

COCONUT ROOT WILT DISEASE: HISTORICAL PERSPECTIVES, MOLECULAR ADVANCES AND INTEGRATED DISEASE MANAGEMENT

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ABSTRACT

Root wilt disease (RWD) is one of the most destructive phytoplasma-associated diseases affecting coconut production in South India, causing substantial yield reduction and long-term economic losses. Although the disease has been recognized for more than a century, significant advances in molecular biology have transformed the understanding of its etiology, epidemiology and diagnosis. This review critically summarizes the progression from early investigations involving fungal, bacterial and nematode hypotheses to the definitive identification of the causal phytoplasma and its molecular classification. Recent developments in nucleic acid-based diagnostics, immunological assays, transcriptomics, proteomics and biomarker discovery have substantially improved disease detection and expanded knowledge of host–pathogen interactions. The review also evaluates current integrated disease management strategies, including cultural, nutritional, chemical, biological and host tolerance approaches, while highlighting their practical limitations under field conditions. Particular emphasis is placed on emerging omics technologies and biomarker-assisted diagnostics that provide opportunities for early disease detection and precision management. By integrating classical pathology with recent molecular and systems biology approaches, this review identifies major research gaps and proposes future directions for developing reliable diagnostics, understanding phytoplasma biology and improving sustainable disease management. The information presented provides a comprehensive scientific framework for advancing research and enhancing coconut health in phytoplasma-endemic regions.

KEYWORDS: Coconut root wilt disease; Phytoplasma; Molecular diagnostics; Proteomics; Biomarker discovery; Integrated disease management.

1. INTRODUCTION

The coconut palm (*Cocos nucifera* Linn.) is a tropical tree widely grown in India, playing a vital role in the economic, social, and cultural lives of small-scale farmers. Often called the “tree of life”, it offers a variety of products used in nutrition, medicine and cosmetics, such as coconut water, milk, sugar, oil and meat. Additionally, nutrient-rich by-products from coconut processing are repurposed into value-added food items, enhancing economic benefits (Karandeep et al., 2019). Globally, coconut is grown in 90 countries, with a total production of more than 65 million metric tonnes as per FAOSTAT (2023). Coconut is cultivated across 2.19 million hectares in India, with an annual production of 20.30 billion nuts and an average productivity of 9,249 nuts ha⁻¹. Kerala, Karnataka and Tamil Nadu together account for the major share of the country's coconut area and production, while Andhra Pradesh records the highest productivity of 16,002 nuts ha⁻¹. All of these states have favourable agroclimatic conditions for coconut cultivation <https://coconutboard.gov.in/Statistics.aspx>, (2024-25).

The 2022-2023 data on coconut production in Tamil Nadu shows significant regional differences. The state cultivated 4,72,711 ha, producing 6.8 billion nuts with an average yield of 14,382.78 nuts/ha. Coimbatore led in production with 1.43 billion nuts, while Madurai had the highest yield at 24,419.05 nuts/ha. The Nilgiris and Tuticorin district had the lowest production and yield respectively. These variations suggest differences in agricultural practices, soil quality and local conditions across districts (DES, 2022-2023). The coconut kernel rich in lipids, proteins and functional dietary components, is a significant contributor to the vegetable oil market and offers various nutraceutical benefits through products like virgin coconut oil, coconut water and coconut milk. These products are gaining popularity as functional foods due to their nutritional and antioxidant properties. Despite its wide range of applications and economic importance, the full potential of coconut is still not fully recognized (Samarajeewa, 2024).

Coconut palms are widely grown and essential for the livelihoods of over 20 million people in coastal regions (Ohler, 1999). Coconut production and yield are adversely affected by a range of biotic and abiotic stresses (Vinod, 2011). In addition, biotic factors such as pests and diseases impose significant stress on coconut palms (Kumar, Rajagopal and Bai, 2006). Pests and diseases alone lead to annual losses of 15 % to 20 % in coconut crops. Despite being hardy, coconut palms are often affected by plant pathogens due to moisture stress and climate. Globally,

over 50 diseases and 173 fungi have been reported, with 35 fungi linked specifically to coconut leaves in India (Brown, 1973). Additionally, bacteria, phytoplasma, viruses and nematodes also cause diseases in coconuts.

Coconut palms face over various diseases globally, among them root wilt disease (RWD) caused by phytoplasma being the most significant and deadly disease. Root wilt disease was first reported from Kerala in 1882 by Butler (1908), RWD can reduce the yield from 35 % to 80 % in severe cases. In India, this disease leads to an estimated annual loss of around 968 million nuts (Manimekalai et al., 2010), making it a major concern for coconut plantations in Kerala and the neighbouring border districts of Tamil Nadu. The Root wilt pathogen was found to infect more than 50 different palm species growing in different continents (Yankey et al., 2018).

The diseased palms can be identified by flaccidity, yellowing and necrosis of leaflets (affects younger palms less severely than older ones), inflorescence necrosis and finally root decay. Root wilt disease symptoms vary by age and condition of the palms (Menon and Nair, 1952; Radha and Lal, 1972; Koshy, 2000). Phytoplasmas are phloem-limited, cell wall-less bacteria that infect several hundred plant species and are responsible for economically important diseases worldwide. Among palms, phytoplasma-associated diseases collectively known as lethal yellowing-type diseases (LYDs) have caused severe economic losses across Asia, Africa, the Caribbean and Oceania. Coconut root wilt disease of India represents a unique non-lethal member of this disease complex, causing chronic decline in palm health and substantial yield reduction rather than rapid palm death (Gurr et al., 2016).

This review provides a comprehensive synthesis of recent advances in the understanding of coconut root wilt disease by integrating historical evidence with contemporary molecular discoveries. Unlike previous reviews, it critically consolidates developments in phytoplasma identification, transcriptomics, proteomics, biomarker discovery and emerging diagnostic technologies while relating these advances to practical disease management. Furthermore, the review highlights current knowledge gaps and proposes future research priorities that support precision diagnostics, molecular breeding and sustainable integrated management of coconut root wilt disease.

2. Identification of Coconut Root Wilt Disease

Coconut root wilt disease (RWD) is one of the oldest and most extensively investigated diseases of coconut (*Cocos nucifera* L.) in South Asia. The disease was first recognized in the state of Travancore, Kerala, around 1874 and became more evident following the severe floods of 1882. Early reports documented independent disease foci at Erattupetta, Kaviyoor - Kallloopara and Kayamkulam, indicating multiple centres of disease occurrence (Butler, 1908; Pillai, 1911; Varghese, 1934). Although the disease was recognized more than a century ago, its etiology remained uncertain for several decades, leading to extensive investigations involving fungal, bacterial, viral and nematode pathogens.

The earliest studies primarily implicated fungi as the possible causal agents. Butler (1973) isolated *Botryodiplodia theobromae* from diseased roots and suggested its involvement in disease development. Later, Menon and Nair (1951) reported the association of *Rhizoctonia solani* and *Rhizoctonia bataticola* with affected palms, while Radha and Menon (1954) observed a stronger association of *R. solani* with diseased palms. Additional fungi, including *Neocosmospora vasinfecta*, *Fusarium equiseti* and *Cylindrocarpon effusum*, were subsequently isolated from infected tissues. Although these fungi induced varying degrees of root damage under experimental conditions, none consistently reproduced the characteristic root wilt disease syndrome, suggesting that they were secondary invaders rather than the primary causal agents (CPCRI, 2015).

The inability to establish fungal pathogenicity shifted attention towards viral etiology. Nagaraj and Menon (1956) demonstrated transmission of a putative infectious agent through sap inoculation and the lace bug *Stephanitis typica*, while Menon (1935) also implicated the insect as a potential vector. However, repeated attempts to isolate or characterize a virus were unsuccessful. Subsequently, *Enterobacter cloacae* were investigated because of its frequent association with diseased palms and its sensitivity to oxytetracycline treatment. Nevertheless, long-term pathogenicity studies failed to reproduce the disease, indicating that the bacterium was not the primary causal agent (CPCRI, 2015).

During the 1960s and 1970s, nematodes were also examined as possible causal organisms or vectors. Weischer, (1967) reported the occurrence of *Xiphinema* and *Longidorus* species in diseased coconut rhizospheres, while Khan et al. (1971) identified additional nematodes, including *Dolichodorus pulvinus* and *Longidorus saginus*. Later, demonstrated that *Radopholus similis* caused root damage but failed to induce typical root wilt disease, indicating that nematodes may aggravate disease severity rather than initiate it Koshy et al. (1999).

A major breakthrough in disease identification was achieved through molecular studies. Sharmila et al. (2004) first reported the association of phytoplasma with root wilt disease through 16S rDNA sequencing. This finding was strengthened by Manimekalai et al. (2010), who consistently detected phytoplasma DNA in symptomatic palms using nested PCR. Subsequently, Manimekalai et al. (2014) conclusively identified the pathogen as a 16SrXI-B subgroup phytoplasma, closely related to '*Candidatus Phytoplasma oryzae*', thereby resolving the long-standing uncertainty regarding the etiology of coconut root wilt disease.

3. Root wilt disease

The root wilt disease of coconut was first identified in 1882 in the Erattupetta area of Meenachil Taluk, Kottayam District and was a significant plant disease that affected coconut palms (Butler, 1908). Symptoms of coconut phytoplasma appear after six to 24 months, occasionally upto three years (Mathen et al., 1990). According to Indian studies, palms affected by root wilt disease exhibited impaired stomatal regulation, leading to excessive water loss and causing flaccidity of leaves (Rajagopal et al., 1986).

The 1985 survey conducted by Central Plantation Crops Research Institute and the Department of Agriculture, Kerala, found that root wilt disease has affected 4,10,000 hectares of coconut palms. It was most severe in Kottayam (75.6 %) and Alappuzha (70.7 %), with lower rates in Thrissur (2.6 %) and Thiruvananthapuram (1.5 %). Sporadic disease appeared in Palakkad, Malappuram, Kozhikode, Kannur, Kasaragod and Tamil Nadu. This disease led to a loss of 968 million nuts annually, reducing yields by 45 % in West Coast Tall and 60 % in D x T hybrids (Koshy, 1999).

Based on the importance of this disease, a survey conducted in the hotspot areas of Kerala viz., Alappuzha, Pathanamthitta, Kollam and Kottayam, revealed about 75 % of Chowghat Green Dwarf (CGD) palms were disease-free, showing higher resistance to root wilt disease compared to West Coast Tall (WCT) palms, which had over 80 % disease incidence. This suggests CGD's greater resistance, while disease-free WCT palms found in affected areas are useful for breeding programs (Krishnakumar et al., 2015).

From 2016 to 2019, a survey conducted in six districts of Tamil Nadu state revealed a significant prevalence of root wilt disease in coconut palms. The disease showed low incidence in Theni (16.15 %) and Tirunelveli (15.77 %), but in few areas like Uthamapalayam (53.00 %) and Tenkasi (30.90 %) had high infection rates. The disease spread slowly to new areas having healthy palms. However, inconsistent monitoring has hindered the full eradication of the disease and the achievement of disease-free coconut plantations in Tamil Nadu (Rajendran et al., 2019).

Kavitha et al. (2023) reported the significant pest and disease issues in coconut plantations, with root wilt being the most severe, especially in Thippiramalai (74.42 %) and Vellimallai (52.63 %) villages of Kanyakumari district, Tamil Nadu.

4. Symptomatology

Foliar symptoms of Coconut root wilt disease are flaccidity of leaves, yellowing and marginal necrosis of leaflets from the central and outer whorls (Varghese, 1934; Menon and Nair, 1952; Menon and Pandalai, 1958). Radha and Lal (1972) identified flaccidity, along with bending or ribbing of leaflets, as the earliest and most consistent visual symptom. Symptom severity varies based on the plant's age, nutritional status, management practices and time since disease onset. Generally, 67-97 % of palms display flaccidity, 38-67 % show yellowing and 28-48 % exhibit marginal necrosis. Young palms (under 10 years) often show 96.8 % flaccidity with minimal yellowing and necrosis, while older palms may exhibit more severe symptoms, including curling and dropping of distal leaf ends (Koshy, 2000).

The disease also causes inflorescence necrosis, inability to produce female flowers and pollen sterility, leading to reduced productivity (Varghese, 1934; Varkey and Davis, 1960). Immature nut shedding may occur early. Advanced cases involve significant root decay, with up to 94.4 % of roots affected (Butler, 1908; Michael, 1964). Diseased palms show reduced root production, degenerated phloem and impaired physiological functions, including water uptake, which is 35 % less than in healthy palms (Ramadasan, 1964). The characteristic symptoms of coconut root wilt disease observed under field conditions are shown in **Figures 1–6**.

Fig. 1 Yellowing of Leaves in Older Palms



Fig. 2 Yellowing of leaves in younger palms

Fig. 3 Flaccidity of leaves

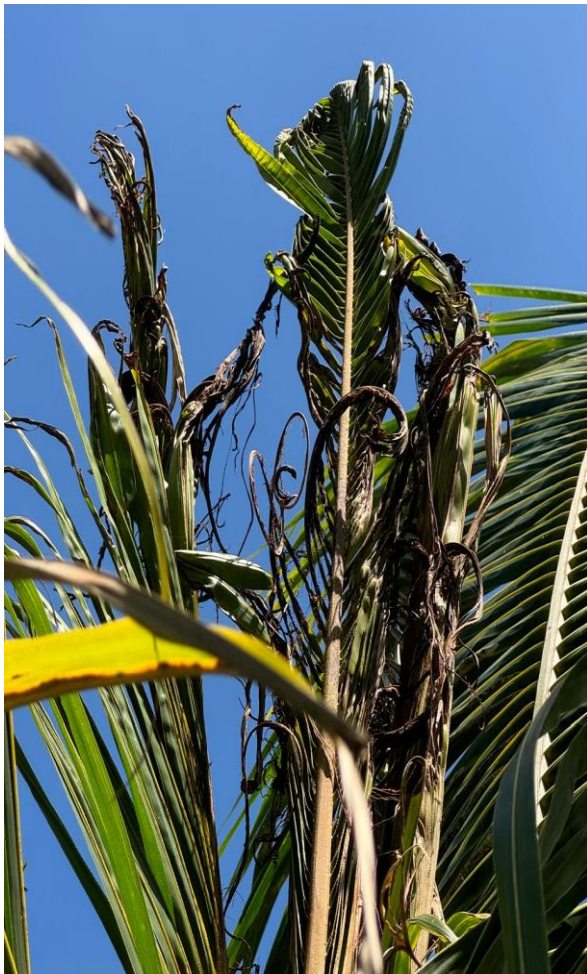


Fig. 4 Marginal necrosis of leaflets (Leaf rot)



Fig. 5 Inflorescence necrosis



Fig. 6 Crown rot

5. Molecular characterization of root wilt phytoplasma

Sharmila et al., (2004) made a deep groundwork for understanding the causative agent of Kerala wilt disease (or root wilt disease, RWD) in coconut palms by cloning and sequencing the associated disease with phytoplasma. But this initial sequence (GenBank accession no. AY158660) showed no homology with known phytoplasmas, it sparked further research into the correct identification and classification of this coconut root wilt disease. Edwin and Mohankumar (2007) subsequently performed phylogenetic analysis and placed the coconut root wilt as phytoplasma in the 16SrIV group. However, due to the unique nature of the sequence, additional studies were required to identify the proper agent of causing disease in coconut.

Based on the ideas of previous study, the present study focused on characterizing the 16S rRNA and secA genes of the RWD phytoplasma for accurate classification. Spindle leaf samples from symptomatic coconut palms in Kayankulam, Kerala, were collected and DNA was extracted using a modified phytoplasma enrichment protocol. Semi-nested/nested PCR was performed with various primers as primer pair (1F7/7R3-1F7/7R2) was found to be the most effective for detecting the RWD phytoplasma, producing consistent results across multiple trials. The sequences were then deposited in NCBI GenBank. The study concluded that the RWD phytoplasma is a '*Candidatus Phytoplasma oryzae*'-related strain and classified it in the 16SrXI-B subgroup. This marks the first report of an association between the 16SrXI-B phytoplasma subgroup and coconut, expanding our understanding of phytoplasma diversity and its impact on coconut palms globally.

Root wilt disease severely affects coconut cultivation in southern India. This study identifies and classifies the phytoplasma associated with the disease in Kerala. Using specific primers, the 16S rRNA and secA genes were amplified and analysed, revealing that the phytoplasma belongs to the rice yellow dwarf group and is related to '*Candidatus Phytoplasma oryzae*'. In silico restriction digestion further classified it into the 16SrXI group, specifically the 16SrXI-B subgroup, aligning it with sugarcane white leaf and arecanut yellow leaf disease phytoplasmas (Manimekalai et al., 2014).

Nair et al. (2016) developed a loop-mediated isothermal amplification (LAMP) assay targeting the phytoplasma 16S rRNA gene for rapid molecular confirmation of root wilt disease. Sequence verification and restriction enzyme analysis confirmed the specificity of the amplified products, while real-time LAMP consistently detected the 16SrXI-B phytoplasma with greater robustness than conventional nested PCR. The assay provided a rapid and reliable molecular tool for confirming phytoplasma infection in symptomatic palms and screening planting material.

Complementing nucleic acid-based diagnostics, Sasikala et al. (2010) standardized a modified Direct Antigen-Coated (DAC)-Indirect ELISA using phytoplasma-specific polyclonal antibodies and leaf-disc antigen. The optimized protocol reduced the assay duration to approximately 7 hours while maintaining 98% sensitivity

compared with visual diagnosis. The assay facilitated the identification of latent infections and has been widely used for screening disease-free mother palms in breeding programmes and confirming disease occurrence in newly affected regions.

Advances in functional genomics further enhanced the molecular understanding of coconut root wilt disease. Rajesh et al. (2018) employed comparative RNA sequencing (RNA-Seq) to investigate transcriptomic differences between healthy and root wilt-infected Chowghat Green Dwarf palms. Differential expression analysis identified 2,718 significantly regulated transcripts involved in cell wall biogenesis, hormone signalling, primary and secondary metabolism, transport processes and plant–pathogen interactions, providing the first comprehensive insight into host responses to phytoplasma infection and identifying candidate genes associated with disease susceptibility and resistance.

Building upon these transcriptomic resources, Verma et al. (2017) developed the first Coconut Transcriptome Database (CnTDB) dedicated to root wilt disease. The database comprises 285,235 assembled transcripts, 22,021 differentially expressed genes, transcription factors, functional annotations, KEGG pathways, and numerous SSR, SNP and InDel markers. This comprehensive genomic resource provides valuable molecular markers and candidate genes for functional genomics, resistance breeding and future molecular investigations of coconut root wilt disease.

Recent advances in proteomics have further strengthened the identification of coconut root wilt disease by enabling the discovery of host protein biomarkers specifically associated with phytoplasma infection. Jayaker et al. (2025) employed comparative proteomic analysis using two-dimensional gel electrophoresis coupled with MALDI-TOF/TOF mass spectrometry to identify proteins that were differentially expressed in healthy and root wilt-infected coconut palms. Among the identified proteins, BTB/POZ domain and ankyrin repeat-containing protein NPR2 and mannan endo-1,4- β -mannosidase were recognized as potential biomarker proteins because of their close association with phytoplasma-induced host responses. Bioinformatic analyses identified unique signature peptides, VLEKCIRRIARSNL (NPR2) and HQVEGFEDAHRD (mannan endo-1,4- β -mannosidase), which exhibited high specificity and antigenic properties. These signature peptides provide molecular targets for developing highly specific antibody-based diagnostic assays capable of distinguishing infected palms from healthy ones.

Unlike conventional PCR-based approaches that directly target phytoplasma DNA and may be limited by low pathogen titre and non-specific amplification, proteomics-based biomarkers exploit host proteins uniquely induced during phytoplasma infection, thereby offering an alternative strategy for early, accurate and reliable identification of root wilt disease. The identification of these disease-specific biomarker proteins represents a significant advancement towards developing rapid, cost-effective and field-deployable diagnostic tools for coconut root wilt disease.

6. Management strategies to control root wilt disease

Despite several decades of research, an effective cure for coconut root wilt disease has not yet been developed because of the obligate nature of phytoplasma. Therefore, current management focuses on minimizing disease spread, maintaining palm vigour and improving productivity through an integrated approach involving cultural, physical, chemical and biological practices together with the use of tolerant planting materials (Maheswarappa and Anithakumari, 2005).

6.1 Cultural methods

Several cultural practices have been recommended to improve the productivity of root wilt-affected coconut gardens. Srinivasan (1999) recommended the removal of severely diseased and uneconomic palms producing fewer than ten nuts annually. Incorporation of green manure crops such as cowpea, sunnhemp and other legumes during April–May followed by incorporation into the soil during September–October improves soil organic matter and enhances beneficial microbial activity. Adequate irrigation (approximately 250 L palm⁻¹ week⁻¹), proper drainage and adoption of suitable intercropping or mixed cropping systems are also essential for sustaining palm health.

Mixed cropping with cocoa has shown considerable economic benefits in root wilt-affected gardens and reported a 27–35% increase in coconut yield under cocoa-based mixed cropping systems, with double hedge planting initially producing higher yields. However, long-term evaluation indicated that single hedge cocoa planting was more productive after ten years (Anon., 1988).

Balanced nutrient management is another important component of disease management. Krishnakumar et al. (2015) recommended annual application of 500 g N, 300 g P₂O₅, 1250 g K₂O and 250 g magnesium sulphate per palm, applied in two equal splits during May–June and August–September. Fertilizer doses for young palms should be adjusted according to age, while micronutrients, particularly boron (120 g borax palm⁻¹), should be applied based on soil analysis and deficiency symptoms.

6.2 Physical methods

6.2.1 Sanitation

Continuous surveillance and identification of disease hotspot areas facilitate early intervention and reduce disease spread to adjoining plantations (Ramjegathesh et al., 2019). Sanitation is an important component of integrated disease management. Removal and destruction of severely infected palms reduce the source of inoculum and help minimize further spread of the disease within plantations (Thomas et al., 2014).

6.2.2 Field hygiene

Regular removal of diseased leaves, fallen debris and infected plant residues reduces potential inoculum sources. Proper disposal of infected plant material further minimizes pathogen persistence within coconut plantations (Thomas et al., 2014).

6.2.3 Drainage improvement

Efficient drainage is essential in waterlogged areas because prolonged soil moisture aggravates disease severity. Construction of drainage channels and improvement of field topography reduce excess moisture and improve root health.

6.2.4 Mulching

Application of organic mulches such as coconut husk, coir pith and green manure conserves soil moisture, moderates soil temperature and improves soil physical properties, thereby enhancing root growth and reducing susceptibility of palms to root wilt disease (Sreekumar et al., 2013).

6.3 Chemical methods

Several chemical treatments have been evaluated to reduce disease severity and improve palm productivity. Dwivedi et al. (1980) reported reductions in leaflet yellowing and flaccidity together with increased nut yield following application of micronutrients, ascorbic acid, phenolic compounds and their combinations. Similarly, CPCRI (Anon., 1986) recommended annual application of 500 g MgO palm⁻¹ to maintain productivity in disease-endemic areas.

Among antibiotics, oxytetracycline hydrochloride has shown temporary remission of disease symptoms. Pillai et al. (1991) and Srinivasan (1999) observed that oxytetracycline treatment reduced symptom severity by lowering phytoplasma populations, although it did not eliminate the pathogen. Monthly root feeding with 100 ml of 1000 ppm oxytetracycline hydrochloride for up to one-year improved palm vigour and nut yield. Since tetracyclines inhibit protein synthesis by binding to the 30S ribosomal subunit, they suppress phytoplasma multiplication rather than eradicate the pathogen, resulting in symptom recurrence after discontinuation of treatment (Ramjegathesh et al., 2016).

6.4 Chemical inducers

Chemical elicitors such as salicylic acid (SA) have been investigated for enhancing host resistance against coconut root wilt disease. Raj et al. (2013) demonstrated that SA activates defence-related enzymes and metabolites, thereby strengthening host defence responses. Likewise, Kumar et al. (2017) reported that SA application significantly reduced disease severity and improved palm productivity. Field studies further showed that foliar application of 100 ppm SA reduced disease incidence by 30–40% and increased nut yield by approximately 25% compared with untreated palms (Kumar et al., 2017).

6.5 Biological methods

Biological management has emerged as an environmentally sustainable strategy for improving palm health in root wilt-affected plantations. Application of *Bacillus subtilis* and *Trichoderma viride* effectively reduced leaf rot severity associated with root wilt disease and improved palm vigour under field conditions (Srinivasan et al., 2010). Similarly, a microbial consortium comprising *P. fluorescens* + *B. subtilis* + *T. viride* (100 g each combined with 5 kg FYM palm⁻¹) enhanced chlorophyll and protein content while reducing stomatal resistance, indicating improved physiological performance and increased tolerance to disease (Ramjegathesh et al., 2016).

Johnson et al. (2017) further demonstrated that a microbial consortium containing *P. fluorescens* Pfl, *B. subtilis* Km1 and *T. viride* effectively managed leaf blight caused by *Lasiodiplodia theobromae* in coconut, with annual application of 300 g consortium palm⁻¹ together with farmyard manure providing the best field performance.

Plant growth-promoting rhizobacteria (PGPR) are also known to suppress plant diseases through multiple mechanisms, including production of antimicrobial metabolites and induction of systemic resistance (ISR). Although limited information is available regarding their direct role against phytoplasma diseases, PGPR-mediated ISR has been well documented in several crops (Beckers and Conrath, 2007). Mixed inoculation of compatible PGPR strains generally provides superior disease suppression compared with single-strain applications because of complementary modes of action (Ramos Solano et al., 2008). Species belonging to *Pseudomonas*, *Bacillus* and *Trichoderma* not only promote plant growth but also activate defence responses and enhance tolerance against diverse pathogens (Harman et al., 2004).

Intercropping and integrated farming systems further contribute to sustainable management of root wilt-affected gardens. Intercropping with cassava, elephant foot yam and greater yam increased coconut yield while reducing disease severity (Menon and Nayar, 1978), whereas mixed cropping systems produced 27–35% higher yields than monocropping (Nair et al., 1975). Integration of irrigation, balanced fertilization and biological approaches for managing associated leaf rot has also been recommended for maintaining productivity in affected plantations (Koshy et al., 2001).

Development of compatible microbial consortia offers greater reliability under field conditions than individual microbial inoculants. The use of antagonists possessing different mechanisms of action reduces variability in biological control and improves efficacy across diverse environments (Grosch et al., 2012). Similar advantages have been demonstrated in several crops using bacterial consortia comprising *Bacillus*, *Pseudomonas*, *Curtobacterium* and *Serratia* species (Raupach and Kloepper, 1998; Asaka and Shoda, 1996; Someya et al., 2000; Suryadi et al., 2011). Commercial formulations based on *Bacillus subtilis* have also shown considerable potential for sustainable disease management (Jayaraj et al., 2005; Mathivanan et al., 2005).

7. CONCLUSION

Coconut root wilt disease continues to represent one of the most challenging phytoplasma diseases affecting coconut cultivation because of its complex biology, prolonged latent period and absence of an effective curative treatment. Progressive improvements in molecular characterization have resolved the long-standing uncertainty surrounding disease etiology and established the phytoplasma as the principal causal agent. The integration of molecular diagnostics, transcriptomics, proteomics and comparative genomic analyses has considerably expanded the understanding of host-pathogen interactions and disease-associated molecular responses. Recent identification of protein biomarkers and candidate resistance-associated genes demonstrates the transition from conventional symptom-based diagnosis toward precision diagnostic approaches. Despite these advances, disease management remains dependent on integrated cultural practices, nutritional management, sanitation, biological interventions and tolerant planting materials that primarily reduce disease impact rather than eliminate infection. The convergence of advanced molecular technologies with sustainable management strategies provides an important opportunity to improve disease surveillance, facilitate early detection and enhance plantation productivity. Collectively, current scientific evidence indicates that combining sensitive diagnostic platforms with molecular breeding and integrated crop management will strengthen long-term control strategies and contribute to the sustainable production of coconut in disease-endemic regions.

8. Future Directions

Future research should prioritize the development of highly sensitive, field-deployable diagnostic platforms capable of detecting phytoplasma during asymptomatic stages to facilitate timely disease management. Multi-omics approaches integrating genomics, transcriptomics, proteomics and metabolomics should be employed to elucidate molecular mechanisms governing host susceptibility, pathogen virulence and disease progression. Functional validation of candidate resistance genes and phytoplasma-responsive proteins using advanced molecular techniques will accelerate marker-assisted selection and resistant cultivar development. Artificial intelligence-assisted disease prediction models, remote sensing technologies and precision agriculture tools offer promising opportunities for large-scale disease surveillance and risk assessment. Investigation of insect vector biology, phytoplasma transmission dynamics and microbial interactions within the coconut microbiome may reveal novel targets for biological intervention. Integrating these emerging technologies with sustainable agronomic practices will establish a comprehensive disease management framework capable of improving coconut productivity and strengthening resilience against root wilt disease under changing environmental conditions.

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10. Credit authorship contribution statement

Akilesh: Writing- review & editing, Writing – original draft, Visualization, software, Resources, Methodology, Formal analysis, Data curation. Dr. S. Sundravadana: Writing- review & editing, Validation, Supervision, Conceptualization. Dr. G. Karthikeyan: Writing- review & editing, Validation, Supervision. Dr. K. Angappan: Writing- review & editing, Validation, Supervision. Dr. C. Sudhalakshmi and Dr. M. Jayakanthan: Writing- review & editing, Validation, Supervision

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