Review Article

评述论文

**Fungal and Bacterial Diseases in Rye: Historical Contexts and Modern Solutions**

**黑麦中的真菌和细菌病害：历史背景与现代解决方案**

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**Abstract:** Rye (*Secale cereale* L.), as an important cereal crop, has historically suffered from severe fungal and bacterial diseases. This study explores the historical context, modern management methods, and future directions for controlling these diseases. By examining major fungal diseases such as ergot, rusts, and smuts, as well as bacterial diseases like bacterial blight and black chaff, it reviews the impact of disease outbreaks on rye production and the evolution of disease resistance. Modern disease management strategies include the use of fungicides and antibiotics, the introduction of biological control agents, breeding for disease resistance, and integrated disease management practices. With the challenges posed by climate change, the control of rye diseases has become increasingly complex. This study integrates historical successes and modern technologies, emphasizing the importance of crop rotation, cultural practices, and biotechnology in future disease management to enhance rye’s disease resistance, ensure food security, and promote the sustainable development of agricultural ecosystems.

**Keywords:** Rye cultivation; Fungal diseases; Bacterial diseases; Disease resistance; Integrated disease management

**1 Introduction**

Rye (*Secale cereale* L.) is a versatile cereal crop known for its resilience to harsh environmental conditions and its ability to thrive in poor soils where other cereals might fail. It is widely cultivated in temperate regions and is used for a variety of purposes, including food production, animal feed, and as a cover crop to improve soil health and prevent erosion (Frost et al., 2019). Despite its hardiness, rye is susceptible to several fungal and bacterial diseases that can significantly impact yield and quality.

Historically, fungal diseases have posed a significant threat to rye cultivation. One of the most notorious diseases is ergot, caused by *Claviceps purpurea*, which has been a problem since the early Middle Ages in Europe. Ergot contamination not only reduces yield but also produces toxic alkaloids that can cause severe health issues in humans and animals (Miedaner and Geiger, 2015; Pitt and Miller, 2017). Another major disease is snow mold, caused by *Microdochium nivale*, which thrives under snow cover and can devastate winter rye crops (Gorshkov et al., 2020; Ponomareva et al., 2022). The historical context of these diseases highlights the ongoing challenge of managing fungal pathogens in rye cultivation.

This study will provide a comprehensive overview of the fungal and bacterial diseases that affect rye, with a focus on their historical impact and the modern solutions being developed, including studying the biology and genetics of major pathogens, the effectiveness of current disease management strategies, and the potential for cultivating disease resistant rye varieties. It will explore the challenges and solutions currently available to address their impacts, with the aim of providing insights for future rye cultivation and conservation strategies.

**2 Historical Context of Fungal and Bacterial Diseases in Rye**

**2.1 Major outbreaks and their consequences**

Rye (*Secale cereale* L.) has historically been susceptible to a variety of fungal and bacterial diseases, which have had significant impacts on crop yields and food security. One of the most notable fungal pathogens affecting rye is *Microdochium nivale*, which causes severe damage and has been poorly characterized at the molecular level until recent studies (Tsers et al., 2021). The susceptibility of rye to this pathogen has led to substantial crop losses, highlighting the need for improved disease resistance. Another significant fungal disease in rye is powdery mildew, caused by *Blumeria graminis* f. sp. *tritici*. The introgression of resistance genes from rye into wheat, such as the *Pm17* gene, has been a common strategy to combat this disease. However, the effectiveness of these resistance genes can be limited by the ancient variation of the corresponding fungal effector genes, which predate the introgression and can lead to rapid resistance breakdown.

The historical context of rye diseases also includes the impact of climate change, which has been shown to exacerbate the emergence and spread of fungal pathogens. Environmental pressures resulting from climate change can lead to the adaptation of fungi to new conditions, increasing their pathogenicity and geographic range (Nnadi and Carter, 2021). This has been observed with various fungal species, which have become more problematic in recent decades due to changing climate conditions.

**2.2 Evolution of disease resistance in rye**

The evolution of disease resistance in rye has been a critical area of research, particularly in the context of breeding programs aimed at enhancing phytoimmunity. Studies have identified several rye genotypes with non-specific resistance to multiple fungal diseases. For instance, research conducted on winter rye genotypes has revealed varieties with slow rusting traits and high resistance to septoria and other fungal infections (Shchekleina and Sheshegova, 2023). These resistant varieties, such as 'Rossiyanka 2', have been crucial in breeding programs to develop new rye cultivars with improved disease resistance.

The identification and characterization of resistance genes have also played a significant role in the evolution of disease resistance in rye. The *Pm17* and *Pm8* resistance genes, originally introgressed from rye into wheat, demonstrate the ancient diversity and evolutionary divergence of resistance genes in cereal crops (Singh et al., 2018). These genes have been isolated and functionally validated, providing valuable insights into the genetic basis of disease resistance and guiding future breeding efforts. The development of novel translocation lines, such as the wheat-rye 1RS·1BL translocation lines, has contributed to the enhancement of disease resistance in rye. These lines exhibit high resistance to stripe rust and other fungal pathogens, offering new genetic resources for wheat and rye improvement programs (Ren et al., 2022).

**3 Fungal Diseases Affecting Rye**

**3.1 Ergot disease**

Ergot disease, caused by fungi in the genus *Claviceps*, is a significant concern for rye cultivation. The most notable species, *Claviceps purpurea*, infects the ovaries of rye flowers, replacing seeds with toxic sclerotia. This disease has been documented in Europe since the early Middle Ages and poses severe health risks due to the alkaloids produced by the fungus, which can affect both humans and animals. In Canada, ergot is a grain-grading factor, impacting grain quality and safety due to the presence of ergot alkaloids (Walkowiak et al., 2022). Breeding efforts have identified several winter rye cultivars with moderate resistance to ergot, which can be utilized to develop more resistant varieties.

**3.2 Rusts and smuts**

Rusts and smuts are other significant fungal diseases affecting rye. Rust diseases, such as stripe rust caused by *Puccinia striiformis*, have historically been a major threat to cereal crops. Although primarily a concern for wheat, rust fungi can also affect rye. The management of rust diseases often involves the use of fungicides and the development of resistant cultivars (Cook et al., 2021). Smut diseases, caused by fungi like Ustilago species, can also impact rye, leading to significant yield losses.

**3.3 Modern fungal disease management**

3.3.1 Fungicide application strategies

Fungicide application remains a critical component of managing fungal diseases in rye. However, the efficacy of fungicides can be limited and weather-dependent, particularly for diseases like ergot (Miedaner and Geiger, 2015). Soil-applied fungicides have shown promise in reducing sclerotia germination and disrupting the ergot disease cycle in perennial ryegrass, suggesting potential applications for rye as well (Dung et al., 2018). The emergence of fungicide-resistant strains of rust pathogens highlights the need for careful management and monitoring of fungicide use.

3.3.2 Breeding for fungal resistance

Breeding for resistance is a sustainable approach to managing fungal diseases in rye. Research has identified several rye cultivars with moderate resistance to ergot, which can be used in breeding programs to develop more resistant varieties. Advances in molecular breeding techniques, such as the use of transcriptomics to understand the genetic basis of resistance, are paving the way for the development of rye cultivars with enhanced resistance to ergot and other fungal diseases (Mahmood et al., 2020). The identification of specific resistance genes, such as those conferring stripe rust resistance, further supports these efforts (Ashraf et al., 2022).

3.3.3 Integrated disease management

Integrated Disease Management (IDM) combines multiple strategies to control fungal diseases in rye. This approach includes the use of resistant cultivars, timely fungicide applications, and cultural practices that reduce disease pressure. For example, the use of gametocides to induce male sterility in rye can enhance the effectiveness of ergot management by preventing pollen contamination and increasing the susceptibility of unfertilized ovaries to fungal infection (Hanosová et al., 2015). IDM practices are essential for sustainable disease management and reducing the reliance on chemical controls alone (Carmona et al., 2020).

**4. Bacterial Diseases in Rye**

**4.1 Bacterial blight**

Bacterial blight in rye is primarily caused by the pathogen *Xanthomonas campestris* pv. *translucens*. This disease manifests as water-soaked lesions on leaves, which eventually turn necrotic, leading to significant yield losses. The pathogen is known for its rapid spread under favorable conditions, such as high humidity and warm temperatures. Similar to rice, where bacterial blight caused by Xanthomonas oryzae pv. oryzae is a major concern, extensive genetic and genomic studies have been conducted to understand the molecular mechanisms of plant-pathogen interactions and to develop resistant varieties (Jiang et al., 2020).

**4.2 Black chaff**

Black chaff, caused by Xanthomonas translucens pv. undulosa, is another significant bacterial disease affecting rye. This disease is characterized by dark streaks on the glumes and leaves, often accompanied by a bacterial ooze. The symptoms can be confused with those of fungal diseases, making accurate diagnosis crucial for effective management. The disease can lead to reduced grain quality and yield. Research on similar bacterial diseases in other cereals, such as rice and wheat, has provided insights into potential control strategies, including the use of resistant varieties and biological control agents (Rojas et al., 2020; Byrne et al., 2022).

**4.3 Advances in bacterial disease control**

4.3.1 Use of antibiotics and biological control agents

The use of antibiotics, such as streptomycin, has been a traditional method for controlling bacterial diseases in crops. However, the emergence of antibiotic-resistant strains and the environmental impact of antibiotics have led to a shift towards more sustainable solutions. Biological control agents, such as endophytic bacteria and fungi, have shown promise in managing bacterial diseases. For instance, Bacillus oryzicola, an endophytic bacterium isolated from rice roots, has demonstrated antimicrobial and systemic resistance-inducing activities, effectively suppressing bacterial blight in rice (Chung et al., 2015). Similarly, the application of beneficial microorganisms could be explored for controlling bacterial diseases in rye.

4.3.2 Development of resistant varieties

Breeding for disease-resistant varieties is a cornerstone of integrated pest management. Advances in molecular biology and genomics have facilitated the identification and incorporation of resistance genes into crop varieties. In rice, extensive research has led to the characterization of resistance (*R*) genes and their interactions with bacterial blight pathogens, enabling the development of varieties with durable and broad-spectrum resistance (Figure 1) (Jiang et al., 2020).

During the infection process of bacterial blight, effector proteins secreted by the pathogen, such as RaxX, bind to the XA21 receptor located on the plasma membrane of rice cells, activating downstream defense responses. This process involves several regulatory proteins, such as OsSERK2, XB24, XB15, and XB21, which play key roles in maintaining XA21 function and regulating its phosphorylation state. This complex protein network effectively enhances rice’s defense against pathogens. Similar approaches can be applied to rye, leveraging genomic tools to identify and introduce resistance genes against bacterial blight and black chaff. The development of resistant varieties not only reduces the reliance on chemical controls but also ensures sustainable crop production.

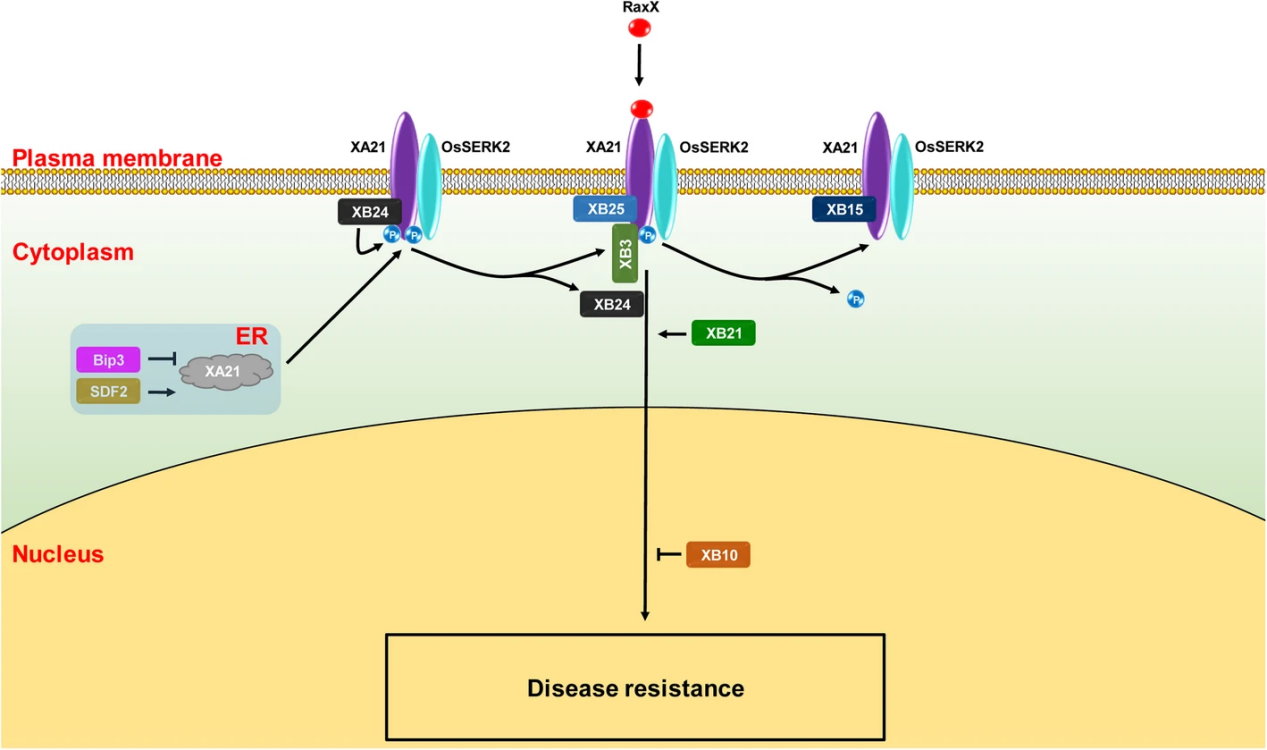


Figure 1 Xa21-mediated immune signaling pathways triggered by *Xanthomonas oryzae* (Adopted from Jiang et al., 2020)

**5 Integrated Disease Management Strategies**

**5.1 Crop rotation and cultural practices**

Crop rotation and cultural practices are fundamental components of integrated disease management (IDM) strategies. These practices help in breaking the life cycles of pathogens and reducing the inoculum levels in the soil. For instance, cover cropping with species like sunn hemp has been shown to suppress soilborne nematodes and fungal pathogens, such as Meloidogyne incognita, Rhizoctonia solani, and Sclerotinia sclerotiorum, especially when combined with deep tillage practices (Marquez and Hajihassani, 2023). However, the use of winter cereal cover crops, such as rye, can sometimes host pathogens that affect subsequent crops like corn, necessitating careful management to mitigate these risks (Bakker et al., 2016). The adoption of perennial grain crops, while beneficial for sustainable agriculture, introduces new disease management challenges that require innovative solutions (Fulcher et al., 2022).

**5综合病害管理策略**

**5.2 Use of resistant varieties and biotechnology**

The development and use of disease-resistant crop varieties are crucial for managing both fungal and bacterial diseases in rye. Research has identified several winter rye varieties with non-specific resistance to multiple fungal diseases, which can be used in breeding programs to enhance phytoimmunity (Shchekleina and Sheshegova, 2023). For example, varieties like 'Rossiyanka 2' have shown high resistance to septoriose and slow rusting traits, making them valuable for breeding efforts. Furthermore, advances in biotechnology, such as genome modification, offer promising avenues for developing crops with enhanced disease resistance. This approach is considered one of the most effective strategies against bacterial diseases, although more research is needed to develop novel management tactics (Sharma et al., 2022).

**5.3 Future directions in disease management**

Future directions in disease management will likely focus on sustainable and environmentally friendly solutions. The increasing concern over the impact of fungicides and bactericides on human health and the environment underscores the need for alternative strategies. For instance, the use of antibiofilm compounds at sub-lethal concentrations offers a potential eco-sustainable strategy to counteract fungal pathogens, reducing the severity of diseases and the selection of resistant forms (Villa et al., 2017). Integrated pest management (IPM) techniques, such as forecasting disease pressure and optimizing fungicide use based on disease resistance and environmental conditions, can help minimize the reliance on chemical treatments while maintaining crop yields (Stetkiewicz et al., 2019). Research must continue to address the challenges posed by emerging pathogens and develop durable, accessible, and sustainable disease management practices (Fones et al., 2020).

**6 Challenges in Managing Rye Diseases**

**6.1 Climate change and disease dynamics**

Climate change significantly impacts the dynamics of fungal and bacterial diseases in rye. The increasing global temperatures and changing precipitation patterns create favorable conditions for the emergence and spread of new pathogens. For instance, climate change can extend the geographic range of pathogenic species or their vectors, leading to the emergence of diseases in areas where they were previously unknown (Nnadi and Carter, 2021). Environmental disruptions such as floods and storms can disperse fungal spores, increasing the incidence of infections.

Emerging fungal pathogens pose a significant risk to global food security, as they can infect staple crops and economically important commodities. The current agricultural systems, which emphasize intensive monoculture practices, further exacerbate the spread of these pathogens (Fones et al., 2020). The adaptation of fungi to higher temperatures due to climate change could lead to an increase in thermotolerant species capable of infecting rye and other crops. Therefore, understanding the role of climate change in disease dynamics is crucial for developing effective management strategies.

**6.2 Resistance development and breakdown**

The development and breakdown of resistance in rye is a complex challenge in disease management. Resistance genes, such as those introgressed from rye to wheat, can be rapidly overcome by pathogens due to the presence of ancient variants of effector proteins in the pathogen gene pool (Müller et al., 2022). This rapid breakdown of resistance highlights the need for continuous monitoring and the development of new resistance genes.

Breeding for resistance to specific diseases, such as snow mold, has shown promise. However, the limited use of resistance sources in contemporary breeding programs has resulted in a scarcity of varieties with moderate to high resistance (Figure 2) (Ponomareva et al., 2022). Identifying and utilizing diverse genetic sources of resistance is essential for enhancing the durability of resistance in rye. The evolutionary divergence of resistance genes, such as *Pm17* and *Pm8*, demonstrates the complexity of resistance mechanisms. These genes, originally introgressed from rye to wheat, show significant diversity, suggesting that orthologous resistance genes can evolve differently in various cereal species (Singh et al., 2018). This diversity can be leveraged to develop novel resistance genes for rye breeding programs.

The experiment in the image is a systematic evaluation of the resistance to snow mold in different rye varieties, aimed at identifying the optimal genetic sources of resistance. By incorporating these high-quality disease-resistant genes into new breeding programs, the resistance of rye to snow mold can be significantly improved. This strategy of enhancing crop disease resistance through genetic diversity is expected to provide more disease-resistant crop varieties for future agriculture, reduce the reliance on chemical pesticides, and simultaneously increase crop yields and food safety.



Figure 2 Rye plots in the nurseries with a natural infection background (NIB) (A) and with an artificially-enriched infection background (AIB) (B) (Photo credit : Ponomareva et al., 2022)

**7 Case Studies of Successful Disease Management**

**7.1 Historical successes in disease control**

Historically, the management of fungal and bacterial diseases in rye and other crops has seen significant advancements. One notable success is the development and application of fungicide treatments. For instance, the use of fungicides such as metalaxyl, pyraclostrobin, fludioxonil, ipconazole, and sedaxane has been instrumental in controlling diseases caused by Pythium, Fusarium, and Rhizoctonia solani. These treatments have been shown to improve seed germination and seedling growth under controlled conditions, highlighting their effectiveness in disease management (Acharya et al., 2018).

Another historical success is the understanding and management of central nervous system infections caused by bacterial and fungal pathogens. The progression of diseases such as cryptococcal meningitis and candidiasis has been well-documented, leading to improved diagnostic and treatment protocols. This historical perspective has provided a foundation for modern disease management strategies (Shih and Koeller, 2015).

**7.2 Modern case studies from different regions**

In recent years, modern approaches to disease management in rye have continued to evolve, incorporating both traditional methods and innovative solutions. For example, the use of fungicide seed treatments in corn, which is often rotated with rye, has shown promising results. Studies have demonstrated that treatments targeting *Pythium* spp. significantly reduce disease incidence and improve seedling health, even in challenging environmental conditions (Acharya et al., 2018).

Global initiatives such as the Leading International Fungal Education (LIFE) portal have facilitated the estimation and management of fungal infection burdens across different regions. This initiative has highlighted the varying prevalence of fungal diseases and the need for region-specific management strategies. By providing accurate data on the burden of serious fungal infections, the LIFE portal has enabled targeted interventions and improved disease outcomes (Bongomin et al., 2017).

These modern case studies underscore the importance of both historical knowledge and contemporary research in effectively managing fungal and bacterial diseases in rye and other crops. By combining these approaches, researchers and farmers can develop robust strategies to mitigate the impact of these diseases on agricultural productivity.

**8 Concluding Remarks**

Historically, fungal and bacterial diseases in rye have posed significant challenges to agriculture, with ergot (*Claviceps* spp.) being one of the most notorious. Ergot has been a known issue since the early Middle Ages, causing severe health problems due to the toxic alkaloids produced by the fungus. Traditional methods to combat these diseases included crop rotation, selection of resistant varieties, and manual removal of infected plants. However, these methods were often labor-intensive and not entirely effective.

In modern times, the approach to managing rye diseases has evolved significantly. Advances in genetic research have led to the identification of resistant genotypes and the development of hybrid varieties with improved resistance to diseases like ergot and rust. Molecular breeding techniques, such as the introgression of effective restorer genes, have shown promise in reducing ergot infection levels. Additionally, fungicide treatments, although limited in efficacy and dependent on weather conditions, have been employed to manage fungal infections.

The use of genome-wide association studies (GWAS) has furthered our understanding of the genetic basis of disease resistance. For instance, research on Fusarium culmorum has identified key SNPs associated with aggressiveness and mycotoxin production, providing valuable insights for resistance breeding. Moreover, the discovery of natural products with antimicrobial properties has opened new avenues for developing biocontrol agents.

The future of rye disease management lies in the integration of advanced genetic tools and sustainable agricultural practices. Continued research into the genetic diversity of rye and its pathogens will be crucial. For example, the identification of novel resistance genes, such as *Pm17* and *Pm8*, and their evolutionary divergence offers potential for developing new resistant varieties. Additionally, the use of resistant germplasm and the selection of distinct donors for breeding programs will enhance the genetic variability and durability of disease resistance in rye.

Biotechnological advancements, such as CRISPR/Cas9, could be leveraged to introduce specific resistance traits into rye cultivars more efficiently. Furthermore, the development of environmentally friendly fungicides and biocontrol agents will play a significant role in sustainable disease management. The integration of these modern approaches with traditional practices, such as crop rotation and proper field management, will provide a holistic strategy to combat fungal and bacterial diseases in rye.

**Acknowledgments**

We express our sincere gratitude to two reviewers.for their suggestions.

**Conflict of Interest Disclosure**

The author affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

**References**

Acharya, J., Bakker, M., Moorman, T., Kaspar, T., Lenssen, A., & Robertson, A. (2018). Effects of fungicide seed treatments and a winter cereal rye cover crop in no till on the seedling disease complex in corn. Canadian Journal of Plant Pathology, 40, 481 - 497. <https://doi.org/10.1080/07060661.2018.1506503.>

Ashraf, R., Johansson, E., Vallenback, P., Steffenson, B., Bajgain, P., & Rahmatov, M. (2022). Identification of a small translocation from 6R possessing stripe rust resistance to wheat.. Plant disease. <https://doi.org/10.1094/PDIS-07-22-1666-RE.>

Bakker, M., Acharya, J., Moorman, T., Robertson, A., & Kaspar, T. (2016). The Potential for Cereal Rye Cover Crops to Host Corn Seedling Pathogens.. Phytopathology, 106 6, 591-601 . <https://doi.org/10.1094/PHYTO-09-15-0214-R.>

Bongomin, F., Gago, S., Oladele, R., & Denning, D. (2017). Global and Multi-National Prevalence of Fungal Diseases—Estimate Precision. Journal of Fungi, 3. <https://doi.org/10.3390/jof3040057.>

Byrne, M., Thapa, G., Doohan, F., & Burke, J. (2022). Lactic Acid Bacteria as Potential Biocontrol Agents for Fusarium Head Blight Disease of Spring Barley. Frontiers in Microbiology, 13. <https://doi.org/10.3389/fmicb.2022.912632.>

Carmona, M., Sautua, F., Pérez-Hernández, O., & Reis, E. (2020). Role of Fungicide Applications on the Integrated Management of Wheat Stripe Rust. Frontiers in Plant Science, 11. <https://doi.org/10.3389/fpls.2020.00733.>

Chung, E., Hossain, M., Khan, A., Kim, K., Jeon, C., & Chung, Y. (2015). Bacillus oryzicola sp. nov., an Endophytic Bacterium Isolated from the Roots of Rice with Antimicrobial, Plant Growth Promoting, and Systemic Resistance Inducing Activities in Rice. The Plant Pathology Journal, 31, 152 - 164. <https://doi.org/10.5423/PPJ.OA.12.2014.0136.>

Cook, N., Chng, S., Woodman, T., Warren, R., Oliver, R., & Saunders, D. (2021). High frequency of fungicide resistance-associated mutations in the wheat yellow rust pathogen Puccinia striiformis f. sp. tritici.. Pest management science. <https://doi.org/10.1002/ps.6380.>

Dung, J., Kaur, N., Walenta, D., Alderman, S., Frost, K., & Hamm, P. (2018). Reducing *Claviceps purpurea* sclerotia germination with soil-applied fungicides. Crop Protection, 106, 146-149. <https://doi.org/10.1016/J.CROPRO.2017.12.023.>

Fones, H., Bebber, D., Chaloner, T., Kay, W., Steinberg, G., & Gurr, S. (2020). Threats to global food security from emerging fungal and oomycete crop pathogens. Nature Food, 1, 332 - 342. <https://doi.org/10.1038/s43016-020-0075-0.>

Frost, M., Haramoto, E., Renner, K., & Brainard, D. (2019). Tillage and Cover Crop Effects on Weed Seed Persistence: Do Light Exposure and Fungal Pathogens Play a Role?. Weed Science, 67, 103 - 113. <https://doi.org/10.1017/wsc.2018.80.>

Fulcher, M., Law, E., Wayman, S., Ryan, M., & Bergstrom, G. (2022). Fungal plant pathogens observed on perennial cereal crops in New York during 2017–2018. Renewable Agriculture and Food Systems. <https://doi.org/10.1017/s1742170521000582.>

Gorshkov, V., Osipova, E., Ponomareva, M., Ponomarev, S., Gogoleva, N., Petrova, O., Gogoleva, O., Meshcherov, A., Balkin, A., Vetchinkina, E., Potapov, K., Gogolev, Y., & Korzun, V. (2020). Rye Snow Mold-Associated *Microdochium nivale* Strains Inhabiting a Common Area: Variability in Genetics, Morphotype, Extracellular Enzymatic Activities, and Virulence. Journal of Fungi, 6. <https://doi.org/10.3390/jof6040335.>

Hanosová, H., Koprna, R., Valík, J., Knoppová, L., Frébort, I., Dzurová, L., & Galuszka, P. (2015). Improving field production of ergot alkaloids by application of gametocide on rye host plants.. New biotechnology, 32 6, 739-46 . <https://doi.org/10.1016/j.nbt.2015.01.008.>

Jiang, N., Yan, J., Liang, Y., Shi, Y., He, Z., Wu, Y., Zeng, Q., Liu, X., & Peng, J. (2020). Resistance Genes and their Interactions with Bacterial Blight/Leaf Streak Pathogens (Xanthomonas oryzae) in Rice (Oryza sativa L.)—an Updated Review. Rice, 13. <https://doi.org/10.1186/s12284-019-0358-y.>

Mahmood, K., Orabi, J., Kristensen, P., Sarup, P., Jørgensen, L., & Jahoor, A. (2020). De novo transcriptome assembly, functional annotation, and expression profiling of rye (*Secale cereale* L.) hybrids inoculated with ergot (*Claviceps purpurea*). Scientific Reports, 10. <https://doi.org/10.1038/s41598-020-70406-2.>

Marquez, J., & Hajihassani, A. (2023). Successional effects of cover cropping and deep tillage on suppression of plant-parasitic nematodes and soilborne fungal pathogens.. Pest management science. <https://doi.org/10.1002/ps.7450.>

Miedaner, T., & Geiger, H. (2015). Biology, Genetics, and Management of Ergot (*Claviceps* spp.) in Rye, Sorghum, and Pearl Millet. Toxins, 7, 659 - 678. <https://doi.org/10.3390/toxins7030659.>

Müller, M., Kunz, L., Schudel, S., Lawson, A., Kammerecker, S., Isaksson, J., Wyler, M., Graf, J., Sotiropoulos, A., Praz, C., Manser, B., Wicker, T., Bourras, S., & Keller, B. (2022). Ancient variation of the Avr*Pm17* gene in powdery mildew limits the effectiveness of the introgressed rye *Pm17* resistance gene in wheat. Proceedings of the National Academy of Sciences of the United States of America, 119. <https://doi.org/10.1073/pnas.2108808119.>

Nnadi, N., & Carter, D. (2021). Climate change and the emergence of fungal pathogens. PLoS Pathogens, 17. <https://doi.org/10.1371/journal.ppat.1009503.>

Pitt, J., & Miller, J. (2017). A Concise History of Mycotoxin Research.. Journal of agricultural and food chemistry, 65 33, 7021-7033 . <https://doi.org/10.1021/acs.jafc.6b04494.>

Ponomareva, M., Gorshkov, V., Ponomarev, S., Mannapova, G., Askhadullin, D., Askhadullin, D., Gogoleva, O., Meshcherov, A., & Korzun, V. (2022). Resistance to Snow Mold as a Target Trait for Rye Breeding. Plants, 11. <https://doi.org/10.3390/plants11192516.>

Ren, T., Jiang, Q., Sun, Z., Ren, Z., Tan, F., Yang, W., & Li, Z. (2022). Development and characterization of novel wheat-rye 1RS•1BL translocation lines with high resistance to Puccinia striiformis f. sp. tritici.. Phytopathology. <https://doi.org/10.1094/PHYTO-07-21-0313-R.>

Rojas, E., Jensen, B., Jørgensen, H., Latz, M., Esteban, P., Ding, Y., & Collinge, D. (2020). Selection of fungal endophytes with biocontrol potential against Fusarium head blight in wheat. Biological Control. <https://doi.org/10.1016/j.biocontrol.2020.104222.>

Sharma, A., Abrahamian, P., Carvalho, R., Choudhary, M., Paret, M., Vallad, G., & Jones, J. (2022). Future of Bacterial Disease Management in Crop Production.. Annual review of phytopathology. <https://doi.org/10.1146/annurev-phyto-021621-121806.>

Shchekleina, L., & Sheshegova, T. (2023). The nature of fungal infection growth in varietal biocoenoses of winter rye and the search for resistant genotypes. Siberian Herald of Agricultural Science. <https://doi.org/10.26898/0370-8799-2023-8-4.>

Shih, R., & Koeller, K. (2015). Bacterial, Fungal, and Parasitic Infections of the Central Nervous System: Radiologic-Pathologic Correlation and Historical Perspectives.. Radiographics : a review publication of the Radiological Society of North America, Inc, 35 4, 1141-69 . <https://doi.org/10.1148/rg.2015140317.>

Singh, S., Hurni, S., Ruinelli, M., Brunner, S., Sánchez-Martín, J., Krukowski, P., Peditto, D., Buchmann, G., Zbinden, H., & Keller, B. (2018). Evolutionary divergence of the rye *Pm17* and *Pm8* resistance genes reveals ancient diversity. Plant Molecular Biology, 98, 249 - 260. <https://doi.org/10.1007/s11103-018-0780-3.>

Stetkiewicz, S., Burnett, F., Ennos, R., & Topp, C. (2019). The impact of fungicide treatment and Integrated Pest Management on barley yields: Analysis of a long term field trials database. European Journal of Agronomy. <https://doi.org/10.1016/J.EJA.2019.02.010.>

Tsers, I., Meshcherov, A., Gogoleva, O., Petrova, O., Gogoleva, N., Ponomareva, M., Gogolev, Y., Korzun, V., & Gorshkov, V. (2021). Alterations in the Transcriptome of Rye Plants following the *Microdochium nivale* Infection: Identification of Resistance/Susceptibility-Related Reactions Based on RNA-Seq Analysis. Plants, 10. <https://doi.org/10.3390/plants10122723.>

Villa, F., Cappitelli, F., Cortesi, P., & Kunova, A. (2017). Fungal Biofilms: Targets for the Development of Novel Strategies in Plant Disease Management. Frontiers in Microbiology, 8. <https://doi.org/10.3389/fmicb.2017.00654.>

Walkowiak, S., Taylor, D., Fu, B., Drul, D., Pleskach, K., & Tittlemier, S. (2022). Ergot in Canadian cereals – relevance, occurrence, and current status. Canadian Journal of Plant Pathology, 44, 793 - 805. <https://doi.org/10.1080/07060661.2022.2077451.>

Yang P.P., and Fu J., 2024, Pantoea ananatis: emerging bacterial pathogen in wheat fields, Molecular Pathogens, 15(2): 83-92. <https://doi.org/10.5376/mp.2024.15.0009>

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