Late blight of tomato and potato (*Phytophthora infestans*) continues to be one of the most challenging diseases to sustainably and proactively manage. Potato early blight (*Alternaria solani*) occurs annually in Wisconsin. Growers spend upwards of $19 million to control these two destructive diseases. Our previous work established a non-destructive method of early late blight detection based on hyperspectral reflectance that can identify infected plants with >85% accuracy 2–4 days before visual symptoms appear during its biotrophic phase. Our objective was to use this methodology to distinguish latent *P. infestans* infection from latent and symptomatic *A. solani* infection. We conducted two growth chamber experiments using *P. infestans*, *A. solani*, co-inoculation, and control, non-inoculated plants to identify significant wavelengths for detection and differentiation. We measured continuous visible to shortwave infrared reflectance (400-2500 nm) on leaves using a portable spectrometer with contact probe at 12–24 hr intervals. We could both detect and distinguish early blight from late blight infection with >80% accuracy at 24 hr post-inoculation, and upwards of 90% accuracy after 48 hr post-inoculation. Shortwave infrared wavelengths (>1300 nm) were important for disease detection and differentiation. Our results support the potential use of hyperspectral reflectance-based predictive models as tools for rapid, early, real-time detection of two important diseases of potato.

The game-changing impact of NGS in Plant Virology

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In the past few years, the rapid development of high-throughput sequencing (HTS) technologies has impacted many research areas. In virology and, in particular, in plant virology, HTS coupled with bioinformatics have dramatically changed the way virus discovery, etiology efforts or viral population analyses are performed. Among the advantages of such approaches is that they offer for the first time the ability to perform the complete viral indexing of a plant sample without the need for any prior knowledge. Protocols for the efficient analysis of a variety of templates including siRNAs, virion-associated nucleic acids (VANA), double-stranded RNAs (dsRNAs), mRNAs or total RNAs, with or without rRNA depletion, are now available, together with efficient pipelines for the bioinformatics analysis of the huge volumes of sequence data involved. As a consequence, a wide range of novel plant viruses have been described, a first glimpse at phytoviromes has been achieved and some viral populations have been described with unprecedented precision and depth. These technologies have a huge potential in certification and for the improvement of the safety of the conservation and movement of plant materials. Still, HTS-based viral indexing has yet to be applied on a large scale in routine diagnostic settings with the need to meet challenges such as validation, comparison of sensitivity with existing techniques or implementation of quality controls.

Bringing potato disease resistance traits to market in the U.S.

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The most widely used French fry potato variety in America, the Russet Burbank, and the most popular chips variety, Atlantic, recently celebrated their 100-year and 40-year anniversaries respectively. In crops where varieties change infrequently, biotechnology tools and traits can readily bring benefits to farmers and consumers. To this end, Simplot Plant Sciences began working within the potato genome to reduce limitations of the widely grown commercial potato. The result is the Innate® potato platform with a stepped approach of increasing trait value from generation to generation. Simplot Innate® technology permits the selective improvement of positive traits or minimization of negative traits without incorporation of foreign genes. The second generation of Innate® potatoes reduce blackspot bruise and asparagine (which reduces the potential for the formation of acrylamide), cold storage capability, and provide foliar late blight resistance against common North American strains. Therefore, Innate® potatoes are genetically engineered with traits appealing to potato growers, packers, processors, retailers and consumers. The talk will mainly focus on the late blight protection trait strategy, how it was selected, a description of benefits, and how to maintain its efficacy. I will also discuss how resistance genes can be combined in various desirable permutations to protect against pathogen populations and provide a preview of future disease traits.

Crop-specific sulfur management for optimizing productivity, quality and plant health

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The implementation of biological know-how into fertilizer practice is a major contribution to fully utilize potential crop yield and quality, and to strengthen crops against biotic stress. Sulfur Induced Resistance (SIR) is one constituent of the complex phenomenon of induced resistance (IR). S fertilization reduced the plant disease index (DI) for various host/pathogen relationships by 5 to 50% (greenhouse) and 17 to 35% (field experiments), for instance *Verticillium* wilt in cotton from 0.708 to 0.375. Effective fertilizer rates can be higher than the physiological S demand and vary crop-specifically between 20 to 40 kg/ha S before winter and 50 to 100 kg/ha S during main vegetative growth in spring; a constant S supply over time provided best protection against soil-borne and foliar plant diseases. The magnitude and efficiency of SIR seems to be regulated by the external plant available S reserves and plant-inherent S pools and fluxes, whereby the strongest response to S can be expected when going from severe S deficiency to sufficiency. S fertilization increases plant S status, content/release of S-containing primary and secondary metabolites (cysteine, glutathione, glucosinolates, H_2S and COS). All components show either a direct fungicidal/fungistatic effect or are involved in the induced resistance response. Based on a profound and robust statistical procedure, critical S concentrations (severe deficiency, optimum supply, toxicity) have been calculated for *Brassica* crops, legumes, pastures, Poaceae and root crops. These are recommended for adjusting fertilizer rates in order to maximize productivity and quality as well as enhance resistance against plant diseases.

Innovative management strategies for Aspergillus spp. and Penicillium spp. on nuts

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In postharvest, chestnuts and hazelnuts can be affected by species of *Penicillium,* agents of blue-green mould, and some species of *Aspergillus*, able to produce mycotoxins. Several strains of *Aspergillus* spp. and *Penicillium* spp. isolated from the chestnut field and production chain were characterized. *A. flavus* resulted the dominant *Aspergillus* species. Forty percent of the *Aspergillus* spp. strains produced AF_S *in vivo,* while most strains were pathogenic on chestnut. A total of 20 species of *Penicillium* spp. were identified, including *P. crustosum*, *P. glabrum*, *P. bialowiezense*, *P. discolor* and *P. expansum*. Around 70% of *Penicillium* spp. isolated were pathogenic on chestnut, while 59% of the strains could produce at least one mycotoxin on chestnut. A new HPLC-MS/MS method was developed to detect twenty metabolites produced by *Penicillium* spp. on nuts. A LAMP assay was developed for *Aspergillus flavus*, while an antibody-immobilized microcantilever resonators was developed for mycotoxin detection. Drying conditions of chestnuts and hazelnuts is a critical point to reduce *Aspergillus* spp. and aflatoxin contamination. Monitoring, prevention and control are the strategies to manage *Aspergillus* spp. and *Penicillium* spp. on nuts. Besides these strategies, traditional static hot air roasting and infra-red rays roasting, together with cold atmospheric pressure plasma could be used for nut detoxification from aflatoxins.