International Journal of Plant Pathology and Microbiology

E-ISSN: 2789-3073
P-ISSN: 2789-3065
Impact Factor (RJIF): 5.78
www.plantpathologyjournal.com
IJPPM 2025; 5(2): 204-212
Received: 15-10-2025
Accepted: 18-11-2025

Sadashiv N Shinde
[1] Department of Botany, Rajarshi Shahu College, Latur, Maharashtra, India
[2] Research Centre, Department of Botany, Science College, Nanded, Maharashtra, India

Venkat S Maske
Department of Botany, B.S. College, Basmatnagar, Dist. Hingoli, Maharashtra, India

Correspondence Author:
Sadashiv N Shinde
[1] Department of Botany, Rajarshi Shahu College, Latur, Maharashtra, India
[2] Research Centre, Department of Botany, Science College, Nanded, Maharashtra, India

Emerging fungal pathogens of horse gram (*Macrotyloma uniflorum*): Epidemiological insights and sustainable management approaches

Sadashiv N Shinde and Venkat S Maske

DOI: https://www.doi.org/10.22271/27893065.2025.v5.i2c.164

Abstract
Macrotyloma uniflorum, commonly referred to as horse gram, is an underexploited leguminous crop with substantial potential for enhancing food security and nutritional standards, particularly in arid and semi-arid ecosystems. This review presents a comprehensive analysis of the current understanding of fungal pathogens affecting horse gram, focusing on their epidemiology, host-pathogen interactions, and the genetic diversity of both the pathogens and the host. Additionally, it explores sustainable management strategies aimed at mitigating disease impact, including integrated pest management, biocontrol agents, and cultural practices that enhance crop resilience. By synthesising research findings, this paper underscores the critical need for effective disease management frameworks that align with sustainable agricultural practices. A multidisciplinary approach that combines plant pathology, agronomy, and molecular biology is essential for harnessing the full potential of horse gram in sustainable food systems. Overall, this review not only highlights the challenges posed by emerging fungal pathogens but also emphasises the importance of horse gram as a resilient crop capable of contributing to global food security.

Keywords: *Macrotyloma uniflorum*, horse gram, fungal pathogens, disease management, sustainable agriculture, food security, epidemiology, genetic diversity

Introduction

Macrotyloma uniflorum, commonly known as horse gram, is an underutilised legume with significant potential to address global food and nutritional security challenges, particularly in arid and semi-arid regions (Aditya *et al*., 2019) [1]. Despite its resilience and nutritional density, its cultivation, production, and productivity have seen a consistent decline over the past two decades (Singh *et al*., 2022) [83]. However, its inherent tolerance to abiotic stressors and high protein content position it as a crucial crop for marginal farmers in low-fertility or rainfed environments (Singh *et al*., 2024) [84]. This dicotyledonous plant, belonging to the Leguminosae family, is widely distributed across South Asia, Australia, the West Indies, and Africa, providing nutritional security through its use as food, livestock supplements, and green manure due to its high nitrogen availability and robust pest resistance (Wu *et al*., 2024) [95]. Initially classified under the genus *Dolichos*, *Macrotyloma uniflorum* was reclassified in 1970 by botanist Verdcourt, a revision that placed it within a genus comprising three economically significant species: *M. uniflorum*, *M. axillare*, and *M. geocarpum* (Fuller & Murphy, 2017) [27]. This taxonomic reclassification has helped to clarify botanical distinctions, especially given prior confusion where *Dolichos biflorus* was erroneously applied to horse gram, leading to misidentification with cowpea types (Fuller & Murphy, 2017) [27].

Its hardy nature and adaptability make it a critical crop for dry and marginal lands, especially for resource-poor farmers in India, where rainfed farming accounts for a substantial portion of agricultural land (Priyanka *et al*., 2021) [64]. As a self-pollinating diploid legume within the Fabaceae family, horse gram demonstrates exceptional tolerance to drought conditions and can thrive in regions where other crops fail (Shirasawa *et al*., 2021; Agnihotri & Rana, 2021) [82, 2]. This drought tolerance, coupled with its ability to grow on marginal soils and saline conditions, positions horse gram as a crucial crop for water conservation and sustainable agriculture in semi-arid environments (Kumar *et al*., 2020) [40]. Its nutritional richness, characterised by high protein and mineral content, further enhances its value as a food security crop, particularly in regions where malnutrition is prevalent (Mahesh *et al*., 2021) [45]. Furthermore, the crop provides an inexpensive protein source for populations relying primarily on vegetarian diets, and its deep penetrating root system contributes to its ability to thrive even in conditions of limited water availability (Patil & Kasturiba, 2019; Sahoo & Mohanty, 2020) [61, 70].

Despite its resilience, fungal pathogens pose significant threats to horse gram cultivation, necessitating effective disease management strategies to maintain yield stability (Priyanka *et al*., 2021) [64]. For instance, various fungal diseases, such as anthracnose and rust, can severely impact horse gram productivity, highlighting the need for robust control measures (Bhardwaj *et al*., 2013) [9]. These measures are critical, as grain mould alone can cause yield losses ranging from 30% to 100%, depending on the specific cultivar and prevailing weather conditions (Kumar *et al*., 2022) [38]. Moreover, integrated pest management approaches, encompassing both cultural practices and the development of resistant varieties, are essential for mitigating these fungal threats and ensuring consistent crop yields (Singh *et al*., 2024) [84]. This review aims to synthesise existing knowledge on Macrotyloma uniflorum, encompassing its taxonomy, genetic diversity, nutritional composition, and agronomic benefits, to elucidate its untapped potential for sustainable agriculture and food security.

Major Fungal Diseases of *Macrotyloma uniflorum*

Macrotyloma uniflorum (horsegram) is susceptible to several major fungal diseases, with anthracnose and powdery mildew being the most significant. Anthracnose is particularly prominent, affecting various leguminous crops, including horsegram. Powdery mildew is another critical disease-causing considerable yield losses proportional to disease severity and infection stage. Seed-borne fungi also pose a significant threat, with studies identifying multiple fungal species, including *Aspergillus niger, A. flavus*, *Fusarium* sp., and additionally, research has identified specific pathogenic fungi like *Macrophomina phaseolina, Phomopsis* sp., *Nigrospora oryzae*, and *Boeremia exigua* that can infect horsegram and reduce crop productivity. Researchers recommend developing disease-resistant varieties and adjusting sowing dates to mitigate these fungal challenges.

Anthracnose: Anthracnose, caused by various species within the fungal genus *Colletotrichum*, represents a significant phytopathological challenge across a diverse array of crops, including horse gram (Ahmad, 2017) [3]. This disease, characterised by necrotic lesions on stems, leaves, flowers, and pods, can lead to substantial yield losses, sometimes reaching up to 50% in severely affected fields (Madhusudhana, 2019) [42]. The ubiquity and genetic variability of *Colletotrichum* species, particularly *C. gloeosporioides*, further complicating disease management strategies due to their broad host range and rapid adaptation to host defences and control measures (Raghavendra *et al*., 2020; Talhinhas, 2023) [65, 86]. Symptoms of anthracnose often manifest as minute, circular to irregular spots on leaves that subsequently enlarge and darken, eventually coalescing into large, necrotic lesions (George *et al*., 2022) [29]. Beyond foliar damage, anthracnose can also induce crown and stem rots, as well as seedling blight, depending on the specific *Colletotrichum* species and environmental conditions (Bellé *et al*., 2019) [8]. In the context of horse gram, *Colletotrichum truncatum* has been identified as a primary etiological agent, exhibiting a broad host range that includes other legumes such as soybean, cowpea, mungbean, limabean, and fababean (Pandit, 2020) [60]. The pathogenic diversity within *Colletotrichum* is further exemplified by species like *C. lentis*, which causes anthracnose in lentils, with distinct races exhibiting specific virulence profiles (Talhinhas, 2023) [86]. The disease significantly impairs crop productivity through qualitative and quantitative losses, particularly under hot and humid conditions conducive to fungal proliferation (Mogali *et al*., 2023) [54].

Leaf Spot and Blight: Leaf spot and blight diseases, primarily caused by *Cercospora* and *Alternaria*species, pose significant phytopathological concerns for horse gram (*Macrotyloma uniflorum*) cultivation, often resulting in substantial yield losses. These fungal pathogens induce a range of symptoms from discrete necrotic spots to extensive blighting, severely impacting photosynthetic efficiency and overall plant vigour (Meena *et al*., 2020) [49]. Early and accurate identification of these pathogens is crucial for implementing effective management strategies and mitigating their economic impact (Shafique *et al*., 2024; Khang *et al*., 2008) [75, 36]. Understanding the specific etiological agents, such as *Alternaria tenuissima*, which is a predominant causal agent of leaf spot in various legumes, is fundamental for developing targeted control measures (Радченко *et al*., 2019) [97]. Moreover, accurate differentiation between *Cercospora* and *Alternaria* infections is vital, as their distinct morphological characteristics, such as angular versus concentric blight spots, influence diagnostic approaches and subsequent disease management protocols (Nazneen *et al*., 2024) [56].

Cercospora species are characterised by their slender, septate conidia and distinct conidiophores, which emerge from stomata or directly from epidermal cells (Basavarajappa *et al*., 2023) [7]. These fungi typically induce circular to angular leaf spots with distinct margins and often a chlorotic halo, differentiating them from the more diffuse lesions caused by *Alternaria* species. Conversely, *Alternaria* species, particularly *A. alternata*, exhibit dark olive-brown to blackish-brown septate mycelia and conidia that are often arranged in long chains, with tapering apices and ranging in colour from light to dark brown or olivaceous green (Magsi *et al*., 2024) [44]. These morphological distinctions, particularly in conidial morphology and sporulation patterns, are critical for microscopic identification and differentiation between *Cercospora* and *Alternaria* infections in host tissues. Furthermore, *Alternaria* spp. are noted for their production of characteristic concentric rings on leaves and pods, leading to significant defoliation and seed loss in severely infected areas (Sharma *et al*., 2023) [80]. The pathogenicity of *Alternaria* species is further evidenced by their ability to induce light to dark brown patches with characteristic concentric zonation, often leading to complete drying and blightening of leaves in severe cases (Anembom *et al*., 2022) [4]. Such symptoms, particularly those associated with *Alternaria tenuissima*, often manifest as small, chlorotic, water-soaked lesions that progressively expand, become necrotic, and coalesce, resulting in a ragged or blighted appearance and subsequent defoliation (Kumar *et al*., 2022) [38]. Molecular approaches, such as multi-locus phylogenetic analyses, further refine species identification within *Alternaria*, revealing distinct clades like *A. arborescens* despite morphological similarities with *A. alternata* and *A. tenuissima* (Elfar *et al*., 2023) [22]. This genetic differentiation is crucial for understanding host specificity and disease epidemiology, especially since morphological markers can be unreliable due to genotype-environmental interactions (Sadia *et al*., 2021) [69].

Root rot and wilt: Root rot, a significant disease in various legumes including horse gram, is primarily caused by soil-borne fungal pathogens such as *Macrophomina phaseolina* and *Fusarium oxysporum* (Kulkarni *et al*., 2019; Hassan & Khalaphallah, 2023) [37, 33]. *Macrophomina phaseolina* is particularly problematic due to its broad host range and enhanced virulence under conditions of low moisture and high heat, leading to significant yield losses (Sadhana *et al*., 2024) [68] (Mohanapriya & Balabaskar, 2017) [55]. This ubiquitous pathogen, first identified in India in 1936, is responsible for a range of disease symptoms, including charcoal rot, dry rot, and seedling blight across more than 500 economically important crops (Princejayasimha *et al*., 2023; Madhusudhana, 2019) [63, 42]. Its necrotrophic nature allows it to survive in soil as a saprophyte in the absence of a host, contributing to its persistence and widespread impact on agricultural systems (Sharma & Pande, 2013) [79].

Rhizoctonia solani, another prevalent soil-borne pathogen, is characterised by its ability to cause damping-off, foliar blight, and root and crown rot in a wide array of hosts globally (Hanif & Dawar, 2016) [32]. This fungal complex, often designated as a species complex due to its genetic diversity, lacks asexual spores and instead propagates through mycelial growth and the formation of sclerotia, allowing it to persist in soil and plant debris for extended periods (Sandhu *et al*., 2023) [71]. The pathogenicity of *Rhizoctonia solani* is further complicated by its extensive host range, encompassing numerous crops and ornamental plants, making its management particularly challenging (Mageshwaran *et al*., 2022) [43]. Furthermore, environmental stressors like soil pH, reduced moisture, and elevated temperatures exacerbate the growth and pathogenic activity of *Rhizoctonia bataticola*, a critical member of this genus causing dry root rot in chickpeas and other legumes (Saxena *et al*., 2022) [72]. This pathogen, also known as *Macrophomina phaseolina*, can cause significant losses in various pulse crops, including mungbean and urdbean, ranging from 30-40% (Swehla *et al*., 2020) [85]. The disease manifests as dark brown lesions at the stem base, accompanied by bark shredding and easily detachable plants due to rotted root portions (Kulkarni *et al*., 2019) [37]. The characteristic symptoms of root rot include scattered necrotic brownish to black lesions in the roots, which progress to rotting and the withering of lateral roots, culminating in prematurely dried, straw-colored foliage (Patil *et al*., 2022) [62]. The disease development is further exacerbated by high temperatures between 25 and 35 ºC and low soil moisture conditions, which are highly conducive to the pathogen's proliferation (Babu *et al*., 2017) [6].

Epidemiology and Disease Dynamics

Globally, food security is paramount, and the continuous emergence and resurgence of crop fungal diseases, exacerbated by climate change and evolving agricultural practices, significantly imperil crop yields and quality (Wang, 2023) [92]. Understanding the epidemiology of these plant pathogens is therefore critical for developing effective management strategies and ensuring sustainable agricultural production, especially given their role in mediating ecosystem processes (Wang, 2023; Miller *et al*., 2022) [92, 53]. Fungal diseases alone contribute significantly to worldwide yield losses, with estimates suggesting up to 40% of crop yields are lost to various pests and pathogens (Djuikem, 2023) [19]. Specifically, fungal pathogens are a major concern due to their prolific spore production, extensive dispersal capabilities, and high mutation rates, which collectively enable rapid adaptation and widespread disease propagation (Taylor & Cunniffe, 2023) [87]. This adaptive capacity is further complicated by the interaction of fungal diseases with environmental factors, such as temperature and humidity, which can dictate the severity and timing of disease epidemics (Vijaykumar *et al*., 2024) [90]. Consequently, comprehending the intricate dynamics of pathogen spread within host populations is essential for anticipating and mitigating the burden of fungal diseases on agricultural productivity (Miller *et al*., 2022) [53]. For instance, arid legumes like horsegram frequently experience stagnant productivity due to their pronounced susceptibility to root diseases, underscoring the urgent need for in-depth pathological investigation (Gautam *et al*., 2016) [28].

Geographic distribution and disease incidence patterns

These patterns are heavily influenced by the diverse ecological conditions prevalent across different regions, particularly in areas like India with its rich biodiversity, where various dispersal methods, including wind, water, and animal vectors, facilitate fungal spread (Dhar *et al*., 2024) [17]. Moreover, certain fungal diseases may exhibit episodic outbreaks driven by generalist pathogens with diverse inoculum sources, leading to sudden yet recurrent epidemics under favourable environmental conditions (Dentika *et al*., 2022) [16]. These dynamics underscore the necessity of accurate disease incidence and severity estimations, which are crucial for assessing the negative impacts on crop quality and for informing timely detection and identification efforts (Hyde *et al*., 2024; Dormatey *et al*., 2020) [34, 20]. Accurate assessments of disease incidence and severity are also vital for understanding the broader ecological implications, such as the potential for fungal pathogens to reduce host fitness and alter plant community structures (Dietzel *et al*., 2019) [18]. In India, where agricultural losses due to pests and diseases are substantial, fungi account for approximately 22% of these losses, with about 85% of plant diseases worldwide attributed to fungal pathogens (Todawat & Rathod, 2025) [88]. These statistics highlight the critical need for a deeper understanding of fungal pathogen dynamics in crops such as horsegram, especially given the increased incidence and severity of diseases in other susceptible legume cultivars in recent years (Pandey *et al*., 2018) [59].

Seasonal occurrence and host susceptibility stages: The interplay between environmental variables, such as fluctuating temperatures and humidity, and the phenological stages of horsegram, significantly dictates the susceptibility to fungal pathogens, often leading to enhanced disease proliferation during specific growing seasons (Nema & Singh, 2025) [57]. This seasonal susceptibility is further compounded by the continuous exposure of plants to biotic stress from both symbiotic and pathogenic organisms, where resistance is typically the rule and disease the exception, a phenomenon known as non-host resistance (Lattanzio *et al*., 2006) [41]. The underlying mechanisms of non-host resistance often involve preformed physical or chemical barriers on the plant surface that prevent pathogen invasion, or a lack of support for the invading pathogen's lifestyle within the host (Lattanzio *et al*., 2006) [41]. However, plants can also synthesize induced defense compounds in response to biotic stress, which are often restricted to the damaged tissue and contribute to the overall defense response (Lattanzio *et al*., 2006) [41].

Disease forecasting models: The development and application of robust disease forecasting models are therefore crucial for predicting disease outbreaks, thereby enabling proactive rather than reactive disease management strategies. These models, often leveraging multi-omics approaches, allow for a detailed account of plant-microbial interactions and can facilitate the development of predictive tools for how microbes and plants respond to stress under environmental changes, thereby identifying novel targets for disease control and improving the development of resistant plant varieties (Hyde *et al*., 2024) [34]. Such models integrate complex data sets, including environmental parameters, host genotypes, and pathogen virulence factors, to offer sophisticated insights into disease risk and progression, thereby refining precision agriculture practices and reducing reliance on broad-spectrum interventions (Sharma *et al*., 2024) [77]. For instance, the severity of fungal diseases like leaf rust and powdery mildew, frequently observed in various regions, has been correlated with erratic rainfall patterns and higher temperatures, underscoring the importance of meteorological data in predictive models (Bijlwan *et al*., 2025) (Vijaykumar *et al*., 2024) [11, 90].

Fungal Disease Management Strategies

Cultural Control: Crop rotation, seed treatment, and residue management are fundamental cultural control methods that disrupt pathogen life cycles and reduce inoculum loads in the soil (Xu, 2011) [96]. Optimised irrigation practices and intercropping further contribute to an unfavorable environment for fungal proliferation while enhancing agroecosystem diversity (Farzana *et al*., 2025; Sharma *et al*., 1997) [78]. For instance, longer crop rotations and managing crop residues are critical for reducing primary inoculum, as fungal pathogens often persist on plant debris or within the soil (Debaeke *et al*., 2014) [14]. Strategic water management, such as the temporary removal of water in rice paddies, has been shown to significantly reduce insect pests and, by extension, the vectors for certain fungal diseases, leading to improved grain yields and biomass ratios (Sharma *et al*., 1997) [78]. Diversified cropping systems, including crop rotation and intercropping, have also been shown to modulate the soil microbiome, thereby enhancing suppressiveness against soil-borne pathogens like Fusarium wilt and reducing the overall abundance of fungal genera that include potential pathogens (Marín-Guirao *et al*., 2025) [48]. Such practices are integral to an integrated pest management approach, which combines various strategies to maintain pest populations below economically damaging thresholds while minimizing environmental impact (Bhattacharjya, 2024) [10]. These integrated strategies often incorporate resistant cultivars and biological controls, alongside judicious pesticide application, to manage disease effectively and sustainably (Bhattacharjya, 2024) [10]. Implementing integrated disease management strategies, which encompass cultural practices like crop rotation and the use of resistant cultivars, along with biological controls, is crucial for minimizing fungicide dependence and mitigating resistance development (Ceresini *et al*., 2024) [12]. Additionally, the strategic arrangement of landscape mosaics at a regional level can prevent unwanted spore dissemination from primary inoculum sources to host plants, thereby reducing overall disease pressure (Debaeke *et al*., 2014) [14]. Furthermore, the careful selection of sowing times and sites can prevent disease outbreaks by avoiding periods or locations conducive to pathogen development or where inoculum is absent (Mendoza-Mendoza *et al*., 2024) [50]. This proactive approach, combined with methods such as burning crop debris, which can drastically reduce inoculum levels by up to 90%, or incorporating residues into the soil through tillage, aims to minimise the initial pathogen burden (Farzana *et al*., 2025) [24]. Crop rotation, specifically, serves to separate crops from pathogens both spatially and temporally, preventing the establishment and proliferation of specialised fungal species that thrive in monoculture conditions (Kerdraon, 2019; West *et al*., 2023) [35, 94]. For example, diversified crop rotations have proven effective in reducing pest populations, such as the wheat midge, by disrupting continuous host availability (Sharma, 2023) [80].

Biological Control: It involves the strategic introduction of beneficial microorganisms or natural enemies to suppress fungal pathogens, offering an environmentally benign alternative or complement to chemical interventions (Guzmán, 2021) [30]. This approach harnesses the power of ecological interactions, utilising antagonistic fungi, bacteria, or even predatory nematodes to outcompete, parasitise, or inhibit the growth of pathogenic fungi, thus minimising disease incidence and severity (Manzoor *et al*., 2024) [47]. For example, the application of various microorganisms can induce systemic resistance in plants, making them less susceptible to subsequent pathogen attacks, while certain endophytes can directly antagonise pathogens through competitive exclusion or antibiotic production. Moreover, biofungicides, derived from naturally occurring microorganisms or their metabolites, are increasingly being developed as potent tools for managing fungal diseases without the ecological drawbacks associated with synthetic chemicals (Ceresini *et al*., 2024) [12]. These biological agents represent a crucial component of integrated pest management strategies, particularly in organic farming systems where synthetic chemical use is restricted (Rojas *et al*., 2018) [67]. The careful selection and deployment of these biocontrol agents are paramount, necessitating a deep understanding of their ecological niche and interaction mechanisms with both host plants and target pathogens to ensure efficacy and environmental compatibility. However, the efficacy of biological control agents can be influenced by environmental factors, pathogen populations, and the availability of suitable antagonists (Hamim *et al*., 2024) [31]. Consequently, further research is needed to develop more robust and consistent biological control strategies that are effective across diverse agricultural settings (Elkhairy *et al*., 2023) [23].

Chemical Control and Its Disadvantages: Despite their effectiveness in preventing crop losses and improving yields, the widespread application of chemical fungicides faces mounting scrutiny due to the emergence of pathogen resistance and concerns regarding environmental accumulation and non-target effects on ecosystems (Seyi-Amole & Onilude, 2021) [74]. Moreover, overreliance on these synthetic compounds can lead to the development of fungicidal resistance in pathogenic fungi, underscoring the urgent need for sustainable and eco-friendly alternatives (Sbai *et al*., 2024; Reddy *et al*., 2024) [73, 66]. This imperative has driven extensive research into biological control agents, which are increasingly recognised as a viable and sustainable alternative for managing fungal diseases in cereals and other crops (Dehbi *et al*., 2023) [15]. For instance, endophytic fungi represent a promising avenue, as they establish symbiotic relationships with host plants, producing an array of bioactive compounds that directly antagonise phytopathogenic fungi while simultaneously promoting plant growth (Manathunga *et al*., 2024) [46]. Furthermore, the non-judicious application of agrochemicals has led to widespread environmental damage, necessitating the exploration of microbial metabolites and other biological control agents as sustainable alternatives for crop protection (Verma *et al*., 2020) [89]. The indiscriminate use of chemical pesticides has also been linked to detrimental effects on human health, including neurological and respiratory disorders, further emphasising the need for safer alternatives (Dehbi *et al*., 2023) [15]. This has spurred significant research into developing novel fungal biocontrol agents and evaluating their efficacy in diverse environmental contexts, offering a more sustainable approach to disease management compared to the environmental consequences and potential for resistance development associated with chemical pesticides (Shaili *et al*., 2025; Menjívar *et al*., 2025) [76, 51].

Integrated Disease Management (IDM): Integrated disease management effectively combines genetic resistance, cultural practices, biological control, and chemical interventions to provide comprehensive and sustainable protection against fungal diseases (Bhattacharjya, 2024; Hyde *et al*., 2024) [10, 34]. This multifaceted strategy aims to optimise disease control while simultaneously reducing the development of fungicide resistance and minimising adverse environmental impacts (Vilvert *et al*., 2021; Fenta & Mekonnen, 2024) [91, 25]. Implementing this approach requires a deep understanding of pathogen biology, host plant genetics, and agroecosystem dynamics to tailor control measures effectively (Sharma *et al*., 1997) [78]. It emphasizes proactive management by utilising predictive models and surveillance to anticipate disease outbreaks and enact timely, targeted interventions, rather than depending solely on reactive measures. Additionally, the integration of host plant resistance through either conventional breeding or genetic engineering provides a fundamental layer of defence, thus decreasing the need for intensive external interventions and enhancing overall crop resilience (Sharma *et al*., 1997) [78]. Advances in gene editing technologies, particularly CRISPR-Cas9, offer promising opportunities for developing disease-resistant plant varieties, further strengthening this foundational layer of defence (Hyde *et al*., 2024) [34]. Such biotechnological innovations enable the rapid development of resilient crops with broad-spectrum resistance to multiple pathogens, marking a significant advancement over traditional single-gene resistance strategies (Wani *et al*., 2022; Dormatey *et al*., 2020) [93, 20].

Knowledge Gaps and Future Research Directions

Despite notable advancements in our understanding of fungal disease mechanisms and the development of control strategies, several knowledge gaps remain, particularly regarding the long-term ecological impacts of novel biocontrol agents and the molecular complexities that drive the evolution of pathogen resistance (West *et al*., 2023) [94]. Continued research is vital to clarify the intricate interactions within the plant microbiome that contribute to disease suppression and to create durable, multigenic resistance strategies in crops through advanced breeding and genomic technologies (Dormatey *et al*., 2020; Wani *et al*., 2022) [20, 93]. This effort includes the enhancement of monitoring and forecasting systems, as well as the selection and breeding of disease-resistant crop varieties, to promote sustainable and high-yield production while minimising environmental impact (Chen *et al*., 2023) [13]. Furthermore, ongoing investigation into plant defence pathways and pathogen virulence factors is crucial for developing more effective and long-lasting resistance mechanisms (Arnon, 1949) [5]. A thorough understanding of disease epidemiology and pathogenesis, combined with timely interventions, is necessary to reduce production costs and environmental risks (Chen *et al*., 2023) [13]. Additionally, exploring novel pest control strategies such as harnessing pathogen population dynamics and examining the role of wild plants in disease epidemiology is essential for achieving sustainable agricultural production (Fielder *et al*., 2024; Michelmore *et al*., 2017) [26, 52].

Conclusion

The resilience of *Macrotyloma uniflorum* (horse gram) positions it as a vital crop for enhancing food security amidst increasing climate variability. Effective control strategies, including integrated pest management and the breeding of resilient varieties, are imperative to mitigate the significant yield losses attributed to fungal diseases. The establishment of sustainable agricultural practices that leverage the genetic diversity and inherent adaptability of horse gram will be crucial in safeguarding its production. Future research should prioritise the exploration of molecular mechanisms underlying host-pathogen interactions as well as the development of biocontrol agents, thereby contributing to the resilience of agro-ecosystems in arid and semi-arid regions. Addressing these research gaps will not only enhance the understanding of *Macrotyloma uniflorum* response to biotic stressors but also promote its cultivation as a cornerstone of sustainable food systems.

References

1. Aditya JP, Bhartiya A, Chahota RK, Joshi DC, Chandra N, Kant L, Pattanayak A. Ancient orphan legume *Horsegram*: a potential food and forage crop of future. Planta. 2019;250(3):891-899.
2. Agnihotri V, Rana S. *Horsegram*, an underutilized legume: a potential source of nutraceuticals. In: Sustainable Agriculture Reviews. Springer International Publishing; 2021. p. 29-45.

3. Ahmad S. Molecular characterisation and phylogenetic analysis of *Colletotrichum* species associated with anthracnose disease. J Bacteriol Mycol Open Access. 2017;5(2):129-136.
4. Anembom C, Tacham WN, Chia GK, Bih JN, Kinge TR. Assessment of leaf spot disease on water leaf (*Talinum triangulare* (Jacq.) Willd) and *in vitro* effect of three medicinal plant extracts on pathogen(s) in the Northwest Region of Cameroon. Afr J Agric Res. 2022;18(9):688-698.
5. Arnon DI. Copper enzymes in isolated chloroplasts. Polyphenoloxidase in *Beta vulgaris*. Plant Physiol. 1949;24(1):1-15.
6. Babu PSSR, Reddy MSPN, Pushpavathi B. Effect of temperature on *Rhizoctonia bataticola* and dry root rot in chickpea. Int J Curr Microbiol Appl Sci. 2017;6(6):3349-3356.
7. Basavarajappa DS, Kumar RS, Nayaka S. Formulation-based antagonistic endophyte *Amycolatopsis* sp. SND-1 triggers defence response in *Vigna radiata* (L.) R. Wilczek against *Cercospora* leaf spot disease. Arch Microbiol. 2023;205(2):119-132.
8. Bellé C, Ramos RF, Gabriel M, Kaspary TE, Brida AL de. *Colletotrichum gloeosporioides* causes leaf anthracnose on *Oxalis corniculata* in Brazil. Australas Plant Dis Notes. 2019;14(1):1-5.
9. Bhardwaj J, Chauhan R, Swarnkar MK, Chahota RK, Singh AK, Shankar R, Yadav SK. Comprehensive transcriptomic study on *Horsegram* (*Macrotyloma uniflorum*): de novo assembly, functional characterization and comparative analysis in relation to drought stress. BMC Genomics. 2013;14(1):647-661.
10. Bhattacharjya S. Shoot fly complex: a significant threat to cereals, and their management. J Entomol Zool Stud. 2024;12(3):241-249.
11. Bijlwan A, Ranjan R, Singh M, Purohit R, Nath AJ, Chakravarty S. Predicting crop disease severity using real-time weather variability through machine learning algorithms. Sci Rep. 2025;15(1):1-14.
12. Ceresini PC, Silva TC, Vicentini SNC, Leite RP, Moreira SI, Castro-Ríos K, *et al*. Strategies for managing fungicide resistance in the Brazilian tropical agroecosystem: safeguarding food safety, health, and environmental quality. Trop Plant Pathol. 2024;49(1):36-50.
13. Chen X, He Y, Wang Z, Niu A, Xue Y, Zhou D, Zhou G, Liu J. Research progress and management strategies of fungal diseases in *Camellia oleifera*. Front Microbiol. 2023;14:1215024.
14. Debaeke P, Mestries E, Desanlis M, Seassau C. Effects of crop management on the incidence and severity of fungal diseases in sunflower. HAL. 2014. Available from: https://hal.inrae.fr/hal-02801511
15. Dehbi I, Achemrk O, Ezzouggari R, Jarroudi ME, Mokrını F, Legrifi I, *et al*. Beneficial microorganisms as bioprotectants against foliar diseases of cereals: a review. Plants. 2023;12(24):4162-4178.
16. Dentika P, Ozier-Lafontaine H, Penet L. *Colletotrichum gloeosporioides*: apparent continuous spore rain may hide local disparities and iterative disease dynamics. HAL. 2022. Available from: https://hal.science/hal-03890339
17. Dhar J, Hazra A, Patra R, Kumar V, Subramaniyan V, Kumarasamy V, *et al*. Unveiling *Curvularia tuberculata*-induced leaf anomalies in *Rhododendron ferrugineum*: implications in cultural-ecological conservation and harnessing microbial intervention in socio-economic advancement. Front Microbiol. 2024;14:1280120.
18. Dietzel K, Valle D, Fierer N, U'Ren JM, Barberán A. Geographical distribution of fungal plant pathogens in dust across the United States. Front Ecol Evol. 2019;7:304-312.
19. Djuikem C. Mathematical modelling and control of perennial plant phytopathogens. HAL. 2023. Available from: https://theses.hal.science/tel-04026720
20. Dormatey R, Sun C, Ali K, Coulter JA, Bi Z, Bai J. Gene pyramiding for sustainable crop improvement against biotic and abiotic stresses. Agronomy. 2020;10(9):1255-1266.
21. Dormatey R, Sun C, Ali K, Coulter JA, Bi Z, Bai J. Gene pyramiding for sustainable crop improvement against biotic and abiotic stresses. Agronomy. 2020;10(9):1255-1266.
22. Elfar K, Bustamante MI, Arreguin M, Nouri MT, Eskalen A. Identification and pathogenicity of *Alternaria* species causing leaf blotch and fruit spot of apple in California. Phytopathol Mediterr. 2023;62(3):467-479.
23. Elkhairy BM, Salama NM, Desouki AM, Abdelrazek AB, Soliman KA, Ibrahim S, Khalil HB. Towards unlocking the biocontrol potential of *Pichia kudriavzevii* for plant fungal diseases: *in vitro* and *in vivo* assessments with candidate secreted protein prediction. BMC Microbiol. 2023;23(1):1-15.
24. Farzana L, Islam SS, Rahman M, Ferdus H, Hossain MM. Addressing *Bipolaris sorokiniana* in wheat: challenges, management strategies, and future directions for sustainable food security. Discover Agric. 2025;3(1):1-12.
25. Fenta L, Mekonnen H. Microbial biofungicides as a substitute for chemical fungicides in the control of phytopathogens: current perspectives and research directions. Scientifica. 2024;2024:5322696.
26. Fielder H, Beale T, Jeger M, Oliver G, Parnell S, Szyniszewska A, *et al*. A synoptic review of plant disease epidemics and outbreaks published in 2022. Phytopathology. 2024;114(8):1717-1728.
27. Fuller DQ, Murphy C. The origins and early dispersal of *Horsegram* (*Macrotyloma uniflorum*), a major crop of ancient India. Genet Resour Crop Evol. 2017;65(1):285-302.
28. Gautam R, Singh SK, Sharma V. Molecular diagnosis and intraspecific genetic variability of root pathogens of arid legumes in Western Rajasthan, India. Rev Biol Trop. 2016;64(4):1565-1575.
29. George ME, Sarada S, M J. Screening of yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt) genotypes for resistance to *Colletotrichum gloeosporioides*. J Hortic Sci. 2022;17(2):293-302.
30. Guzmán MdPR. Soil biodiversity and root pathogens in agroecosystems. In: IntechOpen eBooks. IntechOpen; 2021. p. 1-18.
31. Hamim I, Sipes BS, Wang Y. Editorial: detection, characterization, and management of plant pathogens. Front Plant Sci. 2024;15:1354042.
32. Hanif A, Dawar S. Comparative studies using homeopathic globules for leguminous and non-

leguminous crop management against root rot fungi. J Agric Sci. 2016;8(9):205-212.
33. Hassan N, Khalaphallah R. Root rot/wilt incidence of *Phaseolus vulgaris* and antagonistic effect of *Trichoderma* spp. and *Aspergillus terreus* isolated from rhizosphere soil. SVU-Int J Agric Sci. 2023;5(4):26-35.
34. Hyde KD, Baldrián P, Chen Y, Chethana KWT, de Hoog S, Doilom M, *et al*. Current trends, limitations and future research in the fungi. Fungal Divers. 2024;125(1):1-23.
35. Kerdraon L. Microbial diversity and pathogen-microbiome interactions in crop residues: the case of *Zymoseptoria tritici* and *Leptosphaeria maculans* in a wheat-oilseed rape system. HAL. 2019. Available from: https://pastel.archives-ouvertes.fr/tel-03537777
36. Khang C, Berruyer R, Park S, Kankanala Czymmek K, Kang S, Valent B. Blast interfacial complex, a novel in planta structure that accumulates effector proteins of rice blast fungus *Magnaporthe oryzae*. HAL. 2008. Available from: https://hal.inrae.fr/hal-02752072
37. Kulkarni S, Shobharani M, Ja R. Integrated management of dry root rot of blackgram caused by *Rhizoctonia bataticola*. Int J Curr Microbiol Appl Sci. 2019;8(8):853-860.
38. Kumar MVN, Ramya V, Govindaraj M, Dandapani A, Maheshwaramma S, Ganapathy KN, *et al*. India's rainfed sorghum improvement: three decades of genetic gain assessment for yield, grain quality, grain mould and shoot fly resistance. Front Plant Sci. 2022;13:1056040.
39. Kumar N, Dutta R, Ajay BC, Radhakrishnan T. Alternaria leaf blight (*Alternaria* spp.) - an emerging foliar fungal disease of winter-summer groundnut (*Arachis hypogaea*): a review. Indian J Agric Sci. 2022;92(9):1043-1052.
40. Kumar R, Kaundal SP, Sharma V, Sharma A, Singh G, Sharma RK, *et al*. Development of transcriptome-wide SSR markers for genetic diversity and structure analysis in *Macrotyloma uniflorum* (Lam.) Verdc. Physiol Mol Biol Plants. 2020;26(11):2255-2265.
41. Lattanzio V, Lattanzio V, Cardinali A, Imperato F. Role of phenolics in the resistance mechanisms of plants against fungal pathogens and insects. Phytochem. 2006;23:1-29.
42. Madhusudhana R. Genetics of important economic traits in sorghum. In: Advances in Plant Breeding Strategies: Agronomic, Abiotic and Biotic Stress Traits. Elsevier; 2019. p. 1-28.
43. Mageshwaran V, Gupta R, Singh S, Sahu PK, Singh UB, Chakdar H, *et al*. Endophytic *Bacillus subtilis* antagonises soil-borne fungal pathogens and suppresses wilt complex disease in chickpea (*Cicer arietinum* L.). Front Microbiol. 2022;13:994847.
44. Magsi QA, Saand MA, Kalwar MS, Ghanghro SGS, Shaikh GH, Soomro SAS, *et al*. First report of *Curvularia lunata* and *Alternaria alternata* causing leaf blights on tomatoes in Sindh, Pakistan. Pak J Biotechnol. 2024;21(1):198-204.
45. Mahesh HB, Prasannakumar MK, Manasa KG, Perumal S, Khedikar Y, Kagale S, *et al*. Genome, transcriptome, and germplasm sequencing uncovers functional variation in the warm-season grain legume *Horsegram* (*Macrotyloma uniflorum* (Lam.) Verdc.). Front Plant Sci. 2021;12:758119.
46. Manathunga KK, Gunasekara NW, Meegahakumbura MK, Ratnaweera PB, Faraj TK, Wanasinghe DN. Exploring endophytic fungi as natural antagonists against fungal pathogens of food crops. J Fungi. 2024;10(9):606-619.
47. Manzoor S, Nabi SU, Rather TR, Gani G, Mir ZA, Wani AW, *et al*. Advancing crop disease resistance through genome editing: a promising approach for enhancing agricultural production. Front Genome Ed. 2024;6:1399051.
48. Marín-Guirao JI, Yan D, Gioia FD, Pugliese M, Fernández-Bayo JD. Editorial: soil microbial communities to promote suppressiveness against soil-borne pathogens and diseases. Front Microbiol. 2025;16:1677158.
49. Meena RP, Saran PL, Kalariya KA, Manivel P. Efficacy of fungicides and plant extracts against *Alternaria alternata* causing leaf blight of chandrasur (*Lepidium sativum*). Indian J Agric Sci. 2020;90(2):337-344.
50. Mendoza-Mendoza A, Esquivel-Naranjo EU, Soth S, Whelan HG, Alizadeh H, Echaide-Aquino JF, *et al*. Uncovering the multifaceted properties of 6-pentyl-alpha-pyrone for control of plant pathogens. Front Plant Sci. 2024;15:1420068.
51. Menjívar M, Dominik P, Lidia B, Łukasz S, Agnieszka W, Moniak U, Marcin B. Interfungal antagonism between *Trichoderma* and *Fusarium proliferatum*: metabolomic and DNA-based analyses. J Appl Genet. 2025;66(1):1-15.
52. Michelmore R, Coaker G, Bart R, Beattie G, Bent A, Bruce T, *et al*. Foundational and translational research opportunities to improve plant health. Carolina Digital Repository. 2017. Available from: https://doi.org/10.17615/zsqj-2k45
53. Miller I, Jiranek J, Brownell M, Coffey SM, Gray B, Stahl M, Metcalf CJE. Predicting the effects of climate change on the cross-scale epidemiological dynamics of a fungal plant pathogen. Sci Rep. 2022;12(1):18851.
54. Mogali SC, Balol G, Goudar IV, Bhat SN. Development of genotypes for foliar disease resistance in mungbean (*Vigna radiata* (L.) Wilczek) through recombination and mutation breeding. Legume Res. 2023;46(5):509-518.
55. Mohanapriya R, Balabaskar RNP. Survey, virulence and pathogenicity of root rot incidence of cowpea in selected districts of Tamil Nadu caused by *Macrophomina phaseolina* (Tassi.) Goid. Int J Curr Microbiol Appl Sci. 2017;6(3):694-703.
56. Nazneen H, Das RJ, Das A, Dutta S, Bhattacharya S, Patar S, *et al*. Disease spectrum and its molecular characterisation in the lentil production system of the lower-Indo Gangetic plains. Front Plant Sci. 2024;15:1199016.
57. Nema D, Singh R. Climate change and its impact on crop health in the Sagar region: a study of temperature and rainfall variability (2010-2025). Int J Res Appl Sci Eng Technol. 2025;13(7):2578-2589.
58. Nurturing the crop: recent innovations in vegetable diseases management. Agrobiol Records. 2023;13:101-110.
59. Pandey AK, Burlakoti RR, Kenyon L, Nair RM. Perspectives and challenges for sustainable management of fungal diseases of mungbean (*Vigna*

radiata (L.) R. Wilczek var. radiata): a review. Front Environ Sci. 2018;6:53.

60. Pandit D. Chemical control of anthracnose (*Colletotrichum truncatum*) of *Horsegram* under field conditions. Int J Res Appl Sci Eng Technol. 2020;8(7):2084-2090.
61. Patil AV, Kasturiba B. A study on protein, *in vitro* protein digestibility, antioxidant activity and total polyphenol content of *Horsegram* varieties. Int J Curr Microbiol Appl Sci. 2019;8(2):1936-1945.
62. Patil MS, Sunkad G, Yenjeerappa ST, Kulkarni S, Rao S, Naik N. Metabolic profiling of plant growth promoting microorganisms (PGPMs) from chickpea rhizosphere and their antagonistic activity against dry root rot pathogen *Rhizoctonia bataticola*. Legume Res. 2022;45(7):497-506.
63. Princejayasimha P, Jayalakshmi R, Vemana K, Naidu GM, Varshney RK, Sudini HK. Prevalence of groundnut dry root rot (*Macrophomina phaseolina* (Tassi) Goid.) and its pathogenic variability in Southern India. Front Fungal Biol. 2023;4:1189043.
64. Priyanka S, Sudhagar R, Vanniarajan C, Ganesamurthy K, Souframanien J. Gamma rays induced morphological, flowering and palynological modifications in horse gram (*Macrotyloma uniflorum*). J Environ Biol. 2021;42(5):1363-1371.
65. Raghavendra S, Raghu HS, Chaithra C, Rajeshwara AN. Potency of mancozeb conjugated silver nanoparticles synthesised from goat, cow and buffalo urine against *Colletotrichum gloeosporioides* causing anthracnose disease. Nat Environ Pollut Technol. 2020;19(3):969-976.
66. Reddy BD, Kumar B, Sahni S, Yashaswini G, Karthik S, Reddy MS, *et al*. Harnessing the power of native biocontrol agents against wilt disease of pigeonpea incited by *Fusarium udum*. Sci Rep. 2024;14(1):60039.
67. Rojas EC, Jørgensen HJL, Jensen B, Collinge DB. Fusarium diseases: biology and management perspectives. In: Burleigh Dodds Ser Agric Sci. Burleigh Dodds Science Publishing Limited; 2018. p. 23-45.
68. Sadhana NH, Geethanjali S, Mirchandani R, Natesan S, Senthil-Kumar M. Navigating towards dry root rot resistance in mungbean: impacts, mechanisms, and management strategies. Plant Physiol Rep. 2024;29(3):439-454.
69. Sadia B, Awan FS, Saleem F, Altaf J, Umar A, Nadeem MA, *et al*. Exploring plant genetic variations with morphometric and molecular markers. In: IntechOpen eBooks. IntechOpen; 2021. p. 1-22.
70. Sahoo SC, Mohanty M. *Horsegram* (*Macrotyloma uniflorum*) production technology: a review. Int J Chem Stud. 2020;8(6):2723-2730.
71. Sandhu R, Bangarwa SK, Attri M, Tiwari S, Kohli S, Fayaz S, Chaudhary NK. Effects of biotic stresses and their mitigation strategies in legumes: a review. Legume Res. 2023;46(8):5160-5175.
72. Saxena DR, Kumbhkar R, Saxena M, Tiwari N, Kumar TS, Chauhan A. Morpho-pathogenic and molecular diversity among *Rhizoctonia bataticola* isolates causing dry root rot of chickpea in Madhya Pradesh, India. J Environ Biol. 2022;43(6):852-861.
73. Sbai H, Hajib A, Msairi S, Amalich S, Bouyahya A, Lee L, *et al*. Fungal infections of legume crops: challenges and management approaches. J Agric Food Res. 2024;101:101447.
74. Seyi-Amole DO, Onilude AA. Microbiological control: a new age of maize production. In: IntechOpen eBooks. IntechOpen; 2021. p. 1-18.
75. Shafique S, Shafique S, Attia U, Zamir MSI. *Alternaria arborescens,* identified as a leaf necrosis pathogen of *Vigna radiata* in Pakistan. J Anim Plant Sci. 2021;34(3):652-661.
76. Shaili SJ, Kabiraj UK, Mahedi M. Fungal biocontrol in agriculture: a sustainable alternative to chemical pesticides - a comprehensive review. World J Adv Res Rev. 2025;26(1):2305-2321.
77. Sharma G, Dwibedi V, Seth CS, Singh S, Ramamurthy PC, Bhadrecha P, Singh J. Direct and indirect technical guide for the early detection and management of fungal plant diseases. Curr Res Microb Sci. 2024;7:100276.
78. Sharma HC, Singh F, Nwanze KF, Subramanian V, Reddy BVS, Rattunde HFW, *et al*. Plant resistance to insects in sorghum. 1997;1-58.
79. Sharma M, Pande S. Unravelling effects of temperature and soil moisture stress response on the development of dry root rot butler in chickpea. Am J Plant Sci. 2013;4(3):584-593.
80. Sharma S. Cultivating sustainable solutions: integrated pest management (IPM) for safer and greener agronomy. Corp Sustain Manag J. 2023;1(2):103-110.
81. Sharma VR, Singh N, Yadav HK. Differential response of guar genotypes to *Alternaria* infection. Legume Res. 2023;46(6):5064-5072.
82. Shirasawa K, Chahota RK, Hirakawa H, Nagano S, Nagasaki H, Sharma TR, Isobe S. A chromosome-scale draft genome sequence of horsegram (*Macrotyloma uniflorum*). Gigabyte. 2021;1:30-42.
83. Singh G, Gudi S, Amandeep, Upadhyay P, Shekhawat PK, Nayak G, *et al*. Unlocking the hidden variation from wild repository for accelerating genetic gain in legumes. Front Plant Sci. 2022;13:1012467.
84. Singh N, Maurya V, Sharma A, Kumar R. Exploring salt stress tolerance in horsegram (*Macrotyloma uniflorum*): insights from growth, physiology and biochemical approaches. Res Square. 2024;1-21.
85. Swehla A, Pandey AK, Nair RM. Bioactivity of *Trichoderma harzianum* isolates against the fungal root rot pathogens with special reference to *Macrophomina phaseolina* causing dry root rot of mungbean. Indian Phytopathol. 2020;73(4):787-796.
86. Talhinhas P. Hosts of *Colletotrichum*. Mycosphere. 2023;14:158-171.
87. Taylor NP, Cunniffe NJ. Coupling machine learning and epidemiological modelling to characterise optimal fungicide doses when fungicide resistance is partial or quantitative. J R Soc Interface. 2023;20(201):1-15.
88. Todawat NJ, Rathod VN. Addition of fungal disease of weeds from Marathwada region (M.S.), India. Int J Sci Res Sci Technol. 2025;12(4):1155-1162.
89. Verma C, Jandaik S, Gupta B, Kashyap N, VS S, Kashyap SK, Kerketta A. Microbial metabolites in plant disease management: review on biological approach. Int J Chem Stud. 2020;8(4):2570-2579.
90. Vijaykumar KN, Kulkarni S, Kambrekar DN, Shashidhar TR, Hiremath SM, Balol G. Impact of weather parameters and time of sowing on the severity

of powdery mildew in cluster bean. Legume Res. 2024;46(9):5275-5284.
91. Vilvert E, Olson Å, Wallenhammar A-C, Törngren J, Berlin A. Scientific evidence of sustainable plant disease protection strategies for oats in Sweden: a systematic map. Environ Evid. 2021;10(1):1-21.
92. Wang H. Epidemiology and control of fungal diseases in crop plants. Agronomy. 2023;13(9):2327-2345.
93. Wani SH, Choudhary M, Barmukh R, Bagaria PK, Samantara K, Razzaq A, *et al*. Molecular mechanisms, genetic mapping, and genome editing for insect pest resistance in field crops. Theor Appl Genet. 2022;135(11):3875-3890.
94. West J, Spadaro D, Höfte M. Editorial: insights in disease management. Front Agron. 2023;5:1155058.
95. Wu Y, Chang-Lin G, Xiao Y, Li X, Yu D, Wan Q, *et al*. Physio-biochemical and transcriptomic analysis of *Bacillus amyloliquefaciens* PG-4-induced salt stress tolerance in *Macrotyloma uniflorum*. Front Sustain Food Syst. 2024;8:1386079.
96. Xu L. Soil fungal communities associated with plant health as revealed by next-generation sequencing: PhD thesis. Research Portal Denmark; 2011. p. 1-150.
97. Радченко ЕЕ, Абдуллаев РА, Alpatieva NV, Putina OV, Гасич ЕЛ. *Alternaria* leaf blight of clusterbean. Vavilov J Genet Breed. 2019;23(6):641-647.