

The Role of Comparative Genomic Bioinformatics in Predicting and Managing Wheat Rust Disease in Wheat Crops: A Multi-Omics Approach for Pathogen Genomics and Host Resistance Identification

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ABSTRACT

The yield results of wheat (*Triticum aestivum* L.) suffer critical losses annually from rust diseases including yellow rust, leaf rust and stem rust. The study explores how comparative genomic bioinformatics supports wheat rust disease prevention and control by examining multiple-omic data approaches. The research demonstrates the way genomics, transcriptomics, proteomics and metabolomics assist in discovering genetic markers by presenting host-pathogen relations and producing resistant wheat varieties. This study has discussed diverse technologies such as genome-wide association studies, quantitative trait loci mapping and CRISPR/Cas9 gene editing tools that present critical results which can easily improve disease resistance. The research examines the difficulties faced through the analysis of big omics datasets while handling complex technological factors. The study explained the way multi-omics data applications work for wheat rust prediction, crop management and improvement efforts to present sustainable food production and agricultural bioinformatics progress.

Keywords: Gene Editing Tools, Genomic, Pathogen, And Wheat,

INTRODUCTION

Bioinformatics act as an essential function in genomics to predict and manage diseases from pathogens using contemporary techniques and multi-omic strategies during the modern age. Wheat rust is a major plant disease which annually costs wheat production worldwide in substantial amounts. It has been found by Chen (2020) that rust infection in wheat plants is mainly caused by to fungal pathogen called *Puccinia* sp. Three main types of rust are commonly found in wheat crops leaf (brown) rust by *Puccinia triticina*, stripe (yellow) rust by *Puccinia striiformis*, and stem (black) *Puccinia graminis* rust. The outputs of genomic bioinformatics with early detection help in disease management through producing resistant varieties of crops, application of effective fungicides, and crop rotation process. The technology of genome

sequencing and annotation works for rapid sequencing of genomes and identification of genes to obtain disease resistance methods. Information from the Genome-Wide Association Studies (GWAS) guides for the recognition of genetic loci for the rust prevention through genetic markers on phenotypic traits (Kibe et al., 2020). The mapping of Quantitative Trait Loci (QTL) points out the genome region and polygenic traits to interact with multiple genes. The application of a gene-editing tool as a part of genomics, CRISPR/Cas9 allows precise modifications to the wheat genome to introduce or enhance resistance traits (Elsharawy and Refat, 2023). This research aims to provide a details overview of the multi-omics approach through several omics' technologies such as transcriptomics, genomics, proteomics, and metabolomics. The results of the study will give a detailed view of host-pathogen interactions for the prediction and reduction of diseases. The outcomes of the research paper will evaluate possibilities of comparative genomic bioinformatics integrated with multi-omics data for designing in curing wheat rust diseases. The recommendations will entail new technologies for use in increasing crop production and enhanced wheat production. The study will also describe the difficulties encountered with the integration and management of extensive amount of data generated through single as well as multiple omics technologies, and the distribution of resources.

LITERATURE REVIEW

Comparative genomic bioinformatics in wheat rust disease

Comparative genomic bioinformatics plays a significant role in the understanding and management of wheat rust disease. It is one of the most destructive threats to wheat crops globally. Researchers can identify key genetic variations and evolutionary patterns that contribute to the pathogen's virulence and adaptability by comparing genomic data from different pathogen strains. One such resource is the TrustDB database which focuses on the host-pathogen interactome of Wheat-Stem rust (Kataria and Kaundal, 2022). This comprehensive bioinformatics tool predicts protein-protein interactions as well as functional annotations of proteins involved in the disease. Functional modules for subcellular localization, functional domains, gene ontology annotations and pathogen orthologs help researchers understand the infection's molecular mechanisms and host defense responses. On the other hand, whole-genome resequencing of different pathotypes of *Puccinia striiformis f. sp. tritici* revealed the evolutionary dynamics of pathogen strains (Yadav et al., 2022). The information of pathogenicity-related genes indeed assists the breeders to develop sustainable resistance to several rust strains in wheat. Comparative genomics have an important role to play in revealing more potential fungicide targets and some other approaches to controlling the disease. Obtainable knowledge on genetic basis of pathogen resistance can assist much more enhanced and sustainable support for more efficient prevention to the losses caused by pathogens on the crop reserves of the wheat. Comparative genomic bioinformatics is an invaluable resource of information about the complexity of the rust pathogens in wheat, based on which the targeted, efficient, and sustainable measures for combating the diseases are framed.

Multiple omics on pathogen genomics and host resistance determination

According to Crandall et al., (2020) the multi-omics approach is to identify pathogen genomics and host resistance in wheat crops using genomics, transcriptomics, proteomics, metabolomics, phenomics, and ionomics. This integrated approach gives the basis of understanding fundamental molecular recognition processes in pathogen-host structures. It significantly illustrates the process of the outpatient disease control in rationality. In the context of two organism's complete genome sequencing where different sequences and associated resistance genes can be identified. Transcriptomics is useful in describing the

interactions during infection by analyzing the RNA organisms when they are fighting pathogens. Although proteomics has a major interest in the proteins of these interactions and provides information on the main players in the infection and protection strategies.

Metabolomics investigates the changes that take place within the metabolic system of the host and the Pathogen. The Host interactome identifies the biochemical networks that are targeted by the pathogen (Jain et al., 2024). Phenomics assesses the phenotypic outcomes of these interactions, correlating genetic and molecular signatures with plant performance. Ionomics concerns the quantitation of elements in the plant and their distribution, gain, and loss during infection stress. Therefore, with proper integration of the transcriptomic and genomic data, the specific genes can be highlighted in the resistant varieties. Overall, this multi-omni approach significantly provides a detailed framework for understanding the different factors of pathogen-host interactions.

METHODOLOGY

This research uses a secondary qualitative research approach to examine the genomic, molecular, and environmental landscape of wheat rust disease to pathogen genomics and host resistance. The application of a qualitative analysis of disease severity, pathogen gene expression, and wheat yield patterns is conducted as part of the research study. The secondary qualitative information is collected from academic journals, and articles available on Google Scholar, ScienceDirect, PubMed, newspapers, and government reports. The analysing process of qualitative data incorporates thematic analysis to analyse multi-omics data to understand complex patterns between significant variables or factors such as pathogen genomics, environment, or host-pathogen interaction. Relationships between the detected patterns of gene expression and disease progression with severity are distinguished through information from existing articles and journals. To determine the qualitative effects of environmental factors on the host-pathogen relations, variability in climate, and soil types are taken into consideration.

The comparison across wheat varieties emphasizes narratives of previously working authors based on multi-omics data. These outcomes are drawn by mapping detailed genotypes and phenotypes of existing diseases to genomic and transcriptomic variations and their contextual environment. Morphological and histopathological tools for disease resistance and susceptibility include coding for comparing quality and relative weight between the different wheat varieties and treatment groups. Qualitative case studies include the examples of wheat crops chosen concerning their relationship with rust pathogens in particular conditions. These case studies are obtained from the analysis of transcriptomic and genomic data to highlight how pathogen/host interactions are distinctive. The integration of multi-omics data is considered from a qualitative perspective concerning the genomic, transcriptomic, and environmental findings. This multi-leveled analysis helps to reveal interactions outlining the discussed strategies of resistance and disease modeling and provides a holistic view of wheat rust disease. By adopting the inductive research approach, the study provides an understanding of wheat rust disease, the interactions between pathogen and environment, and host plant resistance. The systematic review of the collected data explains the key findings and methodology used in the selected studies. These results could help to refine future agronomic predictions and recommendations for rust disease suppression.

Analysis

Author	Year	Aim	Methodology	Findings
Tomar et al.,	2021	‘The aim of the	This study has utilised a	This study has found that

		study was to assess the genomic identification and prediction of new loci for resistance to stripe rust disease in wheat'	diverse wheat genotype set such as landraces and breeding lines. Genotyping has been done based on single nucleotide polymorphism markers to make sure entire generic coverage and genome-wide association studies have been conducted to determine loci attached to resistance.	genomic prediction models critically present higher accuracy in analysing resistance to stripe rust which highlights their ultimate potential for utilisation within breeding programs.
Kataria and Kaundal,	2022	'This study seeks to analyse the constructive bioinformatics resource to understand the complete wheat stem rust host-pathogen interactome'	This has analysed the host-pathogen interaction information to determine key genes, pathways, and proteins included within the wheat-stem rust association. Tools have been utilised to visualise and predict protein-protein association.	The collected dataset of this study highlighted molecular mechanisms related to disease resistance in wheat. The findings help in determining the candidate pathways and genes for preparing disease-resistance wheat varieties.
Babu et al.,	2020	'This study intends to understand the integration of genomic tools in wheat breeding to attain durable rust resistance'	The study has integrated a significant throughput sequencing process for mapping and precise identification of rust resistance genes. It has used bioinformatics tools to determine larger genomic datasets in terms of rust-resistance traits.	This study has found that the genomic tools have critically improved the efficiency and precision of the determination of rust resistance genes within wheat.
Semagn et al.,	2022	'The aim of this study was to analyse the genomic prediction for a common bunt, FHB, stripe rust,	This study has tested different sprint wheat genotypes to determine the resistance to the targeted diseases. Furthermore, genotyping-by-sequencing has been used to gather high	This study has revealed that genomic prediction models present medium to high accuracy for the majority of diseases. Higher predictive accuracy has been noted

		leaf rust, and leaf spotting resistance in spring wheat'	molecular marker information.	in terms of leaf rust resistance and stripe rust.
Zhao et al.,	2020	'The aim of this study was to genome-wide identification of effector candidates with conserved motifs from the wheat leaf rust Fungus <i>Puccinia triticina</i> '	This study has determined different features of the determined effector candidates such as their structure, subcellular localisation, potential functions, and	This has found a larger quantity of candidate effector genes from the selected genome such as a variety of proteins included in pathogenicity with different motifs that are relatively common in fungal pathogens. It also presented that the determined effector candidates can be utilised to develop critical wheat cultivars which are resistant to wheat leaf rust.
Wu et al.,	2020	'This study intends to determine the long-read-based de-novo genome assembly and comparative genomics of the wheat leaf rust pathogen <i>Puccinia triticina</i> identifies candidates for three avirulence genes'	This study has utilised long-read sequencing technology to produce high-quality genomic sequencing of <i>Puccinia triticina</i> .	This study has found a set of genes that are involved within the avirulence phenotype important for disease resistance mechanisms in wheat. The overall findings also provided in-depth insights in terms of the genetic diversity in rust pathogens.
Fernandez-Gutierrez and Gutierrez-Gonzalez	2021	'The aim of this study is to determine the bioinformatic-based approaches for disease-	This study has used bioinformatic tools to determine associated disease-resistance genes from different plant genomes. The approaches	Different candidate disease-resistance genes have been determined across wheat which offer critical insights in terms of the genetic basis of

		resistance gene discovery in plants'	used in this study are sequence analysis, gene expression profiling, and gene mining.	disease resistance. It has been found from the study that stress response pathways and plant immune response helped in disease resistance gene identification.
Jamil et al.,	2020	'This study intends to identify the role of genetics, genomics, and breeding approaches to combat stripe rust to wheat'	This study has utilised a review approach to analyse existing studies in terms of the genetics, breeding, and genomics strategies used to determine wheat stripe rust. This study has concentrated on genetic mapping, breeding strategies, and genomic technologies.	This study has identified significant resistant genes for instance Yr genes which as important in terms of breeding resistant wheat crops. It also has been found that genome-wide association studies and next-generation sequencing helped in the determination of significant markers in terms of stripe rust resistance which can be utilised within marker-assisted selection to accelerate the breeding technique.
Xia et al.,	2020	'This study seeks to determine the avirulence gene cluster in the wheat stripe rust pathogen through genetic mapping and whole genome sequencing of a sexual population'	The methodology involved sequencing the genomes of multiple isolates and performing genetic mapping to locate the avirulence genes.	The findings revealed a cluster of genes responsible for avirulence, which can help in understanding the pathogen's interaction with wheat and potentially aid in developing resistant wheat varieties. It examines the role of <i>Puccinia striiformis</i> and <i>tritici</i> , through genetic mapping and whole-genome sequencing of a

				sexual population.
Haile et al.,	2020	‘The aim of this study is to determine the potential of genomic selection and integration of omics data for disease evaluation in wheat’	The methodology involves using genotyping and phenotyping data to predict resistance to rusts and Fusarium head blight (FHB).	Genomic selection (GS) can significantly reduce the time and cost of breeding by selecting new parents based on genomic estimated breeding values before field trials. The integration of phenomics and machine learning further enhances the prediction accuracy for disease resistance.

Table 1: Systematic review
(Source: Self-developed)

The systematic review briefly summarizes the recent studies of wheat rust and other resistance diseases, using genomic, bioinformatics, and breeding strategies. The studies provide an overview of the molecular techniques including single nucleotide polymorphism markers, genome wide association studies (GWAS) and long read sequencing for genetic mapping of resistance loci and avirulence genes. Evaluation for resistance against diseases using genomic prediction models have been presented with high accuracy in breeding programs as shown by Semagn et al. (2022) and Tomar et al. (2021). For instance, the work by Kataria and Kaundal (2022) and Fernandez-Gutierrez and Gutierrez-Gonzalez (2021) employs bioinformatics to read host-pathogen interfaces and disease non-susceptibility channels, respectively. Protein interaction and gene mining utilities expose molecular processes that are significant for developing resistance against diseases. Application of phenomics and the machine learning as used by Haile et al. (2020) for “omics” data integration demonstrate the ability of precision agriculture to increase prediction accuracy. moreover, these results assist for rapid and accurate wheat breeding programmes towards rust resistance.

RESULTS AND DISCUSSION

Result

Marker-assisted selection and genomic selection

It has been observed that traditional breeding has accomplished success in improving wheat rust resistance through resistance allele accumulation over critical cycles of selection. For instance, R-genes have been incorporated into wheat which are *Sr25* and *Sr2/Lr27/Yr30* obtained from *Th. obtusiflorum* and *T. turgidum* respectively. The timelines of traditional breeding are quite lengthy and there is probable loss of some target genes at the time of breeding due to evolution occurring in pathogen races. Diagnosis or linked molecular markers offer supplementary tools to assist conventional resistance breeding (Tong et al., 2024) [figure 1].

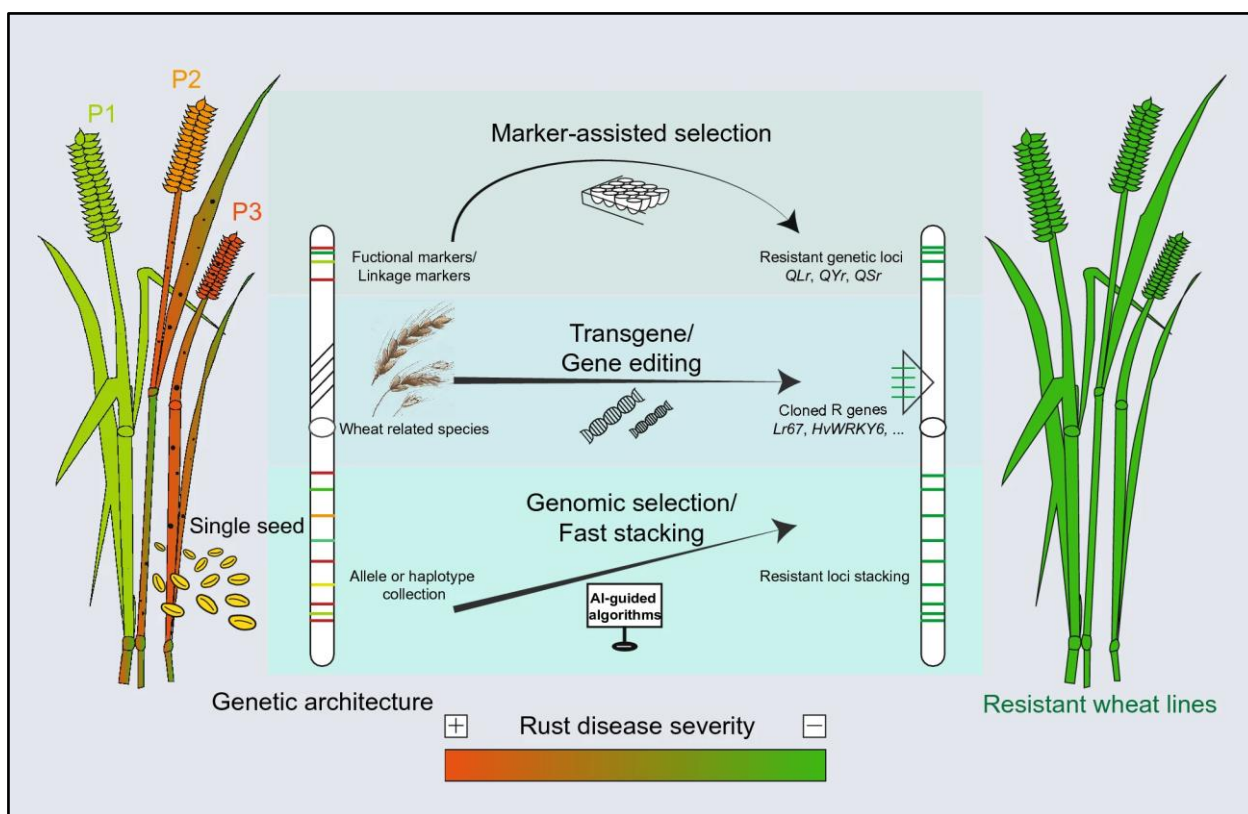


Figure 1: genomic atlas of rust resistance loci in wheat

(Source: Tong et al., 2024)

Diagnostic markers are significant for researchers to determine accessions with novel resistance. The markers for APR genes *Lr67/Yr46/Sr55* and *Lr34/Yr18/Sr57* are utilised to analyse the presence of resistance alleles in the Vavilov wheat diversity pane. These can offer critical insights into appropriate selection. Importantly, knowing the actual resistance genes combination in the overall population can assist in deepening the knowledge of gene impacts with their interactions.

The role of comparative genomic bioinformatics in wheat rust disease prediction

The studies carried out on the genome sequences of different strains belonging to the genus *Puccinia* have presented their genetic nuances among the virulence genes and proteins which control their relative degree of aggressiveness toward the wheat host (Dorostkar et al., 2022). TrustDB which is a specialised database representing host-pathogen interactome in detail assists experimentalists in determining wheat rust infections in a molecular context. Whole-genome resequencing data from *Puccinia striiformis* have contributed significantly to the critical insights about this pathogen. The genomic variations between different pathotypes presented a critical emergence of new virulent strains by analysing the fact that constant monitoring and breeding of resistant wheat varieties are required (Mahmood et al., 2022). The presence of single nucleotide polymorphisms linked with avirulence genes helps to predict disease occurrence and application of focused resistance strategies.

Integration of CRISPR/Cas9 and machine learning in wheat rust resistance

The CRISPR/Cas9 genome editing technology has been evident to be crucial in the management of rust disease in wheat. This works by changing susceptibility genes that help to improve rust resistance in wheat

varieties developed by researchers (Ma et al., 2024). This successful method makes developing resistant crop lines relatively faster by reducing reliance on chemical fungicides. The application of machine learning models helped in the selection of genomic genes in wheat breeding programs. Artificial intelligence algorithms perform typically in predicting disease resistance traits leading to shortened breeding cycles with multi-omics datasets. Predictive modelling in precision agriculture can help farmers in targeted disease management and result in minimal crop losses.

Multi-omics approach to host resistance and pathogen genomics

The application of diverse omics technologies has proven to be a significant approach to studying host-pathogen interactions and breeding disease-resistant wheat cultivars. A coherent framework for the analysis of resistance mechanisms and wheat rust infection has been established through the use of genomics, transcriptomics, proteomics, metabolomics, phenomics, and ionomics (Wu et al., 2022). Whole-genome sequencing has presented the identification of resistance loci and regulatory genes that enhance immune response. Quantitative trait loci associated with rust resistance have been identified using genome-wide association studies (Sirangelo, 2024). Wheat metabolite analysis has resulted in the significance of metabolic shifts based on pathogen interference. Certain secondary metabolites such as flavonoids and phytoalexins have antifungal activity and they are capable of retarding the growth of rust pathogens. Mass-spectrometry-based proteomics provides required data concerning secretory proteins constitutive of wheat immunity. The proteome study highlighted that among the infected and resistant wheat varieties, the resistant plants expressed proteins specific to inhibiting pathogen growth.

Discussion

The results of this study highlighted the importance of multi-omics and comparative genomic bioinformatics in managing wheat rust disease. Multi-omics technologies provide a monitoring tool for determining the mechanisms associated with pathogenic virulence and host resistance (Sehgal et al., 2023). Distinctive genetic loci in terms of resistance traits can be validated and accelerate the breeding of rust-resistant wheat with the help of GWAS and mapping of QTLs. TrustDB and other databases have a significant role in terms of host-pathogen interaction analysis. Whole-genome resequencing used as a pathogen identification technique exhibited that ongoing genomic analysis must be a permanent strategy for identifying new virulent strains. Genetic improvement programs receive significant potential assistance from the successful applications of CRISPR/Cas9 for genome editing.

It has been observed that the use of machine learning techniques to process phenotype data enhances the success of breeding operations as it increases prediction accuracy in practical agricultural systems. Other factors including data integration and limited resources in developing areas have an influence on technology implementation (Chetan et al., 2024). Additional research needs to be done to create bioinformatics workflows which will speed up data analysis and assist these technologies for global wheat breeding work. The prevention and control of wheat rust disease become more effective through the effective combination of multi-omics procedures and comparative genomic bioinformatics databases.

CONCLUSION

It can be concluded from the study that comparative genomics bioinformatics and multi-omics techniques are effective instruments for wheat rust management and prediction. Scientists can evaluate crucial genetic markers for resistance in *Puccinia triticina*, *Puccinia striiformis* and *Puccinia graminis* wheat rust

pathogens through genome sequencing, genome-wide association studies and quantitative trait loci mapping with CRISPR/Cas9 gene editing. The usage of multi-omics generated data faces challenges that include complicated information, inadequate tool development and resource distribution issues. In this study, it has been observed that the need of genomic data is required for enhancing disease resistance. Through these methods, the sustainable solutions generated the potential to enhance levels of global wheat production. The current study progress in integrated bioinformatics and multi-omics research has been fundamental to solving the problems of wheat rust management and improvement in food security.\

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