

## The Journal of Plant Pathology Editors' Choice February 2023

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Papers included in the February 2023 Editors' Choice (EC) section of the Journal of Plant Pathology follow three major themes, ranging from the investigation of disease severity and symptoms on novel hosts, to the understanding of the genetic mechanisms resulting in disease symptoms, and, finally, to the testing of novel strategies to control plant diseases. Papers in each of the three themes, though, are particularly interesting for a variety of reasons. Collectively, the papers in the EC section of this issue come from China, Iran, Kenya, Oman, South Africa and the USA.

The two papers belonging to the first theme focus on a virus and a fungal pathogen, respectively, that are not only little known but are also both vectored by insects. Insect transmission certainly puts these pathogens in a higher-risk category and this epidemiological feature provides an additional reason justifying their inclusion or potential inclusion in the list of regulated pests by the European Union and a few other countries. Detailed information on their host range and symptomatology is thus urgently needed to perfect containment measures and early diagnosis. Genomic data can also be used to reconstruct the movement pathway of disease agents and, in turn, this knowledge can be pivotal to identify differences in disease symptoms and severity caused by strains of different origin, and to understand which commodity or geographic pathways need to be closely monitored to prevent introductions and reintroductions of each specific pathogen.

The knowledge of how a pest causes a disease can provide information that may be essential to identify more aggressive strains and possibly effective disease control strategies. Two papers detail research aimed at understanding the molecular mechanisms responsible for disease development in a staple world crop, potato, and in fruit trees. The paper focusing on Early Blight of potato caused by two *Alternaria* spp. identified a toxin and an elicitor both responsible for disease symptoms development. While it is true that the symptoms studied are normally associated with diseases, in some cases, extreme disease development amounts to what could be called an hypersensitive response, possibly associated with reduced disease progress. The study

identifies several fungal proteins associated with specific plant responses and also leads to a possible conclusion that variable genic expression, leading to substantially difference in the amount of a protein, may result in different disease phenotypes. This result reinforces that resistance can be both a qualitative and/or a quantitative response. The second paper focuses on variability of disease severity by comparing two strains of a phytoplasma and three different fruit tree species. Results point to the presence of significant differences in virulence among strains of the pathogen and in susceptibility among the three fruit tree species tested, and identify an homologue to the SAP11 effector, known to play an important role in pathogenesis. The study allows to make predictions on the severity of disease outbreaks, depending on the phytoplasma strain and on the specific fruit tree species present in orchards.

The correct diagnosis of pathogens, the understanding of host specificity at all taxonomic ranks of a plant, the correlation between certain proteins or metabolites and disease severity are all important, but in the end, they are all meant to help in formulating the best available disease control strategies. The third theme of the EC papers of this issue has to do with disease management. The selected papers truly investigate novel approaches to control disease. Both look at the potential of endophytic organisms to improve crop yield. The first paper focuses on disease control on saline environments. Salinity is currently a mounting problem, exacerbated by intensive cropping systems and by climate change affecting depth of the water table. Solutions to diseases in saline environments are urgently needed, and this EC paper proves that the application of certain endophytic bacteria results in a staggering 82% disease reduction, specifically in saline environments. A second paper, instead, proved the growth promoting potential of two fungal endophytes and identifies volatiles involved in such effects.

A more detailed synopsis of the EC papers follows, with papers grouped by theme. In “Pathogenicity of *Fusarium euwallaceae*, symbiont of the polyphagous shot hole borer beetle, to selected stone fruit trees in South Africa”, de Jager and Roets (South Africa) focused on the aetiology and

epidemiology *Fusarium euwallaceae*, the most relevant and little known fungal associate of the invasive ambrosia beetle *Euwallacea fornicates*. The authors were able to show that both nectarine (*Prunus persica*) and plum (*P. domestica*) are hosts of the pathogen and that the rate of lesion development was independent of both branch diameter and inoculum load. The study adds pivotal pieces of information on this disease and may help reducing uncertainties in risk assessments which are currently ongoing in Europe.

High-throughput sequencing (HTS) on composite survey samples is used by Kinoga and collaborators (Kenya and USA) in the paper titled “Genome characterisation of two complete coding sequences of tomato mild mottle virus from tree tomato and their distribution in Kenya” to provide novel information on a poorly known virus. Tomato mild mottle virus (ToMMV), a whitefly-transmitted member of the *Ipotomovirus* genus was first identified in Yemen in solanaceous hosts in the early 1990's. It has since then been identified in similar hosts in Israel and in Ethiopia. It is today considered a quarantine virus for the European Union and a few other countries. An unpublished entry in GenBank indicated in 2016 its presence in a valuable fruit crop originating from south America, tree tomato (tamarillo, *Solanum betaceum*) in Kenya, prompting the investigation by Kinoga et al. HTS analysis of two pools of samples collected during surveys in 9 tamarillo-growing counties of Kenya revealed the presence of ToMMV and of potato virus Y (PVY) and allowed the assembly of two ToMMV nearly complete genomes. Sequence comparisons indicate that the Kenyan isolates are closely related to an Ethiopian one. RT-PCR assays confirmed the presence of ToMMV and PVY in tamarillo samples from two farms. Unfortunately, all ToMMV-infected plants were also found to be infected by PVY and it was not possible to ascertain the contribution of ToMMV alone to the symptoms observed. The issue of the symptomatology on ToMMV in tamarillo therefore remains an open question. Taken together these results illustrate the power of HTS approaches on composite survey samples for viral surveillance and provide needed information on a quarantine agent for which precious little information is available.

In their study titled "Differential plant response to toxins and elicitor proteins released by the potato and tomato pathogens *Alternaria solani* and *Alternaria alternata*", Jones and Perez (USA) clarified some aspects of pathogenesis and symptoms development of early blight of potato and tomato, which is an economically important disease mainly caused by *Alternaria* spp. The authors were interested in understanding why sometimes necrotic spots on leaves associated with the disease are surrounded by halo of chlorotic tissue. Experiments consisting of infiltration of leaves with *Alternaria*-associated toxins and potential elicitor proteins revealed that two anthraquinones, bostrycin and altersolanon A, elicited a strong necrosis-mediated response. In addition,

infiltration of leaves by *Agrobacterium* to express previously identified putative elicitor proteins demonstrated that *A. solani* Hrip1 induces expanding tissue death and development of chlorotic halos, thereby providing strong evidence in support of the role of this elicitor in the pathogenesis and symptoms development of this relevant disease. We would like to underline the interesting use of transformed *Agrobacterium* to recreate a more realistic genic expression in model pathosystems.

Almond witches'-broom (AlmWB) is a relevant phytoplasma of stone fruit trees associated with the presence of '*Candidatus* Phytoplasma phoenicium' (16SrIX-B) reported from Iran and Lebanon. The team of authors from Shahrood University in Iran investigated the symptom expression of different AlmWB strains. In their paper “Response of *Prunus* species to graft-inoculation by two Iranian strains of almond witches'-broom phytoplasma”, the authors graft-inoculated seedlings of various stone fruit tree species including three almond cultivars. This type of study is rarely performed because biological testing of fruit trees is a long process with many challenges and results that are sometimes difficult to evaluate. The authors showed a differential expression of symptoms by two different AlmWB strains in the tested stone fruit tree species enriching knowledge on the phytoplasma biology. In their effort to link symptom expression with phytoplasma genetic blueprint, they took the analyses a step further. They sequenced a SAP11 homologue from their AlmWB strains and compared them with other SAP11 effector proteins which are known to be important in the phytoplasma symptom development and infection. We are still far from knowing the determinants of AlmWB strain “aggressiveness” and other facets of phytoplasma-host interaction; however, this small step helps building our research foundations.

In "The potential of endophytic bacteria from *Prosopis cineraria* for the control of *Pythium aphanidermatum*-induced damping-off in cucumber under saline water irrigation" Al-Rashdi et al. (Oman) elegantly investigated possible solutions for the cultivation of cucumber in highly saline soils at risk of damping-off caused by *Pythium aphanidermatum*. To maximize the chance of identifying salt-tolerant biological control agents, they screened endophytic and rhizospheric bacteria from *Prosopis cineraria*, a halophyte plant. They were able to identify four bacteria that *in vitro* were active against *P. aphanidermatum*. Among these putative biocontrol agents, the authors identified a strain of *Pseudomonas aeruginosa* that releases volatile compounds active against the pathogen. Greenhouse tests revealed that while soil application of these bacteria had no significant effect on damping-off incidence under non-saline irrigation, they had significant effects and reduced disease incidence, up to 82%, under saline water irrigation. The results presented by Al-Rashdi et al. are particularly relevant because they

provide new options for the disease control under salt-stress conditions, an emerging problem in agriculture.

One of the most intriguing fields of research in the last years is that of the microbiota associated with plants and of its effects on plant health. In the paper titled "Identification of volatile components and growth promoting effects of endophytes of *Tinospora capillipes* Gagnep." by Li et al. (China), endophytes of *Tinospora capillipes* Gagnep. were screened to explore their promoting effects on plants. Two fungal endophytes were identified as possessing various extracellular enzyme activities, phosphorus hydrolysis and low Indole-3-acetic acid (IAA) production capacity. The application of inocula of both fungi, and especially of *Arthrinium phaeospermum*, had obvious promoting effects on soybean seeds rooting, thereby providing the foundation for further testing of these green biocontrol strains.

We hope you will enjoy the papers selected by the Editors for the EC section of the February 2023 issue of the Journal of Plant Pathology and we invite you to join us in complimenting the authors for their achievements.

Matteo Garbelotto, Editor in Chief

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