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SUSTAINABLE CONTROL STRATEGIES IN INTEGRATED MANAGEMENT OF WHEAT STRIPE RUST– AN OVERVIEW

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Abstract

Wheat stripe rust, caused by the fungus Puccinia striiformis f. sp. tritici (Pst), is one of the most devastating diseases affecting wheat production globally. Its epidemic potential, capacity for rapid genetic evolution, and ability to cause significant yield losses make it a persistent threat to global food security. Traditional management approaches, primarily reliant on resistant cultivars and fungicide applications, have been challenged by the emergence of new virulent pathogen races and issues of fungicide resistance. In this context, there is an urgent need to develop and implement sustainable control strategies as part of integrated management systems for wheat stripe rust. Such approaches must balance efficacy, economic viability, environmental stewardship, and social acceptability. This paper provides an in-depth overview of sustainable control strategies within integrated management frameworks for wheat stripe rust, synthesizing recent advances in plant pathology, crop management, energy systems, sustainability science, and digital agriculture. By drawing on cross-disciplinary insights, especially from energy management, industrial process control, and sustainability integration in business and agricultural systems, this review elucidates how innovation in control strategies can address the multifaceted challenges posed by wheat stripe rust.

***Key words**: Puccinia striiformis, wheat, integrated management, control, stripe rust*

INTRODUCTION

Puccinia striiformis f. sp. tritici (Pst), the causal agent of wheat stripe rust (also known as yellow rust), remains one of the most devastating pathogens affecting global wheat (*Triticum aestivum*) production worldwide threatening food security (Chen and Kang, 2017). Ensuring food security is a current global challenge (Bonciu et al., 2021a,b; Paunescu et al., 2023). Bioengineering helps address food security by improving crop yields, creating more resilient crops, and enhancing the nutritional value of food (De Souza and Bonciu, 2022; Ciğerci et al., 2023). *Pst* is an obligate biotrophs that depend on living host tissue to survive and reproduce. The pathogen is favored by cool and moist conditions, non-crop grasses such as *Bromus*, *Aegilops*, *Agropyron*, *Elymus*, *Poa*, and *Lolium* species have been reported to harbor *P. striiformis*, spontaneous flora, including weeds and non-cultivated grasses playing a critical yet often underestimated role in the epidemiology of plant diseases (Răduțoiu, 2022, 2023; Răduţoiu and Băloniu, 2021; Răduţoiu and Stan, 2022; Răduțoiu et al., 2024).

Historically, the wheat stripe rust pathogen has been present on Asian and European continents for thousands of years and on the American continents for more than 100 years (Line, 2002).Owing to its obligate biotrophic life-cycle, *Pst* depends on living host tissues to survive, reproduce, and disseminate — a feature that enables repeated infection cycles in susceptible wheat cultivars under favorable environmental conditions and in the presence of susceptible cultivars, this enables repeated infection cycles and the potential for large-scale epidemics (Chen and Kang, 2017; Carmona et al., 2020).

The pathogen's capacity for long-distance spore dispersal, its genetic adaptability, and the widespread cultivation of genetically uniform wheat varieties have together facilitated the expansion of stripe rust into new agro-ecological zones — including regions that historically had marginal disease risk due to warmer climates (Ju et al., 2022; Chen et al., 2025). Advances in molecular marker technologies and genome-scale analyses have fundamentally improved understanding of the phylogenetic structure and migration dynamics of *Puccinia striiformis* f. sp. *tritici* (Pst) populations. Collectively, these approaches have revealed that stripe rust epidemics are often shaped by long-distance dispersal processes operating across regional and continental boundaries. Early population genetic studies employing amplified fragment length polymorphism (AFLP) markers provided some of the first empirical evidence that genetically related Pst populations can occur across geographically distant European regions, indicating effective long-range migration over distances exceeding 1,500 km (Hovmøller et al. 2002, 2016). Such findings challenged earlier assumptions that stripe rust epidemics were primarily driven by localized inoculum sources. Subsequent work using microsatellite or simple sequence repeat (SSR) markers expanded these insights by demonstrating the repeated introduction and widespread establishment of non-native Pst genotypes throughout Europe, highlighting the continent's vulnerability to exotic incursions and the limited capacity of national boundaries to restrict pathogen movement (Hovmøller et al. 2016). More recently, pathogenomic investigations have provided a global perspective on Pst dispersal, revealing genetic connectivity among populations from Africa, South Asia, and Western Europe. Genome-based comparisons suggest that these populations may arise through recurrent intercontinental migration events or originate from common external inoculum reservoirs, underscoring the globalized nature of stripe rust epidemiology (van Schalkwyk et al. 2022). In parallel, extensive molecular surveillance in China has documented pronounced inter-regional connectivity of Pst populations within one of the world's largest wheat production systems. Studies employing SSR markers, competitive allele-specific PCR–single nucleotide polymorphism (KASP-SNP) assays, or integrated marker platforms have consistently detected substantial gene flow among epidemiological regions (Awais et al. 2022; Zhan et al. 2022; Zhang et al. 2024). These conclusions are further supported by whole-genome sequencing analyses, which provide high-resolution evidence of pathogen movement across major wheat-growing zones (Li et al. 2023). Taken together, these studies underscore the critical role of long-distance dispersal in shaping stripe rust population structure and reinforce the need for coordinated, trans-regional surveillance strategies in managing this globally important disease.

Historically, the impact of stripe rust has been dramatic. Generally, epidemics of stripe rust can result in yield losses ranging from 10% to 30%, even up to 100% in case of severe infection occurring at the early growth stage of highly susceptible wheat cultivars (Beddow et al., 2015; Lan et al., 2017; Buendía-Ayala et al., 2019). Global estimates put annual stripe-rust-attributable yield losses at roughly 5.47 million tonnes, equivalent to nearly US$0.98–1.0 billion per year in lost production value (Roth et al., 2021). More recently, the 2024 wheat disease loss summary estimated that stripe rust reduced U.S. wheat production by 53.9 million bushels (Anderson et al., 2025). Using the U.S. season-average farm price for all-wheat in 2024/25 (about US$5.55 per bushel as reported by USDA/ERS), the 2024 stripe rust loss of 53.9 million bushels converts to roughly US$299.1 million in lost farm (Sowell, 2025). These examples underline that annual economic costs fluctuate widely by year and region, but nonetheless reach hundreds of millions of U.S. dollars in bad years and about ~US$1 billion globally in typical recent estimates — making stripe rust one of the most costly single wheat diseases worldwide (Roth et al., 2021). Beyond yield reduction, the disease can also reduce grain quality, interfere with kernel development, and thus impair both the quantitative and qualitative output of wheat harvests — with downstream effects on livelihoods and food supply.

Given the changing epidemiological landscape, traditional control strategies based solely on host resistance or fungicides are increasingly inadequate. The emergence of more aggressive Pst races, often exhibiting virulence to previously effective resistance genes, has been documented in numerous regions. At the same time, globalized trade and shifting cultivation practices have increased the risk of inter-regional and transcontinental pathogen migration (Chen et al., 2025). Thus, a comprehensive synthesis of historical and recent data is needed. The present review aims to do precisely that: it compiles and assesses global epidemiological records, quantifies agronomic and socio-economic impacts, traces key shifts in pathogen population dynamics, and evaluates the effectiveness and limitations of integrated management options across regions. Such a synthesis can help identify enduring vulnerabilities, emerging threats, and promising strategies — ultimately contributing to more resilient wheat-rust management globally.

MATERIALS AND METHODS

A comprehensive and systematic literature survey was conducted to compile global information on wheat stripe rust epidemiology, impacts, pathogen population dynamics, and management strategies. Peer-reviewed articles were retrieved from major scientific databases including Web of Science, Scopus, PubMed, and Google Scholar. The search was not restricted by geographic region and covered publications from the earliest available records to the most recent literature. In addition to peer-reviewed studies, authoritative datasets and reports were obtained from international and national organizations, including the Food and Agriculture Organization (FAO), the United States Department of Agriculture (USDA), the Crop Protection Network, the Consultative Group on International Agricultural Research (CGIAR), and regional plant protection agencies. These sources provided long-term epidemiological records, yield loss estimates, and economic assessments. Historical and contemporary stripe rust outbreak data were synthesized to identify spatial and temporal patterns of disease occurrence. Epidemics were categorized by region and decade to assess trends in frequency, intensity, and geographic expansion. Where available, climate-associated variables (e.g., temperature regimes, precipitation patterns) reported in the original studies were considered qualitatively to contextualize shifts in epidemic behavior. Yield loss estimates reported in the literature were compiled and expressed as percentage reductions or absolute production losses.

Comparative analyses were used to identify recurring patterns in pathogen evolution, including the breakdown of host resistance and the spread of aggressive or temperature-adapted strains. Published evaluations of stripe rust management were reviewed across multiple scales, including cultivar resistance, fungicide application, cultural practices, and integrated disease management (IDM) frameworks. Management outcomes were interpreted in relation to pathogen population dynamics and epidemiological context, highlighting scenarios in which certain strategies are more or less effective. Management outcomes were interpreted in relation to pathogen population dynamics and epidemiological context, highlighting scenarios in which certain strategies are more or less effective. Rather than performing formal meta-analyses, evidence was synthesized using a narrative integrative approach.

Knowledge gaps and uncertainties were explicitly noted to design future research priorities.

RESULTS AND DISCUSSIONS

Major Recorded Wheat Stripe Rust Epidemics

Wheat stripe rust (*Puccinia striiformis* f. sp. *tritici*, Pst) is a globally pervasive fungal disease that has periodically caused catastrophic epidemics across diverse agro-ecological zones. The spatiotemporal history of severe outbreaks reflects the interplay of pathogen evolution, host susceptibility, climatic drivers, and agronomic practices.

During the time, epidemics have been recorded across Asia, North America, Europe, Africa, and Oceania, often driven by long-distance airborne dispersal.

Two broad mechanisms are involved in race emergence and spread: (i) local evolution—selection on standing genetic variation or mutation within endemic populations that produces new virulence phenotypes (notably common in large, intensively managed production areas such as China); and (ii) long-distance migration/introduction, whereby exotic genotypes are carried between regions by atmospheric transport, trade in infected seed or plant material, or anthropogenic movements (Hovmøller et al., 2002). In many cases, epidemics reflect a combination of both mechanisms.

China has one of the most comprehensive historical records of stripe rust epidemics, owing to its long-standing surveillance and extensive wheat cultivation. Prior to the establishment of systematic monitoring, localized severe outbreaks were reported in the late 1930s and 1940s in southwestern provinces such as Sichuan and Fujian (1939–1940), with yield reductions up to 60% in particularly favorable environments (Zhao and Kang, 2023). Since 1950, at least five nationwide Stripe Rust epidemics have been documented, occurring in 1950, 1964, 1990, 2002, and 2017. The earliest two of these outbreaks were the most expansive, each affecting over 13 million hectares and resulting in estimated yield losses of about 6.0 and 3.2 million metric tons, respectively (Zhao and Kang, 2023). A particularly extensive epidemic in the 2001–2002 season affected approximately 6.6 million hectares in 11 provinces, driven by unusually warm winter temperatures, prevalent susceptible cultivars, and high frequencies of virulent races (e.g., CYR31 and CYR32) (Wan et al., 2004). More recent widespread outbreaks, including a major epidemic in 2019, emphasize the continuous threat of stripe rust in China despite fungicide use and resistance breeding efforts (Zhao and Kang, 2023).

In the United States, historical stripe rust presence was initially concentrated in the Pacific Northwest (Washington, Oregon, and Idaho) and California. However, beginning in the late 20th century and accelerating into the 2000s, stripe rust expanded its range into the south-central states and the central Great Plains (Chen, 2005). The 2000 epidemic was the most widespread in U.S. recorded history, with stripe rust observed in over 20 states. Subsequent severe years (2005, 2010, 2012, 2015, and 2016) underscore the recurrent nature of epidemics in the United States and the challenge of durable management (Singh et al., 2023).

Stripe rust's presence in Africa is relatively recent but has become pronounced in certain agro-ecological systems, particularly those with low fungicide use and susceptible cultivars. The pathogen was absent in South Africa until 1996, when it was first recorded, followed by successive epidemics through the late 1990s and early 2000s in the Free State and other wheat-growing areas (Chen, 2005). In North and East Africa, regional outbreaks have been reported since at least 2009, with high disease pressure noted in countries such as Morocco and across East African low-input farming systems (Esmail et al., 2021).

Although stripe rust was not historically present in Australia and New Zealand prior to 1979, the pathogen's introduction and wind-dispersal from eastern Australia led to widespread national establishment by 1980 (Chen et al., 2025).

In Europe, the epidemiological landscape of stripe rust has evolved significantly since 2000, with the incursion of multiple *Pst* races not originally present in the continent (HovmØller et al. 2016). Thus, the most transformative event in recent European stripe rust epidemiology occurred in 2011 with the emergence of the PstS7 and PstS8 genetic groups, commonly referred to as the *"Warrior"* and *"Kranich"* races, respectively. These lineages exhibited expanded virulence spectra and greater genetic diversity than preceding local clones, enabling them to infect a broader range of wheat genotypes previously considered resistant. They rapidly displaced many of the older European Pst populations and became dominant across northern and western Europe, including the United Kingdom, France, Germany, and Scandinavia (Rodriguez-Algaba et al., 2017). Since the mid-2010s, the PstS10 lineage, also referred to as *"Warrior(−)"* and encompassing multiple race variants, has become the most prevalent genetic group in Europe. Surveillance data indicate that PstS10 now accounts for the majority of isolates collected in European stripe rust surveys, with multiple distinct races within this group detected across national boundaries. At least four distinct races have been identified by integrated phenotypic and molecular genotyping approaches, including those colloquially named *Kalmar*, *Benchmark*, and *Amboise*—names reflecting the varieties or regions where they first caused notable outbreaks (HovmØller et al. 2016). The co-occurrence of multiple races within the PstS10 group suggests that the European Pst population now features within-group diversification, which complicates resistance deployment and race monitoring. In addition to the primary groups (PstS7, PstS8, and PstS10), other genetic lineages have been detected at lower frequencies in recent years. Notably, PstS13 and PstS14 groups, initially reported in field surveys and genotyping efforts spanning southern Europe (e.g., Spain) and other regions, have been increasingly observed (Rodríguez-Vázquez et al., 2023). Analyses from southern Spain demonstrate that PstS10, PstS13, and PstS14 co-occur in recent seasons, with their prevalence shifting spatially and temporally according to local conditions, cultivar deployment, and seasonality of inoculum influx. Also, population genomic and transcriptomic analyses from Serbia illustrate a potential recent shift in dominant Pst races over the past decade. Comparative studies between isolates collected in 2014 and those from the 2022–23 season revealed that earlier populations were dominated by PstS7 (Warrior), whereas more recent isolates cluster within a clade derived from the PstS10 lineage. This shift is mirrored by increased disease severity and altered cultivar responses in field trials, highlighting ongoing evolutionary dynamics within the European Pst population (Zupunski et al., 2024).

Subsequent epidemics have affected wheat production and required increased fungicide applications, reflecting the disease’s capacity to adapt to new geographic zones when climatic and agronomic conditions permit. Therefore, a sustainable management of wheat stripe rust requires an integrated disease management (IDM) approach that combines genetic resistance, agronomic practices, chemical control, biological options, and epidemiological forecasting.

Reliance on single control measures—particularly race-specific resistance genes or fungicides—has repeatedly proven unsustainable due to the high evolutionary potential and long-distance dispersal capacity of *Puccinia striiformis* f. sp. *tritici* (Pst). Consequently, modern stripe rust control strategies increasingly emphasize integration, diversification, and adaptability to local epidemiological conditions (Wilson et al., 2025).

Sustainable Stripe Rust Control Strategies

Durable host resistance

Durable resistance to Pst is most often achieved through polygenic adult-plant resistance (APR) rather than single, race-specific major (R) genes. APR loci typically confer partial, non-race-specific reduction in disease development and, when combined, can produce high levels of field resistance with greater durability. Recent genome-wide association and mapping studies have identified many APR loci and demonstrated the value of pyramiding several APR genes to enhance resistance stability across environments. These strategies reduce selection pressure for single-step virulence mutations and are central to sustainable resistance breeding (Wang et al., 2023).

Breeding programs now routinely use marker-assisted selection (MAS), high-density SNP arrays, genomic selection (GS), and KASP assays to stack APR loci and accelerate selection cycles. Empirical studies confirm that pyramiding APR genes reduces field disease and yield loss compared to single-gene cultivars, and GS allows breeders to select complex quantitative traits more efficiently. However, breeders must guard against unbalanced selection (e.g., sacrificing grain quality or abiotic stress tolerance), and maintain genetic diversity across release portfolios to avoid monoculture vulnerability (Gao et al., 2024).

Mixtures of cultivars with complementary resistance spectra reduce epidemic development at field scale by interrupting pathogen spread and lowering overall inoculum build-up. Recent European and experimental studies indicate that variety mixtures can maintain yield stability and reduce reliance on fungicides, and modeling work shows that landscape-level cultivar diversification (mosaic or temporal rotation of varieties) further reduces selection for highly virulent races. Adoption barriers (seed supply, market standards) need addressing for widescale implementation (Jørgensen et al., 2024).

Fungicide use: optimization for efficacy and resistance management

Fungicides (primarily demethylation inhibitors and QoI/SDHI classes in mixtures) remain essential tools for protecting susceptible cultivars and bridging resistance gaps. Sustainable fungicide use emphasizes *timing, dose optimization, and mixture/rotation of modes of action* guided by disease forecasting systems and economic thresholds rather than calendar sprays. Decision support systems (DSS), which integrate weather data, crop phenology and local disease pressure, have been shown to reduce application frequency and maintain control while minimizing selection pressure. Examples from Europe and Australia demonstrate that DSS-guided programs can reduce fungicide inputs without compromising yield (Jørgensen et al., 2024).

To slow fungicide resistance in Pst and other cereal pathogens, best practices include: (i) using mixtures with effective complementary modes of action; (ii) avoiding repeated applications of the same single-site chemistry within a season; (iii) limiting prophylactic blanket sprays in favor of threshold/DSS-triggered applications; and (iv) integrating non-chemical tools to reduce fungicide dependence. Continuous monitoring of fungicide sensitivity is necessary, and regulatory frameworks should encourage stewardship and incentivize reduced-input practices (USDA Annual Report, 2024).

Cultural and agronomic interventions

Shifting sowing dates to avoid the temporal window when conditions favor Pst infection (e.g., avoiding an early susceptible green canopy during warm, moist autumn/winter periods) can reduce epidemic initiation. This must be balanced with yield potential and other pest/disease trade-offs. Field trials and regional advisories (e.g., GRDC updates) indicate sowing date optimization as a low-cost mitigation measure when combined with other approaches (Simpfendorfer, 2025). Also, reducing inoculum sources by managing volunteer wheat, volunteer grasses, and alternative hosts — and implementing rotations away from cereals where practical — lowers local Pst carryover. In many warm temperate regions overwintering or oversummering hosts maintain local inoculum; targeted removal or strategic rotations can therefore attenuate epidemic start-points (Wilson et al., 2025).

Stubble management and tillage influence microclimate and inoculum survival; in some systems burying infected residue or reducing surface green bridges can lower initial disease pressure. Conversely, conservation tillage that leaves residue may elevate humidity and disease risk — trade-offs with soil health need careful evaluation. Combining residue strategies with resistant cultivars and fungicide timing often yields the best outcomes (Wilson et al., 2025).

Surveillance, pathogenomics and forecasting

Sustained, coordinated surveillance using SSRs, SNP panels (KASP), genotyping-by-sequencing (GBS) and whole-genome pathogenomics is now central to tracking Pst lineage movement and detecting emergent virulence. European networks (RustWatch, national surveys such as UKCPVS) exemplify how systematic sampling and molecular typing provide early warnings of invasive lineages (e.g., Warrior/Kranich/PstS10) and inform breeding and fungicide choices. Investing in routine molecular surveillance at national/regional reference labs is a cornerstone of IDM. Spore-trapping networks combined with atmospheric dispersion modeling (HYSPLIT or local equivalents) identify long-distance inoculum pathways, enabling anticipatory advisories for downwind regions. Coupling trap data with genotyping can link outbreaks to source regions and guide transboundary policy responses. These tools are particularly powerful when integrated into DSS platforms (Wilson et al., 2025). Forecasting systems that combine meteorological forecasts, crop phenology, and real-time surveillance data provide decision-grade outputs for timing fungicide applications and mobilizing extension responses. The European early-warning initiatives and regional DSS pilots demonstrate measurable reductions in unnecessary sprays and quicker response to emergent risk, improving the sustainability of stripe rust control.

Biological control, biostimulants and agritech innovations

Interest in biological control agents (BCAs) — e.g., antagonistic bacteria and fungi or microbial consortia sprayed as foliar treatments — is increasing, but evidence for consistent, field-scale efficacy against Pst remains limited. BCAs may reduce initial spore germination or enhance host defenses and can be part of integrated programs to reduce fungicide loads; however, more controlled field demonstrations and registration pathways are required before widescale reliance (Wilson et al., 2025). Compounds that prime plant defenses (SAR/ISR elicitors) or improve host vigor can lower disease severity and complement genetic resistance. Their role is currently that of adjuncts — helpful in integrated programs but not replacements for robust genetic resistance or targeted fungicides. High-quality trials measuring yield and economic return are still needed. Variable-rate application technologies, remote sensing (multispectral UAV imagery), and disease detection algorithms enable site-specific fungicide application — reducing inputs while maintaining protection. These approaches are most effective where farmers can act on high-resolution maps and when decision systems feed into application equipment. Early adopters reports suggest tangible input savings and similar disease control, but adoption requires capital and extension support. Also, biotechnology offers sustainable solutions (De Souza and Bonciu, 2022). Thus, by developing crops that are naturally resistant to pests and diseases, bioengineering helps increase agricultural productivity and reduce crop loss (Bonciu, 2020, 2023) and environmental impact (Bonciu et al., 2020; Paunescu et al., 2021).

Adopting such a package requires close collaboration among breeders, pathologists, agronomists, extension services, and policymakers to tailor the bundle to local environments and socio-economic constraints.

CONCLUSIONS

Modern stripe rust epidemiology is characterized by the repeated emergence and rapid international dissemination of a relatively small number of high-fitness lineages.

Sustainable management therefore depends on integrating multiple complementary tools — host resistance, optimized fungicide use, cultural mitigation, biological approaches, and robust surveillance/forecasting — in ways that minimize environmental footprint, delay resistance evolution, and remain economically viable for farmers. Recent syntheses argue that IDM that explicitly combines genetics, chemistry, agronomy and information systems is the most promising path to durable control. Continued global sampling, standardized race nomenclature linkage (CYR vs. PstS lineages), and routine pathogenomic surveillance are essential to anticipate shifts in race composition and to design timely, integrated control strategies.

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