

Editorial

# The Genetics and Molecular Biology of Pathogens in Agricultural Crops

Slavica Matic 

Institute for Sustainable Plant Protection, National Research Council of Italy (IPSP-CNR), 10135 Turin, Italy; slavica.matic@ipspp.cnr.it

## 1. Introduction

Despite advances in science and technology, agricultural yield losses due to plant pathogens and pests currently account for 30% of global production [1]. Such losses depend on the genetic structure of the pathogen, which influences its competitiveness, aggressiveness, and spread, as well as on the sensitivity of the host plant and climatic conditions. In addition, market globalization coupled with climate change may increase the risk of the introduction of new emerging pathogens or the reintroduction of existing pathogens with a significant impact on agricultural production [2,3].

The application of new sequencing and bioinformatics technologies brings the continuous discovery of new plant pathogens, providing information about their genomes and genetic variations as well as contributing to the identification of new resistance genes in host plants [4,5]. The molecular mechanisms of the pathogen influence host development through the manipulation of plant hormonal signalling and the targeting of its transcription factors, as well as the host's defence activation [6]. Increased knowledge of the genetics and molecular biology of crop pathogens and their host species will bring new insights into more effective and environmentally friendly plant disease management by combining traditional plant breeding, innovative plant resistance methods and the use of biocontrol agents and natural compounds.

This Special Issue highlights the cutting-edge and innovative proposals addressing these key topics.

## 2. Results

A total of 12 manuscripts were submitted to this Special Issue, with 6 manuscripts accepted and published.

The gradual emergence of harmful plant viruses such as East African cassava mosaic Cameroon virus (EACMCMV) on cassava farms in Côte d'Ivoire along with the presence of African cassava mosaic virus (ACMV) infection represents a dangerous threat to cassava cultivation in this country (Kouakou et al., 2024). The evolutionary dynamics of cassava mosaic viruses and their close phylogenetic affiliation with virus isolates from surrounding countries (Ghana, Burkina Faso, and Nigeria) should be taken into account for a more effective management of the cassava mosaic disease in the future. Genetic variations may play an important role in the adaptability of the cruciferous weed *Cardamine occulta*-infecting populations of *Plasmodiophora brassicae* in Japan, which can significantly contribute to the pathogenesis of this cosmopolitan plasmodiophorid (Lam et al., 2024). It was found that geographical populations of *P. brassicae* from *C. occulta* with a lengthy intron-encoded ORF and putative large subunit mobile elements shared some mutated motifs in polymorphic introns with that from the *Brassica* hosts. Annotation of the 12th chromosome of the forest fungal pathogen *Fusarium circinatum*, the causal agent of Pine Pitch Canker Disease (PPC) and a quarantine pathogen in many countries, can significantly contribute to the management of PPC disease and containment and mitigation strategies (Malewski et al., 2024). At least 14 genes were found to be associated with the pathogenesis/virulence of



**Citation:** Matic, S. The Genetics and Molecular Biology of Pathogens in Agricultural Crops. *Agronomy* **2024**, *14*, 1088. <https://doi.org/10.3390/agronomy14061088>

Received: 10 May 2024

Accepted: 17 May 2024

Published: 21 May 2024



**Copyright:** © 2024 by the author. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

*F. circinatum*, and they may be useful in the establishment of a relationship between this pathogen and hosts. Existing white rust resistance genes are frequently ineffective due to the racial variability of the oomycete *Albugo candida*, the causal agent of white rust, one of the most destructive diseases of Brassicaceae crops. In the study by Mehta et al. (2024), novel sources of white rust disease resistance were found; namely ERJ 39, ERJ 12, and ERJ 15 among introgressed *Brassica juncea* lines and RBJ 18, DRMR 18-36-12, and DRMR 18-37-13 among resynthesized and mutant lines. These new sources of host resistance to *A. candida* will play a crucial role in mustard improvement programs and the identification of resistance-linked markers, QTLs, or genes for the sustainable management of white rust disease in India. Furthermore, barley lines carrying the *Rph7* and *Rph13* genes were found to confer immunity to barley leaf rust, a harmful worldwide disease in barley-growing regions (Danilova et al., 2024). Annual monitoring of the response of *Rph* lines in different climatic conditions, along with virulence studies of *Puccinia hordei*, the causal agent of barley leaf rust disease, is an important measure for efficiently managing this dangerous disease. Finally, one of the most destructive diseases of grapevine in Europe caused by Flavescence Dorée phytoplasma (FDp), a European Union quarantine pathogen, has been diagnosed using a specific loop-mediated isothermal amplification (LAMP) technique (Matić et al., 2024). An in-field LAMP protocol was successfully developed for the sensitive detection of FDp in the insect vector *Scaphoideus titanus*, allowing the monitoring of phytoplasma spread in the field and applying the strategies needed for mandatory and timely pathogen control.

Overall, studies of different resistance genes and genetic variations of economically important harmful plant pathogens, along with the application of innovative point-of-care diagnostic methods for the early identification of pathogens, such as the LAMP method, will certainly contribute to achieving more eco-friendly, efficient, and sustainable plant disease management.

### 3. Perspectives

This Special Issue, entitled “The Genetics and Molecular Biology of Pathogens in Agricultural Crops”, has come to an end. I am very grateful for the hard work and dedication of the journal editors, peer reviewers, and authors. I would also like to thank all readers of *Agronomy* who read and appreciated the articles within. This issue has attracted significant attention in research communities from different domains of plant pathology; I hope it has opened avenues for writing research articles and organizing new Special Issues on similar topics in the future.

**Conflicts of Interest:** The authors declare no conflicts of interest.

#### List of Contributions

1. Kouakou, B.S.M.; Yoboué, A.A.N.; Pita, J.S.; Mutuku, J.M.; Otron, D.H.; Kouassi, N.K.; Kouassi, K.M.; Vanié-Léabo, L.P.L.; Ndougou, C.; Zouzou, M.; et al. Gradual Emergence of *East African cassava mosaic Cameroon virus* in Cassava Farms in Côte d’Ivoire. *Agronomy* **2024**, *14*, 418.
2. Lam, A.T.P.; Sasaki, K.; Yanagi, Y.; Tanaka, S.; Ito, S.-I. Intraspecific Variability and Distribution Difference within the Ribosomal Introns of the Discrete *Plasmodiophora brassicae* Group in Japan: A Case Study for Complex Dynamics of Intron Evolution. *Agronomy* **2022**, *12*, 2154.
3. Malewski, T.; Matić, S.; Okorski, A.; Borowik, P.; Osżako, T. Annotation of the 12th Chromosome of the Forest Pathogen *Fusarium circinatum*. *Agronomy* **2023**, *13*, 773.
4. Mehta, S.; Dhawi, F.; Garg, P.; Rao, M.; Bhattacharya, R.C.; Akthar, J.; Yadav, R.; Singh, M.; Singh, K.; Nallathambi, P.; et al. Potential Source of Resistance in Introgressed, Mutant and Synthetic *Brassica juncea* L. Lines against Diverse Isolates of White Rust Pathogen, *Albugo candida*. *Agronomy* **2023**, *13*, 1215.
5. Danilova, A.; Volkova, G. Efficiency of *Rph* genes against *Puccinia hordei* in Southern Russia in 2019–2021. *Agronomy* **2023**, *13*, 1046.
6. Matić, S.; Candian, V.; D’Errico, C.; Pierro, R.; Panno, S.; Davino, S.; Noris, E.; Tedeschi, R. In-Field LAMP Detection of Flavescence Dorée Phytoplasma in Crude Extracts of the *Scaphoideus titanus* Vector. *Agronomy* **2022**, *12*, 1645.

## References

1. Savary, S.; Willocquet, L.; Pethybridge, S.J.; Esker, P.; McRoberts, N.; Nelson, A. The global burden of pathogens and pests on major food crops. *Nat. Ecol. Evol.* **2019**, *3*, 430–439. [[CrossRef](#)] [[PubMed](#)]
2. Matic, S.; Tabone, G.; Garibaldi, A.; Gullino, M.L. Alternaria Leaf Spot Caused by Alternaria Species: An Emerging Problem on Ornamental Plants in Italy. *Plant Dis.* **2020**, *104*, 2275–2287. [[CrossRef](#)] [[PubMed](#)]
3. Garbelotto, M.; Pautasso, M. Impacts of exotic forest pathogens on Mediterranean ecosystems: Four case studies. *Eur. J. Plant Pathol.* **2012**, *133*, 101–116. [[CrossRef](#)]
4. Nizamani, M.M.; Zhang, Q.; Muhae-Ud-Din, G.; Wang, Y. High-throughput sequencing in plant disease management: A comprehensive review of benefits, challenges, and future perspectives. *Phytopathol. Res.* **2023**, *5*, 44. [[CrossRef](#)]
5. Zhang, C.; Jiang, S.; Tian, Y.; Dong, X.; Xiao, J.; Lu, Y.; Liang, T.; Zhou, H.; Xu, D.; Zhang, H.; et al. Smart breeding driven by advances in sequencing technology. *Mod. Agric.* **2023**, *1*, 43–56. [[CrossRef](#)]
6. Kong, F.; Yang, L. Pathogen-triggered changes in plant development: Virulence strategies or host defense mechanism? *Front. Microbiol.* **2023**, *14*, 1122947. [[CrossRef](#)] [[PubMed](#)]

**Disclaimer/Publisher's Note:** The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.