J.Mycopathol.Res. 63(4) : 715-727, 2025, ISSN : 0971-3719 (Print), 2583-6315 (Online) 10.57023/JMycR.63.4.2025.715

REVIEW

Genome informatics: A perspective towards pathogenicity and diagnostics in fungi

ALOK K. SRIVASTAVA
ICAR-National Bureau of Agriculturally Important Microorganisms (ICAR-NBAIM), Kushmaur Mau, 275103, Uttar Pradesh

Received : 04.07.2025 Accepted : 03.09.2025 Published : 29.12.2025

Advancement of tools and techniques in science has changed the entire face of research. High end instrumentation and high throughput sequencing has generated a huge biological data that could be utilized in deciphering very minute details of biological system. One such aspects is genome informatics. This can be understood as 'bioinformatics for decoding genome'. This has roles in sorting big data for biological purposes, especially for connecting with applied usage. One such applied role is for studying fungal biology and behavior. Analyzing fungal genomes to find characteristics linked to behaviour, disease, infection mechanisms, and diagnostic markers could be key in understanding pathogenicity, and can be utilized in diagnostics as well. Utilizing computational and bioinformatic methods, it becomes easier to examine resistance, host specificity, and virulence.Genome informatics has revolutionized the study of fungal biology, empowering researchers to investigate genetic diversity, pathogenicity, and host-pathogen interactions with remarkable precision. Central to these advancements are molecular tools like Simple Sequence Repeat (SSR) analysis and next-generation sequencing (NGS), which have become foundational for fungal taxonomy, evolutionary insights, and disease management strategies. In this article, the detailed insights in to Genome informatics and its utilization in fungal biology has been discussed at length.

Keywords : Genome informatics, Pathogenicity Mechanisms, Genome-Based Diagnostics, Secretome Analysis, Next-Generation Sequencing (NGS)

INTRODUCTION

Fungi play a dual role in plant ecosystems, acting as both beneficial symbionts and harmful pathogens. While some fungi contribute to plant growth and health through mutualistic associations, others are responsible for severe plant diseases, leading to significant agricultural losses globally.

Plant-associated pathogenic fungi deploy a range of sophisticated mechanisms to infect their hosts, manipulate plant defenses, and extract nutrients (Mishra *et al.* 2024). These infections compromise crop productivity, reduce food security, and increase economic burden. Understanding the molecular basis of fungal pathogenicity is, therefore, critical for developing effective strategies to mitigate their impact on agriculture. Genome informatics has emerged as a transformative tool for studying plant-associated fungi, offering unprecedented insights into their genomes, pathogenic mechanisms, and potential targets for disease control (Kang *et al.* 2022; Higazy *et al.* 2025).

The advent of next-generation sequencing (NGS) technologies has revolutionized fungal research, enabling the rapid sequencing of entire fungal genomes. This technological progress has facilitated the analysis of key genomic features, including genes encoding virulence factors, secondary metabolites, and effector proteins. Genome informatics, which integrates bioinformatics with fungal genomics, allows researchers to unravel the molecular underpinnings of plant-fungal interactions

*Correspondence :
alok.srivastava@icar.org.in; aloksrivastva@gmail.com
21st Sir E. J. Butler Award Lecture organized by Indian Mycological Society delivered on 6th December 2024 during National Conference of IMS in Collaboration with the Department of Botany, University of Calcutta held at Ramakrishna Mission Cultural Centre, Golpark, Kolkata

(Srivastava *et al.* 2023). By comparing genomes of pathogenic and non-pathogenic strains, scientists can identify genes and pathways critical for pathogenicity, such as those involved in host recognition, toxin production, and immune suppression. Moreover, functional genomic approaches, including transcriptomics and proteomics, have deepened our understanding of fungal behaviour during different stages of infection (Muggia *et al.* 2020).

One of the hallmark contributions of Genome informatics to fungal research is the identification of virulence factors and effector proteins (Wu *et al.* 2022). Advances in computational tools have facilitated the prediction of effector candidates and their functional characterization (Lovelace *et al.* 2023). Additionally, the role of secondary metabolite clusters in pathogenicity is becoming clearer through genome mining, revealing insights into the biosynthesis of toxins and other bioactive compounds that contribute to disease severity (Kuhnert *et al.* 2022) (Fig.1). These discoveries hold promise for the development of crop protection strategies targeting specific virulence pathways (Ontoy and Ham, 2024).

Beyond pathogenicity, it has also significantly advanced the field of fungal diagnostics (Tan *et al.*, 2024). Traditional diagnostic methods, often reliant on morphological identification, are slow and prone to misidentification. Genomic approaches, such as whole-genome sequencing, metagenomics, and targeted marker analysis, now enable precise and rapid identification of fungal pathogens. For instance, specific genomic markers such as single nucleotide polymorphisms (SNPs), microsatellites, and effector gene profiles are being employed to differentiate closely related fungal species and track pathogen outbreaks (Singh *et al.* 2023). These genomic tools are especially valuable for early detection of emerging fungal pathogens and monitoring the spread of resistance genes in fungal populations.

This review aims to explore the transformative role of Genome informatics in understanding pathogenicity and enhancing diagnostics in plant-associated fungi. By integrating knowledge from various fungal pathogens, this paper highlights the potential of genome-based strategies to improve disease management and develop sustainable agricultural practices. Genome informatics, as a rapidly evolving field, continues to offer innovative solutions to the challenges posed by plant-associated fungal diseases, ultimately contributing to global food security.

Genome informatics in deciphering pathogenicity

Fungi are among the most destructive pathogens in plants, causing a wide array of diseases that threaten global food security and agricultural sustainability. Understanding the molecular basis of fungal pathogenicity is essential for developing effective disease management strategies. Genome informatics, an interdisciplinary field combining genomics and computational analysis, has revolutionized the study of plant pathogenic fungi by enabling a deeper understanding of the genetic and molecular mechanisms underlying their pathogenicity.

The technological advancement has fostered the sequencing of fungal genomes at an unprecedented pace (Srivastava *et al.* 2018). Through informatics, these sequences are analyzed to identify genes and pathways critical for pathogenicity. Among the most significant discoveries are the genes encoding effector proteins, secondary metabolites, and enzymes involved in cell wall degradation (Higazy *et al.* 2025). Effector proteins, small molecules secreted by fungi, play crucial roles in suppressing plant immune responses and manipulating host cellular processes to establish infection (Wu *et al.* 2022). By mining fungal genomes, researchers can predict effector candidates and study their interactions with host plants, shedding light on their contribution to disease progression (Srivastava *et al.* 2023).

Fungal pathogenicity is also closely linked to the production of secondary metabolites, including toxins that disrupt host cell functions. The tools such as antiSMASH (antibiotics and Secondary Metabolite Analysis Shell) enable identification and analysis of biosynthetic gene clusters responsible for producing these metabolites. Understanding these clusters helps in elucidating the role of fungal toxins in host colonization and disease

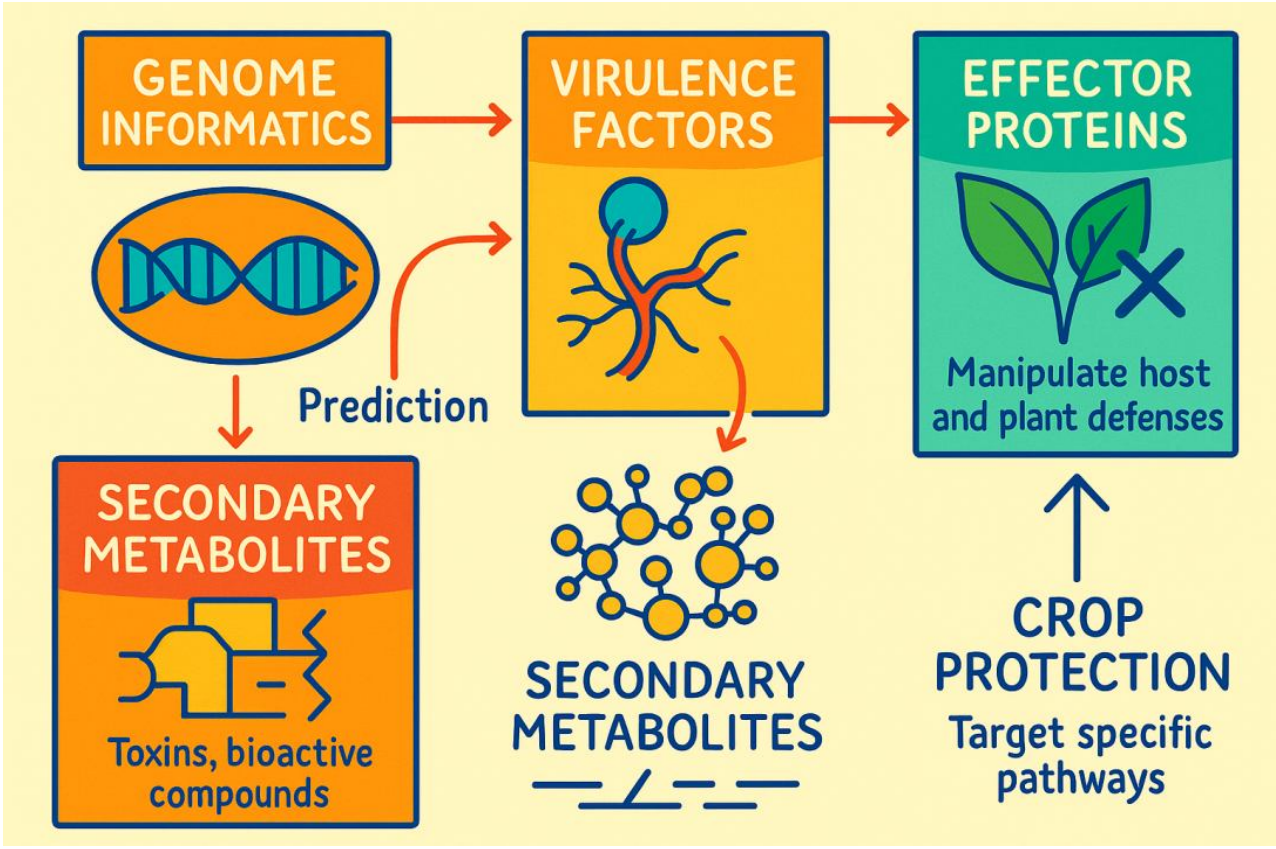

Fig. 1: The diagram illustrates how genome-wide analyses enable the prediction and identification of virulence factors, effector proteins, and secondary metabolite clusters. These elements collectively contribute to host manipulation, toxin production, and disease severity, offering insights for the development of targeted crop protection strategies.

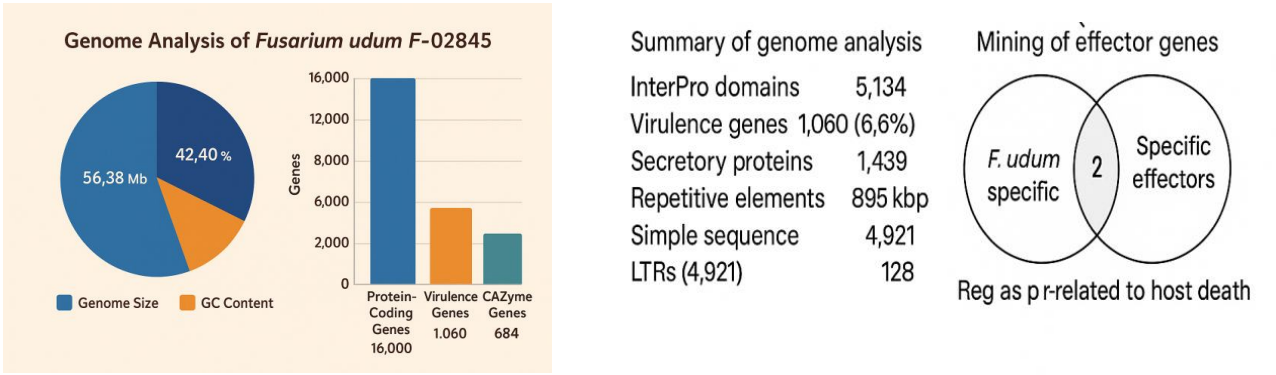

Fig. 2: Genome analysis of *F. udum* F-02845. The pie chart depicts the genome size (56.38 Mb) and GC content (42.40%), while the bar chart summarizes the number of protein-coding genes (16,000), virulence-associated genes (1,060), and CAZyme-annotated genes (684), highlighting key genomic features contributing to the pathogenicity of the pigeon pea wilt pathogen. A Venn diagram shows mining of effector genes with two *F. udum*-specific effectors linked to host cell death.

severity (Mapuranga *et al.* 2022). Similarly, carbohydrate-active enzymes (CAZymes), which degrade plant cell walls, have been identified and characterized through genome analysis (De Coninck *et al.* 2024). These enzymes allow fungi to invade plant tissues and access nutrients, making them a focal point for studying fungal pathogenicity

Genome-Based Insights into Virulence Mechanisms of Fusarium udum

NGS has further broadened the scope of fungal genomics by allowing comprehensive genome-wide analyses. For example, we have made whole genome sequencing (Srivastava *et al.* 2018) and further studies for understanding the

pathogen *F. udum* causing pigeon pea wilt of *Cajanus cajan* (pigeon pea). In this comprehensive genome analysis of *F. udum* F-02845, the genome was sequenced and assembled using a hybrid approach combining long and short reads, resulting in a genome size of approximately 56.38 Mb with a GC content of 42.40% and an N50 length of 0.08 Mb. NGS-based studies identified over 16,000 protein-coding genes, including 1,060 associated with virulence (Srivastava *et al.* 2023). The genome-wide study revealed key secretory proteins annotated with CAZyme. This study also reported genes associated with the pathogen-host interaction, and the virulence effector gene *SIX* (Secreted In Xylem) were also validated *in vitro*. This genomic data offers critical insights into pathogenic mechanisms, revealing proteins involved in cell wall degradation, nutrient acquisition, and immune suppression. These insights into the virulence mechanisms of *F. udum* offer avenues for developing novel strategies to combat wilt disease (Fig.2).

The functional annotation of the whole-genome sequence of *F. udum* F-02845 revealed a variety of protein-coding genes, including secretory proteins and carbohydrate-active enzymes (CAZymes) crucial for its pathogenicity. These enzymes facilitate the degradation of plant cell walls, enabling the pathogen to invade host tissues and utilize plant-derived carbon, which allows it to persist asymptomatically before disease symptoms appear. Effector proteins, critical for host-pathogen interactions, were also identified. These proteins suppress plant defenses and enhance the pathogen's virulence, highlighting their essential role in infection processes

Comparative genomics

Comparative genomics is another powerful application of Genome informatics in fungal research (Tan *et al.* 2024). By comparing the genomes of pathogenic and non-pathogenic fungal strains, researchers can pinpoint the genetic determinants of pathogenicity. Comparative analysis with closely related *Fusarium* species revealed both shared characteristics and unique features of *F. udum* (Srivastava *et al.* 2023). This underscores its distinct pathogenic traits while providing insights into common mechanisms of virulence within the genus. These findings enhance our understanding of *F. udum* and its interactions with host plants, contributing valuable knowledge for disease management strategies.This approach has uncovered genes and pathways unique to pathogenic fungi, such as those involved in host recognition, signal transduction, and stress adaptation. Transposable elements (TEs), often abundant in fungal genomes, are also studied (Tobias *et al.* 2021). These elements contribute to genetic diversity and evolution, enabling fungi to adapt to different hosts and environments and play roles in the regulation of effector gene expression, crucial for infection strategies.

Secretome Analysis and Its Role in Understanding Fungal Pathogenesis

As discussed in previous section, different effector proteins, CAZymes, and host manipulation gene are important in understanding fungal pathogenesis. The secretome analysis help in deciphering this aspect. Secretome analysis has become a pivotal tool in uncovering the molecular mechanisms underlying fungal plant pathogen interactions (Vincent *et al.* 2020). The secretome refers to the collection of proteins secreted by fungi during infection, including enzymes, toxins, and effectors that facilitate host colonization, nutrient acquisition, and immune evasion. For instance, genes associated with pectin-degrading enzymes help the fungus overcome host barriers like pectin in xylem vessels, leading to wilting symptoms (Miyambo, 2020). By studying the secretome, researchers can identify key players in the orchestration of fungal pathogenicity.

One of the primary components of the fungal secretome is carbohydrate-active enzymes (CAZymes), which degrade plant cell walls to penetrate host tissues and release nutrients. These include glycosyl hydrolases, polysaccharide lyases, and carbohydrate esterases. Such enzymes weaken plant structural integrity, aiding fungal invasion. Secretome analysis also identifies small-secreted proteins (SSPs), many of which function as effectors (Ozketen *et al.* 2020). These molecules manipulate host cellular

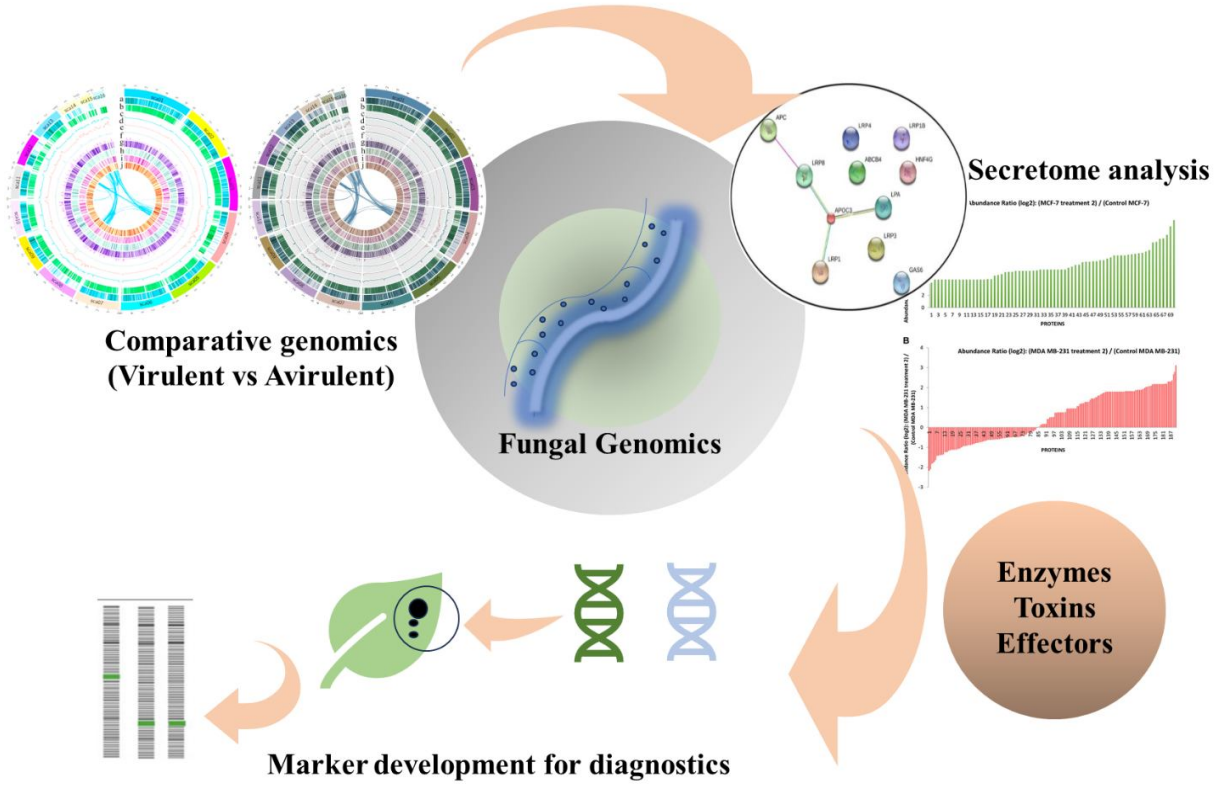

Fig. 3 : Illustration showing Genome informatics approach in understanding fungal behavior.

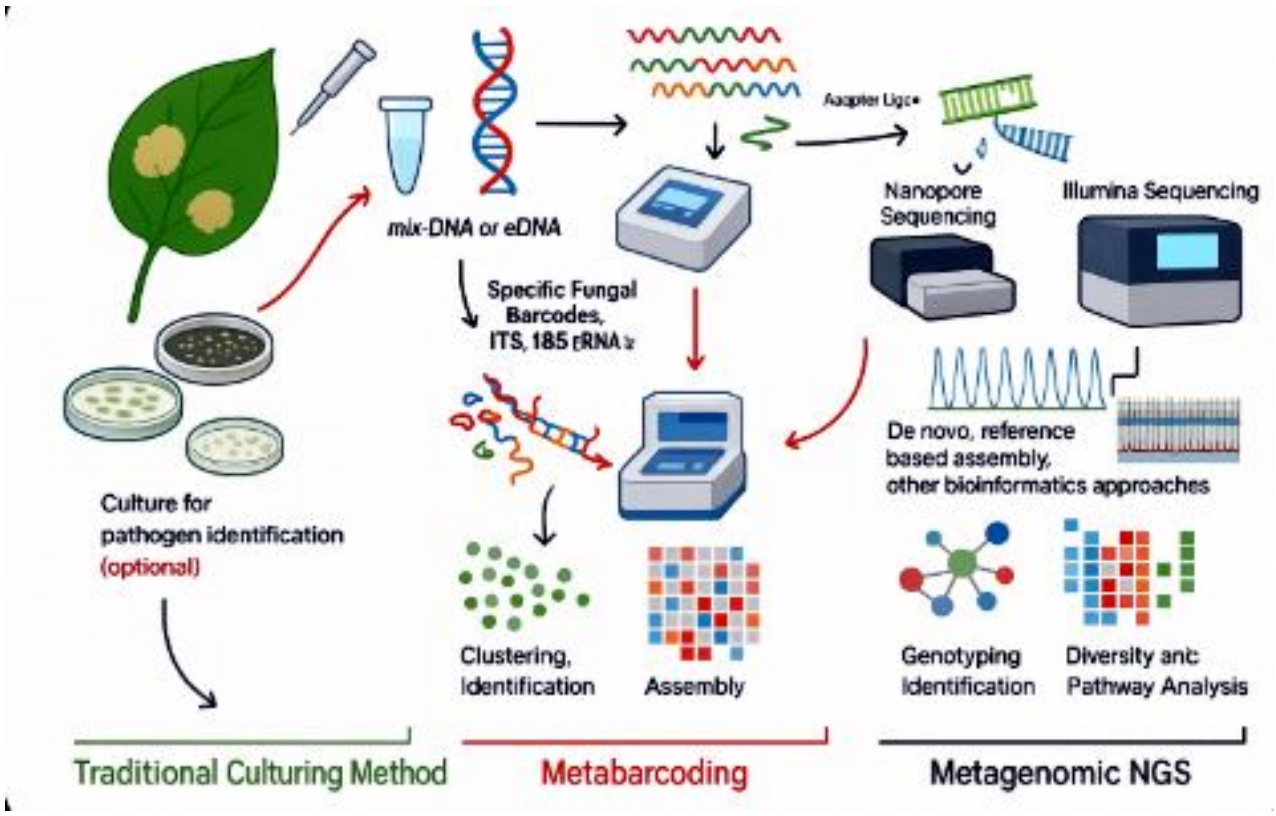

Fig. 4 : Comparative overview of traditional culturing, DNA barcoding, and metagenomic NGS approaches for fungal pathogen identification

processes, suppress immune responses, and create a favourable environment for infection.

Advanced proteomics, coupled with genomic and transcriptomic data, has enabled high-throughput identification of secreted proteins. Bioinformatics tools such as SignalP and EffectorP help predict signal peptides and classify effector proteins (Zhang *et al.* 2020). Comparative secretome analyses among fungal species or strains have revealed host-specific adaptations, such as the diversification of effectors to overcome unique plant defenses.

Insights gained from secretome studies are invaluable for developing disease-resistant crops and novel fungicides. By targeting essential components of the fungal secretome, these strategies can mitigate the devastating impacts of fungal pathogens on agriculture, paving the way for sustainable crop production and food security.

Transcriptomic studies further complement genome-based insights by revealing the expression patterns of pathogenicity-related genes during host infection (Bates *et al.* 2024). RNA sequencing (RNA-Seq) allows researchers to monitor dynamic changes in fungal gene expression, providing a clearer picture of how fungi respond to host defenses and environmental cues. Proteomics and secretome analysis, integrated with genomic data, identify secreted proteins that play critical roles in fungal virulence. The genome analysis provides valuable insights into the virulence mechanisms of plant pathogens. By identifying genes linked to pathogenicity, secondary metabolism, and host interaction, the study offers a foundation for developing strategies to manage diseases at field level. Functional studies on these genes could reveal targets for disease resistance breeding or novel fungicides. The findings also underscore the importance of comparative genomics in understanding pathogen evolution and host specialization.

By decoding the genetic blueprint of plant pathogenic fungi, Genome informatics has not only advanced our understanding of fungal biology but also paved the way for practical applications (Fig.3). These include developing resistant crop varieties by targeting fungal effector genes, designing novel fungicides, and improving diagnostic tools for early detection of fungal pathogens. As genome sequencing and informatics tools continue to evolve, they hold immense potential for addressing the challenges posed by fungal diseases and ensuring sustainable agricultural practices. Figure 3 illustrates how comparative genomics and secretome profiling synergistically contribute to deciphering the molecular basis of fungal pathogenicity and host specificity. The first part depicts comparative genomic analysis between pathogenic and non-pathogenic fungal strains, highlighting differences in gene content, including virulence-associated genes, effector repertoires, transposable elements (TEs), and secondary metabolite gene clusters. These genomic features underpin the adaptation and evolutionary divergence of pathogenic fungi.The second part focuses on secretome profiling, showcasing the identification of carbohydrate-active enzymes (CAZymes), toxins, and small secreted proteins (SSPs), which facilitate host invasion, tissue colonization, and immune suppression. Bioinformatic tools like SignalP and EffectorP help predict and classify secreted proteins with potential roles in causing infection.The third part connects these insights to downstream applications, such as the development of molecular markers for diagnostics, identification of novel antifungal targets, and breeding of resistant crop varieties. Together, this integrated approach provides a holistic view of fungal behaviour, helping to unravel mechanisms of virulence, host adaptation, and ecological fitness.

Genome informatics in diagnostics of plant pathogens

Plant pathogens, including fungi, bacteria, viruses, and nematodes, pose significant threats to global agriculture, reducing crop yields and impacting food security. Early and accurate diagnosis of these pathogens is essential for implementing timely and effective disease management strategies. Traditional diagnostic methods, which rely on visual symptoms, morphological identification, and biochemical tests, are often time-consuming, labor-intensive, and prone to inaccuracies. Genomics-Driven insights, has

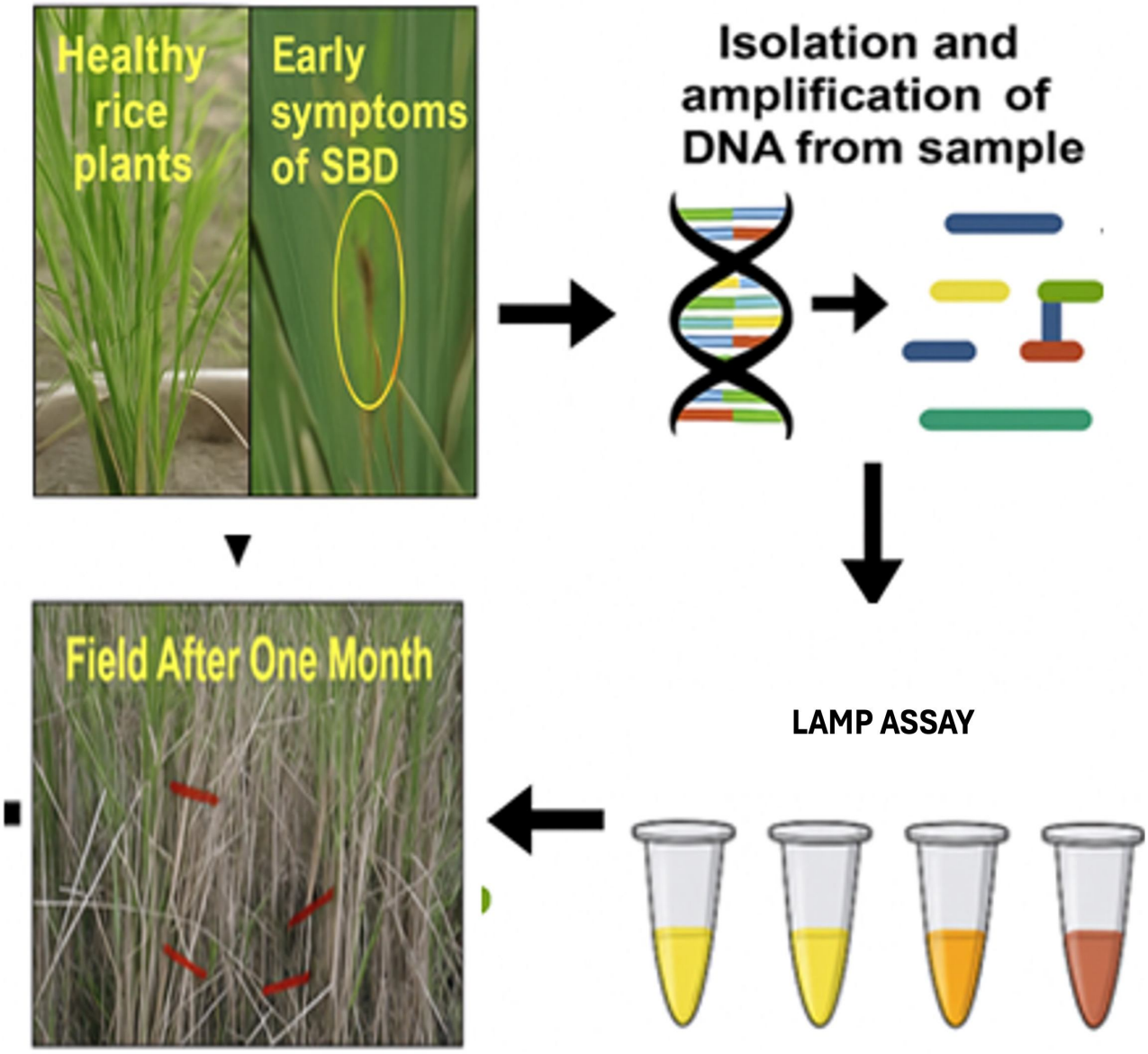

Fig. 5 : Detection of *Rhizoctonia solani* AG-1A causing sheath blight of Rice using LAMP

revolutionized the diagnostics of plant pathogens by enabling precise and rapid identification at the molecular level (Kang *et al.*, 2022).

The advent of next-generation sequencing (NGS) technologies has allowed for the generation of vast amounts of genomic data for plant pathogens. Whole-genome sequencing (WGS) provides a complete picture of a pathogen's genetic makeup, enabling researchers to identify species-specific markers such as single nucleotide polymorphisms (SNPs), insertion-deletion mutations (indels), and unique genes (Srivastava *et al.*, 2023). These markers serve as molecular signatures that can distinguish closely related pathogens and even identify strains with varying levels of virulence. The informatics tools process this data to create comprehensive reference databases, which are invaluable for diagnostic applications.

Metagenomics, a powerful extension of WGS, has transformed the diagnosis of plant pathogens in complex environments, such as soil or infected tissues, where multiple microorganisms coexist (Mohammed and Boyraz, 2022). By sequencing the entire microbial community, metagenomic approaches allow for the detection of pathogens

without the need for prior isolation or culturing. Bioinformatics tools analyze these datasets to identify the presence of specific pathogens and their relative abundances, enabling accurate diagnostics even in mixed infections.

DNA barcoding is an effective and nonspecific molecular tool for fast and reliable identification of living organisms, including fungi. Barcoding is based on short, standardized DNA sequences of typically 400 to 800 base pairs from certain genomic regions and identifies organisms by analyzing the unique patterns their sequences make through computational analysis. There is no single accepted genomic region for barcoding fungi, but the Internal Transcribed Spacer (ITS) region has been the most widely used because it can be amplified from diverse fungal taxa and utilized for ecological and taxonomic studies. The fungal working group acknowledged ITS as the best barcode for fungal plant pathogens in 2011. Barcoding is particularly beneficial if it is difficult to identify morphologically, such as with cryptic life stages or specimens that are degraded (Kashyap *et al.*, 2017).

However, the use of ITS alone is insufficient to resolve species boundaries in some genera, such as *Fusarium, Alternaria,* and *Cercospora*. It is currently unclear as to which additional and alternative markers are the best choices in the contiguous record. There are other markers that have more interspecific variability; species that can be considered are *β-tubulin*, *TEF-1β*, calmodulin, *RPB*1, *RPB*2, *MCM7*, as well as mitochondrial DNA, including cox I and cox II. Kumar, *et al.*, (2013) developed an effective PCR-based diagnostic reaction for the detection of *Alternaria solani*, using *β-tubulin* gene (AS1, AS2) from *A. solani*. The real-time assay developed was highly sensitive, able to detect 0.5 pg/µl of genomic DNA with acceptable linearity (R^2 > 0.987). *In planta* detection was verified from artificial inoculation of tomato plants at several time points. Another study from our group also aimed to compare five genetic markers; RAPD, ERIC, BOX, MAT locus, and microsatellites for assessing virulent *Fusarium oxysporum* f. sp. *ciceri* (FOC) isolates from seven different races of chickpea (Kashyap *et al.*, 2016). In this study, phylogenetic analysis based on *TEF1-α* and ITS regions revealed that isolates formed two major clades. Clade I contained races 1, 2, 5, and 6, and clade II contained races 3, 4, and 7. The MAT-2 locus was present in race 2 isolates, while isolates from race 1 showed the MAT-1 locus. Although PCA demonstrated genetic variation among isolates, there was no association between genotype, race, virulence, or geography. A comparative overview of traditional culturing, DNA barcoding, and metagenomic NGS approaches for fungal pathogen identification is given in Fig. 4.

Marker Development for Diagnostics and Monitoring Pathogen Evolution and Epidemiology

Beyond advancing our understanding of pathogenicity, genomic data has proven indispensable for the development of innovative diagnostic tools. Genome informatics facilitates the identification of molecular markers for pathogen detection. These markers include conserved gene sequences, effector proteins, and pathogenicity-related genes. Once identified, they can be targeted in diagnostic assays such as polymerase chain reaction (PCR), quantitative PCR (qPCR), and loop-mediated isothermal amplification (LAMP). For instance, specific genes encoding virulence factors or secondary metabolites unique to a pathogen can be used as reliable targets for precise detection. The Loop-mediated Isothermal Amplification (LAMP) technology, for example, has shown promise in *Fusarium oxysporum* f. sp. *ciceri,* the causative agent of chickpea wilt. LAMP assays, capable of detecting DNA at concentrations as low as 4.7 pg/µl, provide a rapid, cost-effective detection method crucial for containing fungal spread in agricultural contexts (Fig.5). For the pathogen *Rhizoctonia solani*, which affects rice and maize, researchers designed primers targeting the polygalacturonase (PG) gene; a key virulence factor (Choudhary *et al.*, 2020). These primers enabled specific and sensitive detection of the pathogen using both q-PCR and a LAMP-based colorimetric assay, offering a reliable and timely method for monitoring pathogen presence in the field.

In addition to these approaches, the CRISPR-Cas9 system, originally developed for gene

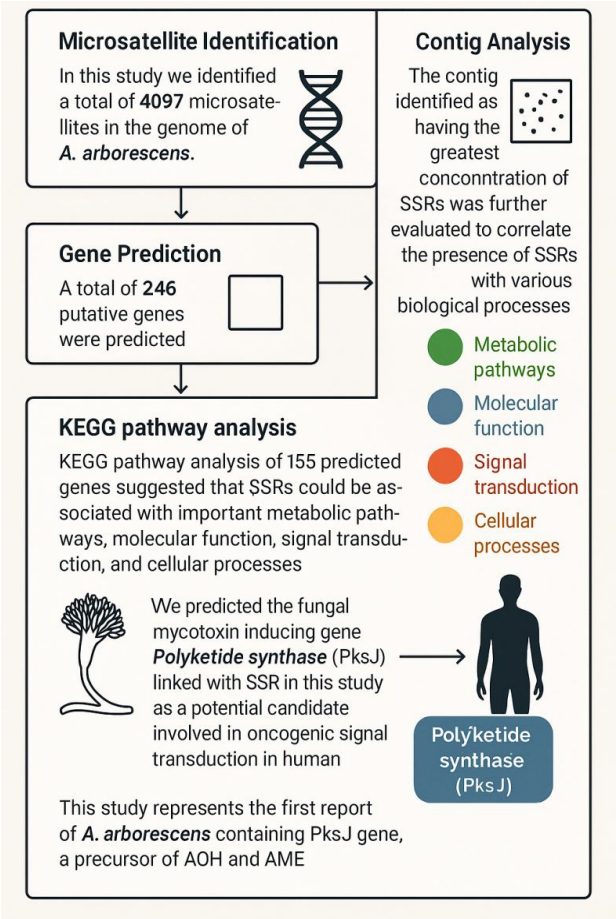

Fig.6 : Genome-wide analysis of microsatellites in *Alternaria arborescens* and elucidation of the function of polyketide synthase

editing, has also been adapted as a diagnostic tool for plant pathogens. Other research groups have used genomic insights in designing CRISPR-based assays by identifying unique pathogen-specific DNA or RNA sequences (Olatunji *et al.* 2024). These assays are highly specific and sensitive, making them ideal for field applications where rapid and accurate results are critical.

These techniques play a crucial role in tracking the evolution and spread of plant pathogens. By analyzing genomic data from different isolates, researchers can identify mutations associated with increased virulence or resistance to fungicides and pesticides. Phylogenomic studies trace the origins and evolutionary pathways of pathogens, revealing how they adapt to changing environments or new host plants (Mitra *et al.* 2022). Such insights are invaluable for predicting disease outbreaks and developing proactive management strategies.

SSR analysis has been particularly instrumental in examining genetic diversity and population structures within fungal species, enabling scientists to track pathogen evolution and identify essential genetic markers for diagnostics (Capote *et al.* 2012). Studies on *Fusarium* species, such as; *Fusarium solani, F. graminearum, F. verticillioides,* and *F. oxysporum* highlight the utility of SSRs in distinguishing microsatellite repeat patterns among species. *F. solani*, for example, displays a high density of trinucleotide repeats, a feature that aids in species identification and enhances understanding of *Fusarium* population dynamics. Given their role as major plant pathogens, these *Fusarium* species contribute significantly to diseases in key crops like legumes, maize and wheat. Similarly, SSRs have been applied to *Alternaria* and *Trichoderma* species to study genetic variation and adaptation to diverse environments. In *Alternaria*, a pathogen responsible for leaf spot and blight diseases, SSR markers have facilitated studies on strain-level genetic variability and the evolutionary tracking of pathogenicity across various host plants. Additionally, SSR markers have been explored for developing diagnostic tools to differentiate closely related species, such as *Alternaria brassicicola* and *A. brassicae*, which affect rapeseed-mustard and are challenging to distinguish morphologically (Singh *et al.* 2014). A total of 8,457 microsatellites were identified in *A. brassicicola* transcript sequences, with trinucleotide repeats being the most common. These transferable SSR markers offer valuable diagnostic tools for differentiating these pathogens in *Alternaria*-induced blight. For *Alternaria* species, a PCR-based diagnostic system was developed using primers for genes such as *nox*B, enabling species-specific detection and enhancing diagnostic accuracy for managing *Alternaria*-related crop diseases (Chakdar *et al.* 2019). Further, these microsatellite markers also indicate a possible relation of the microsatellites with the genes encoding different metabolic processes. For example, we studied the SSR markers in *Alternaria arborescens* causing early blight of tomato, and is also known to produce mycotoxins, such as alternariol (AOH), alternariol monomethyl ether (AME), etc. (Fig. 6) (Choudhary *et al.* 2018).

Comparative genomics has also yielded insights into the evolutionary dynamics of fungal

pathogens, as well as the genetic mechanisms underlying biocontrol properties in certain species. *Trichoderma*, a genus widely used as a biocontrol agent against plant pathogens, has been extensively studied genomically, revealing genes linked to antifungal activity and secondary metabolite production. Using SSR markers, this study characterized genetic diversity in five antagonistic *Trichoderma* species: *T. atroviride, T. harzianum, T. reesei, T. virens,* and *T. asperellum* (Rai *et al.* 2016). Publicly available genome sequences enabled the assessment of SSR distribution, abundance, and density across these species, with *T. asperellum* exhibiting the highest SSR density, followed by *T. reesei* and *T. atroviride*. Trinucleotide repeats predominated, making up approximately 80.2% of the SSRs; a useful marker for strain characterization and optimizing *Trichoderma* strains for improved biocontrol efficacy.

Multi-gene phylogenetic approaches have become essential for accurate species identification in fungal genera with overlapping morphological characteristics. Research on *Bipolaris maydis* and *Curvularia lunata;* pathogens that cause maize leaf blight and related diseases, has highlighted the benefits of multi-gene analyses (Manzar *et al.* 2022). By examining ribosomal DNA regions (ITS, LSU) and protein-coding genes such as GAPDH, they have clarified species boundaries, which is essential for understanding disease epidemiology and improving diagnostic precision. Integrating different omics approaches would be useful in early disease diagnostics, monitoring, and management involving genomics, transcript-omics, proteomics, AI and machine learning, metagenomics (Fig.7). The big data analysis and integration of different approaches could avoid any chances of false positive or negative.

Genomic tools such as whole genome sequencing and SNP analysis enable accurate pathogen identification and tracking. Transcriptomics reveals dynamic gene expression during host-pathogen interactions, while proteomics, particularly secretome profiling, uncovers virulence-associated proteins and metabolic pathways. Metagenomics offers culture-independent detection of pathogens directly from complex environments such as soil or plant tissues. Furthermore, AI and machine learning models enhance predictive diagnostics by analyzing patterns in high-dimensional datasets. The convergence of these data-rich platforms through big data analytics ensures robustness, minimizes false positives/negatives, and paves the way for precision diagnostics and proactive plant disease management.

Artificial Intelligence in plant-fungi interaction

The integration of artificial intelligence (AI) and machine learning (ML) with functional genomics has further enhanced diagnostic capabilities (Zhao *et al.* 2023). AI algorithms analyze complex genomic datasets to identify patterns associated with pathogenicity and resistance. These technologies enable rapid classification of pathogens, prediction of their virulence, and identification of emerging strains. For example, machine learning models can be trained to recognize genetic signatures of resistance in fungal pathogens, aiding in monitoring the spread of resistant strains (Fu *et al.*, 2021). It has enabled the development of portable diagnostic tools for on-site pathogen detection. Nanopore sequencing devices, which provide real-time sequencing data, are becoming increasingly popular for field applications (Ciuffreda *et al.* 2021). These tools, combined with bioinformatics pipelines, allow farmers and plant pathologists to identify pathogens directly from infected samples within hours. Portable devices can analyze small genomic fragments, such as ribosomal DNA or mitochondrial genes, to identify pathogens at the species or strain level, ensuring timely intervention.

The convergence of genomic insights with multi-omics technologies and advanced computational approaches is giving rise to a new era of precision fungal pathogen management. By integrating genomics, transcriptomics, proteomics, secretomics, and metagenomics, researchers can obtain a rather comprehensive molecular portrait of fungal pathogens and their interactions with host plants. The inclusion of artificial intelligence and machine learning further enhances predictive capabilities, allowing for the early detection of emerging threats and real-time

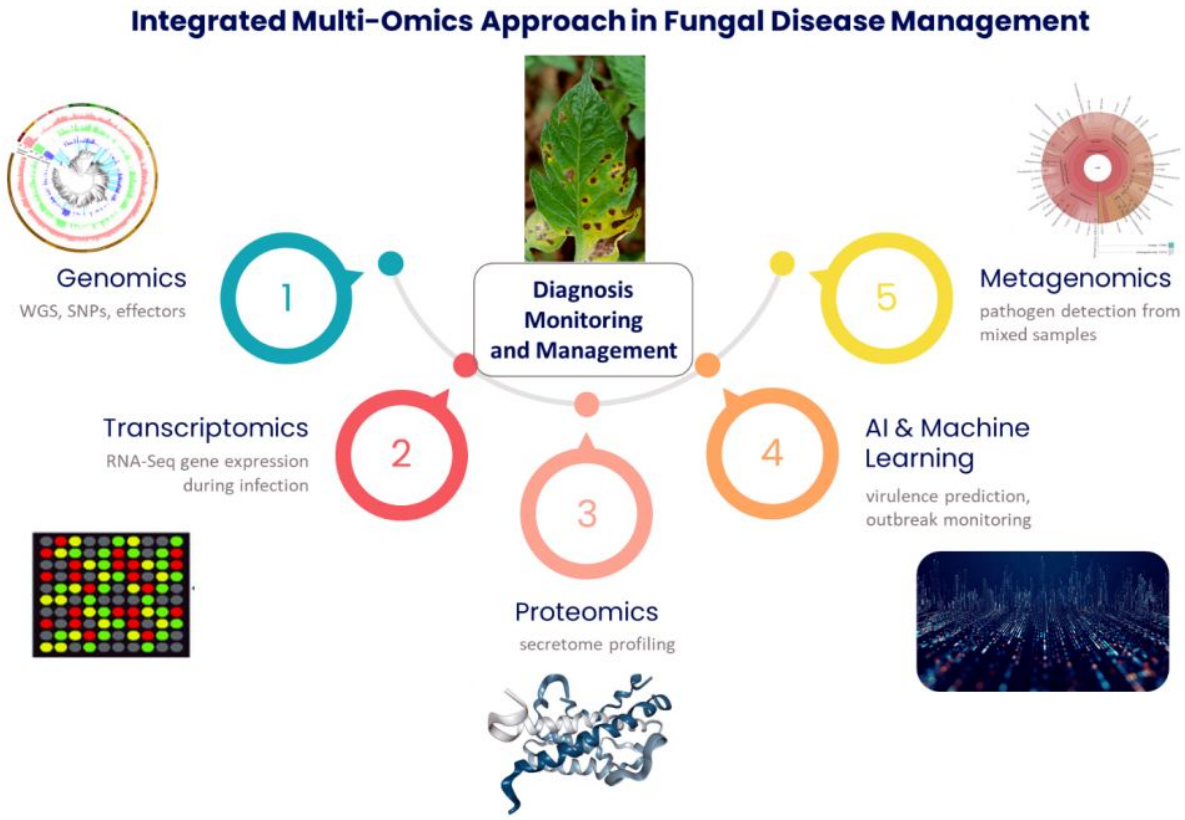

Fig. 7: Integrated multi-omics approach in fungal disease diagnostics, monitoring and management

epidemiological surveillance. Such integrated frameworks not only improve diagnostic accuracy and reduce the risk of false positives or negatives but also inform the rational design of disease-resistant crop varieties and targeted antifungal strategies. These advancements hold immense promise for building sustainable and resilient agricultural systems in the face of evolving fungal threats.

CONCLUSION AND FUTURE PROSPECTS

The integration of SSR analysis, NGS, and molecular diagnostics has greatly enhanced fungal research, especially in disease management and crop protection. By providing insights into fungal genetic diversity, pathogenicity, and evolutionary dynamics, these molecular tools are advancing strategies for developing disease-resistant crops and improved diagnostic tools. Early detection of fungal pathogens is crucial for enhancing crop protection, reducing agricultural losses, and contributing to food security. As fungal genomics continues to evolve, these molecular approaches will remain central to addressing agricultural challenges posed by fungal diseases. Despite its transformative potential, the application of genome informatics in diagnostics faces several challenges. High costs of sequencing, lack of infrastructure in resource-poor regions, and the need for specialized bioinformatics expertise limit widespread adoption. However, advancements in sequencing technologies and the development of user-friendly bioinformatics tools are addressing these barriers.

Conclusively, Genome informatics has emerged as a cornerstone in the diagnostics of plant pathogens, offering unparalleled accuracy and speed. By enabling the identification of pathogens at the molecular level, these approaches enhance our ability to manage plant diseases effectively. As genomic technologies continue to advance, the integration of Genome informatics into routine diagnostics holds immense potential for

safeguarding global agriculture and ensuring food security.

ACKNOWLEDGEMENTS

The author gratefully acknowledges the support and financial assistance provided by ICAR-NBAIM and the AMAAS Network Project. The assistance of Dr. Pramod Kumar Sahu in drafting the manuscript, as well as the contributions of my research team, is also gratefully acknowledged

DECLARATION

Conflict of Interest. Author declares no conflict of interest.

REFERENCES

Bates, H.J., Pike, J., Price, R.J., Jenkins, S., Connell, J., Legg, A., Armitage, A., Harrison, R.J. Clarkson, J.P. 2024. Comparative genomics and transcriptomics reveal differences in effector complement and expression between races of *Fusarium oxysporum* f. sp. *lactucae*. *Front.Plant Sci.* **15**: 1415534.

Capote, N., Pastrana, A.M., Aguado, A. and Sánchez-Torres, P. 2012. Molecular tools for detection of plant pathogenic fungi and fungicide resistance. *Plant Pathol.* **12:**151-202.

Chakdar, H., Goswami, S.K., Singh, E., Choudhary, P., Yadava, J., Kashyap, P.L., Srivastava, A.K., Saxena, A.K. 2019. *noxB*-based marker for *Alternaria* spp.: a new diagnostic marker for specific and early detection in crop plants. *3 Biotech* **9**: 249. https://doi.org/10.1007/s13205-019-1779-4

Choudhary, P., Rai, P., Yadav, J., Verma, S., Chakdar, H., Goswami, S.K., Srivastava, A.K., Kashyap, P.L., Saxena, A.K. 2020. A rapid colorimetric LAMP assay for detection of *Rhizoctonia solani* AG-1 IA causing sheath blight of rice. *Scientif. Reports* **10:** 22022.

Choudhary, P., Kashyap, P.L., Goswami, S.K. Chakdar, H., Srivastava, A.K., Saxena, A.K. 2018. Genome-Wide Analysis of Microsatellites in *Alternaria arborescens* and Elucidation of the Function of Polyketide Synthase (PksJ). *Interdiscip. Sci. Comput. Life Sci.* **10**: 813–822. https://doi.org/10.1007/s12539-017-0251-6

Ciuffreda, L., Rodríguez-Pérez, H., Flores, C. 2021. Nanopore sequencing and its application to the study of microbial communities. *Computat. Struct. Biotechnol. J.* **19:** 1497-1511.

De Coninck, T., Desmet, T., Van Damme, E.J. 2024. Carbohydrate-active enzymes involved in rice cell wall metabolism. *J. Exper. Bot.* **75**: 6206-6227.

Fu, C., Zhang, X., Veri, A.O., Iyer, K.R., Lash, E., Xue, A., Yan, H., Revie, N.M., Wong, C., Lin, Z.Y., Polvi, E.J. 2021. Leveraging machine learning essentiality predictions and chemogenomic interactions to identify antifungal targets. *Nature Commun.* **12**: 6497.

Higazy, S.S., Abdel-Fattah, E.U., Ramdan, R.H., Halawany, B.A., Soliman, M.M., Elsayed, M.M., Hajji-Hedfi, L., Abdel-Azeem, A.M. 2025. "Omics" tools for better understanding the plant-fungi interactions. In: *Forest Fungi* (pp. 83-98). Academic Press.

Kang, S., Kim, K.T., Choi, J., Kim, H., Cheong, K., Bandara, A. , Lee, Y.H. 2022. Genomics and informatics, conjoined tools vital for understanding and protecting plant health. *Phytopathology* **112**: 981-995.

Kashyap, P.L., Rai, P., Kumar, S., Chakdar, H., Srivastava, A.K. 2017. DNA Barcoding for Diagnosis and Monitoring of Fungal Plant Pathogens. In: *Molecular Markers in Mycology. Fungal Biology* (Eds. B.P. Singh, V.K.Gupta). Springer, Cham. https://doi.org/10.1007/978-3-319-34106-4_5

Kashyap, P. L., Rai, S., Kumar, S., Srivastava, A. K. 2016. Genetic diversity, mating types and phylogenetic analysis of Indian races of *Fusarium oxysporum* f. sp. *ciceris* from chickpea. *Arch. Phytopathol. Plant Protect.* **49**: 533–553. https://doi.org/10.1080/03235408.2016.1243024

Kuhnert, E., Collemare, J. 2022. A genomic journey in the secondary metabolite diversity of fungal plant and insect pathogens: From functional to population genomics. *Curr. Opin. Microbiol.* **69**: 102178.

Kumar, S., Singh, R., Kashyap, P.L., Srivastava, A.K. 2013. Rapid detection and quantification of *Alternaria solani* in tomato. *Scientia Horticult.* **151**: 184-189.

Lovelace, A.H., Dorhmi, S., Hulin, M.T., Li, Y., Mansfield, J.W., Ma, W. 2023. Effector identification in plant pathogens. *Phytopathology* **113**: 637-650.

Manzar, N., Kashyap, A.S., Maurya, A., Rajawat, M.V.S., Sharma, P.K., Srivastava, A.K., Roy, M., Saxena, A.K., Singh, H.V. 2022. Multi-gene phylogenetic approach for identification and diversity analysis of *Bipolaris maydis* and *Curvularia lunata* isolates causing foliar blight of *Zea mays*. *J. Fungi*, **8**: 802.

Mapuranga, J., Chang, J., Zhang, L., Zhang, N. ,Yang, W. 2022. Fungal secondary metabolites and small RNAs enhance pathogenicity during plant-fungal pathogen interactions. *J. Fungi* **9**: 4.

Mishra, S., Srivastava, A., Singh, A., Pandey, G.C., Srivastava, G., 2024. An overview of symbiotic and pathogenic interactions at the fungi-plant interface under environmental constraints. *Front. Fungal Biol.* **5**: 1363460.

Mitra, D., Mitra, D., Bensaad, M.S., Sinha, S., Pant, K., Pant, M., Priyadarshini, A., Singh, P., Dassamiour, S., Hambaba, L., Panneerselvam, P. 2022. Evolution of Bioinformatics and its impact on modern bio-science in the twenty-first century: Special attention to pharmacology, plant science and drug discovery. *Computat. Toxicol.* **24**: 100248.

Miyambo, T.M. 2020. Identification and Characterization of Polygalacturonases in *Phytophthora Cinnamomi* [Master's thesis, University of Pretoria (South Africa)].

Mohammed, T.A., Boyraz, N., 2022. Molecular detection of fungal plant pathogens: emphasizing recent advancement. In *2nd International Conference on Sustainable Ecological Agriculture 2.*(p. 422).

Muggia, L., Ametrano, C.G., Sterflinger, K., Tesei, D. 2020. An overview of genomics, phylogenomics and proteomics approaches in Ascomycota. *Life* **10**:.356.

Olatunji, A.O., Olaboye, J.A., Maha, C.C., Kolawole, T.O., Abdul, S. 2024. Next-Generation strategies to combat antimicrobial resistance: Integrating genomics, CRISPR, and novel therapeutics for effective treatment. *Engineer. Sci. Technol. J.* **5**: 2284-2303.

Ontoy, J.C., Ham, J.H. 2024. Mapping and Omics Integration: Towards Precise Rice Disease Resistance Breeding. *Plants* **13**: 1205.

Ozketen, A.C., Andac-Ozketen, A., Dagvadorj, B., Demiralay, B., Akkaya, M.S. 2020. In-depth secretome analysis of *Puccinia striiformis* f. sp. *tritici* in infected wheat uncovers effector functions. *Biosci. Reports* **40**: BSR20201188.

Rai, S., Kashyap, P.L., Kumar, S., Srivastava, A.K., Ramteke, P.W. 2016. Comparative analysis of microsatellites in five different antagonistic *Trichoderma* species for

diversity assessment. *World J. Microbiol. Biotechnol.* **32**: 1-11.

Singh Saharan, G., Mehta, N.K., Meena, P.D. 2023. Molecular Detection and Identification of Pathogens, Pathotypes, and Genes. In: *Genomics of Crucifer's Host-Pathosystem* (pp. 503-593). Singapore: Springer Nature Singapore.

Singh, R., Kumar, S., Kashyap, P.L., Srivastava, A.K., Mishra, S., Sharma, A.K. 2014. Identification and characterization of microsatellite from *Alternaria brassicicola* to assess cross-species transferability and utility as a diagnostic marker. *Mol. Biotechnol.* **56:** 1049-1059.

Tan, K.L., Mohamad, S.B. 2024. Fungal Pathogen in Digital Age: Review on Current State and Trend of Comparative Genomics Studies of Pathogenic Fungi. *Advance. Microbiol.* **63**:23-31.

Tobias, P.A., Schwessinger, B., Deng, C.H., Wu, C., Dong, C., Sperschneider, J., Jones, A., Luo, Z., Zhang, P., Sandhu, K., Smith, G.R. 2021. *Austropuccinia psidii*, causing myrtle rust, has a gigabase-sized genome shaped by transposable elements. *G3*, **11**: p.jkaa015.

Vincent, D., Rafiqi, M., Job, D. 2020. The multiple facets of plant–fungal interactions revealed through plant and fungal secretomics. *Front. Plant Sci.* **10**: 1626.

Wu, Y., Xie, L., Jiang, Y., Li, T. 2022. Prediction of effector proteins and their implications in pathogenicity of phytopathogenic filamentous fungi: a review. *Inter. J. Biologic. Macromol.* **206**: 188-202.

Zhang, Y., Wei, J., Qi, Y., Li, J., Amin, R., Yang, W., Liu, D. 2020. Predicating the effector proteins secreted by *Puccinia triticina* through transcriptomic analysis and multiple prediction approaches. *Front. Microbiol.* **11**: 538032.

Zhao, L., Walkowiak, S., Fernando, W.G.D. 2023. Artificial intelligence: a promising tool in exploring the phytomicrobiome in managing disease and promoting plant health. *Plants* **12**: 1852.