

November 2018. Plant pathology professionals at all levels should promote the IYPH with their counterparts in civil society, industry and government and should consider events and actions to be undertaken during the IYPH.

Molecular Mechanism of Strawberry Fusarium Wilt Suppressive Soil

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Crops lack genetic resistance to most necrotrophic pathogens. To compensate for this disadvantage, plants recruit antagonistic members of the soil microbiome to defend their roots against pathogens and other pests. The best examples of this microbially based defense of roots are observed in disease-suppressive soils in which suppressiveness is induced by continuously growing crops that are susceptible to a pathogen, but the molecular basis of most is poorly understood. Here we report the microbial characterization of a Korean soil with specific suppressiveness to Fusarium wilt of strawberry. In this soil, an attack on strawberry roots by *Fusarium oxysporum* results in a response by microbial defenders, of which members of the Actinobacteria appear to have a key role. We also identify Streptomycetes genes responsible for the ribosomal synthesis of a novel heat-stable antifungal thiopeptide antibiotic inhibitory to *F. oxysporum* and the antibiotic's mode of action against fungal cell wall biosynthesis. Both classical- and community-oriented approaches were required to dissect this suppressive soil from the field to the molecular level, and the results highlight the role of natural antibiotics as weapons in the microbial warfare in the rhizosphere that is integral to plant health, vigor and development.

Identification of a torradovirus-encoded protein that complements the systemic movement of a potyvirus lacking the TGB3 gene

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Cassava torrado-like virus (CsTLV, Family *Secoviridae*) is found in mixed virus infections associated with severe disease symptoms in leaves and roots of cassava (*Manihot esculenta* Crantz, Euphorbiaceae), which is an important staple food crop for Africa, Asia and Latin America. The virus has been reported in Colombia, Peru and Argentina, where it has a significant effect on the accumulation of total sugars in cassava storage roots. CsTLV encodes an atypical Maf/HAM1 domain not found in other torradovirus genomes, but is present in heterologous viruses of the family *Potyviridae* also infecting euphorbiaceous hosts. Most viruses encode RNA silencing suppressors (RSS) to counteract the RNA silencing-based plant defense system. However no RSS has been yet identified in torradoviruses. To advance the characterization of CsTLV, agroinfiltration in *Nicotiana benthamiana* leaves of different viral genes was carried out using GFP as a reporter. Like the Maf/HAM1 domain found in *Cassava brown streak virus* (CBSV; Genus: *Ipomovirus*), the one encoded by CsTLV did not show RSS activity. On the other hand, we found that agroinfiltration of RNA2-ORF1 had a significant effect in the establishment of systemic infection by *Cassava virus X* (CsVX; Genus: *Potexvirus*), a virus lacking one of the Triple Gene Block genes (TGB3), which is involved in potexvirus movement. Although we observed that single infection of CsTLV increased the expression of GUS in of GUS-transgenic cassava lines, none of the CsTLV genes in this study showed RSS activity.

Rice hormone response is involved in the temperature-dependent function of Xa7-mediated bacterial blight resistance

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Bacterial blight, caused by *Xanthomonas oryzae* pv. *oryzae* (Xoo), causes significant losses to global rice production. Bacterial blight disease is more severe during periods of high temperature. However, little is known about the underlying host molecular responses to pathogen infections during high temperature stress. Most known mechanisms of rice resistance to bacterial blight lose efficacy at high temperature, but, notably, one resistance gene, *Xa7*, functions better. To provide insights into how *Xa7* directs the host response at high temperature, we conducted a transcriptomics experiment. Plants exhibiting resistance at high temperature significantly down-regulated the abscisic acid signaling pathway, which is important to abiotic stress responses, while plants in a susceptible interaction did not. Intriguingly, the salicylic acid response – an important pathway in rice defense to Xoo – was down-regulated at high temperatures in all interactions, suggesting that enhanced *Xa7* activity at high temperature is independent of salicylic acid-mediated defense pathways. These results suggest that plants exhibiting *Xa7*-mediated resistance prioritize response to pathogen over response to abiotic stress. This ongoing study is providing insight into the trade-off between disease resistance and plant productivity that will help in the development of rice varieties in a changing climate.

Transcriptome sequencing reveals novel Citrus bark cracking viroid (CBCVd) variants from citrus and their molecular characterization

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Citrus bark cracking viroid (CBCVd) has been identified as an important causative agent on citrus and hop. In this study, we obtained the full-length genomes of different variants of citrus viroids from Pakistan through transcriptome sequencing. CBCVd variants were first found in Pakistan. These newly discovered Pakistani CBCVd variants were provisionally named as 'CBCVd-LSS' for their low sequence similarity (80.9%-88.9%) with the CBCVd RefSeq sequence (NC_003539). Two most predominant CBCVd sequences from Pakistan had the highest, 91% and 88% identity with two CBCVd sequences isolated from hop, respectively. Identification and molecular characterization of CBCVd from citrus in Pakistan and China were also reported. The length of CBCVd from China ranged from 282 to 286 nucleotides, while from Pakistan it ranged from 273 to 277 nucleotides. Based on genetic diversity and phylogenetic analysis, two main CBCVd clades were identified. CBCVd sequences were further divided into six sub-clades. Sequence alignment revealed some nucleotide changes between these sub-clades, and analysis indicated that several mutations could significantly affect the primary and secondary structure of the viroid. Our results indicated that the CBCVd sequences from Pakistan and China were significantly different and Pakistan might be one of the independent geographical origins of CBCVd worldwide.

Global wheat stem rust monitoring: Meeting the challenges of a re-emerging threat to wheat production

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