

# INTERNATIONAL NEWSLETTER ON PLANT PATHOLOGY

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News and announcements from all on any aspect of Plant Pathology are invited for the Newsletter. Contributions from the ISPP Executive, Council and Subject Matter Committees, Associated Societies and Supporting Organisations are requested.

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## Are you appy?

There is, as they say, "an app for everything!" Apps are continuously being developed and revised. But finding the most useful ones can be challenging and frustrating. To make the world of apps easier for us all, I would like to invite reviews on any plant pathology related apps that you have found particularly useful and/or interesting that are of global appeal. I will endeavour to publish these in the next forth coming issues of ISPP Newsletter. You may have noticed the [MyCrop](#) and the [Plant Doctor Game](#) apps were featured in previous issues, and I would love to build on this knowledge of useful and interesting apps that are currently available.

Looking forward to your appy submissions!

Daniel Hüberli

## Plant virus metagenomics: Advances in virus discoveries

"In recent years plant viruses have been detected from many environments, including domestic and wild plants and interfaces between these systems-aquatic sources, feces of various animals, and insects. A variety of methods have been employed to study plant virus biodiversity, including enrichment for virus-like particles or virus-specific RNA or DNA, or the extraction of total nucleic acids, followed by next-generation deep sequencing and bioinformatic analyses. All of the methods have some shortcomings, but taken together these studies reveal our surprising lack of knowledge about plant viruses and point to the need for more comprehensive studies. In addition, many new viruses have been discovered, with most virus infections in wild plants appearing asymptomatic, suggesting that virus disease may be a byproduct of domestication. For plant pathologists these studies are providing useful tools to detect viruses, and perhaps to predict future problems that could threaten cultivated plants."

A new review by M.J. Roossinck, D.P. Martin and P. Roumagnac published in *Phytopathology* in June 2015 (vol. 105, pp. 716-727).

[Read more.](#)

## 3rd International Postharvest Pathology Symposium: Using science to increase food availability, 7-11 June 2015

The 3rd International Postharvest Pathology Symposium, organised by Prof. Antonio Ippolito, University of Bari Aldo Moro, was held in Bari, Italy, from 7-11 June 2015. The theme of the symposium was "Using science to increase food availability." The highly successful symposium was attended by 200 delegates from 41 countries including many students, young scientists as well as known established researchers. This was the biggest

gathering in the field of postharvest pathology ever convened. It was a joint symposium of the Postharvest pathology subject matter committee of the ISPP and the ISHS working group on biological control of postharvest diseases. In the opening ceremony address, Prof. Antonio Ippolito, the convener of the symposium, and Prof. Samir Droby, the chair of the Postharvest Pathology subject matter committee of the ISPP, emphasised the importance of such a symposium in light of the challenges in reducing food losses after harvest. There was also two guest inaugural invited lectures on next generation sequencing for next generation crops given by Prof. Massimo Delledonne and science and social media and how to avoid feeding the troll and save your time given by Lorenzo Mannella.

The scientific program included 58 oral presentations among which 17 were invited speakers and 121 posters. Sessions were dedicated to new advances in various technologies that are changing the way we look at pathogens and the disease process involved in host-parasite interactions. Technical sessions included: Studies on host-pathogen interactions, microorganisms as biocontrol agents, the microbiome and its relation to postharvest pathology, toxic fungal metabolites and postharvest pathology, epidemiology and detection of postharvest pathogens, alternative means for management of postharvest pathogens, and integrated approaches and new products to reduce food waste. There were also two round table discussions about fruit microbiome led by Prof. Samir Droby and innovations in management of table grape postharvest diseases led by prof. Antonio Ippolito.

The social program included symposium gala dinner at a beautiful restaurant on the Adriatic sea shore. During the event three awards for the best posters presented in each of the symposium were given. There was also enjoyable full day tour to Giuliano srl packinghouse, tasting of locally-produced organic food, a visit to Alberobello which is a monumental Trulli village of the 1400's and a UNESCO world heritage site since 1996, and a tour of Polignano a Mare, a fascinating medieval village perched on a high jagged coastline with many caves.

During the business meeting held at the end of the symposium, there was full agreement to establish biannual meetings on the subject of postharvest pathology in order to foster exchange of knowledge and collaboration between members of the international postharvest pathology community. The next meeting will be held in South Africa in 2017.



Attendees at the 3rd International Postharvest Pathology Symposium in Bari, Italy.



Members of the postharvest pathology sub-management committee of the ISPP, left to right, Kerry Everett (Deputy chair), Davide Spadaro (Secretary), Antonio Ippolito (the convener of the symposium), Samir Droby (Chair), and Lisa Korsten (Deputy chair).

(Samir Droby)

### **Population biology of plant pathogens - APS Press book**

Population biology is a constantly evolving sub-discipline of plant pathology, and few comprehensive books have ever been written on the topic, let alone recently. A new title from APS PRESS, *Population Biology of Plant Pathogens: Genetics, Ecology, and Evolution*, fills this information void by explaining in detail how population genetics are applied in plant pathology today.

Author Michael G. Milgroom, a pioneer and leading researcher in this field, offers the very latest information on population biology, population genetics, and the evolution of plant pathogens of all major types, including fungi, oomycetes, bacteria, viruses, and nematodes.

Early chapters of the book address foundational concepts in population genetics, such as genetic markers, genetic diversity, mutation and random genetic drift, natural selection, and migration and population structure. Later chapters cover recombination and clonality; gene-for-gene systems and disease resistance; emerging plant diseases; and applications of population biology in epidemiology and applied agriculture.

Sidebars, a glossary of key terms, summaries of main concepts, a list of commonly used abbreviations, recommended readings, and a comprehensive index are also incorporated for maximize learning and comprehension.

This comprehensive, 414 page book is especially ideal for teachers and students of graduate level plant pathology courses. Researchers and population biologists in plant pathology and related fields will also find this book an important tool. Visit [www.shopapspress.org](http://www.shopapspress.org) to learn more about this and other important titles from APS Press.

(APS Press, Press release)

### **Seven common mistakes in population genetics**

A opinion article by P.G. Meirmans "Seven common mistakes in population genetics and how to avoid them" was published in July 2015 by *Molecular Ecology* (vol. 24, pp. 3223-3231). The abstract is as follows:-

As the data resulting from modern genotyping tools are astoundingly complex, genotyping studies require great care in the sampling design, genotyping, data analysis and interpretation. Such care is necessary because, with data sets containing thousands of loci, small biases can easily become strongly significant patterns. Such biases may already be present in routine tasks that are present in almost every genotyping study. Here, I discuss seven common mistakes that can be frequently encountered in the genotyping literature: (i) giving more attention to genotyping than to sampling, (ii) failing to perform or report experimental randomization in the laboratory, (iii) equating geopolitical borders with biological borders, (iv) testing significance of clustering output, (v) misinterpreting Mantel's  $r$  statistic, (vi) only interpreting a single value of  $k$  and (vii) forgetting that only a small portion of the genome will be associated with climate. For every one of those issues, I give some suggestions how to avoid the mistake. Overall, I argue that genotyping studies would benefit from establishing a more rigorous experimental design, involving proper sampling design, randomization and better distinction of a priori hypotheses and exploratory analyses.

See: <http://dx.doi.org/10.1111/mec.13243>

### **Canadian Phytopathological Society News**

The June 2015 issue of the [Canadian Phytopathological Society News](#) is now available online.

(Deena Errampalli)

### **Mycorrhizae living with mysterious bacteria**

New research sheds light on a class of bacteria found living within mycorrhizal fungi. A Cornell study, published in May 2015 in the [Proceedings of the National Academy of Sciences](#), found these so-called mycoplasma-related endobacteria (MRE) operate with minimal genomes, likely because their fungal hosts provide crucial services for the bacteria's survival. Furthermore, the researchers found that the bacterial genomes had acquired genes transferred from the arbuscular mycorrhizal fungi, which could help the bacteria manipulate their fungal hosts, though more study is needed.

The researchers are conducting experiments to better understand the functional roles of the bacteria in the fungi. Both the host fungi and their endobacteria are very hard to grow in the lab, due to inadequate growth media, so both the fungi and bacteria were grown with plants for study.

Further understanding of these relationships has important implications for developing tools for sustainable agriculture.

(Cornell Chronicle, 27 June 2015)

### **Molecular mechanisms underlying pathogenicity in bacteria and their environmental drivers**

A microreview by C. Bartoli, F. Roux and J.R. Lamichhane titled "Molecular mechanisms underlying the emergence of bacterial pathogens: an ecological perspective" was published online in June 2015 by Molecular Plant Pathology. The abstract is as follows:-

The rapid emergence of new bacterial diseases negatively affects both human health and agricultural productivity. While molecular mechanisms underlying these disease emergences are shared between human and plant pathogenic bacteria, not much effort has been made to date in understanding disease emergences due to plant pathogenic bacteria. In particular, there is a paucity of information in the literature on the role of environmental habitats where plant pathogenic bacteria evolve and on the stress factors to which these microbes are unceasingly exposed. In this micro-review, we focus on three molecular mechanisms underlying pathogenicity in bacteria; namely mutations, genomic rearrangements and the acquisition of new DNA sequences through horizontal gene transfer (HGT). We briefly discuss the role of these mechanisms on bacterial disease emergence and elucidate how the environment can influence the occurrence and regulation of these molecular mechanisms by directly impacting disease emergence. The understanding of such molecular evolutionary mechanisms and their environmental drivers will represent an important step towards predicting bacterial disease emergence and developing sustainable management strategies for crops.

See: <http://dx.doi.org/10.1111/mpp.12284>

### **Yeasts on plums have a plus side**

Some naturally occurring yeasts may be useful for protecting stone fruits against pathogens that attack after harvest. Scientists at the U.S. Department of Agriculture (USDA) looked to the microflora on the surface of the plum to find potential biocontrol agents against brown rot.

At the Agricultural Research Service (ARS) Appalachian Fruit Research Station in Kearneysville, West Virginia, plant pathologist Wojciech Janisiewicz and his colleagues determined that the plum surface harbors several yeast species with excellent potential for use as biological controls against brown rot of stone fruits caused by the fungus *Monilinia fructicola*. Fruit surfaces are naturally colonised by a variety of microbes, including bacteria and yeast. Some of those native microorganisms have been shown to have a beneficial effect on reducing fruit decay after harvest.

In previous efforts, Janisiewicz developed a bacterium normally found on apples into a commercial biological control product that can be used instead of fungicides to control pome fruit diseases. The product is also allowed in organic marketing. A lot of information exists about the benefits of natural fruit microflora on grapes and apples, but for plums, the extent of their potential for biological control of fruit decay remains largely unknown.

The research team identified yeasts naturally colonising plums from early fruit development until harvest and explored their potential for controlling postharvest brown rot, the most destructive disease of stone fruits. Through multiple screenings, Janisiewicz and his colleagues found yeasts with a range of biocontrol activities

against *M. fructicola*, including several isolates that provided complete control on plums from decay caused by this fungus.

Two of the best control candidate species were *Aureobasidium pullulans* and *Rhodotorula phylloplana*. Developing these yeasts into commercial products will provide growers with an alternative approach for combating brown rot after harvest, and this approach should be compatible with requirements for the rapidly growing organic market.

[Read more.](#)

(Sharon Durham, AgResearch Magazine, June 2015)

### **Plant receptors with built-in decoys that make pathogens betray themselves**

The research group headed by Professor Jonathan Jones at The Sainsbury Laboratory has discovered plant receptors carrying built-in decoys that detect pathogens and raise the cell's alarm during infection.

Pathogens target the plant's defense machinery to stop immune response. Plants have evolved to display these targets on receptors that are primed to set off their alarm system. When the pathogen binds, the receptor starts the process of shutting down the cell to contain the pathogen and stop it from spreading. The research of Professor Jones' group shows one way in which plants perceive pathogens, which is essential to their immunity.

Professor Jones hopes that the group's discovery could lead to bioengineering new receptors carrying decoys to perceive and trigger a defense to virtually any pathogen. Professor Jones said, "This is a very exciting discovery. It turns out as we survey the genomes of other plants we can see many more such "integrated decoy" domains associated with immune receptors, so we believe this observation will turn out to be of widespread significance."

Read the paper '[A plant immune receptor detects pathogen effectors that target WRKY transcription factors.](#)'

(The Sainsbury Laboratory News, 21 May 2015)

### **New vacant position**

Senior Plant Pathologist, IITA, (Ref No: DDG-R4D/SPP/07/14) [read more](#)

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