Investigating the Impact of Climate Change on the Dynamics of Fungal Plant Pathogens

Abstract

Fungal plant pathogen dynamics have been revealed to be significantly influenced by climate change, which has important ramifications for global agriculture and food security. This review explores the multifaceted impact of rising temperatures, altered precipitation patterns, and extreme weather events on the prevalence, geographic distribution, and virulence of fungal pathogens. The key topics include the mechanisms of fungal adaptation to climatic variability, the interactions between fungal pathogens and host plants, and the challenges in developing sustainable management strategies. Additionally, developments in biological control methods, molecular diagnostics, and predictive modeling are further explored, emphasizing their function in reducing the negative consequences of fungal diseases in the face of shifting environmental circumstances. In order to address the growing threats posed by fungal infections in a warming environment, this review highlights the necessity of multidisciplinary research and policy initiatives.

Keywords: Biological control; Climate change; Fungal disease; Host-pathogen interactions; Pathogen dynamics; Sustainable disease management.

Introduction

Fungal plant infections pose a serious worldwide threat as they may infect horticulture crops, wild plants, and important commercial agricultural plant species. Fungi are recognized to cause the majority of plant and agricultural illnesses (Fisher et al. 2020; Ramudingana et al., 2025). Food, fiber, and other goods may be wasted as a result of these diseases, which might render yields unmarketable. Early findings suggested that some infections had particular host ranges or geographic distributions, but more modern genetic and experimental methods have shown a growing variety of fungal-plant relationships (Attia et al. 2022; Deresa & Diriba, 2023). Therefore, in order to control a disease or create crop cultivars that are resistant to it, it is very essential to comprehend the ecology and host-pathogen interactions of each component of the disease triangle (El-Baky & Amara, 2021; Upadhyay et al. 2023). Facultative and obligate fungi cause a range of plant diseases such as root and fruit rots, wilts, damping-off, powdery mildew, rust, and smut. The ongoing and dynamic co-evolution between plants and fungal pathogens is of increasing interest to evolutionary biologists and researchers involved in plant pathology (Bernardo-Cravo et al. 2020; Borer et al. 2022; Páez & Fleming-Davies, 2020). There have been accounts of the existence of pleomorphic, anamorphic, and distinct teleomorph phases for some species due to interest in the behavior of some specialists when they "jump" to a new host in response to changing temperature or maybe host physiological or genetic makeup (Yu et al. 2022; Guégan et al. 2024; Yadav and Ravichandran, 2024).The significance of such distinct infection systems to biology and, on the other hand, the economic significance of particular fungal pathogens in connection with crop disease management will be somewhat quantified by longer-planned multicenter research on the frequency and population analyses of relevant data. The potential implications of changing temperatures or increased CO_2 on the interactions between plants and their pathogens have been a topic of investigation as part of a broader concern over the influence of climate change on global plant pathology (Wahid et al. 2020; Singh et al. 2023; Lahlali et al. 2024).

Plants are affected by a broad spectrum of diseases caused by different types of fungi that are found in a wide range of taxonomic groups and are among the most important, diverse, and economically damaging pathogens of plants (El-Baky & Amara, 2021; Fernandez-San et al. 2021). Plant pathogenic fungi manipulate the physiology of plant hosts by a multitude of mechanisms, such as the secretion of proteins that suppress host immunity to respond against pathogen attack, adding enzymes and other proteins to infected plant cells, scavenging important nutrients from plant tissue in order to fuel their growth (Grabka et al. 2022). They can be split into different types of pathogens based on their life cycle and the ways they infect plants. For example, rust fungi are pathogens with complex life cycles, whereas powdery mildews have relatively simple life cycles compared to rust fungi even though they both are biotrophic fungi (Précigout et al. 2020; Mapuranga et al., 2022). An example of a necrotrophic fungal pathogen is the soil-borne take-all fungus, while monogenic pathogens have life cycles similar to biotrophic pathogens, they are not adapted, therefore, unable to spread from one host species to another (Précigout et al. 2020). Biotrophic fungal pathogens can also cause a range of diseases when they switch from being parasitic to saprotrophic towards the end of their life cycle. This transition can result in the reduction of crop quality by pre-harvest diseases (Précigout et al. 2020). On the other hand, there are saprotrophs, which have adapted to exploit plants after they die, by aiding in the return of nutrients to the underlying soil.

Fungi can reproduce either sexually through fruiting structures or asexually through the production of different types of spores that are adapting to their dispersal capabilities and suitable host tissues (Wijayawardene et al., 2022). Fungal spores are produced in a wide range of varieties, and each strategy has its own genetics and evolution, maintaining the maximum capacity for spore germination during the correct conditions (Jayawardena et al. 2021). Some fungi that occur naturally in the environment can also become invasive pathogens, causing severe disease on a range of plants (Leroy et al. 2021; Yigezu Wendimu, 2021; Rathnayaka et al. 2024). In this review, fungal lifestyle strategies were described in more detail before moving to the mechanisms of fungi that allow them to interact with their plant hosts. Agriculture, in particular, is one of the key practices that has been influenced by fungi, and the loss of crop yield due to fungal diseases is a significant threat to food security in a changing climate. The horticultural and forestry industries invest time and energy in controlling a wide range of plant diseases in addition to producing food. The economy is greatly impacted by the harm that pathogenic fungus do. If some of the most dangerous viruses spread more widely as a result of climate change, the impact might be much more severe. An overview of the basics pertaining to this taxonomic group of creatures is given in this review, which also serves as a backdrop for understanding how climate change may affect their interactions with plants.

Climate Change and its Effects on the Environment

According to the European Environment Agency, climate change is any sustained change in observable patterns of the climate that is caused by either anthropogenic or natural variability, such as trends toward global warming or cooling. Global ecosystems are impacted by a number of climate change-related factors. For example, among the known consequences of climate change are an increase in the frequency of infrequent but catastrophic weather events and a rise in the average world temperature (Belazreg et al. 2023). According to the most cautious projections, the world's temperature is expected to increase by 1.5 to 4.5 °C by 2100 (Keppas et al. 2021). In addition, other consequences predicted in response to climate change include altered precipitation patterns, such as more rainfall in some regions but less in others or variations in seasonal timing, as well as a rise in the incidence of extreme meteorological events (Chen et al. 2023; Zhu et al. 2024).

The impact of climate variations on fungal plant pathogens remains difficult to predict because of the complex interaction between several factors. As an example, temperature, humidity, precipitation patterns, and extreme weather events (Garrett et al. 2021). Higher temperatures are predicted to favor some parasitic fungi by enhancing soil health and increase plant debris decomposition (Wang et al. 2020). Besides, a decrease in precipitation frequency combined with longer, more intermittent dry periods are negatively affecting fungal pathogens by reducing the duration of leaf wetness and availability of water-soluble nutrients that are essential for their growth (Aguilar-Paredes et al. 2023). Furthermore, it is predicted that a rise in the intensity and occurrence of extreme weather events would be detrimental to agriculture mainly because of expected losses in crop yield (Thakur et al. 2022; Khalid et al. 2024; Liu et al. 2024). From the point of view of the impact on global agriculture, these consequences could lead to food shortages and, in turn, make all living organisms face malnutrition problems (Ristaino et al. 2021). Therefore, many researchers consider that it is of the utmost importance to study soil pathogens to prevent such catastrophes (Trivedi et al. 2020). With the increasing trend of climate change, the environment is expected to be different from the environment familiar to human populations. Therefore, it is critical to explore the new environment to anticipate the challenges that will face plant health (Ashraf et al. 2021; Singh et al. 2023).

Global Warming and Climatic Variability

Global warming is an unanimously accepted overarching cause of climatic variability which could have impacts on a variety of ecological and agricultural systems. It has been noticed that climate-related modifications at the poles are more extreme than those found in other locations globally, with rising global and ocean temperatures are now known to result in a multitude of alterations to ecosystems (Romero et al. 2022). The rise in extreme events and weather-related disasters, such as hurricanes and tropical storms, is another important result of this change. Such variability may raise ground atmospheric temperatures in many tropical, subtropical, and temperate regions where some of the planet's most important crops are grown. Climatic variability can influence the intensity of plant fungal disease and reduce food crop quality. Since many fungi have considerable advantages for survival and proliferation in these altered or variable conditions, climatic variability can have a substantial influence on fungal-plant disease (Gadre et al. 2022; Singh et al. 2023; Lahlali et al. 2024). This rise in infections was especially noteworthy during the 2000s, as unusual warmth weakened potato host resistance. Research has also shown an increase in the fruiting body production of pollen allergenic fungus during the milder Christmas period. Although suitable forage is vital for honey bee strength and survival during foraging, studies have shown that higher upland temperatures help to spread the infection to forage sets (Borowska-Beszta et al. 2024; Dixit et al. 2024; Zhong et al. 2024).

Although floods produce relatively cold and moist infection settings in some places in addition to photosynthesis and plant development, drought increases temperatures that can both directly and indirectly affect host resistance systems (Ali et al. 2022). In addition to lower air temperatures, unseasonably cooler weather characterized by strong winds induces wet plant foliage, leading to much faster availability of adequate moisture for germination of soil-borne spores (McDowell et al. 2022). The replacement of outdated host plant species with more resilient and stress-tolerant clones can also promote infection by pathogenic fungi in a variety of crops. Such interactive impacts obviously need to be considered by developing predictive models that are poised to mirror the sophisticated interactions occurring in larger agricultural environments containing several simultaneous climate transformations and their organisms, either offering or hindering control over plant diseases (Lahlali et al. 2024).

Interactions Between Fungal Plant Pathogens and Host Plants

Numerous fungal plant diseases possess the capacity to form intricate connections with their hosts as a result of various internal and exterior morphological changes. Internally, both plants and diseases may change gene activity to adjust for environmental fluctuation (Bhunjun et al. 2021; Antonio López-Quílez, 2025). The majority of fungi cause infection by penetrating plant cell walls by mechanical pressure, the attacking fungus's osmotic potential, or the release of enzymes and other secondary metabolites that break down cell walls (Jayawardena et al. 2021). The fungus typically subsequently enters the plant tissue through the cell wall's natural holes or open wounds. Certain fungi have a tightly controlled genetic mechanism for infecting plants, which includes the production of hormones and other secondary metabolites as soon as the fungus detects the presence of a certain root exudate from a host plant (Chiquito-Contreras et al. 2024; Rathnayaka et al. 2024).

Numerous lines of evidence demonstrate the variety of tactics viruses might use to get past host defenses. Reactive oxygen species buildup is one of the tactics used by wound-invading fungal infections. These tactics entail a unique host response that is prepared during the pathogen and host's evolution (McLaren and Callahan 2020). Practical, durable disease resistance can only result from the full comprehension of the underlying mechanisms that characterize the interaction of host, pathogen, and environmental factors (Paludan et al. 2021). Plant diseases will ultimately cause irreversible harm to the environment and the economy. Research in this area should receive a lot of financial and moral support in a society where hunger and violence are ongoing threats. It should be remembered that host-pathogen interactions can have vicarious effects on broad ecosystems, therefore their ecological ramifications extend beyond zootechnical and agricultural dangers (Liu et al. 2022; Smith et al. 2023).

Infection Mechanisms and Disease Development

The infection of the targeted hosts is one of the key stages of the life cycle of most plant pathogens. The various infection mechanisms of fungal plant pathogens have been well described in such research. As the mechanisms of invasion are the only component of the pathogen life cycle where external environmental factors may potentially influence the outcome of a host-pathogen interaction, a brief overview of this topic provided here (Meile et al. 2020; Mapuranga et al. 2022). It is important to note, however, that no clear divisions exist between all of these modes of entry; many pathogens have a combination of all of these modes in their life cycles, adopting different strategies depending on host and environmental conditions, while others are specialized to use only one of these strategies. For example, the hemibiotrophic fungi use appressorium-mediated penetration into unopened fruit, whereas they may rely on a germ tube tip-growth strategy to enter leaves. Following the infection of the host, the pathogen interacts with the plant at the cellular and molecular level to enable establishment and disease progression (Dutt et al. 2021; Palmieri et al. 2022; Yan et al. 2023).

An important approach in plant–disease ecology is to examine the role of the environment in the development of the disease, i.e., the time frame from infection to expression of symptoms (Camenzind et al. 2022; Wang et al. 2022). The outcome of the interaction at the cellular and molecular level may result in necrosis and/or the development of combinations of other symptoms including chlorosis, gall formation, cankers, or induced plant growth. Disease initiation is the period following a successful infection event, while disease progression is the period following the onset of the first symptoms. Large discrepancies exist in the environmental requirements for the asexual sporulation of many fungi between initiation and progression events. Additionally, the influx of nutrients and energy by use of the necrotrophic lifestyle points to supposed advantages of inducing necrosis immediately upon infection to hasten the initiation of disease. The role of environmental cues in the timing of symptoms is reviewed in the next section (Wijayawardene et al. 2022; Hyde et al. 2024).

Current Methods for Studying Fungal Plant Pathogens

Interest in the study of the dynamic interactions between fungal plant pathogens and their natural environments has increased enormously over the last decade. However, to adequately understand the various facets of these often-complex interactions, researchers need a diverse array of appropriate investigative tools. The capacity to better understand microbial pathogens, including the use of molecular diagnostic and identification tools to detect and monitor pathogen populations, has enabled the investigation of ecological dynamics at finer temporal and spatial resolutions (Peng et al. 2021; Palmieri et al. 2022). Classical and modern research methodologies have cumulative or complementary attributes, and the outcomes of separate investigations—each undertaken at different resolutions—add valuable information concerning complex ecological interactions. This approach is consistent with the replicability and falsifiability principles of the scientific method, and unequivocal conclusions about the behavior of plant pathogens are therefore highly valuable in scientific research (Fernandez-San et al. 2021; Liu et al. 2022).

Classical methods of pathogen investigation primarily focused on pathogen identification techniques. These techniques used visual examination of the fungus and cultural characteristics that often raised the taxonomic status of the pathogen to a morphospecies. Among the advent and development of molecular diagnostics, pathogen identifications could, within limits, be made with greater sensitivity and specificity (Carney et al. 2020; Tiedje et al. 2022; Wensel et al. 2022). Environmental studies of fungal pathogen dynamics may now be conducted more robustly thanks to these recently made accessible technologies. In conclusion, direct sampling from field surveys as well as experimental manipulations or inoculation investigations conducted in glasshouse and/or controlled-environment facilities are both incorporated into modern pathogen inquiry methodologies. Field experiments are then used to validate the use of that knowledge in order to capture significant facets of pathogen behavior in empirical investigations. Knowledge derived from field and laboratory studies can therefore be more accurately applied to current disease dynamics, advancing the overall understanding of pathogen ecology (Deng et al. 2021).

Molecular Techniques and Pathogen Identification

In plant pathology, the species of plant pathogens are usually determined on the basis of morphological criteria provided by experienced taxonomists. This is often a challenging and even impossible task when relying on morphological traits because parasites collected in the wild can grow differently in culture from the type material, be in different life stages, undergo cell wall modifications due to exposure to host plants or fungicides, be mixed in culture products and thus misidentified, and be undergoing genetic changes (Buja et al. 2021; Hariharan and Prasannath 2021). The advent of molecular techniques in the late 1970s, however, has revolutionized our capabilities of identifying and characterizing plant and human pathogens globally. Techniques such as DNA barcoding and next-generation DNA sequencing, combined with sequences derived from reference fungal cultures or unknown species available in public and subscription-based repositories, do much to resolve diagnostic dilemmas about cryptic fungal pathogen species (Kulik et al. 2020)

The major advantages of molecular diagnosis are that researchers and practitioners are no longer required to retrieve and grow pathogens from culture, they can rapidly identify the presence and absence of pathogens in substrates such as air, water, and soil. Additionally, they can identify plant pathogens from infected plant tissues that might have been colonized by bacterial symbionts, viruses, and viroids. Furthermore, molecular diagnosis facilitates the analysis of soil and root systems that can reveal the presence of secondary and environmental contaminants and saprophytes in the laboratory and nursery environment. These capabilities support effective management and control outbreaks as they occur. High-throughput next-generation DNA diagnostics, especially metagenomic techniques combined with reverse transcription-quantitative PCR and advanced host-induced gene silencing have significantly innovative the study of disease dynamics and emergence. Having a molecular reference database sitting at the end user’s desktop or secure server manned by competent curators is extremely important (Sahajpal et al. 2021; Suminda et al. 2022; Zhao et al. 2024). This can result in faster pathogen spread rates or a reduction in the effect of management actions themselves over time, eventually making a data-based management program obsolete. Next-generation sequencing has increased our understanding of pathogen diversity around the world, along with the selective pressures influencing its evolution and that of its host plants. Random gene and core-genome sequence selection combined with genome-resolved studies of microbe communities in plant pathology provide a way of understanding the true nature of pathogen and commensal biology on diseases such as Panama disease of banana and the impact of protection agents in sustainable development. In addition to molecular detection, pathogen activity can be tracked using molecular assays. The field is now embracing gene expression of actively growing fungal spores and mycelium directly exposed to commercial control products in addition to the development of dried down spore-based gene assays (Garcia-Garcia et al. 2021; Liu et al. 2023; Altindiş & Kahraman Kilbaş, 2023).

Climate Change Adaptations of Fungal Plant Pathogens

Global climate change has been causing more frequent and intense weather events that are a major factor in the emergence of diseases and famine in natural and agricultural ecosystems. Because of their great variety and host essentiality, fungi are already recognized as a class of plant diseases that can tolerate harsh environmental conditions. Some fungi that cause plant diseases may change to a more virulent form in order to live and procreate in a different climate. In reaction to climate change, they could also directly or indirectly alter their host selection. Moreover, due to their short life spans and large life cycles, there is also a chance of a dynamic shift of fungal plant pathogens (Rienth et al. 2021; Singh et al. 2023; Lahlali et al. 2024).

Numerous investigations on how pathogen dynamics are affected by climate change have been carried out to date, and a number of these research have been examined. The ecological and epidemiological ramifications of the fungal infections that arise in response to these conditions are yet unknown, despite the fact that the effects of climate change on bacterial, viral, and nematode pathogens have drawn increasing attention. The adaptive response of fungal plant diseases to climate change and the impact of warmer and more variable weather on host-pathogen interactions are the main topics of this succinct and topical study. It discusses topics such as potential interactions, including temperature and physicochemical effects, and hypotheses to predict the ecological and epidemiological implications of changing host-pathogen interactions corresponding to changes in climate regimes. This review also addresses that ongoing and future research on dynamic fungal pathogens will be essential to establish and assess the validity of these assumptions and to develop practical strategies to minimize the effects of crop losses from pest management as well as human and animal parasitic fungi (Fones et al. 2020).

Shifts in Geographic Distribution

In response to climate change, substantial attention has been given to the expansion and contraction in the geographic distribution of wildlife. Several pathogens have already undergone marked shifts in their distribution as a consequence of climate change. These distributional alterations often occur when pathogens that attuned to specific climatic conditions are exposed to altered conditions (Stokholm et al. 2020; Vollset et al. 2022; Baker et al. 2022). One well-documented example of this phenomenon is the northward spread of avian malaria in New Zealand: tighter minimum temperature constraints at the northern limit may prevent transmission and disease in native land birds. Similarly, emerging human diseases are often reported to be moving into areas that have historically been considered disease-free because of unsuitable environmental conditions (Legge et al. 2022; Wen et al. 2022).

Ectotrophic root and bark fungi have very strict environmental requirements, and their species composition often varies according to more macro-climatic variables only, such as latitude and altitude. Many fungi will be adapted to specific temperature minima and maxima, as well as humidity and other specific micro-climatic variables. A change in temperature, or in precipitation and humidity regimes, may affect the abundance of ascospores post-dispersal and in the atmosphere, while water circulation below ground within the host plant root system may also be affected. Warmer temperatures may also affect whole tree phenology, which in turn may affect the invasion and colonization potential for root and shoot pathogens (Saidi et al. 2023). Climate change and other processes that increase the likelihood of cross-boundary movement can facilitate biological invasions by pathogens. Another possible outcome of the international commerce in plant products is the introduction of new diseases into the host plants' natural range. These invasion processes may result in increased competition amongst diseases, with the victor frequently relying on certain co-evolutionary characteristics. To protect and preserve the world's food supply, it is imperative to detect and examine worldwide patterns in the emergence of these novel and alien infections in order to track the possible effects of future disease risks (Potapov et al. 2022).

Climate and geographic shifts can result in new pathogens colonizing new hosts. This is important both in terms of disease risk to new hosts and to the potential evolutionary implications for the newly colonizing pathogen. It is noticeable that many of the newly emerging pathogens are becoming established on new host plants in areas where they could not initially (Baker et al. 2022). This probably occurs through selection of more generalist races to the previously confined hosts. Infected material along with global shipping and travel continue to be the main causes of emerging and new plant pathogens (Kafle et al. 2020; Hauser et al. 2021; Singh et al. 2023). New pathogens in new host ranges and distribution limits in native pathogens are important to understand in light of current climate change so that invasive pests can be quickly reported and controlled outside their native host range to slow the natural spread and minimize impacts on native plant, forest, and crop systems (Boeger et al. 2022). Monitoring of disease aliens and use of computer-based models to predict the potential spread and impacts of future disease threats, including expected climate warming scenarios, is essential for improved evaluative and management procedures (Brooks et al. 2022; Jiranek et al. 2023; de et al. 2023; Casu et al. 2024).

Case Studies of Fungal Plant Pathogens in Changing Climates

Case Study 1:

A Warming Mediterranean Basin Warmer winters are reducing the snowpack in the Sierra Nevada and decreasing moisture in the transition zone. Along with the increase in several pests throughout the state, *Phytophthora cinnamomi* appears to be spreading northward. (Serrano et al. 2021). The fact that accessible soil moisture for several months of the year has been inversely connected with illness in various parts of the region makes this rather contradictory. The pathogen's human mobility on nursery stock may be influencing its northward expansion (Noah et al. 2021; Gustafson et al. 2022). From a global standpoint, eucalypts are a host of this disease, which mostly affects oaks and other trees in the Fagaceae family and is a severe issue in many natural and ornamental environments. The forestry sector in Australia is significantly impacted by this. Climate may further restrict the pathogen's distribution in Tasmania, the only significant eucalypt-growing location where it is thought to be nonexistent. It may be especially pertinent in the context of this study since the pathogen's distribution is limited by variables other than climate, and because it has been shown to evolve several strategies for long-term survival in less-than-ideal environments, meaning changes may be gradual and intricate (Sáenz-Romero et al. 2020; Woodward et al. 2022)

Case Study 2:

In the Midwestern United States, the northern range limit of white pine pathogen was positively correlated with increased winter temperatures. In addition to the range limit expansion, the timing of disease in terms of spring temperatures relative to leaf emergence was also shown to be of epidemiological significance, influencing the buildup of the inoculum within host tissues to cause an epidemic and recognition of resistance mechanisms (Dudney et al. 2020; Lalande et al. 2020; Schoettle et al. 2022). Many factors establish the ability of a new infection center to become established each year. Other speculate that *S. tsugae* may spread most successfully with significant cultural or economic aid. More data is needed to increase our understanding of these and other factors driving pathogen and its population distributional ranges, and behavior during future exotic introductions and developing research, especially internationally, is focusing on the area (Kichas et al. 2020; Stern et al. 2021; Six et al. 2021; Cardinal et al. 2022; Sniezko et al. 2024).

Impact on Agricultural Systems

Given the evolving mechanisms by which infections influence disease prevalence, the scientific community is extremely concerned about the emergence of novel fungal epidemics in agricultural systems. These particular effects of fungal plant diseases' dynamic response to climate change will be the main topic of this subsection. A changing population structure in the range or share of different fungi and breeding types will have suboptimal effects on the host's external disease prevalence (Fones et al. 2020; Fisher et al. 2020; Ristaino et al. 2021). If a higher fraction of a pathogen population of a given type is part of a coordinated group of individuals, there will be increased links, such as parallel epidemics, that may elevate external disease prevalence relative to the disease that would occur with the same average pathogen population size. This disease prevalence is removed from the total pathogen population and left as sub-optimally low seeds. Similarly, if the increased fraction of a pathogen type changes the proportion of the pathogen population that seeks to make links inside the host rather than create offspring through asexual reproduction, it will increase growth. A pathogen atop a target under specific conditions with changing temperature can affect a wide range of other suboptimal conditions, having more aggregate effects on total transmission pathways (Belgacem et al. 2021).

In modern agriculture, handling diseases and pathogens are generally reactive rather than proactive. Production systems are usually designed to increase crop yield and hence economic profit rather than withstand ecologically driven perturbations such as climate change. Now that the most acute consequences of climate change on food security are being addressed, greater understanding will enable adaptation. A lack of inclusion of the response of plant pathology to climate change suggests that these changes will not be addressed in time to avert damage to food security (Fisher et al. 2020).

Disease management is a significant factor in shaping adaptive capacity in agroecosystems, especially in less developed regions due to limited technology and lack of infrastructure for pathogens and disease research for development. In the twenty-first century, fungal diseases are estimated to have destroyed 125 million tons of major crops, worth $70 billion. From cotton to coffee to cacao, fungal diseases affecting crops impact the rural poor. Current approaches to mitigating the impact of existing and emergent diseases are costly, and resistance development is one of the largest expenses in the vegetable industry (Khakimov et al. 2020; Shukla et al. 2022; Masih 2024). If resistant crop varieties are not provided for specific diseases, disease can be expected to cause small losses in crop yield. For example, under a specific scenario, there is a 90 % likelihood of an increase of 0–5% in rice disease incidence in Asia, which will produce a 1.2–2.1% decrease in global caloric availability. These direct yield losses are further added to yield reductions caused by climate change, even though the combined effects of climate change and pathogens are subject to significant uncertainty, compounded by seed sensitivity to increased temperatures (Mahadevakumar and Sridhar 2021). For an average farm situated in a specific scenario, out of a base of 4–16 beats equal costs or above that of the standard management scenario. The magnitude of these combined effects on a per-hectare basis seems less significant; the estimated loss only exceeds the 2.5% standard error from the yield and price averaging technique for durum wheat and rapeseed, as higher seed prices are balanced by lower pesticide expenses (Fones et al. 2020).

Predictive Modeling of Fungal Pathogen Dynamics in a Changing Climate

Ongoing climate change poses a novel and complex ecological challenge for both plant pathologists and the society that relies on agricultural production. Innovative and integrative research is desperately needed to keep up with the rapid emergence of new and more aggressive biotic threats. This section examines the role that climatic variables have in risk assessment and predictive modeling of fungal plant pathogen dynamics. Predictive, mechanistic, and eco-physiological modeling are highlighted, along with a discussion of various alternative ecological and statistical methodologies that have been employed (Occhibove et al. 2020; Jeger et al. 2021; Singh et al. 2023). Several studies have predicted range expansion, local adaptation of strains along climate-induced gradients, or have projected the expected evolution or spread of pathogens under different increasing future scenarios. Understanding the general biology and ecological context of the examined pathogen through separate experimental research is a crucial prerequisite for assessing the prediction value of these methods (Gullino et al. 2022). Linking and integrating the two different levels of modeling could form the basis for developing new tools to study changes in biotic interactions (Lahlali et al. 2024)

A vital part of verifying and implementing any new scientific achievement is its possible societal value. In the context of producing food, predictive modeling studies can play a prominent role in planning and implementing forward-looking strategies for coping with a shifting climate and pathogen landscape at field, regional, and global levels. Such scenarios already hold the potential to inform management decisions such as whether or which new crop or new agricultural practice can be tried or developed for a given area within a certain time frame (Sheng et al. 2021; Rolnick et al. 2022). On the other hand, predictive modeling approaches may suffer from significant statistical uncertainty, as they include some sources of variation that interact in unpredictable ways. The models must be carefully validated and regarded as an evolving enterprise. Their speculative nature necessitates close interdisciplinary cooperation and comparison with experimental and on-field surveys (Gomez-Zavaglia et al. 2020; Rellstab et al. 2021; Ridwan et al. 2021)

Simulation and Data Analysis Techniques

This section provides an overview of different types of simulation and data analysis techniques that might be used for predictive modeling of fungal plant pathogens. It outlines the various computational tools and software that can be used to model pathogen dynamics under different climatic variables and how to represent these climatic variables (Gökalp et al. 2021; Zhang et al. 2023). It also talks about how creating a trustworthy data-driven model requires the use of high-quality data. A model's outputs must be interpreted using mathematical or statistical techniques, which address uncertainty and validate the model's dependability. A summary of the several simulation and data analysis methods that may be applied to data-driven modeling is given (Fisher et al. 2020; Liu et al. 2022; Adeniran et al. 2024).

The simulation techniques used in predictive modeling produce computer-generated approximations of the outputs of an experiment or a model at a given time. One of the main purposes of using simulation tools to investigate pathogen progress under varying climatic conditions is to shine light on areas of parametric or structural sensitivity that require more investigation. The combination of the model's biological assumptions and input parameters is one of the fundamental suggestions that need investigation. An important factor that has to be considered is the step-by-step examination of the many model components that are thought to affect the pathogen dynamics as triggered by the environmental variables (Delplace et al. 2022; Lahlali et al. 2024). There is different validation procedures associated with simulation techniques, and their role is to evaluate the level of trustworthiness of the estimated outputs.

Model validation provides one possible answer to the question, how good is our model? Sensitivity analysis as part of the simulation techniques allows for the reduction of the model's complexity and practical constraints. Simulations are used to take into account the random occurrence of each event when predicting pathogen behavior under varying climatic variables (Motamedi et al. 2022; Singh et al. 2023). Model flexibility is important in ensuring that the model is a viable decision-making tool for agriculture. The validation of our data and model predictions can be tested to demonstrate the model's robustness for future projections. Given this, the use of real-world case studies is an essential part of our approach. Two case studies are provided to present the function of the simulation techniques, in which they cover examples of the plant pathogens (Ristaino et al. 2021; Salahshoori et al. 2024)

Mitigation Strategies for Managing Fungal Plant Pathogens in a Changing Climate

It seems sense to create suitable mitigation methods to reduce risks while examining the possible effects of climate change on plant pathogen dynamics. The creation and upkeep of reliable monitoring systems will help anticipate shifts in pathogen behavior and enable the effective distribution of resources to control disease outbreaks when they happen. This information will then be utilized to guide extension initiatives that try to get stakeholders ready for preventative measures (Singh et al. 2023; Olatunji et al. 2024)

In the absence of a 'silver bullet' that would reduce risk across all systems, a combination of management strategies is likely to be the most useful. Integrated pest management programs are often recommended as a way of attacking the pathogen on multiple fronts and are also likely to be better suited to tackling the complexities of a changing disease scenario. Developing resistant cultivars to lower the danger of pathogen establishment and dissemination is the primary goal of breeding and biotechnology in the fight against fungal plant diseases for public use (Baker et al. 2020). By engaging and funding research that increases the capacities of all stakeholders, a range of local and landscape-specific management strategies to lessen the effects of a changing climate may be developed. Plant disease dynamics models and/or farm-level and/or regional weather monitoring systems most certainly played a part. For example, utilizing information on recent local disease observations to forecast when a fungicide treatment is necessary (Deguine et al. 2021). Knowledge-based decision-making is made possible by the creation and upkeep of monitoring and reporting systems, the evaluation of possible effects of modifications to support well-informed management choices, and the incorporation of the effects of biotic and abiotic factors in plant disease simulation models for both primary producers and policymakers. Involving stakeholders in research is essential to ensuring that end users can properly receive the management methods that have been discovered.

To address any possible obstacles to the adoption of proactive or preventative measures, social and agricultural science disciplines should do research on the socioeconomic and adaptive behavioral concerns related to the application of management systems. Sustainable management of a shifting pathogen environment requires long-term approaches that address pathogen life-cycle obstacles and agricultural systems' general vulnerability, maybe by leveraging host resistance. Making sure legislators understand the advantages of the management alternatives discussed might lead to adjustments that protect delicate agricultural systems and eventually lessen the effects of fungal diseases on crop yields (Aiello et al. 2022; Singh et al. 2023)

In an increasingly competitive market, pressure is on all agricultural producers to increase production costs and efficiency while meeting standards for food safety and quality. Although the multiplicative structure of models may be used to overlook relatively unusual events, agricultural components like vineyards, the dairy sector, and flowers cultivated for export might have significant economic imperatives to demonstrate that disease pressures and management apply throughout full seasons. The primary economic engine of the agricultural sector, broadacre cropping, has been the focus of early research on the effects of climate change on disease (Harries et al. 2020; Khanal et al. 2021). Developing and adapting research outcomes to different horticultural cropping industries, organic clients, and outdoor versus undercover fruit and vegetable growers will build on this initial work and further develop adaptive innovation practices. The use of such long-term negative binomial processes for disease dynamics in this sector will also be encouraged by the provision of solid data on the effects and tactics in specific horticultural agricultural businesses (Bondad et al. 2023)

Biological Control Methods

Biological control is one of the fundamental management techniques that may be used to the enormous problem of managing fungal plant diseases in agriculture worldwide. The term "biological control" refers to the use of a natural antagonist that either directly results in high plant pathogen death or inhibits the activities of diseases. Beneficial bacteria and fungi in particular are known to generate or stimulate a variety of hydrolytic and other antifungal chemicals that can aid in suppressing soil pathogens and, as a result, have the ability to lower infection. In many instances, it is still necessary to comprehend the processes by which these biological control agents operate (Palmieri et al. 2022). Three fungal infections are said to be controlled by these, either in fields or in the natural habitat of plants. Depending on ecological particularity, they can be used in low- or high-input agriculture. Probiotics may have unintended side effects, and appropriate bioformulations will need to be investigated.

It is advised that probiotics be used in conjunction with other management techniques like companion planting and farmyard waste to make their use low input and sustainable over the long run (Tariq et al. 2020). Meanwhile, one of the easiest biological control agents for farmers to use has been *Bacillus subtilis* rods, which contain the small protein lipopeptide surfactants iturin and fengycin. These compounds penetrate the fungal spore coat and plasma membrane, causing death for the spores and fungal mycelia to shrink. A marginal note here on biological control in general is that currently, while there has been significant groundwork done to assess their effectiveness, there are no published efficacy figures on using biocontrol for pathogen management in the wild or in commercial agriculture using a sustainable farming approach (Tariq et al. 2020). Nonetheless, it is essential to talk about real-world examples of enhancing crop resilience in various systems. The way biocontrol integrates with the plants' natural habitat, the right dosage, and the treatment window are some important success elements that might affect how effective biocontrol is in agriculture. Increasing the ability for beneficials to spread from the carrier system is the aim of interacting with the local microecology of soils and the plant being cultivated. However, in order for biocontrol or other tactics to be successful in their farming, farmers will want sound guidance on these factors (Ons et al. 2020; Palmieri et al. 2022).

Genomic Approaches in Pathogen Research

The use of genomic techniques in research on fungal plant diseases has grown in recent years. Full-genome sequences of a variety of pathogenic fungal strains, including those belonging to the most economically significant pathogen families, are now possible due to rapid advancements in sequencing technology and significant cost reductions. Whole-genome sequencing is important because it not only allows the identification of candidate pathogenicity and virulence factors either through a de novo approach or through homology search, but it also increasingly reveals fundamental aspects of the biology of the pathogen of interest, such as life history, population connectivity, and selective pressures acting on the pathogens, which are important facets of pathogen population genetics and evolutionary studies (Palmieri et al. 2022).

Because targeted mutation may be more readily carried out in gene areas that lack functional similarity in the host, the availability of genomic information can enhance genetics research. Furthermore, the availability of whole-genome sequences can aid in the creation of more resilient crop varieties by controlling marker-assisted selection of host gene alterations at will. Thus, the availability of a full set of reference sequences for host and pathogen, combined with a better understanding of gene conservation, can be exploited to propose cataloging of genes highly conserved between host and pathogens, which can be used as effector targets for enhancing crop resistance in the long term and safe allele selection for gene deployment and conventional breeding of new crop cultivars in the short term. Finally, the described research can be carried out in parallel with field trials and data acquisition, which, if relevant to the constructed parameters, can be directly added to the model to provide a comprehensive view of pathogen dynamics. Integrating high-throughput, methodical methodologies to patshogen research present a number of significant hurdles (El-Baky & Amara, 2021). One of these challenges is the interpretation of these mixed data requires robust computational tools that can identify, link, and prioritize candidate genes in high data dimensionality. Furthermore, there is some historical precedent for the ethical issues raised by the use of pathogen sequencing data. Indeed, one can and should argue that out of respect for public safety, such studies should only be undertaken with the utmost caution by a well-regulated research community living up to its responsibilities (Hariharan and Prasannath 2021). Nevertheless, using cutting-edge molecular genetic technologies is an identified responsibility under European law. At this point, it is difficult to envisage any significant advances in our understanding of pathogens available to researchers not exploiting genomics or similar cutting-edge molecular genetic approaches. Arguably, there are wider societal benefits to such studies, particularly those that provide feasible alternatives and safe research to undertake (Yadav et al. 2023; Chethana et al. 2021).

RNA-sequencing (RNA-seq) technology has been widely used to provide important insights into the interactions between plants and pathogens (Nibedita and Jolly, 2017). Accurate recording of host transcriptome responses during infections is made possible by this method. Consequently, RNA-seq is a sophisticated technique to unravel the molecular mechanism behind these interactions, as evidenced by the hundreds of transcriptome profiling studies that have been conducted too far (Tyagi et al., 2022). These methods would also help with the ongoing discovery of novel resistance genes, which is essential for enhancing resistance to biotic stressors and laying the groundwork for future breeding initiatives (Zambounis et al., 2020, Doddaraju et al., 2021). For example, the pomegranate genome has 186 R2R3-MYB transcription factors (TFs) that regulate defensive responses, metabolite accumulation, and plant growth; the U-box gene family, which is implicated in abiotic stressors, has a similar function (Chen et al., 2023; Suo et al., 2023). These days, expenses are going down and RNA-seq technology is becoming more useful because to the use of cutting-edge next generation sequencing (NGS) platforms like Illumina and Single-molecule realtime (SMRT) sequencing (Li et al., 2018; Naidoo et al., 2018). There is currently a study vacuum in the transcriptional profiles of pomegranate fruits following challenge with *C. granati*, despite the fact that similar methods have recently been used on the fruits and petals of other deciduous trees to understand the defense responses against fungal infections (Aci et al., 2024; Tsalgatidou et al., 2024a,b).

Future Research Directions and Emerging Technologies

Due to a combination of rising temperatures, increased moisture availability, and shifting natural and agricultural environment acclimatizations, most diseases are predicted to grow, which has drawn attention to plant pathology. As a result, in addition to thoroughly outlining the dynamics connected to every patho-system and agro-ecosystem, future study will necessitate other methodologies from those presented in this review and created thus far (Baker et al. 2022). These alternatives can be broken down into at least five: the use of machine learning and artificial intelligence to analyze accumulated data; basic research on the genetics of pathogens and their evolution; use of various technologies to decipher metabolic and signaling pathways that are important for pathogens; interdisciplinary and multidisciplinary approaches; and the need to involve practitioners and intermediaries in developing data-based predictive models (Mora et al. 2022)

For the study of system pathologies, which were defined by constant communication between practitioners and modelers, a number of networks have recently been formed. These efforts have to be expanded and based on collaboration with transdisciplinary and multidisciplinary organizations in addition to practitioners and modelers (Rehman et al. 2022). Needless to mention, but it should be said, all of the above priorities imply an integration of research skills in the same research team rather than the sum of results obtained by distinct researchers who work independently but interchange comments about the results (Van et al. 2021).

Finally, however, the co-evolution of plants and a changing environment has not yet been addressed. It is likely that changing climate patterns and new farming practices will challenge the control strategies currently in place. In fact, there are indications that, for example, quantitative resistance will behave differently in a changed climate (Syed et al. 2022).

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