Plant Health 2022
Abstracts of Presentations

Abstracts submitted for presentation at the APS Plant Health 2022 Annual Meeting held in Pittsburgh, Pennsylvania, August 6–10, 2022. The recommended format for citing annual meeting abstracts, using the first abstract below as an example, is as follows:

Gonzalez-Giron, J. L., and Smart, C. D. 2022. Characterization of bacterial spot of tomato in New York show a predominance of *X. perforans* and offers an insight into copper tolerance. (Abstr.) Phytopathology 112:S3.1. https://doi.org/10.1094/PHYTO-112-11-S3.1

The abstracts are published as a supplement to *Phytopathology* for citation purposes. They were not reviewed by the *Phytopathology* Editorial Board and were not edited by the APS editorial staff.

https://doi.org/10.1094/PHYTO-112-11-S3.1
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Characterization of bacterial spot of tomato in New York show a predominance of *X. perforans* and offers an insight into copper tolerance
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Bacterial spot dramatically reduces the productivity and marketability of tomato and pepper crops across the US. The disease is predominantly attributed to two species in the *Xanthomonas* genus comprising three pathovars, *X. euvesicatoria* pv. *euvesicatoria*, *X. euvesicatoria* pv. *perforans*, and *Xanthomonas hortorum* pv. *gardneri*. While *X.h. gardneri* has been associated with spot outbreaks across the Midwest, the *X. euvesicatoria* pathovars have been reported as being prevalent in warmer regions. Recent population analyses show evidence of a shift towards *X.e. perforans* being the predominant causal agent of bacterial spot, however, it is not the only species present. To understand pathogen diversity in New York, 48 isolates collected between 2003 and 2020 across the State were identified, showing both *X.h. gardneri* and *X.e. perforans*. A phylogeny resulting from a whole-genome analysis of a subset of New York isolates and 190 publicly available bacterial spot genomes showed diversity within the isolates collected, which might correspond to inoculum being introduced in seeds or transplants. Additionally, we observed the presence of large operons containing genes for heavy metal efflux pumps and other biocides, which correlated to resistance in a growth assay on copper-amended media. Overall, we show that bacterial spot in New York is caused by two bacterial species, similar to what has been observed in other locations. Future studies will enable a further understanding of the causal organisms of bacterial spot of tomato in New York.

Data standardization can boost collaborative efforts in plant pathology research: Current state of the art with application to SDS prediction modeling
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Disease onset in field crops is affected by several factors, including environment, pathogen intensity, host genetics, and management practices. These factors impose an immense parameter space that needs to be explored and understood to facilitate efficient mitigation efforts. Addressing this task necessitates a collaborative approach within the agricultural community, which can be hampered by a myriad of data sources, formats and notations used by the participating groups. Data standardization platforms streamline collaborations, enable efficient research progress, and help capitalize on the availability of large datasets. This presentation will provide an overview of available research data standardization tools and explain the underlying data management principles. Using the Axiom platform (by Agmatix) as an example, observational data of sudden death syndrome (SDS, caused by *Fusarium virguliforme*) in soybean from 7 states in the US and Canada (2472 observations), collected between 2013–2016, was used to develop a machine learning prediction model. The model, built as an ensemble of decision trees, was able to predict SDS occurrence with an accuracy of 80% across the different production environments. Sensitivity analysis found the key factors affecting SDS in our data: i) crop genetics,

Resistance to SDHI fungicides in *Alternaria* populations was reported rapidly after their registration and use on pistachio. In California, six mutations, among which SdhC-H134R and SdhB-H277Y were the most frequent, are associated with fungicide resistance. A real-time PCR (qPCR) assay to quantify the frequency of these mutations within the *Alternaria* populations was developed. Primers were designed and standard curves that allow quantification of DNA for wild-type and mutant genotypes were established. The qPCR assay was verified using known densities of DNA mixtures. The qPCR protocol was then applied to determine the fungicide resistance levels in California orchards. The frequency of both mutants was determined by qPCR and compared with that obtained using a fungicide discriminatory dose. The frequency of H134R mutants was much higher than that of H277Y mutants. Orchards with the highest mutant frequencies also had the highest proportion of resistant isolates. The effect of two commercial fungicide programs on the resistance levels was also studied using this protocol. One program used products formulated with SDHI and QoI fungicides, while the other program used DMI and AP fungicides. The program using SDHI fungicides did not significantly increase the frequency of resistant mutants and controlled Alternaria late blight disease better than the DMI/AP program. A qPCR protocol to quantify the frequency of mutant conferring SDHI resistance was developed. This will serve to monitor resistance levels in the orchards and design management strategies accordingly.

Translating cropland and trade connectivity for mitigation of emerging pathogens: Priority locations globally and focusing on the Americas

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Analyses of crop-specific cropland and trade network structures provide a first step for guiding strategies to manage emerging crop pathogens, for iterative improvement as more detailed data become available. We analyzed global to regional cropland and trade networks for the potential spread of emerging pathogens in twelve crops key to food sustainability. We identified which locations have high cropland connectivity globally, and in a more detailed analysis for Central America. A location with high cropland connectivity is more likely to have an important role in epidemics, and so is a candidate for prioritizing mitigation. In epidemic scenario analyses to evaluate relative risk for each crop, we identified countries in the Americas with cropland patterns more likely to result in high levels of pathogen establishment, and so more likely to need focused attention to manage invasions. Country-specific trade networks indicate how invasion risk varies among crops and pathogens, and which components of the network merit particular phytosanitary attention. Using these maps of risk for planning in advance can inform phytosanitary strategies globally, regionally, and within countries, for an efficient response to epidemic invasion. Integrating cropland and trade connectivity with other geographic factors – such as weather conduciveness, management landscapes, regional transportation, local trade, and international phytosanitary networks, will strengthen pest risk assessment and mitigation.

The *diageotropica* (*dgt*) mutation contributes to tomato resistance to *Ralstonia solanacearum* through an SA-independent mechanism

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Bacterial Wilt (BW) is among the most devastating plant diseases in the world. This disease is caused by the soilborne plant pathogen *Ralstonia solanacearum* (*Rs*) and affects more than 200 species of plants. In tomato, resistance to *Rs* is quantitative and the result of many genes and no resistance genes to the US *Rs* strain K60 have been identified in tomato. Transcriptomic analysis of resistant tomato roots showed that at 48 hours post inoculation with *Rs*K60, genes involved in auxin transport and signaling pathways are downregulated. A tomato mutant defective in auxin transport and signaling, known as *diageotropica (dgt)* has enhanced resistance to *Rs*K60. Auxin acts antagonistically with the plant hormone Salicylic Acid (SA), and we have found that *dgt* roots have endogenously higher levels of SA and a strain of *Rs* that can degrade SA is partially virulent on *dgt*. However, after inoculation with *Rs*K60, the expression of SA-dependent response genes is not activated and the SA-deficient double mutant *dgtxNahG* is still resistant to *Rs*K60. In addition, inoculation with *Pseudomonas syringae* pv *tomato* has shown that both *dgt* and its wildtype background are susceptible to this foliar pathogen. Our research suggests that the resistant response to *Rs*K60 of the *dgt* mutant may be due a SA-independent mechanism in roots, and that the *DGT* gene and proper auxin transport and signaling is important for susceptibility to *Rs*K60 in tomato roots. Understanding the role of DGT, auxin, and SA in defense responses to *Rs* in tomato is important for Solanaceae crop improvement.

Transcriptomic changes induced by exogenous NAD^+ in snap bean against *Pseudomonas syringae* pv. *phaseolicola* revealed by RNA-sequencing

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