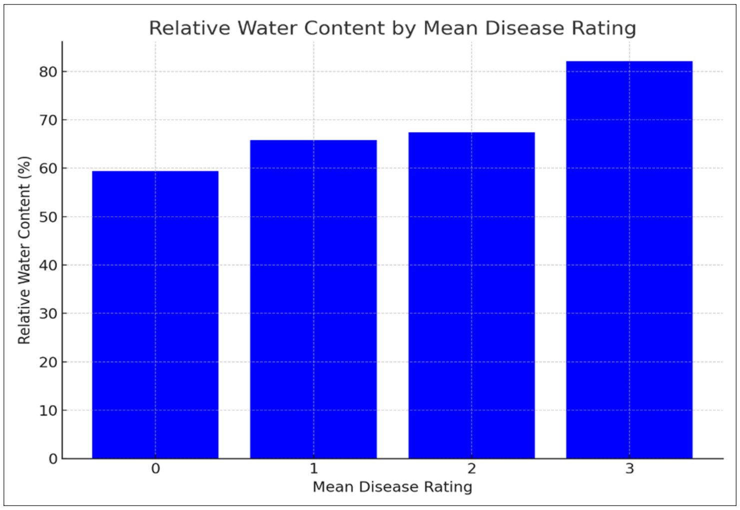

Figure 5. Relationship between Relative water content and Disease rating.

Correlation between growth traits and disease severity

Spearman's rank correlation analysis was conducted to explore relationships between seedling height, RCD, and disease rating (Table 8). The results revealed a strong, positive correlation between height and RCD ($p < 0.001$), indicating that seedlings with greater height also tend to exhibit thicker stem bases, reflecting coordinated structural growth. Additionally, moderate positive correlations were observed between height and disease rating ($p < 0.001$), and between RCD and disease rating ($p < 0.001$). These findings suggest that while vigorous growth is generally associated with improved structural traits, it may also coincide with increased susceptibility or exposure to brown spot needle blight. The presence of these statistically significant associations emphasizes the need to balance growth vigor with disease resistance in early seedling evaluations.

Visualizing correlation trends among growth variables and disease

The relationships between seedling height, RCD, and disease severity were further illustrated through scatterplots with fitted trend lines.

The height vs RCD plot displayed a clear positive linear trend, visually reinforcing the strong correlation observed statistically ($\rho = 0.629$, $p < 0.001$). This alignment indicates that taller seedlings generally develop thicker stem bases, reflecting balanced structural growth (Figure 2). In the height vs disease rating plot, a modest upward trend was evident, with seedlings exhibiting greater height tending to show slightly higher disease ratings ($p < 0.001$). While many tall seedlings remain healthy or mildly infected, the data suggests that vigorous vertical growth may coincide with elevated exposure or

Table 4. Summary statistics for disease susceptibility based on families

Family	Sample size(n)	mean_disease (0-4 rating)	*sd_disease	min_disease	max_disease	Rank
F13	176	0.585	0.617	0	2	1
F14	178	0.596	0.684	0	2	2
F8	163	0.620	0.747	0	3	3
F9	162	0.623	0.669	0	3	4
F2	170	0.629	0.752	0	3	5
F17	179	0.631	0.694	0	2	6
F12	169	0.633	0.642	0	2	7
F6	171	0.643	0.716	0	3	8
F1	163	0.644	0.709	0	2	9
F4	166	0.645	0.739	0	3	10
F16	180	0.650	0.689	0	3	11
F5	155	0.684	0.709	0	2	12
F11	160	0.694	0.761	0	3	13
F10	167	0.695	0.683	0	3	14
F7	170	0.700	0.687	0	3	15
F3	154	0.708	0.722	0	3	16
F15	171	0.731	0.718	0	3	17

*sd: Standard deviation

Table 5. Dunns's post hoc comparison for differences in seedling height.

Comparison	Z*	P. adj**
F10 - F2	-4.34971	0.001854
F11 - F2	-4.58044	0.000631
F14 - F2	-4.03914	0.007296
F15 - F2	-4.3386	0.00195
F17 - F2	-4.23654	0.003
F10 - F3	-4.35594	0.001802
F11 - F3	-4.58213	0.000626
F14 - F3	-4.0517	0.006915
F15 - F3	-4.34451	0.001898
F17 - F3	-4.24391	0.002987
F3 - F5	3.586774	0.045532
F1 - F6	-5.70863	1.55E-06
F10 - F6	-6.85419	9.75E-10
F11 - F6	-7.05791	2.3E-10
F12 - F6	-3.63354	0.03802
F13 - F6	-4.77676	0.000242
F14 - F6	-6.58335	6.26E-09
F15 - F6	-6.85805	9.49E-10
F16 - F6	-5.69453	1.68E-06
F17 - F6	-6.78454	1.58E-09
F4 - F6	-3.77498	0.021763
F5 - F6	-6.01543	2.44E-07
F2 - F7	4.148752	0.004546
F3 - F7	4.159557	0.004337
F6 - F7	6.66422	3.62E-09
F6 - F8	5.154404	3.46E-05
F6 - F9	4.147825	0.004565

*Z: Z value, **P. adj: Adjusted p-value

Table 6. Dunns's post hoc comparison for differences in seedling RCD

Comparison	Z	P. adj
F1 - F13	-5.773	1.06E-06
F10 - F13	-4.984	8.49E-05
F11 - F13	-6.548	7.94E-09
F1 - F14	-4.78	0.000238
F10 - F14	-3.982	0.00929
F11 - F14	-5.561	3.64E-06
F1 - F15	-4.09	0.00588
F11 - F15	-4.867	0.000154
F1 - F16	-3.886	0.0139
F11 - F16	-4.674	0.000402
F13 - F2	3.881	0.0141
F1 - F3	-4.126	0.00503
F11 - F3	-4.883	0.000142
F1 - F4	-4.705	0.000346
F10 - F4	-3.919	0.0121
F11 - F4	-5.474	5.99E-06
F11 - F6	-3.638	0.0374
F13 - F7	4.998	7.87E-05
F14 - F7	3.992	0.0089
F4 - F7	3.929	0.0116
F13 - F8	5.629	2.47E-06
F14 - F8	4.635	0.000485
F15 - F8	3.946	0.0108
F16 - F8	3.741	0.025
F3 - F8	3.986	0.00916
F4 - F8	4.562	0.000689
F11 - F9	-3.787	0.0208

*Z: Z value, **P.adj.: Adjusted p-value

susceptibility to brown spot needle blight under certain conditions (Figure 3).

The RCD vs disease rating plot showed a similar moderate positive association ($\rho = 0.443$, $p < 0.001$), where seedlings with thicker stems were also somewhat more likely to display signs of infection. This trend could reflect increased pathogen contact due to greater tissue mass or other correlated factors such as microclimate effects or family-level traits. Together, these visualizations corroborate the statistical findings and emphasize that while strong growth traits like height and root collar diameter are generally desirable, they may also be associated with increased disease occurrence, emphasizing the importance of integrated trait selection in breeding programs.

Relationship between disease rating and RWC by plot and families

A mixed-effects model (DiseaseRating ~ RWC + MonthIdx + Family + Plot) was used to partition variance and test RWC effects while controlling time and family effects. The results showed that each 1% increase in tissue relative water content corresponds to a 0.012-point drop in disease rating, holding month constant ($t = 13.21$, $p<0.001$) (Table 9). However, disease severity rises by an approximate 0.08 point per month from March to November ($t = 10.86$, $p <0.001$). As disease progresses, damaged needles may retain more water, altering the water dynamics (Figure 5). All predictors are significant at the 95% confidence interval. The high t value with $p < 0.05$ across all terms indicates that these effects are highly significant. The model shows approximately 65% of variability in disease rating suggesting a strong joint influence of water status and seasonality. Families F11 and F2 showed the highest RWC (~75-85%) with F17 and F14 at the lower end (~60-65%) (Figures 4A, 4B).

DISCUSSION

The study reveals pronounced differences in *Lecanosticta acicola* susceptibility among loblolly pine families, with some lines exhibiting markedly lower disease severity than others. Our results corroborate earlier work documenting differential susceptibility among pine taxa, underscoring genetic diversity as a critical buffer against epidemic outbreaks (Jones & Smith, 2021; Carter & Johnson, 2021). The negative relationship between RWC and disease rating (co.ef = -0.012, $t = -8.63$, $p < 0.001$) indicates that better-hydrated needles are more resistant to *Lecanosticta acicola* infection, aligning with studies linking high relative water status to reduced foliar pathogen colonization (Agrios, 2005). However, as infection advances, damaged needles might retain more water (for example, by disrupting cuticular function) thereby artificially inflating measured RWC (Huber & Gillespie, 1992). This suggests that selecting or managing families with superior water retention could mitigate brown spot needle blight impact. The positive MonthIdx (month progression factor) effect captures the seasonal epidemic curve, reflecting cumulative inoculum build-up and favorable summer conditions for sporulation (Sinclair & Lyon, 2005). Although plot-to-plot random effects (variance = 0.016; SD = 0.13) indicate only modest baseline differences among sites, incorporating RWC and time into predictive models greatly enhances our ability to forecast disease progression. Practically, these findings support integrating water status monitoring and targeted irrigation management into BSNB control strategies, and emphasize the value of phenological timing (e.g., focusing treatments just before the steepest disease incline in early summer). In conclusion seedlings of different loblolly pine families exhibit varying tolerance response to BSNB. Inoculum pressure, environmental factors as well as inherent genetic variations of the seedling groups play a role in determining their tolerance levels. The results underscore the importance of selecting resistant loblolly pine families for reforestation and management practices aimed at mitigating the impact of BSNB.

Table 7. Summary statistics for height, RCD and disease rating of seedlings based on plots.

Plot	Sample size (n)	mean_height (cm)	*sd_height	mean_rcd** (mm)	sd_rcd	mean_disease (0-4 rating)	sd_disease
10	574	50.6	27.5	6.16	1.45	0.646	0.68
11	568	48	24.1	5.99	1.35	0.579	0.632
12	594	43.3	19.3	5.09	0.978	0.552	0.656
13	558	45.8	10.8	5.71	1.28	0.731	0.76
14	560	48.8	12.3	6.8	17.3	0.762	0.754

*sd: Standard deviation, **rcd: Root collar diameter

Table 8. Correlation between growth traits and disease severity.

Variables Compared	Spearman's ρ (rho)	Strength	Direction	p- value
Height vs RCD	0.629	Strong	Positive	0.001
Height vs Disease Rating	0.454	Moderate	Positive	0.001
RCD vs Disease Rating	0.443	Moderate	Positive	0.001

Table 9. Regression table at 95% confidence interval for the relationship between relative water content and monthly disease progression with plot-to-plot variability.

	Coef*	Std. Err**	t-value	p-value	95% CI Lower	95% CI Upper
Intercept	1.850	0.140	13.21	< 0.001	1.588	2.120
RWC	-0.012	0.001	-8.63	< 0.001	-0.014	-0.010
Monthldx	0.076	0.007	10.86	< 0.001	0.062	0.090

*Coef: Regression co-efficient, Monthldx: Monthly disease progression factor, Std. Err**: Standard error, CI: Confidence Interval, Model fit statistics: $R^2 = 0.65$, Adj. R = 0.64, $p < 0.05$