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Editorial

Molecular Variability of Crop Pathogens

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Crops account for over 80% of the human diet; however, plant diseases and pests are responsible for up to 40% of the loss in food production worldwide, costing approximately EUR 200 billion [1]. There are four main types of plant pathogens and pests affecting crops, namely bacteria, fungi, viruses and nematodes. These have a major impact on food production worldwide, especially when they affect staple crops, such as rice, wheat, maize and potatoes, on which vulnerable populations are deeply dependent, leading to food insecurity [2]. Additionally, as food demand continues to increase, agricultural production is further threatened by environmental pressures that result from current and predicted climate change scenarios [3]. Thus, it is becoming ever more relevant to look at the effect of these factors on the genetics, prevalence and virulence of crop-pathogenic organisms to enable the development of efficient tools to decrease losses and improve food availability worldwide.

Disease management is improving with the aim of increasing efficiency, allowing for early detection, and efficacy, thus ensuring that crop loss is avoided. Recent advances highlight the importance of epigenetic regulation in plant immunity and phenotypic variation in plant–microbe dynamics. Gene-editing technology is also rapidly advancing to develop crops with plant disease resistance. Other molecular-based strategies, such as the sequencing of pathogen populations, transcriptome analysis to identify virulence-related gene expression, or proteome analysis to identify proteins involved in pathogenicity may help in anticipating the emergence of virulent populations and prevent disease outbreaks. These virulence mechanisms may also be analyzed through metabolomic studies that, by looking at primary and secondary metabolite changes, can determine key resistance/susceptibility-associated pathways in the plant–microbe interaction. Finally, biocontrol agents have been increasingly used as sustainable counterparts to the application of chemical pesticides and antibiotics that endanger environmental and human health safety.

This Special Issue aimed to explore the influence of genetic and environmental factors on the molecular variability of crop pathogens that underpin disease incidence and spread. It focused on the molecular mechanisms involved in the crosstalk between pathogens and crops that could support effective disease management strategies. This collection contains six published papers addressing key bacterial and fungal pathogens in coffee, sorghum, tomato, triticale, rice and kiwifruit plants. They report two main disease management strategies, biocontrol agents [4,5] and molecular-based [6–9].

As recently reviewed [10], *Trichoderma* species are effective biocontrol agents not only against phytopathogens but also abiotic stresses. Indeed, in the papers published in this Special Issue, further evidence was presented regarding the *Trichoderma* mode of action in disease control. Specifically, in [4], the diversity of *Trichoderma* species present in **coffee plants** was characterized. The major knowledge gap addressed was the lack of data on the application of this biocontrol method in tropical perennial crops. The authors identified and characterized 175 isolates of *Trichoderma*, which corresponded to 16 putative species. These were screened for their potential as a biocontrol agent against coffee wilt disease, caused by the fungal pathogen *Fusarium xylarioides*. Based on in vitro assays, three isolates were

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selected as the most effective against the infection agent—*T. asperellum* AU71, *T. asperellum* AU131 and *T. longibrachiatum* AU158. In [5], the authors adopted a two-branched approach by testing two *Trichoderma* isolates against *Fusarium oxysporum f. sp. lycopersici* and *Rhizoctonia solani* in **tomato plants**, firstly under in vitro conditions and secondly in greenhouse trials. The main innovation of this study was the selection of new strains from *T. atrobrunneum* and *T. simmonsii*, which are species with few studies for this application. The authors identified isolates from both species with a strong antagonistic effect against the pathogens and also showed that a positive plant-promoting growth effect may occur in stressed plants.

As regards the studies based on molecular techniques, Ref. [6] used phenotyping combined with a targeted gene expression analysis to understand the mechanisms of resistance of 36 **sorghum** accessions against pathotype 5 of *Sporisorium reilianum*. The authors observed that the expression of chitinase- and PR10-encoding genes may be key in the mechanism behind this plant's pathosystem. To select multi-resistant **triticale** genotypes, the study developed in [7] tested the genetic variation of 656 triticale cultivars for their resistance to powdery mildew, leaf rust, yellow rust, stem rust and Fusarium head blight. This large-scale experiment advanced knowledge on the phenotypic data available for triticale species' disease resistance and evidenced the importance of understanding these pathogens' incidence dynamics in response to climate change. In [8], the authors used transcriptome sequencing and analysis to understand the molecular mechanisms behind brown planthopper infection in **rice plants**. The large transcriptome data obtained showed alterations in different biologically relevant gene classes and allowed the identification of differentially expressed genes commonly triggered in three rice varieties after insect damage, paving the way for future resistance screening studies. Finally, Ref. [9] reviews the mitigation strategies for controlling bacterial plant pathogens, using *Pseudomonas syringae* pv. *actinidiae* (Psa) as a case study. Efforts to control Psa, the pathogen causing bacterial canker in **kiwifruit** orchards, have focused on understanding Psa population structure, virulence mechanisms, and plant defense strategies. While eradication has not been achieved, a steady coexistence has been established through integrated approaches in orchard management, which include the development of biochemical and molecular approaches for pathogen identification, understanding pathogen epidemiology, the improvement of orchard management using prophylactic treatments and reducing the influence of environmental factors, and anticipating pathogen dispersal using remote sensing and modelling approaches. The most effective and sustainable strategy for managing plant diseases is host resistance; however, achieving this requires a comprehensive grasp of plant regulatory mechanisms. This not only includes ground-breaking high-throughput approaches on topics such as pathogen recognition, triggered immunity, plant antioxidant response, phytohormone regulation, and primary and secondary metabolism, but also conducting meta-analyses to harness the wealth of molecular evidence accumulated over the past decade.

In conclusion, the sustainable management of crop pathogens must include optimized agricultural practices that prevent or delay the appearance of pathogens, including molecular approaches aiming for early detection, effective crop protection, and enhancing plant tolerance. These efforts must be temporally and spatially dynamic to account for the constantly shifting genetics of bacterial populations and respective plant hosts. Although mitigating crop pathogens with minimal impact on food production and sustainable resource utilization is challenging, it can be achieved through effective knowledge transfer and collaboration among producers, researchers, and policymakers.

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