

EDITORIAL

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# Welcome to *Phytopathology Research*: a new platform for sharing research advances in plant pathology

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Rapid advances in molecular biology and biotechnology have substantially transformed the research field of phytopathology during past two decades. The establishment of the fundamental framework of plant innate immunity (Dodds and Rathjen, 2010) has provided a springboard for molecular dissection of the interactions between key crop species and diverse phytopathogens. The application of next-generation sequencing technologies in major domains of phytopathology research has advanced the understanding of the transcriptome reprogramming of plant disease resistance or susceptibility, the composition of plant-associated microbiomes, and the genetics underlying the quantitative variation in disease resistance across host populations. Successful examples of engineering disease resistance by editing host susceptibility gene (Wang et al., 2014) or interfamily transfer of pattern recognition receptors (Lacombe et al., 2010) have opened new avenues for the development of durable resistance in crop species that can be integrated into sustainable disease management. On the other hand, certain previously considered minor crop diseases may have emerged as major concerns for yield production and plant pathologists (Zhang et al., 2014); likewise, increasingly enhanced connectivity among countries, regions, and continents may raise new challenges for phytopathologists to prevent the spread of devastating plant pathogens. Hence, phytopathology is still an expanding discipline full of exciting prospects and challenges that calls for close communication among scientists.

To embrace the dynamic changes in the field and rapid increase in the number of publications, the Chinese Society for Plant Pathology (CSPP), affiliated with China Agricultural University (CAU), in collaboration with the leading Open Access brand BMC (part of Springer Nature), launch the journal of *Phytopathology*

*Research (PR)*. The journal aims to provide an excellent platform on which phytopathologists from worldwide can exhibit insightful discoveries by publishing high-quality original research papers and review articles on both fundamental and applied research on all aspects of plant pathology. For details of the Aims and Scope of the journal, please check with our website: <https://phytopatholres.biomedcentral.com>. Currently, PR is preparing a thematic series on the Virus-Host interaction, and will subsequently release other thematic series as needed.

We have assembled an international Editorial Board consisting of a group of highly experienced frontline scientists whose commitments to the journal guarantee the unbiased, constructive, and timely delivery of peer reviews. All contributions will be published online promptly after acceptance and proofreading. It is not possible to deliver the first batch of articles of this brand new journal without the joint efforts of all the dedicated editorial board members, enthusiastic authors, and international colleagues. We truly appreciate those who gave us strong support in the preparation for launching of the journal.

We are publishing several review and full research articles to mark the launch of *Phytopathology Research*.

In *NAC transcription factors in plant immunity*, Yuan et al. have summarized recent progress of NAM, ATAF, and CUC (NAC) transcription factors (TFs) in plant immunity, and drawn up a list of each NAC acting as an activator or a suppressor on a specific pathogen via particular defensive pathways as well as target genes. NAC TFs have been shown to be modulators of plant hypersensitive responses and stomatal immunity, players of phytohormones-related signaling, targets of pathogen effectors, and components of the regulatory complex. NAC TFs enable binding to diverse DNA elements regulating many target genes and also are regulated at transcriptional and post-transcriptional levels. Yuan et al. also pointed out the directions for further studies for the

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molecular mechanism of NAC TFs in plant defense responses and their potential application in the improvement of disease resistance.

In the research article **A glycine-rich protein MoGrp1 functions as a novel splicing factor to regulate fungal virulence and growth in *Magnaporthe oryzae***, Gao et al. report functional characterization of a novel gene encoding a glycine-rich RNA-binding protein, MoGrp1, that has an N-terminal RNA recognition motif (RRM) and a C-terminal glycine-rich domain with four Arg-Gly-Gly (RGG) repeats, in the rice blast fungus *Magnaporthe oryzae*. The authors showed that deletion of the gene had pleiotropic effects on fungal development, stress responses, and virulence. An elegant series of experiments on its nuclear localization, interaction with splicing factors, and binding activity to poly(U) strongly suggest the importance of MoGrp1 in splicing-related processes and fungal development. These findings would provide new insights into the molecular mechanism of RNA splicing and pathogenicity in the rice blast fungus.

Morris and colleagues have investigated the host range tests for 134 strains of *Pseudomonas syringae*, representing eight phylogroups, on many plant species in **The overlapping continuum of host range among strains in the *Pseudomonas syringae* complex**. The authors have observed that the individual strains in the *P. syringae* complex constitute an overlapping continuum of potential host ranges with roughly equal representation of those with narrow, intermediate and broad host ranges. The authors present an alternative perspective to the current most acceptable understanding of pathotypes of *P. syringae*. The authors also observed that the extent of host range is positively correlated with the capacity of strains to swarm on semi-solid agar medium and with the abundance of genes in biosynthetic clusters and is inversely correlated with the abundance of genes for proteins with transmembrane domains in their genomes. This is an interesting association, which needs an experimental test. The interesting observations and interpretations of the host range of *P. syringae* by Morris et al. will surely stir further discussion in this important topic to advance our understanding of bacteria and plant interactions.

We hope you enjoy reading the first series of papers, and cordially invite you to share with other readers your experiences, discoveries, and insights on phytopathology research. We look forward to your submissions.

#### Authors' contributions

The authors read and approved the final manuscript.

#### Competing interests

The authors declare that they have no competing interests.

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#### References

- Dodds PN, Rathjen JP. Plant immunity: towards an integrated view of plant-pathogen interactions. *Nat Rev Genet.* 2010;11:539–48.
- Lacombe S, Rougon-Cardoso A, Sherwood E, Peeters N, Dahlbeck D, van Esse HP, et al. Interfamily transfer of a plant pattern-recognition receptor confers broad-spectrum bacterial resistance. *Nat Biotechnol.* 2010;28:365–9.
- Wang Y, Cheng X, Shan Q, Zhang Y, Liu J, Gao C, et al. Simultaneous editing of three homoeoalleles in hexaploid bread wheat confers heritable resistance to powdery mildew. *Nat Biotechnol.* 2014;32:947–51.
- Zhang Y, Zhang K, Fang A, Han Y, Yang J, Xue M, et al. Specific adaptation of *Ustilaginoidea virens* in occupying host florets revealed by comparative and functional genomics. *Nat Commun.* 2014;5:3849. <https://doi.org/10.1038/ncomms4849>.

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