

Review article

Cashew Fusarium wilt: Status and management

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Abstract: The cashew nut crop, *Anacardium occidentale* L., is one of the most important export cash crops in Tanzania, contributing to the national income and that of over 500,000 households. Cashew yields have been recorded as low for the last three decades. Biotic restrictions, including insect pests and diseases, have predominantly contributed to the recorded yield loss. Despite efforts to develop cashew protection technologies and new high-yielding, disease-tolerant cashew varieties, the situation has remained unchanged for the last decade. Fusarium wilt caused by *Fusarium oxysporum* is the major soilborne fungal pathogen affecting cashew in Tanzania. The devastating waves of Fusarium wilt epidemics have been observed in a diversity of crops globally, affecting both production and productivity. The infestations caused by Fusarium wilt may result in a loss of up to 100 percent if no precautionary measures are taken promptly. Presently, no pathogenic races are reported in the cashew crop despite the variation in symptoms exhibited in cashew plants. The development of molecular tools (specific primers) to distinguish between formae speciales and or pathogenic races is of paramount importance towards the establishment of precise and accurate management strategies. This is accompanied by an incorporation of a molecular breeding programme, which involves techniques for identifying molecular markers linked to genes controlling Fusarium wilt. However, integrated disease management, which encompasses cultural, chemical, and biological control, is also of paramount importance in preventing Fusarium wilt of cashew.

Keywords: Cashew, Disease status, *Fusarium oxysporum*, Fusarium wilt, Fungal pathogen

Introduction

Overview of cashew crop

Cashew *Anacardium occidentale* L. is an evergreen tree nut crop widely cultivated across tropical and subtropical regions (Masawe and Kapinga, 2016). Native to

tropical Central and South America, its center of origin is believed to be in northeastern Brazil (Asna and Menon, 2024). The generic name *Anacardium* was assigned by Linnaeus, inspired by the heart-shaped appearance of its pseudo fruit. Cashew belongs to the family Anacardiaceae, which comprises over 60 genera and approximately 400 species of trees

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and shrubs (Masawe and Kapinga, 2016). According to Mitchell and Mori (2020), the genus *Anacardium* includes eight tropical American species. Botanically, cashew is a medium-sized evergreen tree that can grow up to 20 meters in height. It develops a robust root system, characterized by a prominent taproot and an extensive network of lateral and sinker roots. Cashew thrives in loamy, sandy, or well-drained soils, although its growth is influenced by environmental factors such as temperature (ranging from 7 °C to 40 °C) and annual rainfall (between 300 and 4,000 mm).

Cashew is among the most economically significant export crops globally, with major production occurring across three continents: America, Africa, and Asia. Leading producers include Brazil, India, Vietnam, Mozambique, Côte d'Ivoire, Benin, Ghana, Nigeria, Tanzania, Togo, Burkina Faso, Gambia, Guinea-Bissau, the Philippines, Senegal, Sri Lanka, and emerging producers such as Ethiopia and Zambia. In Tanzania and other countries, such as Kenya, Mozambique, Madagascar, Uganda, Malawi, and Zambia, cashew serves as a vital source of income for smallholder farmers.

In Tanzania, cashew is a key export crop, supporting the livelihoods of over 500,000 households (Lilai *et al.*, 2022). Initially cultivated in coastal regions of Lindi, Mtwara, Ruvuma (Tunduru district), Coast, and Tanga, these areas are recognized as traditional cashew-growing zones. Due to its economic importance, cultivation has expanded into inland regions previously not associated with cashew farming. Today, cashew is grown in more than 17 regions, including Morogoro, Dodoma, Singida, Tabora, Kigoma, Katavi, and Mbeya. Despite this expansion, approximately 80% of Tanzania's cashew production still originates from the southeastern regions of Lindi, Mtwara, and Tunduru (Masawe and Kapinga, 2017).

Like other crops, cashew is vulnerable to a range of diseases, notably powdery mildew *Oidium anacardii* (Mboya and Sijaona, 2013), leaf and nut blight *Cryptosporiopsis* spp. (Majune *et al.*, 2018), and anthracnose

Colletotrichum gloeosporioides (Bukari *et al.*, 2025). Other diseases of lesser economic impact include dieback *Phomopsis anacardii*, Pestalotia leaf spot *Pestalotia heterocornis*, and macro-fungi linked to cashew wilt *Parasitoidus cashewii* (Mbasa *et al.*, 2025). These diseases have been recognized as major constraints to cashew production since the 1970s (Martin *et al.*, 1997), with potential yield losses ranging from 70% to 100% if not properly managed (Martin *et al.*, 1997; Sijaona *et al.*, 2006). Fortunately, diagnostic and management strategies for these diseases are now available to farming communities, thanks to the contributions of experienced cashew pathologists.

Currently, *Fusarium wilt* has emerged as the most devastating disease affecting cashew, significantly reducing both yield and productivity (Tibuhwa and Shomari, 2016; Lilai *et al.*, 2021). The disease causes complete wilting of trees and can lead to total crop loss (Mbasa *et al.*, 2020; Tibuhwa and Shomari, 2016). A five-year prevalence survey conducted between 2018 and 2023 revealed that *Fusarium wilt* resulted in the loss of approximately 49.6 metric tonnes of raw cashew nuts, translating to an estimated monetary loss of 133,354,560 Tanzanian shillings (approximately USD 53,341.82).

Since Tanzania's independence in 1961, cashew production has experienced fluctuations due to various factors, including policy and market regulations, particularly those affecting exports, as well as other non-sectoral influences (Mitchell, 2004). However, biotic stresses, especially diseases, have remained the most persistent constraints.

Cashew production saw a remarkable recovery from its near collapse in the 1980s, with output rising from 29,868 metric tonnes in 1990/91 to 121,207 metric tonnes in 1999/2000. This resurgence was largely driven by the 1986 economic reforms, particularly trade liberalization, which allowed farmers to export raw cashew nuts and receive timely payments. This financial empowerment enabled them to invest in agricultural inputs, such as sulfur dust, which was crucial for managing powdery mildew at the time (Mitchell, 2004).

Despite historical fluctuations, current cashew yields have surpassed 300,000 metric tonnes annually (Bank of Tanzania, 2018), although this remains below the crop's full potential. The recent yield improvements are attributed to enhanced cashew technologies, including the breeding of disease-resistant varieties and the adoption of advanced crop protection strategies (Salifou and Masawe, 2018; Lukurugu *et al.*, 2022).

While breeding and protection efforts have significantly boosted cashew productivity, the industry still faces challenges due to unstable production. The primary limiting factor remains the crop's susceptibility to biotic and abiotic stresses, particularly fungal diseases like *Fusarium* wilt. Therefore, developing robust cashew protection technologies and breeding varieties resistant to major diseases is a top priority for cashew research programs. This review focuses on the current status and management strategies for *Fusarium* wilt in cashew.

Fusarium wilt

Fusarium wilt is currently one of the most devastating soilborne diseases affecting cashew production in Tanzania. Its impact extends beyond cashew, affecting other economically important crops such as chickpeas, bananas, tomatoes, and sesame, thereby contributing to increased poverty and food insecurity on a global scale (Tushemereirwe *et al.*, 2004; Tibuhwa and Shomari, 2016; Mbasu *et al.*, 2020; Lilai *et al.*, 2021; Dyussebayev *et al.*, 2021). Historically, *Fusarium* wilt in Tanzania has been reported primarily in annual crops, including banana, tomato, and cotton (Machang'u *et al.*, 2021; Kibani and Hillocks, 1998). In cashew, the disease was first observed in 2012, with the causative agent identified in 2016 in Magawa village, Mkuranga district, located in the Coast region (Tibuhwa and Shomari, 2016).

Following its initial detection, a rapid increase in infections was recorded across southeastern Tanzania, particularly in districts such as Liwale, Nachingwea, Ruangwa, and Mtama in Lindi region, and Tandahimba,

Newala, Masasi, and Mtwara Rural in Mtwara region (Lilai *et al.*, 2021). More recently, the disease has also been reported along the northeastern coast of the Indian Ocean, notably in Pangani district of Tanga region (Mbasu *et al.*, 2025).

Currently, the incidence of *Fusarium* wilt in cashew is escalating, with new cases emerging in previously unaffected growing areas. Moreover, reinfestation has been observed in earlier hotspots, especially in bordering cashew fields. For instance, a recent prevalence survey conducted in early 2024 recorded approximately 55 cashew trees dead and another 101 showing clear symptoms of *Fusarium* wilt. This trend underscores the urgent need for enhanced surveillance, early detection, and integrated disease management strategies to curb further spread and mitigate losses.

Biology and causal agent

Fusarium wilt of cashew is caused by *Fusarium oxysporum*, a soilborne fungal pathogen (Fang *et al.*, 2012; Lilai *et al.*, 2021). Its taxonomical position is as follows: Kingdom Fungi; Phylum Ascomycota; Class Ascomycetes; Subclass: Sordariomycetidae; Order: Hypocreales. The pathogen is a complex entity, encompassing distinctive features of anamorphic, filamentous, and morphologically undifferentiated fungal species, comprising saprophytes, antagonists, and pathogens of plants, animals, and humans (O'Donnell and Cigelnick, 1999). As a phytopathogen, it causes vascular wilt, damping off, and root rot. *F. oxysporum* comprises all the species, varieties, and forms recognised by Wollenweber and Reinking (1935) within an intragenic grouping called section *Elegans*. It is an anamorphic species that encompasses numerous plant pathogenic strains, causing wilt diseases in a wide range of crops (O'Donnell *et al.*, 2009; Mostert *et al.*, 2017). Aoki *et al.* (2013) detailed the taxonomy and current position of *F. oxysporum* year by year, since Snyder and Hansen (1940). In their review, they detailed the concept of *forma specialis*, which was first introduced into *Fusarium* taxonomy by Snyder and Hansen (1940, 1941, 1945), based on

the specialization of pathogenicity plant genera and families. The emergence of several variants under the *F. oxysporum* species complex has management implications for Fusarium wilt (Patel *et al.*, 2022).

Pathogenesis

Pathogenesis is the overall process of disease development that occurs within the host. It is the sequence of events from initial infection to symptom generation (Lucas, 1998; Groenewald, 2006). One of the most critical steps in the fungal infection is the response mechanism to plant stimuli, which induce important physiological changes, including morphogenic and biochemical alterations. The root exudates released by host plants are among the important stimuli to infecting pathogens. During pathogenesis, the fungal pathogen penetrates the first line of defence made of plant cell walls. Before entry, the fungal pathogen secretes important hydrolytic enzymes for the lysis of plant cell walls. These enzymes include cellulases, proteases, and pectinases (Verlent *et al.*, 2004). In the plant cell, the fungal pathogen manipulates the host plant physiology to its own benefit through the secretion of toxins (Knogge, 1996).

Disease symptoms

Externally, Fusarium wilt in cashew typically begins with the gradual loss of chlorophyll in green leaves, leading to chlorosis that progresses to yellow discoloration. This symptom often appears branch-wise, corresponding to the infected root system, and eventually spreads to entire branches, followed by brown discoloration before the plant succumbs. In some cases, leaf symptoms may begin with pale brown to deep brown discoloration, accompanied by gum exudation on the stem bark, ultimately leading to plant death (Mbaso *et al.*, 2021).

Diagnosing Fusarium wilt remains challenging due to its symptom overlap with other soilborne diseases and abiotic stresses such as water deficiency or nutrient imbalance. The delayed onset of leaf symptoms further complicates diagnosis, necessitating internal examination of root and stem tissues through

cross-sectional or longitudinal cuts. Infected vascular tissues typically exhibit distinct brown discoloration. Early and accurate detection of Fusarium wilt across host species is critical for effective disease management (Cahill, 1999; Dyussebayev *et al.*, 2021; Patel *et al.*, 2022).

Fusarium wilt symptoms can easily be mistaken for those caused by other pathogens or environmental factors. For example, in cashew, leaf yellowing due to Fusarium infection may resemble symptoms of water stress or nutrient deficiency. Therefore, a thorough field assessment is essential to accurately identify vascular wilt caused by *F. oxysporum* and distinguish it from other potential causes.

Disease cycle and infection dynamics of Fusarium wilt in cashew

The spread of Fusarium wilt in cashew fields is primarily facilitated through the introduction of pathogens via water runoff, infected planting materials, and various human-related activities. These include the inadvertent use of contaminated tools in previously uninfected areas, contributing significantly to disease transmission (Sankaran *et al.*, 2010; Mbaso *et al.*, 2020).

Fusarium oxysporum, a spore-forming pathogen, is particularly resilient due to its ability to persist in the soil as chlamydospores for over 30 years. These spores remain dormant until favourable environmental conditions trigger their virulence (Lilai *et al.*, 2021; Rafiq *et al.*, 2020). The pathogen typically enters the cashew plant through injured roots, where it proliferates and obstructs the xylem vessels, disrupting water and nutrient transport (Fig. 1).

According to Lucas (1998) and Groenewald (2006), once the hyphae adhere to the root surface, the pathogen may penetrate either indirectly through wounds or directly via the apical root region, where the endodermis is not fully developed. This allows the pathogen to reach and colonize the developing protoxylem. The root cap and elongation zone have also been identified as key entry points in various host crops such as cabbage, cotton, and banana (Rodriguez-Gálvez and Mendgen, 1995; Groenewald, 2006; Rafiq *et al.*, 2020).

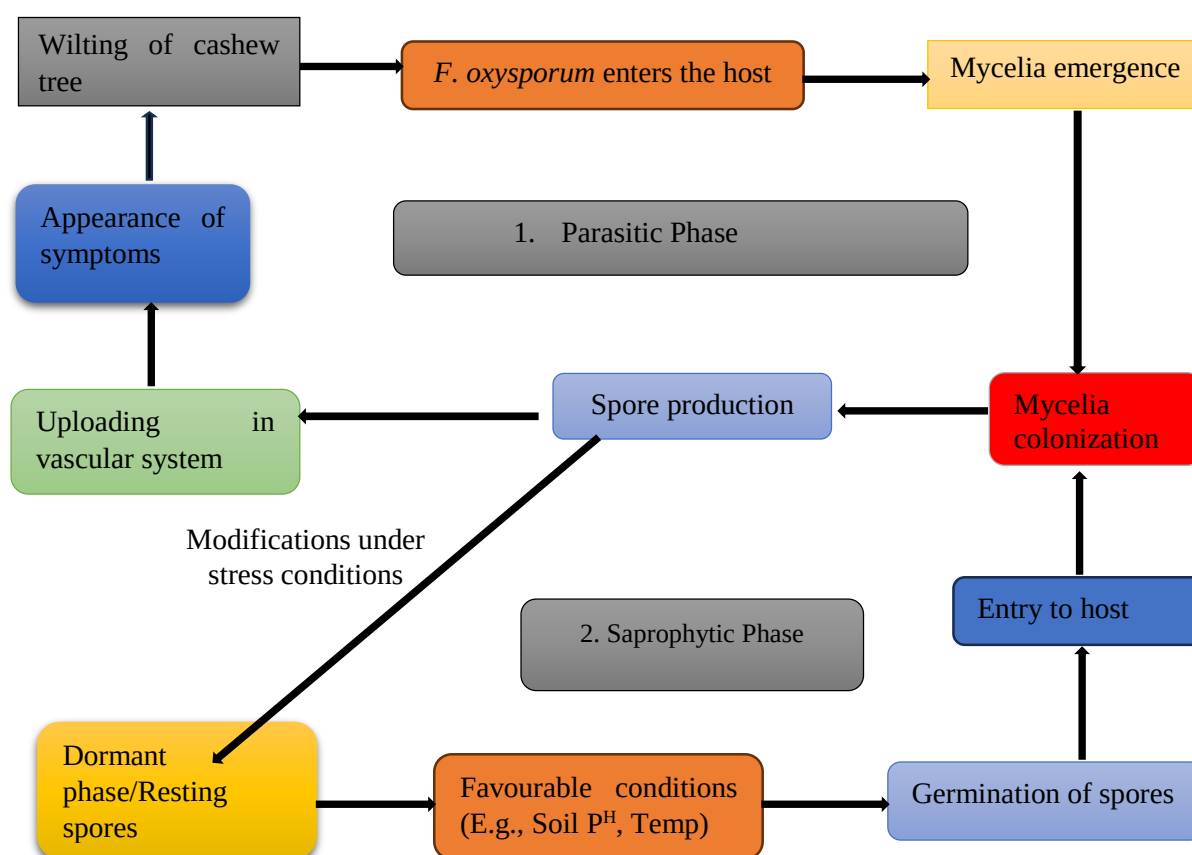


Figure 1 Life cycle of *Fusarium oxysporum* in cashew crop, modified from Rafiq *et al.* (2020). 1. Parasitic phase or infective stage which begins after pathogen entry into the host, colonizing, producing spores and finally uploading in the vascular system. 2. Saprophytic phase begins after spore production, ending with dormant stage before resuming its virulence when favourable conditions are available.

Tibuhwa and Shomari (2016) further emphasized that the pathogen's impact is predominantly observed in the vascular tissues, reinforcing the root as the primary route of infection. The disease can spread to previously healthy cashew fields through multiple pathways, including the movement of infected plant parts, water runoff, and interconnected root systems. Natural root injuries within the rhizosphere facilitate this underground transmission.

Additional vectors include surface water, contaminated soils, infected planting materials, farm equipment, clothing, and footwear. Similar transmission mechanisms have been documented in banana plantations affected by *F. oxysporum* f. sp. *cubense* (FOC), where

footwear and surface water played significant roles in pathogen dissemination (Stover, 1962; Ploetz, 2015).

Moreover, certain field conditions, such as light-textured soils, the presence of multiple water streams, and low microbial diversity in the rhizosphere, can exacerbate the spread and severity of *Fusarium* wilt epidemics (Lilai *et al.*, 2021; Orr and Nelson, 2018; Fang *et al.*, 2012).

Genetic variability of *Fusarium oxysporum*

The virulence form of *F. oxysporum* comprises several different races and pathotypes (Edel-Hermann and Lecomte, 2019; Chen *et al.*, 2024; Yang *et al.*, 2024). The designation of pathogenic races primarily follows Koch's

postulates; i.e., the presumed pathogenic isolates are subjected to pathogenicity tests to induce wilting symptoms. Hence, the variation in the virulence among isolates of *F. oxysporum* is used to designate the pathogenic races. Pathogenic races may differ based on geographical distribution; for example, a study conducted by Dita et al. (2018) revealed the distribution of *F. oxysporum* f. sp. cubense pathogenic races (Foc R4) in the tropics and subtropics. Likewise, Jimenez-Gasco et al. (2004) and Jimenez-Diaz et al. (2015) revealed the presence of pathogenic races of *F. oxysporum* f.sp. *ciceris* affecting chickpea in different geographic locations.

Unlike in other crops, the *F. oxysporum* infecting the cashew crop has yet to be well established as to whether it has genetic variants, i.e., pathogenic races and pathotypes. In cashew, the commonly used genetic markers (genetic markers) in phylogenetic analysis and characterization of *F. oxysporum* are elongation factor-1 α (*EF-1 α* , O'Donnell et al., 1998). Tibuhwa and Shomari (2016) used the EF1/EF2 primer pairs, which are useful in a wide variety of filamentous ascomycetes. The primers targeted an ~700 bp region of EF-1 α , which is over half of the amplicon's length in all known fusaria. It's consistent as a single-copy gene in the genus *Fusarium*, which shows a high level of sequence polymorphism among its closely related species, making this gene one of the important genetic marker regions. Therefore, they used a standard Polymerase Chain Reaction (PCR) protocol to amplify the *EF-1 α* gene region using ef1 (forward primer: 5'-ATGGGTAAGGA(A/G)GACAAGAC-3) and ef2 (reverse primer: 5'-GGA (G/A)GTA CCAGT(G/C)ATCATGTT-3') designed by O'Donnell et al. (1998).

Recent investigations by Mbaso et al. (2024) identified over 20 genetically distinct *Fusarium* isolates collected from infected cashew-growing regions in Tanzania. The isolates were artificially inoculated on various host plants, including mango, tomato, cotton, pigeon peas, banana, and cashew seedlings, and examined for the induction of symptoms,

which included chlorosis, leaf yellowing, and wilting. They were then further subjected to molecular analysis. Therefore, the pathogenicity tests revealed that *Fusarium* isolates from different locations induced wilting symptoms in cashew seedlings, while no symptoms were observed in other host plants. This proves that *F. oxysporum* is host-specific; however, molecular identification assays are still underway.

The characterization and identification of *F. oxysporum* races in all cashew-growing areas affected by the pathogen is of paramount importance, particularly in establishing management strategies for the disease (van Dam et al., 2017). For example, developing resistance cashew cultivars against *Fusarium* wilt as part of a breeding program is only possible after accurate identification of pathogenic races.

Nonetheless, the identification of genetic variants using Koch's postulates appears time-consuming and may be misleading, as it involves a robust conventional bioassay. Therefore, to fill this gap, it is imperative to devise appropriate, rapid, consistent, and reproducible testing methods for determining pathogenic races. Such diagnostic methods involve the designation of specific primers that accurately identify forma specialis and their pathogenic races (Fig. 2).

Therefore, to manage *Fusarium* wilt in cashew, a proper diagnostic method needs to be established, particularly the deployment of molecular tools, which have proven effective in many studies.

Management of *Fusarium* wilt

Similar to other crops, managing cashew *Fusarium* wilt is challenging, as it requires a combination of control strategies. The major driver of the development of *Fusarium* wilt of cashew is the primary inoculum of the pathogen. Thus, the management practices for the disease should focus on excluding or reducing the initial pathogen inoculum. Therefore, to achieve this goal, the following control strategies should be smartly followed:

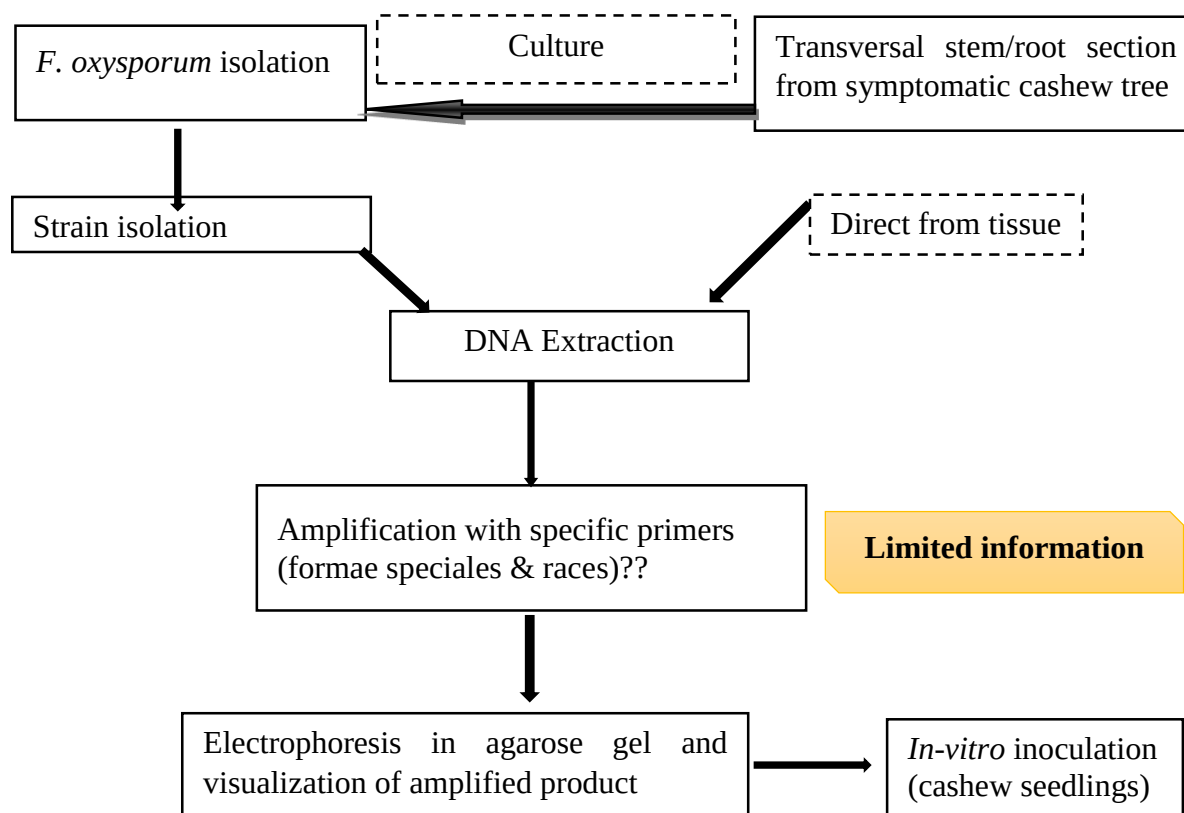


Figure 2 A stepwise PCR identification of *F. oxysporum* causing cashew wilt with specific primers.

Eradication or reduction of the inoculum in soil

Soil harboring a high-density inoculum is a prime source of disease severity. Therefore, such soil can be recovered for agricultural production by reducing its inoculum levels below the threshold level of disease severity. Thus, to achieve this goal, the following methods have been used in the control of Fusarium wilt of cashew.

(i) Chemical Control

Chemical control has proven effective in managing Fusarium wilt in cashew. Field trials conducted by Mbasia *et al.* (2020) demonstrated the efficacy of Carbendazim and Azoxystrobin in reducing disease impact. Specifically, Carbendazim applied at a rate of 10 g/L of water resulted in a 49.4% recovery of cashew plants from an initial disease severity of 50%, while

Azoxystrobin at 15 g/L of water achieved a higher recovery rate of 65.2% under similar conditions. This control strategy has also been applied to other crops, including banana, tomato, oil palm, and cotton (Perez-Vicente, 2014; Landeros *et al.*, 2017). For example, chemical fungicides such as Prothioconazole, Tebuconazole, Prochloraz, Fludioxonil, Guazatine, Captan, Thiram, Mancozeb, Thiophanate-Methyl, Thiabendazole, and Iprodione have also been used to control *Fusarium* species (Mihajlović *et al.*, 2017). Nevertheless, the prolonged use of fungicides harms the rhizosphere microbiome, leading to reduced soil fertility and productivity (Dubey *et al.*, 2007). Emphasizing this, many studies have demonstrated adverse soil effects associated with the frequent use of fungicides, including the lowering of soil enzyme activities, which are of utmost importance as indicators of soil health.

Disturbances in biochemical reactions, such as the mineralization of organic matter, ammonification, and nitrification, also occur in this process. Thus, the extreme use of chemical fungicides has implications for the environment and microbial ecology, leading to their unsustainability. However, studies have shown reduced effects on other biota in the case of controlling *Fusarium* wilt of cashew (Mbasa *et al.*, 2024).

(ii) Biological control

The use of biological control agents (BCAs) has been widely recognized as an effective strategy for managing a range of soilborne and foliar diseases (Lilai *et al.*, 2022; Oiuphisittraiwat, 2024). These agents offer a sustainable and environmentally friendly alternative to chemical pesticides, particularly in controlling soilborne pathogens such as *Fusarium*, *Rhizoctonia*, *Pythium*, and *Phytophthora* (Sellappan *et al.*, 2009). BCAs consist of beneficial microbes that suppress pathogens through various mechanisms, including competition, antibiosis, parasitism, and the induction of plant defense responses (Köhl *et al.*, 2019).

Their inhibitory potential is primarily attributed to their ability to colonize the rhizosphere, where they compete for space and nutrients while producing metabolites that are toxic to invading pathogens (Valarmathi, 2020). Commonly used BCAs include *Trichoderma* spp., known for their antagonistic activity against soilborne pathogens and their role in promoting plant growth; *Bacillus* spp., which produce antibiotics and enzymes that inhibit fungal development; and *Pseudomonas* spp., recognized for their production of siderophores and antifungal compounds (Lilai *et al.*, 2025a). Additionally, Arbuscular Mycorrhizal Fungi (AMF) contribute to improved nutrient uptake and systemic resistance in host plants (Umer *et al.*, 2025).

Unlike chemical control methods, BCAs leave no toxic residues and are ecologically safe (Dubey *et al.*, 2007). Their efficacy has been demonstrated in both controlled and field conditions. For instance, *Bacillus* strains and

Trichoderma asperellum have been evaluated for their potential to suppress *F. oxysporum*, the causal agent of cashew wilt. Under screenhouse conditions, cashew seedlings treated with these bioformulations showed significantly lower disease severity (0–7.54%; $p < 0.05$) compared to untreated seedlings, which recorded severity levels ranging from 0 to 27.27%. Field trials conducted over two consecutive seasons (2019/2020 and 2020/2021) further confirmed their effectiveness, with treated cashew trees exhibiting reduced disease severity (0–11.49% and 0–12.98%) compared to untreated controls (60.05% and 59.71%; $p < 0.001$) (Lilai *et al.*, 2022).

Supporting evidence from other studies reinforces these findings. Nautiyal (1997) demonstrated the *in vitro* efficacy of *Pseudomonas fluorescens* in suppressing *F. oxysporum* f. sp. *ciceris*, while Herrera-Téllez *et al.* (2019) reported the protective role of *Trichoderma asperellum* in enhancing tomato plant resistance against *F. oxysporum*. These results highlight the colonization competence of BCAs in soils with high pathogen inoculum density, proving their effectiveness in reducing inoculum levels to non-damaging thresholds.

(iii) Cultural practices

Cultural control practices represent invaluable components of an integrated disease management strategy, particularly for smallholder and commercial farmers. These methods focus on preventing the establishment and spread of pathogens by modifying the environment to create conditions that are unfavorable for disease development (Perez-Vicente, 2014a). Through practices such as crop rotation, sanitation, proper spacing, and soil management, cultural controls aim to suppress the survival and proliferation of soilborne inoculum. Ultimately, their goal is to reduce pathogen levels in the soil to below the threshold required for disease expression, thereby minimizing the risk of outbreaks and enhancing crop resilience. Some of the cultural practices used in the prevention of *Fusarium* wilt of cashew are included.

Screening of resistance cashew cultivars

The use of resistant cultivars remains one of the most effective and economically viable strategies for managing soilborne diseases. This approach has proven successful in controlling Fusarium wilt in crops such as chickpea and banana (Dita *et al.*, 2010; Xu *et al.*, 2022; Visen *et al.*, 2024). Resistant varieties not only reduce dependence on chemical inputs but also contribute to long-term yield stability and environmental resilience (Panth *et al.*, 2020).

In cashew, resistance to *F. oxysporum*, the pathogen responsible for wilt disease, varies across cultivars and is shaped by both genetic and physiological factors. Advances in plant pathology have uncovered key resistance mechanisms that can guide screening and selection in cashew breeding programs. Insights from other crops have identified several resistance genes that may serve as molecular markers in cashew. These include Nucleotide-Binding Site–Leucine-Rich Repeat (NBS-LRR) genes, which trigger hypersensitive responses upon pathogen detection; Pathogenesis-Related (PR) genes such as PR-5 (NP24) and β -glucanase, which contribute to systemic acquired resistance through cell wall degradation and defense signaling; and genes involved in Reactive Oxygen Species (ROS) production, including NAD (P)H oxidases, which mediate oxidative bursts to inhibit pathogen colonization (Dmitriev *et al.*, 2017). Additionally, RNA interference (RNAi)-based resistance, particularly Host-Induced Gene Silencing (HIGS), has shown promise in tomato by targeting *F. oxysporum* fasciclin-like protein genes (FoFLP1, FoFLP4, FoFLP5) (de Lamo and Takken, 2020; Dmitriev *et al.*, 2017).

Although these genes have not yet been fully characterized in cashew, their functional analogs may exist and could be identified through transcriptomic or comparative genomic studies. Complementing molecular approaches, resistance screening should also incorporate field and greenhouse trials under controlled inoculation to evaluate disease severity and recovery rates. Histological assessments of vascular discoloration, root integrity, and tissue

colonization, as well as studies on endophyte interactions, are equally important. Notably, non-pathogenic strains such as *F. oxysporum* Fo47 have been shown to elicit localized immune responses and suppress virulent strains independently of classical SAR/ISR pathways (Chauhan and Rajam, 2024).

Currently, screening and selection of cashew cultivars for resistance to Fusarium wilt is underway at the Tanzania Agricultural Research Institute–Naliendele experimental center. However, the deployment of resistant cultivars may require additional time due to the complexity of screening procedures, which involve both laboratory and field evaluations, as well as challenges related to undesirable agronomic traits in some candidate cultivars.

Physical removal of crop residues

This practice involves the removal and destruction of wilted cashew trees, which, in infected fields, act as reservoirs for the resting spores (chlamydospores) of *F. oxysporum*. To effectively reduce the inoculum load, affected trees are felled, their branches segmented into smaller pieces, gathered at a designated site, and thoroughly incinerated (Tibuhwa and Shomari, 2016).

Sanitation

Sanitation in cashew farming encompasses maintaining field hygiene and ensuring the cleanliness of farm tools and equipment. Soil particles clinging to boots, shoes, and cutting tools such as chainsaws should be thoroughly cleaned and, where necessary, sterilized using disinfectants like sodium hypochlorite. Additional measures include the removal and destruction of infected plant residues and fallen nuts, as well as minimizing movement between diseased and healthy cashew fields without proper decontamination of footwear and clothing. Regular disinfection of tools is essential to prevent the spread of *F. oxysporum* spores, as well as other soilborne pathogens, such as *Phytophthora* spp., *Verticillium* spp., and various *Fusarium* species (Perez-Vicente *et al.*, 2014).

Cover crops

One of the important cultural control practices is the use of a cover cropping system to prevent the upsurge of pathogens. This is a disease-suppression method that involves the use of suppressive cover crops. For example, in the control of cashew *Fusarium* wilt, crops such as mucuna, cowpea, soybean, and green gram are used to enrich soils with low fertility. This has been observed to increase the number of rhizosphere microbes exponentially, hence enhancing competition with pathogens. In addition, the cover crops have also been observed to elevate the total soil nitrogen, available phosphorus, and potassium. The disease assessment also showed that the cover crops have been able to reduce the inoculum level below the threshold of disease severity (Lilai *et al.*, 2025b). Similarly, studies conducted by Perez-Vicente *et al.* (2014), Yang *et al.* (2023), and Cao *et al.* (2024) revealed that mineral nutrition elements and pH are potential factors for suppressing *Fusarium* wilt in banana. For instance, the presence of high Phosphorus content in the soil reduces the incidence of *Fusarium* wilt (Woltz and Jones, 1981) while the low level of soil nitrogen increases the incidence of *Fusarium* wilt (Lilai *et al.*, 2021).

Intercropping

In cashew farming, we encourage mixed plantings whenever possible, particularly with annual crops that do not harbor insect pests or vectors of disease-causing pathogens. For example, cashew can be intercropped with cowpea, green gram, mucuna, and other economically important crops. It has been observed that the incidence of disease is often lower in intercropped cashew fields than in monocultures (Lilai *et al.*, 2025b). The reason behind this is that the distance between similar plants is greater than in more intensive growing systems, thus it is less likely that inoculum or vectors of pathogens will successfully move from one host to another. The plants intercropped pose physical barriers to the spread of aerial pathogens or their vectors. However, the intervening crops may serve as reservoir

hosts, which is alarming for future infestations. Therefore, precautionary measures should be taken, particularly during the harvest or crop rotation (Yousefi *et al.*, 2024; Cucu *et al.*, 2025).

Breeding measures

In fact, the breeding method for *Fusarium* wilt resistance in the cashew crop is far behind current prevention practices. However, in the cashew crop, some cultivars have been released for resistance to other cashew diseases, including cashew leaf and nut blight, as well as powdery mildew diseases. However, breeding efforts are underway to identify cashew cultivars resistant to *Fusarium* wilt of cashew. Similar to other crops, a breeding program for the cashew crop must pass through three important phases: genetic variation, selection within that particular variation, and evaluation of the selected lines. A breeding program can be performed either conventionally or by integrating genomic technologies (molecular breeding program). Conventional breeding takes time to complete, as it involves tedious crossing (hand pollination) and mass selection of desirable traits against pathogens, whereas molecular breeding takes a shorter period of time compared to the former. In molecular breeding, the selection of segregating plant materials involves either the construction of genetic maps or the use of Marker-Assisted Selection (MAS) (Hasan *et al.*, 2021; Singh *et al.*, 2024; Nair *et al.*, 2024; Kumar *et al.*, 2024). However, the effectiveness of MAS depends on several factors, including a high level of polymorphism and the localization of saturated genomic regions (Hasan *et al.*, 2021).

Conclusions and recommendations

The taxonomic complexity within the genus *Fusarium* presents significant challenges in developing and implementing effective management strategies for *Fusarium* wilt across various crops. Pathogenic species within this genus often induce similar symptoms in host plants, complicating accurate diagnosis and targeted control. In cashew, for example, *F. oxysporum* exhibits diverse symptomatology. In some cases,

infection begins with the yellowing of green leaves, progressing to brown discoloration and eventual wilting, and is occasionally accompanied by gum exudation on the stem bark. In other instances, symptoms initiate with pale brown leaf discoloration that deepens before wilting occurs (Mbaso *et al.*, 2020). This variability suggests the presence of distinct variants within *F. oxysporum*, including different formae speciales and pathogenic races.

Further complicating diagnosis, studies by Perez-Vicente *et al.* (2014) and Jimenez-Fernandez *et al.* (2011) have shown that other *Fusarium* species, such as *F. redolens* and *F. oxysporum* f. sp. *ciceris* (Foc), can produce wilting symptoms indistinguishable from those caused by *F. oxysporum* in chickpea (Bogale *et al.*, 2007). Additionally, similar symptoms may arise from root rot caused by nematodes, bacterial wilt, or fungal-like pathogens such as oomycetes, including *Phytophthora* spp. (Biruma *et al.*, 2007; Ristaino *et al.*, 2020).

To establish effective management strategies for *Fusarium* wilt in cashew, it is essential first to clarify the disease's etiology and epidemiology. This requires the development of accessible molecular protocols capable of accurately identifying and differentiating pathogenic *Fusarium* species into their respective formae speciales and races. Such precision in pathogen identification across different agroecological zones will be instrumental in breeding and deploying resistant cashew cultivars.

Screening for resistance among cashew genotypes should therefore be prioritized, supported by the development of robust molecular markers for Marker-Assisted Selection (MAS). These tools will enhance the efficiency of selecting promising cultivars with durable resistance. Meanwhile, cashew farming communities are advised to adopt precautionary measures, particularly when planting in fields with a known history of high pathogen inoculum. Avoiding low-lying, poorly drained areas where *Fusarium* wilt incidence tends to be higher remains a critical preventive strategy (Mbaso *et al.*, 2024).

Conflict of interest

The authors have no relevant financial or non-financial interests to disclose

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پژمردگی فوزاریومی بادام هندی: وضعیت و مدیریت

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چکیده: محصول بادام هندی، *Anacardium occidentale* L. یکی از مهم‌ترین محصولات صادراتی در تانزانیا است که به درآمد ملی و بیش از ۵۰۰۰۰۰ خانوار کمک می‌کند. عملکرد بادام هندی در سه دهه گذشته پایین بوده است. محدودیت‌های زیستی، از جمله آفات و بیماری‌های حشرات، عمدتاً در کاهش عملکرد ثبت شده نقش داشته‌اند. علی‌رغم تلاش‌ها برای توسعه فناوری‌های محافظت از بادام هندی و گونه‌های جدید بادام هندی با عملکرد بالا و مقاوم در برابر بیماری، وضعیت در دهه گذشته بدون تغییر باقی‌مانده است. پژمردگی فوزاریومی ناشی از *Fusarium oxysporum*، پاتوژن قارچی اصلی خاکزی است که بادام هندی را در تانزانیا تحت تأثیر قرار می‌دهد. امواج ویرانگر اپیدمی‌های پژمردگی فوزاریومی در طیف وسیعی از محصولات کشاورزی در سراسر جهان مشاهده شده است که بر تولید و بهره‌وری تأثیر می‌گذارد. در صورت عدم انجام اقدامات احتیاطی به‌موقع، هجوم ناشی از پژمردگی فوزاریومی ممکن است منجر به از دست رفتن تا ۱۰۰ درصد محصول شود. در حال حاضر، علی‌رغم تنوع علائم مشاهده شده در گیاهان بادام هندی، هیچ نژاد بیماری‌زایی در محصول بادام هندی گزارش نشده است. توسعه ابزارهای مولکولی (آغازگرهای اختصاصی) برای تمایز بین گونه‌های خاص و نژادهای بیماری‌زا از اهمیت بالایی برای ایجاد استراتژی‌های مدیریتی دقیق و صحیح برخوردار است. این امر با گنجاندن یک برنامه اصلاح نژادی مولکولی همراه است که شامل تکنیک‌هایی برای شناسایی نشانگرهای مولکولی مرتبط با ژن‌های کنترل‌کننده پژمردگی فوزاریومی است. با این حال، مدیریت تلفیقی بیماری، که شامل کنترل زراعی، شیمیایی و بیولوژیکی است، در جلوگیری از پژمردگی فوزاریومی بادام هندی نیز از اهمیت بالایی برخوردار است.

واژگان کلیدی: بادام هندی، وضعیت بیماری، فوزاریوم اکسیسپوروم، پژمردگی فوزاریومی، عامل بیماری‌زای قارچی