Postprint: Correlation between Abnormal Leaf Coloration and Leaf Endophytic Bacteria in Loropetalum chinense var. rubrum

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Date: 2024-02-07T00:00:00+00:00

Abstract

To investigate the correlation between leaf endophytic bacteria and seasonal abnormal leaf color phenomena in Loropetalum chinense var. rubrum, this study employed plate isolation and culture method and 16S rDNA sequence characteristic analysis to isolate and identify endophytic bacteria from five types of abnormal leaf color and normal red leaves of L. chinense var. rubrum, and analyzed the differences in bacterial diversity, community structure, and functional bacteria levels among leaves with different colors. The results showed that: (1) The endophytic bacterial biomass was higher in leaves with the five types of abnormal coloration, and the 906 isolated bacterial strains were identified and classified into 26 genera and 40 species. (2) Small-leaf type leaves harbored the most diverse endophytic bacterial species with a uniform community structure, whereas the red-yellow type showed opposite results. (3) Comparison of the bacterial flora between abnormal leaf color leaves and normal red leaves revealed not only significant differences in dominant genera and species, but also enrichment of large quantities of Methylobacterium and Pseudomonas bacteria in abnormal leaf color leaves, particularly a notable increase in Pseudomonas oryzihabitans. (4) Abnormal leaf color leaves (small-leaf, red-spot, and red-yellow types) were enriched with bacteria possessing phosphate solubilizing, nitrogen fixing, IAA producing, and salt tolerant functions, among which four strains exhibited all four functions simultaneously; this enrichment of functional bacteria is highly likely associated with the abnormal leaf color phenomenon. This study reveals that the abnormal leaf color phenomenon in L. chinense var. rubrum is closely related to the enrichment of specific endophytic bacterial communities, providing clues for research on the formation mechanism of abnormal leaf color in L. chinense var. rubrum and holding important applied value for the high-quality and efficient cultivation of this species.

Full Text

Correlation Between Abnormal Leaf Color Phenomenon and Endophytic Bacteria in *Loropetalum chinense* var. *rubrum*

DOI: 10.11931/guihaia.gxzw202310023

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Abstract

This study investigated the correlation between leaf endophytic bacteria and seasonal abnormal leaf coloration in *Loropetalum chinense* var. *rubrum*. Using plate isolation culturing and 16S rDNA sequence analysis, we isolated and identified endophytic bacteria from five types of abnormally colored leaves and normal red leaves, analyzing differences in bacterial diversity, community structure, and functional bacteria across leaf color types. The results revealed: (1) Abnormally colored leaves harbored higher endophytic bacterial biomass, with 906 isolated strains classified into 26 genera and 40 species. (2) Small-leaf type leaves exhibited the highest species richness and most uniform community structure, while red-yellow type leaves showed the opposite pattern. (3) Comparative analysis between abnormal and normal red leaves revealed significant differences in dominant genera and species, with substantial enrichment of *Methylobacterium* and *Pseudomonas* in abnormal leaves, particularly *Pseudomonas oryzihabitans*. (4) Abnormally colored leaves (small-leaf, red-spot, and red-yellow types) were enriched with bacteria possessing phosphorus solubilization, nitrogen fixation, IAA production, and salt tolerance functions, including four strains exhibiting all four functions simultaneously. This enrichment of functional bacteria likely correlates with the abnormal leaf color phenomenon. These findings demonstrate that abnormal leaf coloration in *L. chinense* var. *rubrum* is closely associated with enrichment of specific endophytic bacterial communities, providing insights into the formation mechanisms of abnormal leaf pigmentation and offering valuable resources for high-quality, efficient cultivation.

Keywords: *Loropetalum chinense* var. *rubrum*, abnormal leaf color, endophytic bacteria, bacterial diversity, community structure

Introduction

Loropetalum chinense var. *rubrum*, commonly known as red-flowered loropetalum, belongs to the family Hamamelidaceae and genus *Loropetalum*. As a renowned native colorful-leaf plant in Hunan Province, it holds significant value for ornamental landscaping, ecological protection, and medicinal applications (Guo et al., 2022). In recent years, the phenomenon of abnormal leaf coloration in *L. chinense* var. *rubrum* has attracted increasing attention from researchers. Zhang et al. (2022) observed that this seasonal abnormal coloration causes no apparent harm to the plants, manifesting most prominently during summer and autumn while gradually diminishing or disappearing in winter and spring. Some researchers have attributed this phenomenon to plant viruses, though the specific causative factors remain unclear (Wang and Zhu, 2007). Wang (2023) investigated the triggers of five typical abnormal leaf types—small-leaf, red-yellow mosaic, yellow-green mosaic, complete yellowing, and red-spot types—defined by Xu et al. (2021), concluding that bacterial diseases, fungal pathogens, or nutrient deficiencies were not responsible. However, current research on *L. chinense* var. *rubrum* has primarily focused on cultivation, breeding, physiological characteristics, and chemical composition, with studies on abnormal leaf coloration limited to phenotypic characterization, photosynthetic properties, and disease aspects (Xu et al., 2021; Zhang et al., 2022). No studies have yet examined endophytic bacterial diversity in this species or explored the relationship between the frequent abnormal coloration phenomenon and leaf endophytic bacterial communities.

Plant endophytes are microorganisms that reside within plant tissues without causing apparent disease or immediate harm. Under suitable internal plant conditions, endophytes exhibit high diversity, low dominance, and uniform species distribution (Stone et al., 2000; Jiang et al., 2008; Gu et al., 2021; Meng et al., 2023). Moreover, their symbiotic relationship with host plants enhances stress resistance, disease control, growth promotion, nitrogen fixation, and bioremediation capabilities (Wani et al., 2015; Daniel et al., 2016; Bak and Gaj, 2016). Previous studies have demonstrated that bacterial invasion, shifts in bacterial communities, and bacterial diseases can cause localized or whole-plant color abnormalities, with bacterial microorganisms inducing leaf color changes observed in citrus and rice (Xie et al., 2021; Chen and Chen, 2022). We therefore hypothesize that abnormal leaf coloration in *L. chinense* var. *rubrum* may relate to changes in the endophytic bacterial environment or community composition. The unique physiological responses of *L. chinense* var. *rubrum* leaves may alter the internal leaf environment, which in turn modifies endophytic bacterial diversity, dominance, and species distribution. These bacterial community shifts subsequently affect plant growth and development, ultimately causing phenotypic changes (Hou et al., 2020). Clarifying the differences in microbial communities and diversity between normal red leaves and abnormally colored leaves will help determine whether bacterial community changes represent a co-evolutionary response to the "stress" of leaf color abnormality or actually induce the abnormal

pigmentation, while also enabling screening for superior bacterial resources.

This study examined both abnormally colored and normal red leaves of *L. chinense* var. *rubrum* using plate isolation culturing and 16S rDNA sequence analysis. Through diversity analysis, community structure analysis, and functional bacterial screening, we compared differences across leaf color types to address three key questions: (1) What are the diversity and community structure characteristics of endophytic bacteria in *L. chinense* var. *rubrum* leaves? (2) How do endophytic bacterial species and structures differ among various leaf color types? (3) How do functional bacterial communities shift under abnormal leaf color conditions? These investigations aim to identify microorganisms closely associated with abnormal leaf coloration, establish a foundation for elucidating the underlying mechanisms, and discover functional bacteria from enriched leaf endophytes as valuable resources for promoting cultivation.

Materials and Methods

1.1 Materials

1.1.1 Plant Materials Samples of five abnormal leaf color types and normal red leaves were collected from the *L. chinense* var. *rubrum* 'Dayehong' cultivar at the Hunan Agricultural University flower base. Samples were obtained from areas exhibiting frequent abnormal coloration and from regions without such phenomena. Plant materials are illustrated in Figure 1 [Figure 1: see original paper].

Figure 1 [Figure 1: see original paper]: Abnormal leaf color and normal red leaf of *Loropetalum chinense* var. *rubrum*.
A. Normal red leaf (ZC); B. Red-yellow mosaic leaf (HH); C. Yellow-green mosaic leaf (HL); D. Completely yellowed leaf (QH); E. Small leaf (XY); F. Red-spotted leaf (HB).

1.1.2 Culture Media

- **Endophytic bacteria isolation media**: R2A and NA media (Reasoner & Geldreich, 1985; Hao, 1992)
- **Phosphorus solubilization screening medium**: Pikovskaya's medium (Solarbio)
- **Nitrogen fixation screening medium**: Ashby nitrogen-free medium (Solarbio)
- **IAA production screening medium**: King' s medium B (Lin et al., 2022) with Salkowski reagent (1.5 mL of 0.5 mol·L^{-1} $FeCl_3$, 30 mL H_2SO_4, 50 mL distilled water)

1.2 Methods

1.2.1 Leaf Endophyte Isolation One gram of normal red or abnormally colored leaves was weighed, washed with tap water, surface-sterilized in 75%

ethanol for 30 seconds, treated with 0.1% $HgCl_2$ for 8 minutes, and rinsed five times with sterile water. The final rinse water was plated as a blank control to confirm successful surface sterilization. Sterilized leaves were thoroughly ground and serially diluted (10^{-1} to 10^{-5}). One hundred microliters from each dilution were spread on R2A and NA plates in triplicate and incubated at 28°C for 7 days. Colony morphology (size, color, surface characteristics) was recorded. The dilution yielding well-isolated colonies with maximum countable numbers was used for biomass calculation. Single colonies were purified through three successive subcultures, transferred to R2A and NA slants, assigned unique codes (format: "Medium Type-Leaf Type-Strain Number"), and stored at 4°C for molecular identification.

1.2.2 Genomic DNA Extraction and Bacterial Identification Genomic DNA was extracted using the boiling method (Pérez-Montaño et al., 2014). The 16S rDNA gene was amplified using universal primers 27F (5' -AGAGTTTGATCCTGGCTCAG-3') and 1492R (5' -GGTTACCTTGTTACGACTT-3'). PCR reactions contained: 25 L 2×Phanta Max Buffer, 1 L dNTP Mix (10 mM), 18 L ddH_2O, 2 L primer F (10 mM), 2 L primer R (10 mM), 1 L template DNA, and 1 L Phanta Max Super-Fidelity DNA Polymerase. Cycling conditions: initial denaturation at 95°C for 3 min, followed by 35 cycles of denaturation at 95°C for 15 s, annealing at 53°C for 15 s, extension at 72°C for 1 min, and final extension at 72°C for 5 min. Amplified products were verified by 1% agarose gel electrophoresis, and clear bands were sequenced by Tsingke Biotechnology. Sequences were submitted to EZBioCloud (https://eztaxon-e.ezbiocloud.net/) for taxonomic identification and deposited in GenBank. Phylogenetic analysis was performed using MEGA6.0 with the neighbor-joining method (Kimura 2-parameter model, 1,000 bootstrap replicates).

1.2.3 Diversity Analysis Community structure characteristics were analyzed using Shannon-Wiener (H) and Simpson (D) diversity indices (Xu et al., 2011):

$$H = -\sum_{i=1}^{S} P_i \ln P_i$$

$$D = 1 - \sum_{i=1}^{S} P_i^2$$

where S represents total species number and P is the proportion of the ith species.

1.2.4 Functional Characterization of Endophytes **Test strains**: Forty distinct endophytic bacterial species isolated from abnormal and normal red leaves of *L. chinense* var. *rubrum*.

Functional assays: - **Phosphorus solubilization**: Following Zhao et al. (2015) - **Nitrogen fixation**: Following Luo et al. (2023) - **IAA production**: Following Patten & Glick (2002) - **Salt tolerance**: Strains were inoculated on NA medium supplemented with NaCl (0.5%, 3%, 6%, 9%, 12%, 15%) and incubated at 30°C for 8 days with three replicates. Growth was recorded at each concentration.

1.3 Data Analysis

Statistical analysis and graphing were performed using Microsoft Excel 2016, SPSS 21.0, and GraphPad Prism 8.

Results

2.1 Quantity and Distribution Characteristics of Endophytic Bacteria in *L. chinense* var. *rubrum* Leaves

Endophytic bacterial biomass is presented in Table 1 . The R2A medium yielded higher bacterial counts than NA medium across all six leaf types, making it the reference for biomass calculations. Endophytic bacterial biomass in *L. chinense* var. *rubrum* leaves ranged from 3.50$×10^{2}$ to 1.60$×10^{4}$ CFU · g^{-1} on R2A medium. Normal red leaves (ZC) showed the lowest biomass, while red-yellow mosaic leaves (HH) exhibited the highest at 1.60$×10^{4}$ CFU · g^{-1}.

Table 1 : Biomass of endophytic bacteria in various leaf types of *Loropetalum chinense* var. *rubrum*

Leaf Type	Endophytic Bacteria Biomass (CFU · g^{-1})
	R2A Medium
ZC	350.00$±144.91*c*|200.00±117.04*c*||*HH*|16000.00±1154.70*a*|333.00±41.80*c*||*HL*|5000.00±375

Note: Data are mean ± standard deviation (n=3). Different lowercase letters indicate significant differences (P<0.05).

2.2 Molecular Identification of Leaf Endophytic Bacteria

Following preliminary classification based on colony morphology, 16S rDNA sequence analysis and phylogenetic tree construction were performed (Figure 2 [Figure 2: see original paper]). A total of 906 bacterial strains were isolated across all leaf types (Table 2), with quantities ranking: HH > HL > HB > XY > QH > ZC. Taxonomic analysis identified 6 genera and 6 species from normal

red, red-yellow, and yellow-green leaves; 13 genera and 15 species from small leaves; 4 genera and 5 species from completely yellowed leaves; and 7 genera and 12 species from red-spotted leaves.

Table 2 : Number of endophytic bacteria isolated from various leaf types of *Loropetalum chinense* var. *rubrum*

Leaf Type	Bacteria Number (Strains)
ZC	150
QH	120
HH	200
HL	180
XY	130
HB	126

Figure 2 [Figure 2: see original paper]: Phylogenetic trees of endophytic bacteria based on 16S rDNA sequences.
A. ZC leaf; B. QH leaf; C. HH leaf; D. HL leaf; E. XY leaf; F. HB leaf.

2.3 Diversity and Community Structure Analysis of Endophytic Bacteria Across Leaf Types

Diversity indices are summarized in Table 3 . Shannon-Wiener and Simpson indices ranged from 0.39–1.79 and 0.02–0.81, respectively. The Shannon-Wiener index, representing community richness, was significantly higher in small leaves (XY) than other types, including normal red leaves, indicating highest bacterial richness. The Simpson index, representing community evenness, was highest in normal red leaves (ZC) at 0.81, indicating concentrated bacterial communities, while red-yellow leaves (HH) showed the lowest value (0.02), reflecting imbalanced communities.

Community structure at genus and species levels revealed distinct differences between normal and abnormally colored leaves (Figure 3 [Figure 3: see original paper]A, 3B). Dominant genera varied among leaf types: HH leaves were dominated solely by *Methylobacterium* (98.4%), whereas ZC, HL, XY, QH, and HB leaves each harbored multiple dominant genera, with the most abundant being *Massilia* (27.3%), *Sediminibacterium* (49.1%), *Methylobacterium* (52.8%), *Bacillus* (70.8%), and *Curtobacterium* (56.6%), respectively. Comparative analysis identified *Methylobacterium* and *Pseudomonas* as shared genera across all five abnormal leaf types. *Pseudomonas oryzihabitans* was identified as a shared species among abnormal leaf types but was absent from normal red leaves.

Table 3 : Bacterial diversity indices in different leaf types

Leaf Type	Shannon-Wiener Index	Simpson Index
ZC	1.41$±0.17*b*|0.81±0.01*a*||*HH*|0.39±0.17*c*|0.02±0.01*b*||*HL*|1.30±0.12*b*|0.67±0.21*a*||*XY*|1.79	

Note: Data are mean ± standard deviation (n=3). Different lowercase letters indicate significant differences (P<0.05).

Figure 3 [Figure 3: see original paper]: Endophytic bacterial community structure in *Loropetalum chinense* var. *rubrum* leaves.
A. Genus-level classification; B. Species-level classification.

2.4 Functional Analysis of Endophytic Bacteria

2.4.1 Phosphorus Solubilization Capacity Among 40 tested strains, seven exhibited phosphorus solubilization on inorganic phosphate medium (Table 4 , Figure 4 [Figure 4: see original paper]). *Pseudomonas oryzihabitans* NXY1-1 from small leaves showed the strongest activity. Strains isolated from abnormal leaf types (HH, XY) demonstrated higher phosphorus solubilization than those from normal red leaves.

Table 4 : Phosphorus solubilization ability of endophytic bacteria

Strain Number (Species)	Halo/Colony Diameter Ratio
RZC1-2 (*Aquincola tertiaricarbonis*)	1.29$±0.07*bc*||*NHH*1 − 1(∗*Labedellagwakjiensis*∗)|1.45±0.19*b*||*NHH*2− 2(∗*Bacillustequilensis*∗)|1.38±0.08*bc*||*RHL*2− 2(∗*Ralstoniapickettii*∗)|1.24±0.07*c*||*NXY*1− 1(∗*Pseudomonasoryzihabitans*∗)|1.81±0.19*a*||*NXY*3− 4(∗*Rhizobiumsoli*∗)|1.42±0.07*b*||*RHB*1− 2(∗*Curtobacteriumalbidum*∗)|1.22±$0.05c

Note: Data are mean ± standard deviation (n=4). Different lowercase letters indicate significant differences (P<0.05).

2.4.2 IAA Production Capacity IAA production analysis (Figure 5 [Figure 5: see original paper]) identified 9 low-producing strains (<17 mg · L^{-1}), 5 moderate-producing strains (17-80 mg · L^{-1}), and 26 high-producing strains (>80 mg · L^{-1}). Small leaves (XY) and red-yellow mosaic leaves (HH) showed broader IAA production ranges than normal red leaves. High-producing strains RXY2-6 (*Flavobacterium acidificum*), RHH2-2 (*Pantoea anthophila*), and NXY1-1 (*Pseudomonas oryzihabitans*) were all isolated from abnormal leaves, indicating enrichment of growth-promoting IAA-producing bacteria.

2.4.3 Nitrogen Fixation Capacity Nitrogen fixation assays (Table 5) showed that 50% of nitrogen-fixing bacteria originated from dominant species in abnormal leaves. Small leaves (XY) and red-spotted leaves (HB) contained more nitrogen-fixing bacteria (17.5% and 10%, respectively) than other types, suggesting that diverse abnormal leaf bacterial communities possess stronger nitrogen fixation capacity than normal red leaves.

2.4.4 Salt Tolerance Capacity All 40 strains grew in low-salt medium (0.5% NaCl), but viable counts decreased with increasing salinity (Table 5). Abnormal leaf endophytes tolerated up to 12% NaCl, whereas normal leaf bacteria failed to grow above 9% NaCl, demonstrating superior salt tolerance in abnormal leaf endophytic communities.

Table 5 : Nitrogen fixation and salt tolerance of endophytic bacteria

Note: + indicates positive function; - indicates negative function.

Discussion and Conclusion

This study systematically isolated and identified endophytic bacteria from five typical abnormal leaf types and normal red leaves of *L. chinense* var. *rubrum*, revealing substantial differences in bacterial quantity, diversity, community composition, and functional bacteria distribution across leaf color types. The data demonstrate that abnormal leaves consistently harbor higher endophytic bacterial biomass than normal red leaves, a pattern also observed in studies of healthy versus diseased leaves in tea and citrus, where diseased (discolored) leaves contained greater bacterial populations (Chen, 2009; Gao, 2017). Previous research indicates that bacterial abundance correlates negatively with anthocyanin content in *L. chinense* var. *rubrum* leaves (Zhang et al., 2022), similar to findings in tea leaves (Wang et al., 2016) and other plant fruits (Rogez et al., 2012), where high anthocyanin levels inhibit microbial growth. Consequently, the lower anthocyanin content in abnormal leaves may release this inhibition, allowing increased bacterial proliferation.

Diversity analyses revealed that, except for small leaves, abnormal leaf types exhibited lower endophytic bacterial diversity than normal red leaves, consistent with findings in diseased leaves of *Idesia polycarpa* and giant sequoia showing reduced diversity compared to healthy leaves (Yue et al., 2020; Zhou et al., 2022). Small leaves are unique in that both color and leaf size are altered. Previous studies have shown that leaf color and endophytic communities in *L. chinense* var. *rubrum* respond to environmental factors like light and temperature (Fei et al., 2008; Huang et al., 2017; Yang et al., 2021). The drastic size reduction in small leaves decreases photosynthetic area, potentially prompting enhanced plant-microbe cooperation to maintain adequate photosynthetic capacity for normal growth and development. This may occur through increased endophytic diversity and enrichment of specific functional bacteria that improve environmental adaptation.

Abnormal leaves showed higher relative abundance at genus and species levels, more imbalanced community structures, and enrichment of *Methylobacterium* and *Pseudomonas*, particularly *Pseudomonas oryzihabitans*. Similar patterns have been reported in diseased leaves of *Eupatorium adenophorum* and tea plants, where community structure and relative abundance differed significantly from healthy leaves (Zhou et al., 2010; Chen et al., 2023). *Pseudomonas* and *Methylobacterium* species can cause color changes and lesions in other plants, with *P. oryzihabitans* specifically inducing brown discoloration in rice grains (Feng, 2017; Hou et al., 2020), suggesting these genera may contribute to leaf color changes in *L. chinense* var. *rubrum*.

Functional analysis demonstrated that abnormal leaves were enriched with bacteria possessing superior phosphorus solubilization, salt tolerance, nitrogen fixation, and IAA production capabilities compared to normal leaves, with four strains exhibiting all four functions simultaneously. The enriched genera *Pseudomonas* and *Bacillus* have been previously isolated from wheat and *Caragana* and confirmed to have strong phosphorus solubilization and salt tolerance (Zumft, 1998; Dai et al., 2012; Ju, 2014; Kushwaha et al., 2020). The 26 high IAA-producing strains from *L. chinense* var. *rubrum* exceeded production levels reported in wheat and *Coptis chinensis* endophytes (Malik et al., 1997; Xiang et al., 2023), likely due to the unique microbial enrichment in abnormal leaves. Despite these community shifts, the enriched functional bacteria appear to assist plant growth rather than become pathogenic, merely causing phenotypic changes.

In conclusion, *L. chinense* var. *rubrum* leaves harbor rich endophytic bacterial communities, with abnormal leaves showing enrichment in both total and functional bacteria. Changes in bacterial quantity, diversity, community structure, and functional groups occurred, with enriched dominant communities potentially inducing color changes. This specific bacterial enrichment likely correlates with abnormal leaf coloration. The substantial endophytic and functional bacterial resources isolated in this study provide a reference for elucidating the mechanisms of abnormal leaf color formation and hold important application value for high-quality, efficient cultivation of *L. chinense* var. *rubrum*.

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Note: Figure translations are in progress. See original paper for figures.