Wadi Alshatti University Journal of
Pure and Applied Sciences

مجلة جامعة وادي الشاطئ
للعلوم البحتة والتطبيقية

Volume 4, No. 1, January-June 2026   Online ISSN: 3006-0877   المجلد 4، الاصدار 1، يناير - يونيو 2026

REVIEW ARTICLE **PLANT PATHOLOGY**

Wheat Fungal Diseases: A Review

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ARTICLE HISTORY
Received 16 January 2026
Revised 10 February 2026
Accepted 15 February 2026
Online 19 February 2026

KEYWORDS
Wheat rust;
Powdery mildew;
Strip rust;
Fungal resistance gene.

ABSTRACT

Wheat is a global dietary staple, supplying one of world's grain production and serving as a primary source of carbohydrates, protein, as well as essential micronutrients. However, its productivity remains increasingly jeopardized via biotrophic fungal pathogens obligate parasites that severely compromise plant health and grain yield. This review critically examines four major diseases: *(Puccinia graminis* f. sp. tritici) stem rust, (*P. striiformis* f. sp. tritici) stripe rust, (*P. triticina*) leaf rust, and (*Blumeria graminis* f. sp. tritici) powdery mildew, which collectively threaten food security across diverse agroecosystems. Moreover, central to sustainable control is genetic resistance, which operates through two paradigms: race-specific (qualitative) as well as non-race-specific (quantitative or adult plant resistance). Furthermore, the novelty of this work lies in its integrative synthesis of global pathogen distribution, virulence evolution, for instance, Ug99 and TKTTF lineages), as well as the strategic deployment of resistance genes from landraces and wild relatives. In addition, this synthesis supports next-generation wheat improvement aimed at stabilizing yields under escalating disease pressure.

الأمراض الفطرية التي تصيب القمح

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الكلمات المفتاحية
صدأ القمح
البياض الدقيقي
الصداء الأصفر
الجينات المقاومة في الفطريات

الملخص

يُعدّ القمح غذاءاً أساسياً عالمياً، إذ يُساهم في إنتاج أحد أكبر قطاعات الحبوب في العالم، ويُشكّل مصدراً رئيسياً للكربوهيدرات والبروتين، فضلاً عن العناصر الغذائية الدقيقة الضرورية. مع ذلك، لا تزال إنتاجيته مُعرّضة للخطر بشكل متزايد بسبب الفطريات المُتطفّلة التي تُلحق ضرراً بالغاً بصحة النبات وإنتاجية الحبوب. تُحلّل هذه الدراسة أربعة أمراض رئيسية: صدأ الساق *Puccinia graminis* f. sp. tritici، وصدأ الخطوط *P. striiformis* f. sp. tritici، وصدأ الأوراق *P. triticina*، والبياض الدقيقي *Blumeria graminis* f. sp. tritici، والتي تُهدّد مجتمعةً الأمن الغذائي في مختلف النظم الزراعية. علاوةً على ذلك، يُعدّ التحكّم الجيني عنصراً أساسياً في المكافحة المُستدامة، حيث يعمل وفق نموذجين: التحكّم النوعي (الخاص بالسلالة) والتحكّم الكمّي (غير الخاص بالسلالة أو المُقاومة في النبات البالغ). علاوة على ذلك، تكمن حداثة هذا العمل في تكامله الشامل لتوزيع مسببات الأمراض عالميًا، وتطور ضراوتها ، على سبيل المثال، سلالات Ug99 TKTTF، فضلًا عن التوظيف الاستراتيجي لجينات المقاومة من السلالات المحلية والأقارب البرية. كما يدعم هذا التكامل تحسين الجيل القادم من القمح بهدف تثبيت المحاصيل في ظل تزايد ضغط الأمر

Introduction

Wheat is an essential food product in human nutrition because of the primary source of dietary carbohydrates and metabolic energy. Moreover, it contains several beneficial health components such as vitamins (B), protein, dietary fiber, as well as phytochemicals [1,2]. Wheat is economically, socially, culturally, historically, and archaeologically valuable as a primary food production. Therefore, it was significantly affected and evolved via various civilizations throughout history. Wheat production in (2025) reached 771 million tons worldwide, among the leading global producers of wheat are China, India, Russia, and the United States, with Turkey consistently [4]. Despite a steady rise in wheat output, the land area dedicated to its cultivation has shown a gradual decline in recent years. This trend occurs against the backdrop of a projected global population of approximately nine billion via 2050 [5]. Recently, rising demand for wheat-based foods across numerous Asian nations coupled with evolving grain nutritional quality with global efforts.These demographic and dietary shifts, annual cereal production is anticipated to surpass current levels via more than one billion metric tons. Wheat constitutes approximately 19% of global grain crop output underpinning its critical role in food security [6]. In light of projected population growth and escalating demand for staple food commodities, a 40–60% increase in wheat productivity is deemed necessary over the coming four decades to satisfy the nutritional needs of future generations. However, this target is substantially via both biotic and abiotic stressors [7,8]. According to these, fungal pathogens

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https://doi.org/10.63318/waujpasv4i1_20

particularly biotrophic diseases types represent a primary constraint, significantly diminishing yields and widening the gap between current production levels and theoretical yield potential [7]. Plant diseases represent a significant challenge for cultivators globally, resulting in considerable economic losses. Wheat is highly adaptable to diverse environmental conditions, capable of thriving in both dry and wet climates [8]. As a staple cereal crop, wheat production is critical for meeting human nutritional requirements. However, obligate parasitic fungi such as *Puccinia graminis* f. sp. *tritici*, *Puccinia striiformis* f. sp. *tritici*, *Puccinia triticina*, and *Blumeria graminis* f. sp. *tritici* adversely affect plant physiology and morphology. These pathogens ultimately compromise cereal production by significantly reducing crop yields [9].

Literature Review

Wheat Rust

Fungal diseases of wheat represent a major global concern, with causal agents broadly categorized based on their nutritional strategies. Obligate biotrophs are highly specialized pathogens that depend entirely on living host tissue infect wheat through diseases, for instance, the three rusts (stem, leaf, as well as stripe rust), powdery mildew, as well as bunts and smuts as presented in Figure 1. Moreover, necrotrophy, are responsible for conditions including *Septoria tritici* blotch, *Stagonospora nodorum* (*Septoria nodorum*) blotch, spot blotch, tan spot, as well as *Fusarium* head blight which is known as scab as in Figure 2. The obligate biotrophs exhibit remarkable genetic diversity in virulence traits, often linked to their ability to overcome host resistance genes. Furthermore, this adaptive potential arises through mechanisms, for instance, long-distance pathogen migration, spontaneous mutations, as well as genetic recombination, with strong selective pressures particularly evident in rusts as well as powdery mildew fungi driving the emergence of novel virulent races. Consequently, considerable research efforts have been directed toward elucidating the genetic underpinnings of disease resistance as well as developing wheat cultivars with durable resistance to fungal pathogens [10]. Rust fungi, classified as obligate biotrophs, depend exclusively on living host cells for their growth, development, as well as reproduction [11]. Their capacity to rapidly circumvent host resistance mechanisms has been well demonstrated that rust spores can traverse vast distances via wind dispersal, facilitating swift global spread. For instance, genetically similar isolates of *Puccinia striiformis* f. sp. *tritici* the causal agent of wheat yellow rust were detected across North America, Australia, Europe within a span of fewer than three years. Moreover, a distinct strain exhibiting an identical virulence profile but differing in two AFLP markers emerged independently in Europe (circa 2000–2001) as well as was subsequently identified in Western and Central Asia as well as the Red Sea region, although the precise timing of its initial appearance in the latter areas remains uncertain [12].

Yellow Rust (Stripe rust)

Over the past 15 years, wheat stripe rust also known as yellow rust due to the characteristic yellow-orange urediniospores produced during its asexual phase on wheat has emerged as the foremost biotic constraint on global wheat production, posing a serious threat to food security. Current estimates indicate that approximately 88% of the world's wheat area is planted with varieties vulnerable to this disease, leading to annual yield losses amounting to roughly five million metric tons, valued at around US$1 billion [13]. Consistent with this trend, Schwessinger [14] announced that *Puccinia striiformis* f. sp. *tritici*, the causal agent of stripe rust, has become the most significant biotic limitation to wheat cultivation worldwide in the twenty-first century. Furthermore, contemporary isolates of the pathogen exhibit heightened aggressiveness also an expanded virulence spectrum, enabling them to infect wheat cultivars previously regarded as resistant thereby facilitating swift and widespread dissemination across regions. The causal agent, *Puccinia striiformis* f. sp. *tritici* (Pst), is an obligate biotrophic fungus whose agricultural threat stems from three interrelated attributes: exceptional genetic diversity driven largely via sexual recombination predominantly occurring in the Himalayan region efficient long-distance dispersal via both natural, for instance, windborne spores; and anthropogenic pathways, and a capacity for rapid local adaptation through stepwise evolutionary shifts that sequentially overcome individual host resistance genes [15] Genetic analyses have revealed varying degrees of diversity among *Puccinia striiformis* f. sp. *tritici* (Pst) populations across different regions. These areas are now recognized as key hotspots for the generation of novel yellow rust genotypes through sexual reproduction [15,16].

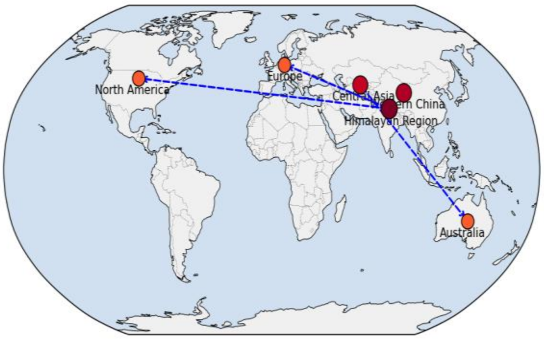

Figure 1: Global Distribution of *Puccinia striiformis* f. sp. *tritici* Populations and Dispersal

Stripe rust

The causal agent based on wheat stripe rust is taxonomically classified within the kingdom Fungi, phylum Basidiomycota, class Urediniomycetes, order Pucciniales (formerly Uredinales), family Pucciniaceae, as well as genus *Puccinia*. Specifically, *Puccinia striiformis* f. sp. *tritici* (Pst) remains an obligate parasite that colonizes only the photosynthetically active tissues of susceptible hosts including leaves, leaf sheaths, glumes, as well as awns as announced by [16]. Infection can occur at any growth stage, from young seedlings with a single leaf to fully mature plants, provided that green, metabolically active tissue remains present as announced by [17]. In addition, the broader species *Puccinia striiformis* Westend. comprises at least nine formae speciales, differentiated via their host-specific interactions across various grass genera. Among these, Pst primarily targets cultivated wheat (*Triticum aestivum* L.), durum wheat (*T. turgidum* var. durum L.), domesticated emmer wheat (*T. dicoccum* Schrank), wild emmer (*T. dicoccoides* Körn), and triticale. Although certain barley (*Hordeum vulgare* L.) as well as rye (*Secale cereale* L.) cultivars may also serve as incidental hosts, Pst rarely initiates large-scale epidemics on these species [16].

Stripe rust, caused via *Puccinia striiformis* f. sp. *tritici*, produces vivid yellow–orange urediniospores (20–30 μm) with echinulate walls that germinate rapidly at 7–12 °C in the presence of leaf moisture, forming linear pustules between veins and on other aerial parts. In resistant wheat, infection is often restricted via a hypersensitive response, manifesting as chlorosis or necrosis instead of spore production [18].

Wheat stem rust

Wheat stem rust, caused via *Puccinia graminis* f. sp. *tritici* Eriks. & E. Henn. (Pgt), affects both durum wheat (*Triticum turgidum* L. ssp. durum) as well as bread wheat (*T. aestivum* L.). Historically, severe epidemics have been documented across major global wheat-producing zones [19]. Early historical accounts, interpreted via Chester [20], suggest that stem rust or a disease phenotypically consistent with it has afflicted cereal crops for many centuries. Although *Puccinia graminis* maintains a near-global distribution, it is generally less prevalent than leaf as well as stripe rusts [21,22]. Furthermore, the pathogen distribution in warm, humid environments, with infection typically manifesting as brick-red uredinial pustules on stems, leaf sheaths, glumes, as well as awns as announced by Kolmer [23]. In the mid-20th century, recurrent stem rust outbreaks were a primary catalyst for the Green Revolution, which prioritized the development of semi-dwarf wheat varieties incorporating durable resistance to this disease as declared by Figueroa et al. [24]. On the other hand, in recent decades, the emergence of novel virulent Pgt races most notably Ug99 as well as its derivatives has undermined the resistance of many widely cultivated wheat genotypes, leading to a resurgence based on stem rust as a critical threat to global food security [25]. Although stem rust has been effectively managed in many wheat-producing regions through breeding as well as surveillance, modelling studies that assume the absence of durable resistance project average annual global yield losses of at least 6.2 million metric tons, with substantially higher losses possible during severe epidemics of particular concern is the emergence as well as spread of novel virulent lineages of *Puccinia graminis* f. sp. *tritici* (Pgt). For instance, a Yr9-virulent strain initially detected in eastern Africa disseminated in a stepwise fashion over approximately a decade, traversing the Middle East as well as West Asia before reaching South Asia, triggering significant epidemics route [10]. The Ug99 lineage, first identified in Uganda in 1999, represents one of the most formidable threats to global wheat production [26]. It is estimated that up to (90%) of currently cultivated wheat varieties lack effective resistance to Ug99 as well as its derivatives, heightening concerns about food security [27]. Members of the Ug99 race group have been confirmed in multiple regions, including eastern, southern, as well as northern Africa, the Middle East, Central Asia, and parts of Europe, underscoring its transcontinental reach as well as adaptive potential [25,28]. Non-Ug99 lineages of *Puccinia graminis* f. sp. *tritici* have also emerged with significant virulence, diminishing the efficacy of recently deployed as well as widely distributed resistance genes [29]. These novel races possess the capacity to disperse into major global wheat production zones, raising concerns about their potential impact [30].

Wheat leaf rust

Wheat leaf rust commonly referred to as brown rust is incited via the obligate fungal pathogen *Puccinia triticina* Erikss. (Pt). This pathogen is globally widespread, exhibits a highly dynamic and genetically diverse population structure, as well as demonstrates a remarkable capacity to rapidly evolve new virulent races capable of overcoming widely deployed resistance genes in modern wheat cultivars [31]. The disease presents a persistent management challenge due to the pathogen's extensive genetic variability, the continuous emergence of novel virulence phenotypes, as well as its physiological adaptability across a broad thermal range [32]. Wheat leaf rust exerts considerable agronomic and economic pressure across nearly all major global production zones, including North as well as South America, Africa, Europe, Asia, and Australia, affirming its role as well as high-impact disease in wheat systems [33]. The taxonomy of wheat leaf rust has undergone significant refinement since the 19th century initially grouped wheat as well as rye leaf rusts under the name *Puccinia dispersa*, the primary global host of *Puccinia triticina* is hexaploid bread wheat (*Triticum aestivum*) [12].

However, the pathogen also infects several related species, including tetraploid durum wheat (*T. turgidum* ssp. durum), wild emmer (*T. dicoccoides*), cultivated emmer (*T. dicoccum*) [34]. Specialized variants of *P. triticina* have been identified on non-wheat hosts: Yehuda et al. [35] described a distinct isolate in Israel that was recovered exclusively from the diploid grass *Aegilops speltoides* as well as showed no virulence on common wheat. Similarly, specific pathotypes of *P. triticina* have been found infecting *Aegilops cylindrica* (common goatgrass) in the southern Great Plains of the United States. These observations highlight a pronounced degree of telial host specificity within the *P. triticina* complex. Indeed, strains adapted to durum wheat or *Ae. speltoides* exhibit genetic divergence as well as non-overlapping host ranges compared to those infecting hexaploid wheat, suggesting they may represent distinct formal specials within the broader *P. triticina* lineage [36].

Powdery Mildew

Powdery mildew (PM) remains a widespread fungal disease that colonizes the aerial tissues of both wild and cultivated higher plants, often resulting in yield losses of up to (30%) in affected crops. Taxonomically, PM fungi belong to the order Erysiphales within the phylum Ascomycota. They constitute a monotypic family, Erysiphaceae, which is further subdivided into five major clades corresponding to the tribes and subtribes Erysipheae, Golovinomycetinae, Cystothecieae, Phyllactinieae, as well as Blumerieae as well as encompasses more than ten recognized genera [37]. With over 500 species reported to infect more than 1,500 plant species [38]. The Erysiphaceae represent one of the most ecologically as well as economically significant families of plant pathogens. Key agricultural and horticultural hosts include wheat, barley, grapevines, apples, and a wide array of vegetable and ornamental crops grown both in open fields and protected environments, for instance, greenhouses. Despite decades of research into their infection mechanisms, disease dynamics, as well as management strategies, powdery mildew fungi continue to pose persistent and serious challenges in global crop production systems. Powdery mildew of wheat, caused via *Blumeria graminis* f. sp. *tritici* (Bgt), ranks as the sixth most significant fungal disease affecting global wheat production and is responsible for the eighth-largest yield loss worldwide among all plant pathogens as well as pests [39]. The disease is capable of persisting year-round in many wheat-growing regions, with reported yield reductions varying considerably via geography and epidemic severity up to 35% in Russia, 62% in Brazil, as well as 40% in China further documented that losses fluctuate seasonally and regionally [40]: for instance, up to 20% in the United Kingdom during peak outbreaks, typically 10–15% in Western Europe, as well as 5–17% in North Carolina, though epidemic conditions can elevate these figures to 30–35% in Russia, over 60% in Brazil, as well as 30–40% in China. Unlike many foliar diseases that favor humidity, powdery mildew thrives in relatively cool, dry climates as well as is endemic across major wheat zones including China, Europe, and the Southern Cone of South America [40].

Given its economic impact, timely and precise assessment of disease incidence and severity is essential for effective monitoring and management. Graeff as well as Claupein [41] explored the potential of leaf spectral reflectance as a non-invasive diagnostic tool, demonstrating that changes in reflectance patterns during Bgt infection and in comparison with take-all disease could be leveraged to quantify disease intensity and differentiate between pathogen-specific symptoms. Among the spectral regions examined, the wavelength ranges of 490–780 nm exhibited the highest sensitivity to foliar damage caused via both powdery mildew as well as take-all pathogens. These findings suggest that targeted reflectance measurements within specific wavelength intervals could serve as a reliable basis for early pathogen detection as well as differentiation in wheat.

Figure 2: Major Symptoms of Fungal Diseases of Wheat; (A) Stripe rust (*Puccinia striiformis* f. sp. *tritici*); (B) Leaf rust (*Puccinia triticina*); (C) Stem rust (*Puccinia graminis* f. sp. *tritici*, including Ug99); (D) Powdery mildew (*Blumeria graminis* f. sp. *tritici*);(E) *Septoria nodorum* blotch in wheat

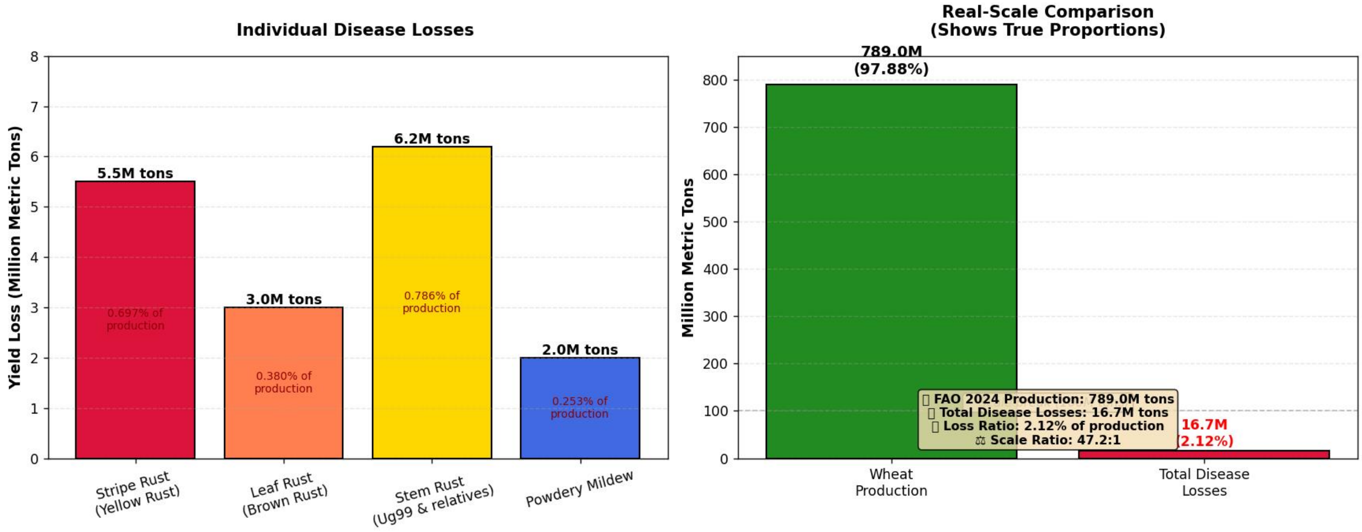

Figure 3: Global Impact of Major Biotrophic Diseases on Wheat Cultivation Annual Yield Loss [49].

Figure 3 presents a comprehensive quantitative assessment of global wheat yield losses attributed to major biotrophic fungal pathogens based on FAO 2024 [49] production data (789 million metric tons), illustrating both disease-specific impacts and their cumulative effect relative to total production. The left panel delineates individual pathogen contributions, with stem rust (Ug99 & relatives) causing the highest losses at 6.2M tons (0.786%), followed by stripe rust at 5.5M tons (0.697%), leaf rust at 3.0M tons (0.380%), and powdery mildew at 2.0M tons (0.253%), collectively representing 16.7M tons of avoidable losses. The right panel employs real-scale visualization to contextualize these losses against global wheat production, revealing that despite the seemingly modest aggregate loss ratio of 2.12%, the absolute magnitude translates to substantial food security implications affecting millions of tons of grain. This dual-perspective representation underscores the critical importance of disease management strategies, as the 47.2:1 production-to-loss ratio masks the significant economic burden and nutritional deficits imposed by these pathogens on global agricultural systems. Consequently, this visualization serves as empirical evidence justifying the research imperative for developing sustainable disease control measures, resistant cultivars, and integrated pest management approaches to safeguard wheat production capacity in the face of evolving pathogen threats. [9]. Continuous pathogen evolution necessitates global surveillance, deployment of diverse resistance genes, and integration of molecular breeding to safeguard wheat production.

Fungal Resistance Genes in Wheat

Wheat production faces persistent threats from biotrophic fungi, particularly stem rust (*Puccinia graminis* f. sp. *tritici*), stripe rust (*P. striiformis* f. sp. *tritici*), leaf rust (*P. triticina*), and powdery mildew (*Blumeria graminis* f. sp. tritici). While race-specific, gene-for-gene resistance has historically protected crops exemplified via cloned genes like Sr35, Rmg8, and PmHHXM its durability is limited due to rapid pathogen evolution. In plant pathology, resistance is scientifically defined as any heritable trait in a host that mitigates the adverse effects of a pathogen or pest. A continuum from apparent immunity to extreme susceptibility with effective resistance often judged not merely via the absence of symptoms, but via the prevention of economically significant damage within a relevant timeframe [42,43]. Given the persistent threat posed via pathogens as well as pests to global food security, durable disease resistance is a cornerstone of sustainable crop production. The past few decades have underscored the urgent need to broaden as well as diversify the genetic arsenal deployed in wheat cultivars. Recent breakthroughs in genomics and functional genetics have revealed a rich spectrum of resistance mechanisms in wheat ranging from race-specific to broad-spectrum, qualitative to quantitative the potential for more resilient as well as adaptive breeding strategies to meet future production demands [44]. Genetic resistance to rust diseases is often described as oligogenic when it is governed via one or a few genes, each exerting a relatively modest effect on the phenotype. Functionally, resistance is typically defined through epidemiological parameters, for instance, reduced infection frequency, slower disease progression, otherwise diminished sporulation rather than complete immunity. In the context of wheat rusts, resistance mechanisms are broadly categorized as either race-specific (also termed seedling or qualitative resistance) otherwise non-race-specific (often adult plant or quantitative resistance), depending on their interaction with specific pathogen races as announced by [45]. More than 70 resistance loci conferring reactions to *Puccinia striiformis* f. sp. *tritici* (Pst) have been formally designated as yellow (stripe) rust resistance genes as found in leaf rust (*P. triticina*) and stripe rust in bread wheat (*Triticum aestivum*) can be achieved through the pyramiding of several partially effective, non-hypersensitive genes that act additively [33]. In breeding schemes, this has been pursued via crossing parental lines exhibiting mild to strong slow-rusting phenotypes, followed via top-crossing the F_1 progeny with a third high-yielding but rust-susceptible parent to combine agronomic performance with partial resistance. Among the known sources of durable defense against leaf rust in wheat, the adult-plant resistance (APR) genes Lr13 as well as Lr34 whether deployed individually or in combination have demonstrated the most consistent and long-lasting effectiveness across diverse global environments. Early cytogenetic work localized key resistance loci, including Lr1, Lr3, as well as Lr11, to specific wheat chromosomes. Approximately 80 distinct leaf rust resistance genes or alleles have been identified and characterized across bread wheat (*Triticum aestivum*), durum wheat (*T. turgidum* ssp. durum), as well as related diploid wheat species. Advances in molecular marker techy particularly enzymatic assays, PCR-based approaches, and microsatellite (SSR) markers have greatly facilitated the mapping and tracking of these loci in breeding populations. Resistance mechanisms in wheat operate [42]resistance (ASR), historically referred to as seedling resistance, typically involves single, major-effect genes that trigger a hypersensitive response as well as confer immunity across all growth stages. However, this form of resistance is generally race-specific and vulnerable to pathogen evolution. In contrast, APR is usually governed via multiple minor-effect genes, exhibits partial also progressive suppression of disease development, and is largely non-hypersensitive and race-nonspecific characteristics that collectively contribute to its durability This horizontal, polygenic nature render [46]. APR a preferred strategy for sustainable rust management in modern wheat improvement programs. However, the majority of known Lr (leaf rust resistance) genes confer major-effect, race-specific resistance that operates at the seedling stage through a classic gene-for-gene interaction, typically triggering a hypersensitive response (HR) a form of localized programmed cell death that restricts pathogen spread. A durable protection in the field is often underpinned via a limited set of adult plant resistance (APR) genes. Therefore, Lr34 and Lr46 have proven especially valuable in breeding programs due to their broad-spectrum, long-lasting efficacy across diverse environments as well as against multiple *Puccinia triticina* (Pt) pathotypes [46]. *Puccinia triticina* (Pt) isolates analysing infection phenotypes at the seedling stage, the authors were able to infer the likely presence of specific resistance genes based on established reaction patterns. Of the 50 cultivars tested, 39 exhibited resistances to at least one Pt race as well as were found to carry one or more of 13 known Lr genes: Lr1, Lr18, Lr3ka, Lr15, Lr26, Lr20, Lr14a, Lr30, Lr2a, Lr11, Lr34, Lr46, as well as Lr68. In contrast, the remaining 11 genotypes displayed susceptibility across all tested pathotypes and showed no evidence of harboring any of the characterized Lr resistance loci.

Among the Ethiopian wheat cultivars surveyed, Lr1 as well as Lr46 were the most prevalent resistance genes, each identified in 13 accessions, followed via Lr34 in Lr12. Less frequently observed were Lr26 (in five cultivars), Lr30, Lr18 (four each), Lr15, Lr3ka, and Lr2a (three each). Lr68 was detected in two cultivars, while Lr11, Lr20, as well as Lr14a each appeared in only a single genotype offering tentative. Lr21 of the evaluated cultivars exhibited slow-rusting resistance, a phenotype typically associated with durable, partial resistance at the adult plant stage. Complementary molecular screening approaches have also been employed in other germplasm collections. wheat landrace ‘Aus26582’ exhibits seedling-stage resistance against both durum- as well as bread wheat-specific *Puccinia triticina* (Pt) pathotypes. Similarly, Singh et al. [33] reported the identification of LrARK12c, a novel resistance locus from spelt wheat cv. Greenhouse-based seedling assays using three Pt isolates revealed a monogenic inheritance pattern, and subsequent segregation analysis mapped the resistance locus to the distal region of chromosome arm 7BS a genomic interval previously devoid of known leaf rust resistance genes. This novel locus was formally designated Lr72. As announced by Park et al. [42] observed an unexpected resistance pattern in the historically susceptible cultivar ‘Morocco’, which, despite uniform susceptibility towards the most global Pt isolates, exhibited resistance towards an Australian Pt isolate collected in (2004). On the stem rust front, *Puccinia graminis* f. sp. *tritici* (Pgt) has historically caused devastating yield losses in North America, in the US as well as Canada, until the widespread adoption of resistant cultivars after (1955) brought the disease under effective control. However, this stability was disrupted via the emergence in Uganda in (1999) of the virulent Pgt race Ug99 (TTKSK), which overcomes Sr31 as well as several other widely deployed stem rust resistance genes [47]. Severe epidemics in East Africa have been linked to the breakdown of the race-specific resistance gene SrTmp, which had been introgressed into popular cultivars , for instance, ‘Digalu’ in Ethiopia as well as ‘Robin’ in Kenya [33]. In response, efforts to broaden the resistance base have intensified 1,061 accessions of *Triticum monococcum* and 205 of T. urartu against the Ug99 race TTKSK and four additional Pgt races (TTTTF, TRTTF, QFCSC, and MCCFC), successfully identifying new sources of stem rust resistance for future breeding use. The resistant accessions included 55 *T. monococcum* accessions (6.4% of the total) that were also resistant to the other four races. Screening of *Triticum monococcum* germplasm revealed resistance against multiple *Puccinia graminis* f. sp. *tritici* (Pgt) races, suggesting the presence of broad-spectrum resistance factors. High-resolution mapping and GWAS have accelerated the discovery of novel QTLs and resistance genes, including Sr62 from wild relatives and Pm63 from landraces. Marker-assisted pyramiding of 4–8 effective Yr genes significantly improves stripe rust resistance, with combinations like Yr30 + Yr48 showing epistatic enhancement. Screening of global germplasm , for instance, Aegilops tauschii, Ethiopian, and Chinese cultivars reveals valuable untapped diversity, including broad-spectrum resistance in lines like TRI 1796 and HHXM. Yr10, Yr18, and Pm30 are widely deployed, yet susceptibility remains high: ~71% of Chinese breeding lines lack adequate resistance. Durable protection increasingly relies on pleiotropic APR genes and strategic gene stacking to delay resistance breakdown. Advances in genomic tools, such as the LPmerge-based consensus map, enable precise introgression of resistance from wild progenitors into elite backgrounds. This integrative approach combining phenotyping, genomics, and evolutionary insight underpins efforts to secure global wheat yields against emerging pathotypes like Ug99 and TKTTF [48].

Conclusion

This study quantifies the devastating impact of major biotrophic fungal pathogens on global wheat production, revealing cumulative annual losses of 16.7 million metric tons, representing 2.12% of the 789 million metric tons produced globally in 2024. Stem rust (Ug99 and relatives) emerged as the most destructive pathogen causing 6.2 million tons of losses, followed by stripe rust (5.5M tons), leaf rust (3.0M tons), and powdery mildew (2.0M tons), underscoring the urgent need for durable resistance strategies. The substantial 47.2:1 production-to-loss ratio demonstrates that while percentage losses appear modest, the absolute magnitude poses critical threats to global food security and economic stability. Given the rapid evolution of virulent pathotypes like Ug99 and TKTTF that overcome race-specific resistance genes, this research validates the imperative shift toward quantitative adult plant resistance (APR) sourced from wild relatives such as *Aegilops* species, *Triticum monococcum*, and synthetic wheats. The integration of genomic tools including marker-assisted selection and genome-wide association studies, combined with multi-environment phenotyping, enables effective pyramiding of pleiotropic resistance loci like Lr34/Yr18/Sr57/Pm38 to achieve broad-spectrum, long-lasting protection. These findings emphasize that developing resilient, high-yielding cultivars through such integrated breeding approaches is essential to mitigate the 2.12% production losses and safeguard wheat's role as a cornerstone of global nutrition under evolving pathogen pressures and changing climatic conditions. The empirical evidence presented herein provides a compelling rationale for sustained investment in durable resistance breeding programs to ensure wheat production stability and food security for future generations.

Suggestions and Recommendations

1. Given the recurrent “boom-and-bust” cycles associated with race-specific seedling resistance, national and international breeding initiatives should systematically integrate pleiotropic APR genes such as Lr34/Yr18/Sr57/Pm38 and Lr67 into high-yielding elite backgrounds. These genes confer partial but broad-spectrum, long-lasting protection against multiple biotrophic pathogens and are less vulnerable to pathogen evolution.
2. Breeders should deploy molecular markers linked to validated resistance loci (e.g., Yr5, Yr15, Sr2, Sr35, Pm30) to pyramid multiple effective genes into single cultivars. Combining three to eight complementary resistance genes especially those with additive or epistatic interactions can significantly elevate resistance thresholds and delay pathogen adaptation.
3. Continuous surveillance and phenotypic screening of wheat collections including landraces, synthetic hexaploids, and wild relatives (*Aegilops*, *Triticum monococcum*) in pathogen diversity centers (e.g., the Himalayan region, East Africa, and Central Asia) are essential to identify novel resistance sources before virulent races emerge at scale.
4. High-density consensus maps and genome-wide association studies (GWAS) should be coupled with multi-environment field trials to validate QTL effects under real-world conditions. This integration enhances the accuracy of genomic selection for quantitative resistance traits.

Author Contributions: **Soliman** has collected the research material from the electronic database. **Shlibak** and **Zencirci** have done conceptualization and methodology, writing original draft preparation, review editing, and English proofreading. All authors have read and agreed to the published version of the manuscript."

Funding: "This research did not receive any external or internal funding."

Data Availability Statement: “Electronic databases were used to support this study.

Acknowledgments: " The authors are fully thankful for Prof. Dr. Nusret ZENCİRCİ guidance and academic support in completing this work.

Conflicts of Interest: "The authors declare that they have no conflict of interest."

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