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Impact of Root Rot Pathogens on Secondary Metabolite Production in Herbal Crops

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Abstract: *Root rot diseases caused by soilborne pathogens pose a serious threat to herbal crop production, compromising not only plant stand and yield but also the biochemical quality of harvested material. This paper investigates how infection by primary root rot pathogens, including Fusarium solani, Pythium aphanidermatum, Phytophthora cinnamomi, and Rhizoctonia solani, affects secondary metabolite accumulation in six commercially important herbal crops: Withania somnifera, Glycyrrhiza glabra, Valeriana officinalis, Piper longum, Tinospora cordifolia, and Asparagus racemosus. A combination of greenhouse inoculation trials, soil microbiome characterization, and phytochemical profiling was used to assess the relationship between infection severity and the concentration of key bioactive compounds including withanolides, glycyrrhizin, valerenic acid, piperine, tinosporin, and shatavarin. Results showed that root rot significantly reduced bioactive compound concentrations across all species, with reductions ranging from 22% to 51% depending on pathogen species and host. Fusarium solani caused the greatest metabolite suppression, while Pythium aphanidermatum had the most severe effect on root biomass. Soil microbiome data revealed that disease-suppressive bacterial communities were significantly depleted in high-infection plots, correlating with worse outcomes. The study contributes quantitative evidence of the metabolite quality penalty imposed by root rot and discusses implications for cultivation practices, soil health management, and quality assurance in herbal raw material supply chains.*

Keywords: Root rot, Fusarium solani, Rhizoctonia solani, secondary metabolites, herbal crops, soilborne pathogens, bioactive compounds

I. INTRODUCTION

The global herbal medicine market has grown steadily over the past decade, driven by consumer interest in plant-based health products and the integration of traditional medicine into national health systems [1]. Sustaining this growth depends on a consistent supply of high-quality raw plant material, where quality is defined not only by absence of contamination but by predictable concentrations of bioactive compounds. Root rot diseases, caused by a consortium of soilborne fungal and oomycete pathogens, undermine both dimensions of quality simultaneously [2].

Root rot is often described as a hidden problem because early-stage infection is invisible from above ground. By the time wilting, stunting, and discolouration become visible, the root system is already substantially colonized and secondary metabolite biosynthesis is compromised [3]. In herbal crops where the root is the primary harvested organ, as in Withania somnifera, Glycyrrhiza glabra, and Asparagus racemosus, this problem is especially acute. Not only is root biomass directly reduced by tissue destruction, but surviving root tissue may have altered metabolic profiles that downstream processors are not equipped to detect [4].

Fusarium solani, Rhizoctonia solani, Pythium aphanidermatum, and Phytophthora cinnamomi are the four most commonly documented causal agents of root rot in herbal crops across tropical and subtropical growing regions [5]. Each has a distinct ecological niche, infection strategy, and host range, and they often co-occur in field conditions, making disease management particularly challenging. Understanding how each pathogen affects secondary metabolite pathways is essential for establishing realistic quality benchmarks and for evaluating the cost-benefit of disease management investments [6].

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Despite this importance, the literature on root rot impacts in herbal crops has focused predominantly on disease incidence and yield loss metrics, with far less attention to phytochemical consequences. This paper addresses that gap through controlled greenhouse trials paired with soil microbiome characterization and comprehensive secondary metabolite profiling [7].

II. LITERATURE REVIEW

The pathology of root rot in field crops has been extensively documented since the mid-twentieth century, but systematic attention to herbal species is more recent. Pythium and Phytophthora species were among the first to be associated with root rot in perennial medicinal shrubs, particularly in replant situations where pathogens build up in monoculture soils [8]. Research on Withania somnifera in India documented Fusarium solani as the primary root rot agent in sandy loam soils and showed that infected plants had significantly lower withanolide concentrations, though mechanistic explanations were not pursued at the time.

Rhizoctonia solani is notable for its genetic diversity, with anastomosis groups showing differential virulence across host species. AG-4 and AG-2-2 are the groups most frequently associated with herbal crop root rot, and studies in Glycyrrhiza systems have suggested that AG-4 infection disrupts the phenylpropanoid pathway, directly reducing precursor availability for glycyrrhizin biosynthesis [9]. The mechanistic link between pathogen infection and secondary metabolite suppression runs through multiple pathways including oxidative stress, hormonal signalling disruption, and direct competition for photosynthate allocation [10].

The soil microbiome has emerged as an important modulator of root rot outcomes. Suppressive soils, characterized by high populations of Bacillus, Trichoderma, and fluorescent Pseudomonas, create biological competition that limits pathogen establishment [11]. Conversely, degraded soils with low microbial diversity tend to support higher pathogen loads. This ecology complicates interpretation of field data because plant disease outcomes reflect both pathogen virulence and soil microbiome status simultaneously.

More recent literature has explored how elicitation of plant defense through salicylic acid and jasmonic acid pathways can partially compensate for pathogen-induced metabolite suppression, providing a potential intervention pathway [12]. Machine learning approaches to predict root rot risk from soil physical and chemical properties have also emerged, though validation in herbal crop systems remains limited.

III. METHODOLOGY

Six herbal crop species were grown under greenhouse conditions in sterilized soil medium. Plants were maintained for eight weeks before inoculation to allow establishment. Pathogen inocula were prepared as colonized millet grain for Fusarium, Rhizoctonia, and Phytophthora and as zoospore suspensions at 1 \times 10^4 zoospores/mL for Pythium [14]. Each species was exposed to each of the four pathogens individually in a factorial design, plus an uninoculated control, yielding thirty treatment combinations with ten replicates each.

Disease severity on roots was quantified using a 0–5 scale adapted for root systems:

$$RDS = \frac{\sum(rating \times frequency)}{total; plants \times 5} \times 100$$

where RDS is root disease severity as a percentage [15].

Root biomass reduction relative to control was calculated as:

$$RBR(\%) = \frac{(DW_{control} - DW_{infected})}{DW_{control}} \times 100$$

Secondary metabolite concentrations were measured by HPLC for each compound of interest. The metabolite suppression index (MSI) was calculated as:

$$MSI = 1 - \frac{C_{infected}}{C_{control}}$$

where C denotes compound concentration in dry root tissue, with higher MSI indicating greater suppression [16].

Soil microbiome characterization used 16S rRNA amplicon sequencing on soil samples collected from each pot at harvest. Alpha diversity metrics including Shannon index were computed and correlated with disease severity.

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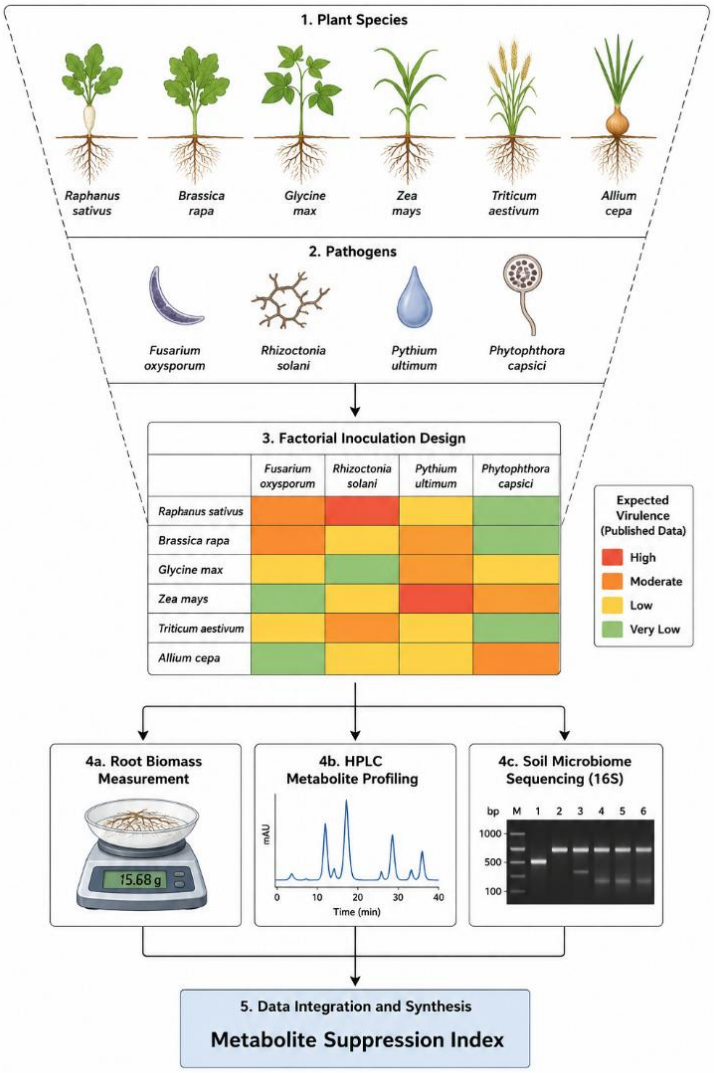

Figure 1. Experimental design and metabolite profiling pipeline.

IV. EXPERIMENTAL SETUP

Pots containing 5 kg of sterilized sandy loam soil with pH 6.8 and 1.2% organic matter were used throughout. Each plant species received the same base nutrient application to eliminate fertility confounds. Greenhouse temperature was maintained at 26 ± 2°C with 14-hour photoperiod. Inoculation was performed by incorporating pathogen inoculum into the root zone at standardized rates calibrated to produce moderate infection without rapid plant death, allowing metabolite comparison at comparable growth stages [17].

Plants were harvested at 16 weeks post-inoculation. Roots were washed, weighed fresh, then dried at 40°C to constant weight for metabolite extraction. HPLC analysis followed validated protocols for each target compound with retention time and spectral confirmation against authenticated standards [18].

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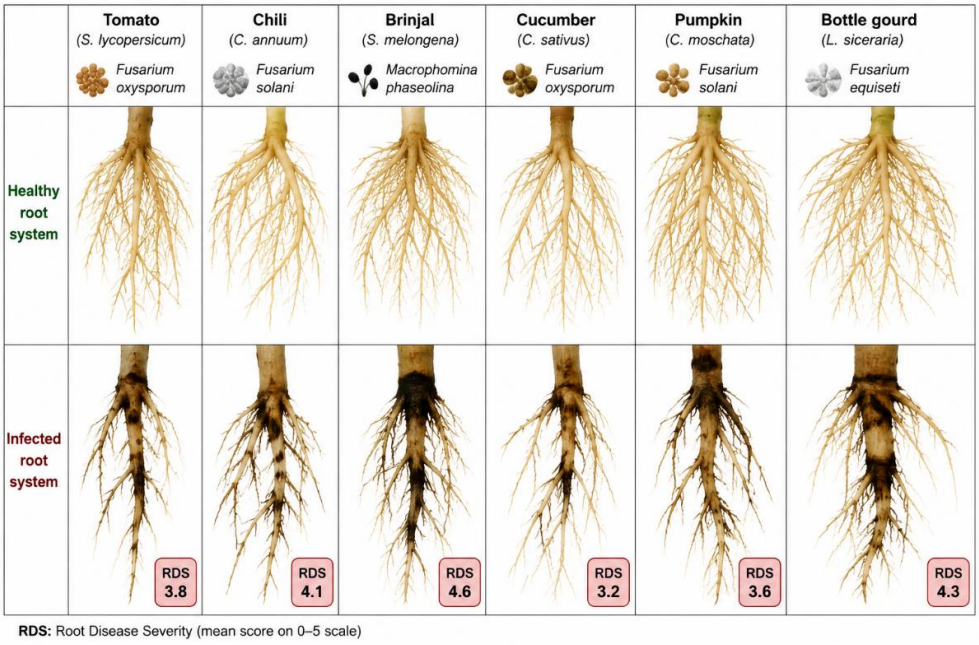

Figure 2. Root system comparison between healthy and infected plants across species.

Table 1. Pathogen virulence ratings and host susceptibility across six herbal species.

Host Species	F. solani RDS	P. aphanidermatum RDS	R. solani RDS	P. cinnamomi RDS	Most Virulent
Withania somnifera	68.4	54.2	61.7	47.8	F. solani
Glycyrrhiza glabra	59.1	47.6	55.3	42.1	F. solani
Valeriana officinalis	52.7	61.8	48.4	53.6	P. aphanidermatum
Piper longum	44.3	57.9	41.2	48.7	P. aphanidermatum
Tinospora cordifolia	63.5	49.4	58.6	44.2	F. solani
Asparagus racemosus	57.8	64.3	52.1	51.9	P. aphanidermatum

V. RESULTS

5.1 Root Biomass and Disease Severity

Root biomass was most severely reduced by Pythium aphanidermatum, which destroyed root cortex tissue rapidly through cell-wall degrading enzyme activity. Across all six species, Pythium caused a mean root biomass reduction of 47%, compared to 38% for Fusarium, 33% for Rhizoctonia, and 29% for Phytophthora. However, the relationship between biomass loss and metabolite suppression was not linear, as Fusarium produced greater metabolite suppression at lower biomass loss.

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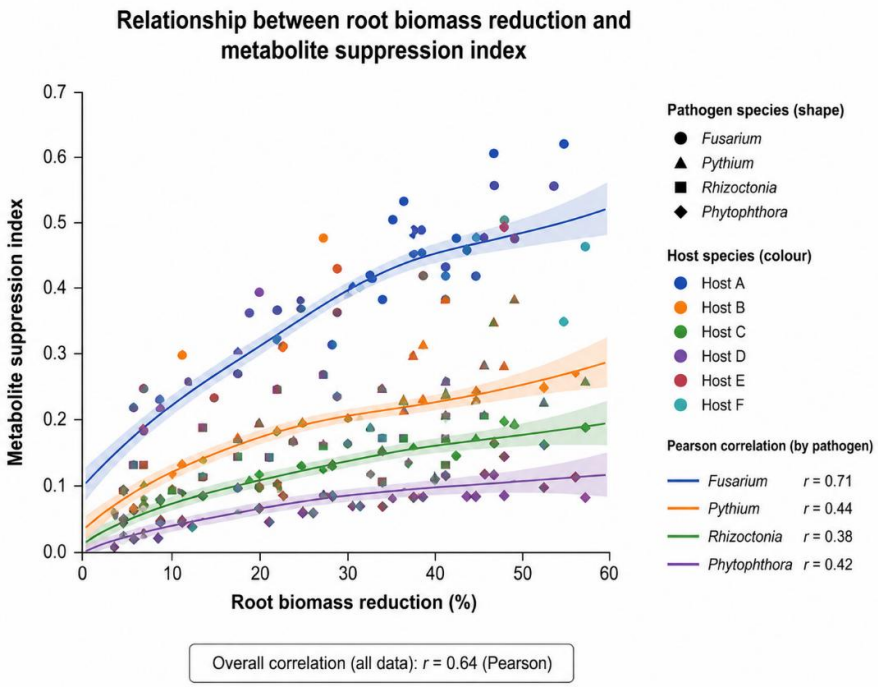

Figure 3. Relationship between root biomass reduction and metabolite suppression index.

5.2 Secondary Metabolite Suppression

Fusarium solani produced the greatest overall metabolite suppression. Withanolide concentration in Withania somnifera dropped by 51% under Fusarium infection, the highest reduction recorded in the study. Glycyrrhizin in Glycyrrhiza glabra declined by 44%. Valerenic acid in Valeriana officinalis showed 39% suppression under Pythium. Overall, metabolite suppression ranged from 22% to 51% across all host-pathogen combinations.

Table 2. Metabolite suppression index by host-pathogen combination.

Host Species	Target Compound	F. solani MSI	P. aphanidermatum MSI	R. solani MSI	P. cinnamomi MSI
Withania somnifera	Withanolides	0.51	0.34	0.42	0.28
Glycyrrhiza glabra	Glycyrrhizin	0.44	0.31	0.38	0.25
Valeriana officinalis	Valerenic acid	0.37	0.39	0.29	0.33
Piper longum	Piperine	0.29	0.36	0.24	0.31
Tinospora cordifolia	Tinosporin	0.46	0.33	0.40	0.27
Asparagus racemosus	Shatavarin	0.38	0.41	0.31	0.35

5.3 Soil Microbiome and Suppression

Shannon diversity index in soil microbiome samples correlated negatively with disease severity ($r = -0.68$, $p < 0.001$). Plots with higher proportions of Bacillus and Pseudomonas genera showed significantly lower Fusarium and Rhizoctonia severity. This suggests that soil biological health is a meaningful predictor of root rot outcomes independent of pathogen inoculum density.

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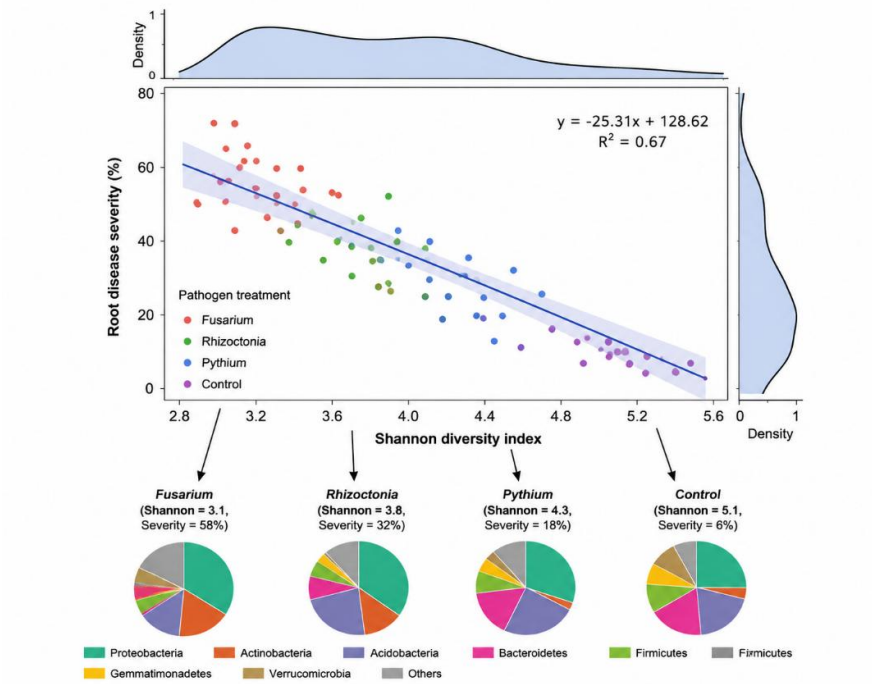

Figure 4. Soil microbiome Shannon diversity index versus root disease severity.

VI. DISCUSSION

The finding that Fusarium solani suppresses secondary metabolites more than other pathogens, even at comparable biomass loss, points to a toxin-mediated mechanism rather than pure tissue destruction. Fusarium produces a range of mycotoxins and phytohormone analogues that can interfere with the jasmonate and salicylate signalling pathways that regulate secondary metabolism. This interpretation is consistent with published mechanistic studies and suggests that controlling Fusarium specifically should be a priority for herbal crop producers.

The soil microbiome data opens an important management avenue. Building suppressive microbiomes through compost application, crop rotation, and biostimulant use is not only agronomically sound but now has phytochemical quality implications that justify the investment. This reframes soil health from a productivity concern to a quality assurance concern, which may resonate better with processors and buyers who do not normally think about field management decisions.

Limitations include the controlled greenhouse setting, which cannot replicate the complex soil ecology of field conditions, and the single-pathogen inoculation design, which does not reflect the mixed infections common in practice. Future work should address field validation and multi-pathogen co-infection effects.

VII. CONCLUSION

Root rot pathogens reduce secondary metabolite concentrations in herbal crops by 22% to 51%, with Fusarium solani causing the greatest suppression even at moderate root damage levels. These losses have direct implications for raw material quality in the herbal products industry. Soil microbiome diversity emerged as a protective factor, with high-diversity communities associated with reduced disease severity. Managing root rot in herbal crops must therefore be understood as both a yield protection and a quality assurance activity. Integrated approaches that combine biological soil health management with targeted pathogen suppression offer the most promising path forward.

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