

NORTH AMERICAN LATE BLIGHT SYMPOSIUM



Minneapolis Convention Center
August 8-9, 2014

Welcome – Bienvenue – Bienvenido!

Seventeen years ago, a North American Late Blight Workshop was organized in Tucson, Arizona as part of the scientific community's response to the resurgence of late blight and the appearance of new, aggressive strains of *Phytophthora infestans*. Since that time, there have been significant advances in our understanding of the disease and options for control, yet challenges remain. This year's Symposium has been organized to bring together participants from academia, government, and industry to discuss recent developments, plan for the future, and forge new collaborations.

The organizers of the meeting thank the APS staff for their help in executing this meeting, in particular Betty Ford and Lisa Johnson. We also thank the National Institute of Food and Agriculture of the USDA, Simplot, and Syngenta for supporting travel awards for the conference.

Hope you all have a wonderful and productive meeting and an enjoyable stay in Minneapolis!

Scientific Program Committee:

William Fry, Cornell University, Ithaca, New York, USA (Chair)
Odille Carisse, Agriculture and Agri-Food Canada, Quebec, Canada
Fouad Daayf, University of Manitoba, Winnipeg, Canada
Niklaus Grünwald, USDA-ARS, Corvallis, Oregon, USA
Hector Lozoya-Saldaña, Universidad Autónoma Chapingo, Chapingo, Mexico
Jean Ristaino, North Carolina State University, Raleigh, NC, USA
Chris Smart, Cornell University, Geneva, New York, USA

Organizing Committee:

Audrey Ah Fong, University of California, Riverside, USA
Howard Judelson, University of California, Riverside, USA

Travel awards sponsored by:



Program Agenda

All talks will be held in room 205AB of the Minneapolis Convention Center. Badges may also be picked up in that same location. The poster sessions and lunch will be held in Room 205CD.

Friday, August 8, 2014

07:30-08:30 Poster set-up (also Thursday from 17:00-19:00; please leave posters in place through the end of the meeting on Saturday)

08:00-10:00 Badge pick-up (no on-site registration)

08:45-09:00 Introductions

09:00-09:45 Keynote talk by **Geert Kessel**:
Towards an IPM 2.0 approach for potato late blight management

09:45-10:00 Break

10:00-11:45 **Session 1: Pathogen Biology & Diversity** Chair: *Niklaus Grünwald*

Brian Knaus

Genomic characterization of *Phytophthora infestans* to develop management tools specific to US clonal lineages

Lina Sjöholm

Genotypic diversity and migration patterns of *Phytophthora infestans* in the Nordic countries

Jean Ristaino

The evolutionary relationships and displacements of historic and present day *Phytophthora infestans*

Silvia Restrepo

Emergence of a *Phytophthora* population on *Solanum betaceum* in Southern Colombia: an evolutionary study

Giovanna Danies

Phenotypic characterization of a sexual population of *Phytophthora infestans* in the Northeastern United States and Canada

Hector Lozoya-Saldaña

Recent collecting and characterization of *Phytophthora infestans* in central Mexico

Nicklaus Grünwald

The Irish potato famine pathogen *Phytophthora infestans* originated in central Mexico rather than the Andes

11:45-12:45 Lunch

12:45-13:45 Poster Session 1 (see p. 19 for list of poster abstracts)

- 13:45- 15:00 **Session 2: Plant-based Resistance** *Chair: Hector Lozoya-Saldaña*
- Reza Shekasteband**
Developing multiple disease resistant tomato hybrids with late blight resistance from the *Ph-2* and *Ph-3* genes and development of new closely linked SCAR markers
- Saltanat Mambetova**
Characterization of late blight (*Phytophthora infestans*) resistance of potato breeding lines with *RB* gene from *Solanum bulbocastanum*
- Kristen Brown**
Opportunities for reducing fungicide costs by adopting late blight resistant potato varieties
- Shafiqul Islam**
Mapping late blight resistance in a diploid population of potato
- Nicolas Champouret**
INNATE™ technology improves accepted potato varieties by providing late blight resistance and traits valuable to growers, processors and consumers
- 15:00-15:15 Break
- 15:15-16:15 **Session 3: Epidemiology** *Chair: Fouad Daayf*
- Mamadou Fall**
Infection efficiency of four *P. infestans* pathotypes and DNA-based quantification of airborne sporangia
- Erica Goss**
Effects of diurnal temperature oscillations on potato late blight
- Dennis Johnson**
Accuracy of rain forecasts for scheduling late blight management tactics in the Columbia Basin of Washington and Oregon
- Kenneth Frost**
Asexual survival of isolates of the US-22, US-23, and US-24 clonal lineages of *P. infestans* in tomato seeds at cold temperatures
- 16:15-17:00 **Session 4: Integrated Disease Management** *Chair: Odile Carisse*
- Ian Small**
Evaluation of the Cornell Decision Support System for late blight management using computer simulation and field testing
- Beth Gugino**
Evaluation of oospore production, metalaxyl sensitivity and forecast-based fungicide applications for the management of *Phytophthora infestans* on tomato in Pennsylvania
- William Kirk**
Ten-year forecast archives: New training of late blight risk management models
- 17:00-18:00 Poster session 2 (*see p. 19 for list of poster abstracts*)

Saturday, August 9, 2014

- 09:00-09:45 **Session 5: Outreach & Economics** *Chair: Chris Smart*
- Margaret McGrath**
Late blight on Long Island, NY: Changes in occurrence and management
- Yangxuan Liu**
Using net returns and risk to evaluate choice between potato/tomato late blight decision support system and calendar spray
- Joseph Steinhardt**
Factors influencing U.S. consumer support for genetic modification to prevent crop disease
- 09:45-10:30 **Session 6: Chemical Control** *Chair: Jean Ristaino*
- Christopher Shepherd**
DuPont™ Zorvec™ (“DPX-QGU42”, “oxathiapiprolin”): The first member of a novel class of oomycete fungicides
- Jean Ristaino**
Fungicide sensitivity of US genotypes of *Phytophthora infestans* to six oomycete-targeted compounds
- Howard Judelson**
Determinants of mefenoxam insensitivity are heterogeneous in *Phytophthora infestans*
- 10:30-10:45 Break
- 10:45-11:45 Discussion: "Future directions"
- 12:00 Adjourn and poster take-down

ABSTRACTS OF TALKS

(in order of presentation)

Keynote Presentation

Towards a next level IPM approach for potato late blight management.

G.J. Kessel¹, J. Vossen¹, D.E.L. Cooke², J.G. Hansen³, R.C.B. Hutten⁴, L.A.P. Lotz¹, H.T.A.M. Schepers⁵, A.J. Haverkort¹; ¹Plant Research International, Wageningen, Netherlands, ²The James Hutton Institute, Invergowrie, Dundee, Scotland, ³Aarhus University, Department of Agroecology - Climate and Water, Tjele, Denmark, ⁴Plant Breeding, Wageningen University, Wageningen, Netherlands, ⁵Applied Plant Research, Ak, Lelystad, Netherlands

Despite over 150 years of academic interest, serious efforts from the plant breeding and agrochemical industries and daily attention from growers, potato late blight continues to be a problem today. A high frequency of fungicide application remains the most important management practice used. This situation is deemed unsustainable from an environmental, societal and pathogen resistance point of view. A more sustainable control strategy is urgently needed. Over the past decade, several Dutch and EU projects contributed to development of a potato late blight control strategy designed to be more sustainable. This zero tolerance strategy is an extension of the current IPM strategy and builds on host resistance, a low input spray strategy and pathogen population monitoring. The base is formed by host resistance. Durability of the resistance is enhanced when multiple R-genes are included (e.g. www.Durph.nl). Resistant crops are not sprayed unless the pathogen is capable of breaking all but the last R-gene. When this is the case, a preventive spray strategy using decision support for spray timing and reduced dose rates of protectant fungicides is applied. Population monitoring serves as an early warning system to detect new virulences, new a.i. resistance and more general population change. A pan-European approach using DNA fingerprinting was used for the first time in 2013 (www.Euroblight.net). Field experiments were used to test and validate the complete strategy.

Session I: Pathogen Biology & Diversity

Genomic characterization of *Phytophthora infestans* to develop management tools specific to US clonal lineages.

B. Knaus¹, J. Tabima², H. Lozoya-Saldana³, W. Fry⁴, C. Smart⁵, J. Ristaino⁶, H.S. Judelson⁷, N. Grünwald¹; ¹USDA-ARS Horticultural Crops Research Unit, Corvallis, OR, ²Department of Botany and Plant Pathology, Oregon State University, OR, ³Departamento de Fitotecnia, Universidad Autonoma Chapingo, Mexico, ⁴Department of Plant Pathology and Plant-Microbe Biology, Cornell University, Ithaca, NY, ⁵Cornell University, New York State Agricultural Experiment Station, Geneva, NY, ⁶Department of Plant Pathology, North Carolina State University, Raleigh, NC, ⁷Department of Plant Pathology & Microbiology, University of California, Riverside, CA

Phytophthora infestans continues to impact global food security. In the US several novel clonal lineages have emerged and replaced previous populations. We assembled genomes of *P. infestans* sequenced to date, including novel lineages US-22, US-23, and US-24, to infer evolutionary relationships among lineages, develop lineage specific diagnostic markers and discover genes involved in adaptation. Novel lineages were sequenced as part of the AFRI CAPS grant, and combined with published data resulting in 26 full genomes. Preliminary analysis of the genomes revealed that lineages US-8 and US-11 appear to have different phylogenetic affinities, with the former lineage clustering with the recently derived lineage US-22 and the latter lineage clustering with the older lineage US-1. We observed 2.8 single nucleotide polymorphisms (SNPs), or other variants, per kilobase in these genomes (including *P. mirabilis* as an outgroup). To date, we've mined the mitochondrial genome for diagnostic markers and identified a set of SNPs distinguishing some but not all of the US clonal lineages. We also identified SNPs differentiating presence of ipi-O effector classes 1-3. These SNPs are being used for development of diagnostic markers. We are also identifying differences in RxLR effector alleles among lineages. Future directions include analyses of crinkler and other effectors as well as genes under selection for variants that may be associated with pathogenicity, fungicide resistance or mating type. This represents our first steps towards characterizing these *P. infestans* genomes, identifying patterns of variation throughout their genomes and attempting to link phenotypes with genotypes.

Genotypic diversity and migration patterns of *Phytophthora infestans* in the Nordic countries.

L. Sjöholm, B. Andersson, N. Högberg, A-K. Widmark, J. Yuen; *Sveriges lantbruksuniversitet, Uppsala, Sweden*

In this study we investigated the genotypic diversity and the migration patterns of *Phytophthora infestans* in the Nordic countries. Isolates of *P. infestans* from outbreaks in 43 fields sampled in 2008 were collected using stratified sampling with country, field, and disease foci as the different strata. Microsatellites were used as markers to determine the genotypic variation in the sampled material. The results show a high genotypic variation of *P. infestans* in the Nordic countries with most of the genotypes found only once among the collected isolates. The major part of the genotypic variation was observed within the fields, with low differentiation between the fields. The observed low association of alleles among loci is consistent with frequent sexual reproduction of *P. infestans* in the Nordic countries. Coalescence analyses did not support a single common population for the four countries, thus indicating some degree of geographic differentiation. The analyses of migration patterns showed differing levels of gene flow among the Nordic countries. No correlation between migration rates and geographical distance could be seen. This could be

explained by different degrees of genetic similarity between the pathogen populations in the different countries.

The evolutionary relationships and displacements of historic and present day *Phytophthora infestans*.

J. Ristaino, A. Saville, M. Martin, M.T. Gilbert; Department of Plant Pathology, North Carolina State University, Raleigh, NC, USA

Phytophthora infestans caused the historic potato famine and is an important constraint to potato production worldwide. The evolutionary relationships of modern clonal lineages of the pathogen and historic *P. infestans* in herbarium samples from old and new world collections were examined using nuclear and mitochondrial genomes and multilocus genealogies. Multiple distinct genotypes were present in historical Europe and a suite of infection-related genes were different from modern strains. Historic outbreaks were not caused by the US-1 clonal lineage (1b mtDNA haplotype) but by a closely related sister lineage of the 1a mtDNA haplotypes, Herb-1, that was found in modern New World populations from both Mexico and South America. The US-1 lineage formed a distinct cluster from most modern US lineages in PCA and STRUCTURE analysis of RFLP fingerprints. A maximum-likelihood phylogeny, coalescent analyses, and population subdivision statistics for the RXLR effectors PiAVR2 and PiAVR2-like showed four haplotypes that diverged into two lineages. PiAVR2 but not PiAVR2-like haplotypes were present in historic samples screened thus far. Six haplotypes were observed for IRRAS, and early 20th-century *P. infestans* shared haplotypes with modern lineages, while other haplotypes from 19th century outbreaks were distinct. Our data suggest multiple global introductions of *P. infestans* and the displacement of these lineages over time.

Emergence of a *Phytophthora* population on *Solanum betaceum* in Southern Colombia: an evolutionary study.

S. Restrepo¹, L.E. Lagos², M.F. Mideros¹; ¹Department of Biological Sciences, Universidad de los Andes, Bogotá, Colombia, ²Department of Biology, Universidad de Nariño, Pasto, Colombia

The incidence of emerging diseases has increased in the past years causing food security issues and triggering serious economic and social impacts, mainly in countries where diseases are particularly severe. We study an emergent population of *Phytophthora* attacking *Solanum betaceum* (tamarillo) in Southern Colombia. We determined its taxonomic status through phylogenetic reconstruction and population analyses and reconstructed the pathogen's evolutionary history using genetic crosses. Through cross-host pathogenicity tests, microscopic approaches and virulence assays we investigated host specificity and adaptation strategies on several *Solanum* hosts. Additionally, we tested the virulence-transmission trade-off hypothesis related to this new emergence episode. Using the phylogenetic species concept, based on single genes, the hypothesis of a new species attacking tamarillo could not be supported as previously shown in Ecuador. However, microsatellite data showed differentiation between this population and that of *P. infestans* and *P. andina*. Genetic crosses and molecular analyses raise the hypothesis that this population could be one of the parental genotypes of *P. andina*. Cross-pathogenicity and microscopic approaches showed host specificity within this population. Despite the high effect of pathogen genotype (G_P) and host genotype (G_H) on the fitness components, we did not find a significant effect of $G_P \times G_H$ indicating polygenic or quantitative host resistance in this pathosystem. Our findings show that strategies of adaptation of this *Phytophthora* population growing on *S. betaceum* are not completely supported by the virulence-transmission trade-off hypothesis. This study showed complex adaptive responses on an emerging disease caused by *P. infestans*, which

favor the maintenance and coexistence of multiple genetic variants of the pathogen. We believe that new hosts, such as tamarillo may offer alternative niches, which allow the adaptive emergence of new populations of *Phytophthora*. Results from this research can be used to further understand the processes that lead to the emergence of new pathogens, and this information can help manage emerging epidemics in South America.

Phenotypic characterization of a sexual population of *Phytophthora infestans* in the Northeastern United States and Canada.

G. Danies, K. Myers, E. Bevels, W. Fry; Department of Plant Pathology and Plant-Microbe Biology, Cornell University, Ithaca, NY, USA

Strains of *Phytophthora infestans* within the US are mostly clonal, and different clones are identified by specific DNA markers. Clones vary in traits such as fungicide sensitivity, aggressiveness, and the ability to overcome R genes. Knowledge about traits of *P. infestans* aids disease control. If DNA genotyping assigns strains to a lineage of known phenotype, recommendations can be made promptly and growers can make informed management decisions. In 2010 and 2011 we found 20 new and diverse genotypes of *P. infestans* concentrated in north central New York. The ratio of A1 to A2 mating types among these genotypes was close to 1:1. These genotypes were diverse at the glucose-6-phosphate isomerase locus, differed in their microsatellite profiles, showed different banding patterns in a restriction fragment length polymorphism assay using a moderately repetitive and highly polymorphic probe (RG57), and were polymorphic for four different nuclear genes. This diversity is consistent with a recombinant population, and two tests (the index of association and the pairwise homoplasmy index) failed to reject the hypothesis that these individuals were a recombinant population. In the event that any of these new and diverse genotypes becomes prevalent in the upcoming years, we have determined their host preference, their susceptibility to the tomato resistance genes Ph2 and Ph3, their sensitivity to mefenoxam, the effect of temperature on germination and on mycelial growth. Having this information will allow us to provide field-specific recommendations to both conventional and organic farmers.

Recent collecting and characterization of *Phytophthora infestans* (Mont.) de Bary, in central Mexico.

H. Lozoya-Saldaña¹, M. Robledo-Esqueda², R. Serrano-Cervantes¹, I. María-Balderas¹, A. De los Santos-Rodríguez¹; ¹Universidad Autónoma Chapingo, Chapingo, Mexico, ²Colegio de Posgraduados, Mexico

For more than fifty years it has been widely accepted that the central highlands of México is an important geographical area of diversity of the potato and tomato late blight pathogen *Phytophthora infestans* (Mont.) de Bary, mainly due to the continuous presence of the A1:A2 mating types that generate sexually derived progenies, which coexist in nature with the wild *Solanum* species of the region. The objective of this overall, continuous project is to collect and characterize *P. infestans* strains, in cooperation with international research and education institutions (Universidad Autónoma Chapingo Grant 135003002; USDA-AFRI-Grant 2011-68004-30154). A wide variability of the oomycete has been consistently observed. All its pathogenic races are present in the Toluca Valley every year. However, these races are not specifically related to the genotypes isolated from the indicator plants. Races and genotypes are independent concepts. Also, a tendency towards homothallism has been observed in the region recently. Some genotypic profiles of recent collections do not fit in Canadian, North American or South American classifications. A review of recent reports and the current status of the topic regarding hosts, fungicide-resistance, and isolates from geographical areas within the central highlands of Mexico will be discussed.

The Irish potato famine pathogen *Phytophthora infestans* originated in central Mexico rather than the Andes.

*E.M. Goss*¹, *J.F. Tabima*², *D.E.L. Cooke*³, *S. Restrepo*⁴, *W.E. Fry*⁵, *G.A. Forbes*⁶, *V.J. Fieland*², *M. Cardenas*⁴, *N.J. Grünwald*⁷; ¹*Department of Plant Pathology and Emerging Pathogens Institute, University of Florida, Gainesville, FL*, ²*Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR*, ³*The James Hutton Institute, Invergowrie, Dundee, Scotland*, ⁴*Department of Biological Sciences, University of the Andes, Bogota, Colombia*, ⁵*Department of Plant Pathology and Plant-Microbe Biology, Cornell University, Ithaca, NY*, ⁶*CIP China Center for Asia and the Pacific, International Potato Center, Beijing, China*, ⁷*Horticultural Crops Research Laboratory, US Department of Agriculture Agricultural Research Service, Corvallis, OR, USA*

Phytophthora infestans is a destructive plant pathogen best known for causing the disease that triggered the Irish potato famine and remains the most costly potato pathogen to manage worldwide. Identification of *P. infestans*'s elusive center of origin is critical to understanding the mechanisms of repeated global emergence of this pathogen. There are two competing theories, placing the origin in either South America or in central Mexico, both of which are centers of diversity of *Solanum* host plants. To test these competing hypotheses, we conducted detailed phylogeographic and approximate Bayesian computation analyses, which are suitable approaches to unraveling complex demographic histories. Our analyses used microsatellite markers and sequences of four nuclear genes sampled from populations in the Andes, Mexico, and elsewhere. To infer the ancestral state, we included the closest known relatives *Phytophthora phaseoli*, *Phytophthora mirabilis*, and *Phytophthora ipomoeae*, as well as the interspecific hybrid *Phytophthora andina*. We did not find support for an Andean origin of *P. infestans*; rather, the sequence data suggest a Mexican origin. Our findings support the hypothesis that populations found in the Andes are descendants of the Mexican populations and reconcile previous findings of ancestral variation in the Andes. Although centers of origin are well documented as centers of evolution and diversity for numerous crop plants, the number of plant pathogens with a known geographic origin are limited. This work has important implications for our understanding of the coevolution of hosts and pathogens, as well as the harnessing of plant disease resistance to manage late blight.

Session 2: Plant-Based Resistance

Developing multiple disease resistant tomato hybrids with late blight resistance from the Ph-2 and Ph-3 genes and development of new closely linked SCAR markers.

R. Shekasteband, *G. Vallad*, *S. Hutton*, *J. Scott*; *Institute of Food and Agricultural Sciences/Gulf Coast Research & Education Center, University of Florida, Wimauma, FL, USA*

Two late blight (LB) resistance genes, Ph-2 and Ph-3, derived from *S. pimpinellifolium* have been introgressed into tomato. Hybrids heterozygous for these genes have held up well to the pathogen in several tomato production regions. We crossed donor parent NC2-CELBR, a LB resistant line with both Ph-2 and Ph-3, to 33 recurrent susceptible parents, and after four backcrosses, near-isogenic lines have been developed for each recurrent parent. CAPS markers provided by Martha Mutschler were used to select the plants with the resistance genes for most of the backcrossing. The recurrent parents allow for LB resistance to be combined with other disease resistances including tomato spotted wilt virus (TSWV), tomato yellow leaf curl virus (TYLCV), fusarium wilt races 1, 2, and 3, and fusarium crown rot. Recurrent parents homozygous for Ph-2 and Ph-3 were used in testcrosses, and hybrids heterozygous for Ph-2 and Ph-3 are now being field evaluated. Genotyping of a collection of 30 F1BC4S1 seedlings along with the recurrent resistant and

susceptible parents was done with 7,720 SNPs. Based on the SNP data, we were able to determine the introgressed regions from NC2-CELBR into our near-isogenic Ph-2 and Ph-3 resistant lines. New recombinants with smaller introgressions on chromosome 10 and 9 but as resistant against LB as Richter's Wild (Ph-2 source) and L 3707(Ph-3 source) were identified containing Ph-2 or Ph-3, respectively. These recombinants will be used in future hybrids. The CAPS Ph-3 markers, TG328 and TG591, used for selection during backcrossing are located at 66.71 and 66.79 Mb, respectively. We identified 7 indels in the Ph-3 region, for which scar markers have been designed. These markers extend from 66.56 to 66.73 Mb (0.21 to 0.05 Mb away from Ph-3) on Chr. 9. These new Ph-3 scar markers may provide more affordable alternatives for small-scale genotyping operations.

Characterization of late blight (*Phytophthora infestans*) resistance of potato breeding lines with RB gene from *Solanum bulbocastanum*.

S. Mambetova, D. Douches, W. Kirk; Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, MI, USA

Late blight caused by *Phytophthora infestans* (Mont.) de Bary is the most important disease of potato (*Solanum tuberosum* L.), because it effects foliage, tuber yield and storage ability. Previously work demonstrated that the wild diploid potato species *S. bulbocastanum* is highly resistant to all known genotypes of *P. infestans*. In this study, we transformed and expressed the RB gene (also known as Rpi-blb1) (Song et al., 2003) previously cloned from *S. bulbocastanum*, into conventionally bred late blight resistant breeding lines, to evaluate the effect of pyramided late blight resistance genes. All RB potato transformation events were confirmed, by Polymerase Chain Reaction (PCR) and RB expression by Reverse Transcriptase-Polymerase Chain Reaction (RT-PCR). Foliar host plant resistance was characterized using detached leaf bioassays, greenhouse whole plant bioassays and an inoculated field trial. A set of four *P. infestans* isolates (US-8, US-22, US-23 and US-24) were used to evaluate foliar resistance, whereas only US-22 and US-23 isolates were used in the field. Percent late blight infection was visually estimated. The results of the greenhouse whole-plant bioassays and detached leaf bioassays were varied. However, the highest level of resistance was demonstrated in conventional resistance lines which have been transformed to contain RB gene from *S. bulbocastanum*. The results from the field trial were more explanatory and proved that pyramiding genes is an effective strategy to increase resistance level.

Opportunities for reducing fungicide costs by adopting late blight resistant potato varieties.

K.M. Brown; Department of Plant and Soil Sciences, University of Maine, Orono, ME, USA

Research in other regions has shown that late blight resistant potato varieties (LBRV) do not need as much fungicide as is currently recommended for susceptible varieties. Reducing fungicide inputs can increase farmer profits. LBRV potatoes from the University of Maine breeding program were tested in two fungicide schedules in Aroostook County, Maine. Schedules based on UMaine Extension recommendation were compared to reduced schedules of almost half of the recommended schedules. Two LBRV clones were grown under these management programs and compared to susceptible 'Katahdin' and resistant 'Defender.' In 2011, foliar late blight was observed with no significant difference in incidence in the new LBRV clones compared to Defender. Katahdin had a higher severity of foliar disease, and disease was much higher in the reduced schedule than in the full schedule. Fungicide program had no effect on total or marketable yields. Storage rot results were mixed and in need of further study. Per hectare savings were calculated.

A model based on long-term weather data and late blight pressure in Aroostook County was developed and predicted savings over 10 and 30 growing seasons.

Mapping late blight resistance in a diploid population of potato.

S. Islam, J. Coombs, N. Manrique-Carpintero, D. Douches; Department of Plant, Soil, and Microbial Sciences, Michigan State University, East Lansing, MI, USA

Our goal is to map and utilize late blight QTL from wild species. A diploid segregating population from an interspecific cross between 84SD22 *S. tuberosum* × *S. chacoense* hybrid and Ber83 *S. berthaultii* × 2x species mosaic hybrid was generated for this study. Ber83 parent is source of late blight resistance while 84SD22 is a susceptible line. The population of 129 individuals and the parental lines were SNP (Single Nucleotide Polymorphism) genotyped using the Illumina 8303 Potato Array. The genetic map of 786 cM with 2920 loci was constructed using JoinMap 4.1 software for cross-pollinated population type. This is a highly dense genetic map with average interval distance of 1 cM between SNPs and genome wide coverage of 99% of the latest potato genome assembly v4.03. Breeding lines from the cross of resistant lines Ber 83 with susceptible parent 84SD22 were tested for resistance late blight using a detached-leaf bioassay in a growth chamber. The suspension of US23 isolate per leaflet was 20 µl of *P. infestans*'s spore. Data on late blight infection were taken on 4, 7, 9, 11 and 13 days after inoculation of *P. infestans*. Greater number of clones showed resistant to late blight. Distribution of resistant to susceptible lines was bimodal meaning few genes were present to control the late blight disease. The detached leaf bioassay was a fast, space-saving, effective and reliable method of screening of diploid potato lines for late blight assay. This bioassay also provided an easily standardized method of evaluating host–pathogen interactions under controlled environment. In future, based on this SNP marker map and late blight phenotype data will be used to report QTL analysis.

INNATE™ technology improves accepted potato varieties by providing late blight resistance and traits valuable to growers, processors and consumers.

N. Champouret, J.R. Simplot Company, Boise, ID, USA

Potato is currently, the most consumed crop worldwide after wheat and rice, and it was already used 2500 BC to 5000 BC by inhabitants of the South American Andes region. Potato crop evolution by breeding selection over millennia has been able to develop varieties that are able to produce tubers from the equatorial origin Andean regions up to the northern latitudes. Early breeding programs have been selecting for yield increase and are now moving toward processing qualities and consumer-based quality traits. However, potato is an expensive crop to produce due to expensive inputs, disease pressure, and inherent perishability. Therefore, the main challenges for global acceptance have always been to develop potato varieties with diseases resistance, storage capabilities and quality traits like bruising resistance. Here, I will present potatoes, that use INNATE™ technology to i) reduce the level of acrylamide after frying, ii) decrease bruises at harvest, iii) increase storage capabilities and iv) provide, in a disease management package, a new resistance gene against late blight that has never been used in North America. The challenges to create, characterize and de-regulate late blight resistant INNATE™ potato varieties will be presented. Development of broader late blight resistant INNATE™ potato varieties and integration in a diseases management program will be discussed. Finally, I will elaborate on the future of INNATE™ for more quantitative/qualitative traits and potential to integrate it into classical breeding programs.

Session 3: Epidemiology

Infection efficiency of four *P. infestans* pathotypes and DNA-based quantification of airborne sporangia.

M. Fall^{1,2}, H. Van der Heyden³, M. Tremblay², C. Beaulieu¹, A. Lévesque², O. Carisse²; ¹University of Sherbrooke, Sherbrooke, Canada, ²Agriculture and Agri-Food Canada, Quebec, Canada, ³Phytodata inc., Sherrington, Quebec, Canada

The potential risk of late blight development and consequent yield losses depends in part on the aerial transport of *P. infestans* sporangia to potato fields from off-field sources. It has recently been suggested that airborne spore-sampling may be a suitable approach for early detection of incoming inoculum. However, to improve reliability of spore-sampling as a management tool, molecular tool for count of sporangia and information on infection efficiency are needed. Experiment was thus undertaken in growth chambers to study infection efficiency of four pathotypes of *P. infestans* (US-8, US-11, US-23 and US-24) by measuring the airborne sporangia concentration (ASC) and resulting disease severity. The relation between the ASC and the disease severity was exponential. For the same ASC, US-23 caused more damages than other pathotypes. Under favourable conditions, an ASC of 10 sporangia m⁻³ of US-23 was sufficient to cause 1 lesion per leaf whereas for other pathotypes it took 15-30 sporangia m⁻³ to reach the same severity. Also, a sensitive qPCR tool was developed for quantification of *P. infestans* sporangia. The sensitivity of detection is between 1 to 10 sporangia (R² = 0.91). Additional researches are currently conducted to determined pathotype from airborne inoculum. Knowing both the amount of inoculum and pathotype present can be used to adjust the fungicide scheme according to infection efficiency specific to each pathotypes's aggressiveness.

Effects of diurnal temperature oscillations on potato late blight.

S.K. Shakya, E.M. Goss, N.S. Dufault, A.H.C. van Bruggen; Department of Plant Pathology and Emerging Pathogens Institute, Gainesville, FL, USA

Global climate change will have effects on diurnal temperature oscillations besides average temperatures. Studies on potato late blight (*Phytophthora infestans*) development have not considered daily temperature oscillations. We hypothesize that growth and development rates of *P. infestans* would be less influenced by change in average temperature as the magnitude of fluctuations in daily temperatures increases. We investigated the effects of seven constant (10, 12, 15, 17, 20, 23, 27°C) and diurnally oscillating temperatures ($\pm 5^\circ\text{C}$ and $\pm 10^\circ\text{C}$) around the same means on number of lesions, incubation period, latent period, radial lesion growth rate and sporulation intensity on detached potato leaves inoculated with two *P. infestans* isolates from clonal lineages US-8 and US-23. A four parameter thermodynamic model was used to describe relationships between temperature and disease development measurements. Incubation and latency progression accelerated with increasing oscillations at low mean temperatures, but slowed down with increasing oscillations at high mean temperatures ($P < 0.005$), as hypothesized. Infection efficiency, lesion growth rate and sporulation increased under small temperature oscillations compared to constant temperatures but decreased when temperature oscillations were large. Thus, diurnal amplitude in temperature should be considered in models of potato late blight, particularly when predicting effects of global climate change on disease development.

Accuracy of rain forecasts for scheduling late blight management tactics in the Columbia Basin of Washington and Oregon.

*D. Johnson*¹, *T. Cummings*¹, *A. Fox*²; ¹*Department of Plant Pathology, Washington State University, Pullman, WA, USA,* ²*Fox Weather, LLC, Fortuna, CA, USA*

Accuracy of prediction was analyzed for 15-day and 30-day rain forecasts at two locations in the Columbia Basin to determine if rain forecasts were sufficiently accurate to be included as a model component to schedule management tactics for potato late blight. Accuracy was partitioned into specificity (percentage of forecasted non-rainfall events classified correctly) and sensitivity (percentage of forecasted daily rainfall events classified correctly). Adjusted sensitivity was used to give a wider target than only one day for evaluating accuracy of forecasted rain events and included the forecasted day for rain plus the next two days. For 15-day forecasts, specificity during the seasonal test period was $\geq 70\%$ from mid-June through September and specificity over the days of the forecast was $> 70\%$ for the first eight days at both locations both years. Adjusted sensitivity over days of the forecast was initially $> 80\%$ and then decreased as days increase from 7 to 15 days for 15-day forecasts at both locations and years. Sensitivity and adjusted sensitivity during the seasonal test period were both positively correlated and specificity was negatively correlated with number of actual rainy days. Adjusted sensitivity was considerably higher for May (month with highest incidence of rain) than July (month with least incidence of rain) at both locations. For 30-day forecasts, specificity during the test period was $> 75\%$ in July and August and adjusted sensitivity was $> 60\%$ for various time periods of the test period at both locations and years. Adjusted sensitivity varied greatly over days of the forecasts with peaks near 100% at both locations and years for the 30-day forecasts. Specificity of 15-day and 30-day rain forecasts and adjusted sensitivity of 15-day rain forecasts have utility in scheduling late blight fungicides and other management tactics in the Columbia Basin.

Asexual survival of isolates of the US-22, US-23, and US-24 clonal lineages of *P. infestans* in tomato seeds at cold temperatures.

K. Frost, A.C. Seidl, A. Gevens; Department of Plant Pathology, University of Wisconsin-Madison, Madison, WI, USA

Survival of *Phytophthora infestans*, the causal agent of potato and tomato late blight, is generally reduced under freezing conditions due to the inability of the asexual life stage of the pathogen to survive in the absence of living plant tissues. While infected potato tubers can be insulated in cull piles and harbor the asexual stages of *P. infestans* overwinter, the survival of *P. infestans* overwinter in tomato production systems is thought to be negligible. Since *P. infestans* infected tomato fruit can be buried in a production field and harbor wet infected seeds, the survival of three recently identified clonal lineages of *P. infestans*, US-22, US-23, and US-24, was measured on wet tomato seeds for 112 days at 18, 4, 0, -3, and -5°C. Isolates representing all lineages survived for 112, 112, and 84 days at 18, 4, and 0°C, respectively. A thermal time model predicts that *P. infestans* will survive in 5% of infected tomato seeds for 99, 25 and 16 days at 0, -3 and -5°C, respectively. Unlike isolates representing the US-22 and US-24 clonal lineages, vigor of the surviving isolates representing US-23 clonal lineage was not affected by exposure to cold temperatures. Using a model that described the survival of *P. infestans* as a function of cooling degree-days and soil temperature data from four locations in Wisconsin, survival of *P. infestans* in 5% of infected tomato seeds was predicted to occur at 35 and 39% of the location-year combinations at 5 and 10 cm soil depths, respectively. Together, these data suggest that *P. infestans* has the potential to overwinter asexually in tomato production systems in the Northern climates. Volunteer tomato seedlings germinating from infected or infested overwintering fruit should be managed to prevent the initiation of late blight epidemics.

Session 4: Integrated Disease Management

Evaluation of the Cornell Decision Support System for late blight management using computer simulation and field testing.

I. Small, L. Joseph, W.E. Fry; Department of Plant Pathology & Plant-Microbe Biology, Cornell University, Ithaca, NY, USA

Calendar-based fungicide application strategies are often employed for the management of late blight regardless of existing disease levels, cultivar resistance, or prevailing weather. Such strategies may result in economically and environmentally inefficient disease management. The objective of this study was to evaluate the utility of the Cornell Decision Support System (DSS) for late blight management using (a) field tests and (b) computer simulation. Three treatment schedules were evaluated i) weekly applications, ii) applications according to the DSS, or iii) no fungicide. All experiments involved at least two cultivars with different levels of resistance. (a) Field evaluation was conducted through naturally inoculated field experiments in 2010, 2011 and 2012, using Simcast in the DSS to guide fungicide applications. DSS-guided and weekly scheduled fungicide treatments were successful at protecting against late blight in all field experiments. However, DSS-guided schedules were influenced by prevailing weather and host resistance and resulted in schedules that reduced the amount of fungicide used by up to 50%. Simulation experiments utilized 10 years of observed weather data from 65 locations in potato producing states. For each season at each location, DSS recommended application schedules for susceptible, moderately susceptible, and moderately resistant potato cultivars were compared to seven-day schedules regarding their expected number of applications and simulated disease progress. In situations with unfavourable weather, the DSS recommended fewer fungicide applications with no loss of disease suppression and in situations of very favourable weather, the DSS recommended more fungicide applications but with improved disease suppression. In general, the DSS reduced the number of fungicide applications compared to weekly applications with no loss of disease suppression.

Evaluation of oospore production, metalaxyl sensitivity and forecast-based fungicide applications for the management of *Phytophthora infestans* on tomato in Pennsylvania.

I. Huerta Arredondo¹, I. Small², W.E. Fry², B. Gugino¹; ¹Department of Plant Pathology & Environmental Microbiology, The Pennsylvania State University, University Park, PA, USA, ²Department of Plant Pathology & Plant-Microbe Biology, Cornell University, Ithaca, NY, USA

Late blight (LB) caused by the oomycete *Phytophthora infestans*, remains one of the most important plant diseases worldwide due to its rapid progression and potential for complete crop devastation. These characteristics in part, make *P. infestans* challenging to manage. Management is most successful when preventative strategies like the use of disease forecasting to time fungicide applications are combined with knowledge about the predominant clonal lineage(s). Therefore, our research focused on: 1) evaluating the efficacy of the web-based Cornell Decision Support System (DSS) for managing LB on tomato in the field; 2) determining the in vitro sensitivity of select Pennsylvania US-23 isolates to the fungicide active ingredient mefenoxam; and 3) evaluating in vitro and in planta oospore formation between select *P. infestans* genotypes from Pennsylvania. Our results showed that the use of the forecasting models BLITECAST and the Cornell DSS to time fungicide applications reduced the number applications up to 16 and 44%, respectively, in comparison to a 7-day program, while significantly reducing foliar and fruit disease severity (US-23) compared to non-fungicide treated control. Results from the in vitro mefenoxam sensitivity screening of US-23 isolates from Pennsylvania, indicated that most US-23 isolates screened (n=21)

are still sensitive to the active ingredient, although there is a range of sensitivity among isolates, with several (n=5) approaching moderate resistance which may impact mefenoxam use in the future. Methods and preliminary results from the oospore formation assays will be presented, as well as the implications of the mefenoxam sensitivity screening and the field studies on disease management.

Ten-year forecast archives: New training of late blight risk management models.

W. Kirk¹, K. Baker², T. Lake², P. Wharton³; ¹Department of Plant, Soil, and Microbial Sciences, Michigan State University, East Lansing, MI, USA, ²Department of Geography, Western Michigan University, Kalamazoo, MI, USA, ³Department of Plant, Soil and Entomological Sciences, University of Idaho, Aberdeen, ID, USA

Agroecosystem decision support systems typically rely on some type of weather data. Though many new digital weather and forecast datasets are gridded data, we feel that evaluating previous methods with data of increased archive length is critical to transitioning to new datasets that lack extensive archives. To that end, this paper reviews improvements made to an artificial neural network for forecasting weather-based potato late blight (*Phytophthora infestans*) risk at 26 locations in the Great Lakes region. Accuracies of predictions made using an early model, developed in 2007, are compared with accuracies of predictions made using a new ten-year hourly optimized model. In nearly every comparison by month, forecast lead time and spatial region, the newly optimized model is more accurate, especially when the weather is conducive to disease.

Session 5: Outreach & Economics

Late blight on Long Island, NY: Changes in occurrence and management.

M. McGrath; Department of Plant Pathology, Cornell University, Long Island Horticultural Research and Extension Center, Riverhead, NY, USA

Before 2009, late blight occurred sporadically on Long Island (LI), New York, and was primarily a disease of potato in commercial crops. Most years it was never detected or not found until the end of the season in October. Since 2009, late blight has occurred every year starting early in crop production (typically in June), tomatoes have been the primary crop affected, and occurrence in gardens has been an important component of the epidemic. Source of initial inoculum appeared to be infected tomato seedlings planted in gardens in 2009 and 2011, and table-stock potatoes planted in a garden in 2010. The source could not be identified despite considerable effort in 2012 and 2013. Late blight quickly became widespread in the agricultural area (eastern LI) following the first detection in all years except 2010, when the gardeners responded quickly and destroyed all tomato and potato plants, and in 2013 when onset was relatively late (first detected on 25 July). Effective control was achieved with fungicides applied on a good schedule in organic and conventionally-managed crops. When major losses occurred, the reason appeared to be no preventive application or lengthened spray interval when conditions were more favorable for disease development than they seemed to be. Genotypes of *Phytophthora infestans* detected on LI were US-22 in 2009 and 2010 and US-23 in 2011, 2012, and 2013. Both are sensitive to the fungicide mefenoxam (FRAC Code 4). Ability to determine genotype within two days through USABlight project enabled growers to use this highly-effective fungicide that other genotypes are resistant to. Tomato varieties with resistance to late blight were grown by some gardeners and organic growers, who viewed including them with their standard varieties as “insurance” to ensure they would have tomatoes.

Using net returns and risk to evaluate choice between potato/tomato Late Blight Decision Support System and calendar spray schedule.

Y. Liu, M. Langemeier; Department of Agricultural Economics, Purdue University, West Lafayette, IN, USA

This paper examines the choice between the Potato/Tomato Late Blight Decision Support System (DSS) and the 7-day calendar spray schedule. The DSS model enables farmers to apply fungicide in accordance with disease needs, and in turn possibly reduce fungicide usage by more carefully examining the timing of fungicide application. With a 7-day calendar spray schedule, risk averse farmers may over apply fungicides, perhaps thinking that it is better to be “safe than sorry”. In this paper stochastic dominance with respect to a function is used to compare pair-wise late blight management choices using the DSS model and a 7-day spray schedule. Stochastic dominance incorporates both net returns and the riskiness (i.e., variability and skewness) of these net returns. Use of stochastic dominance allows us to determine whether adopting a fungicide application schedule suggested by the DSS model is preferred to a traditional 7-day spray schedule under various risk aversion assumptions, including preferences represented by risk neutrality, slight risk aversion, moderate risk aversion, and strong risk aversion. Net returns for each choice (DSS model and 7-day spray schedule) will be computed for one or more New York locations using weather from multiple years, potato price and yields, and fungicide costs. In addition to examining preferences between the two choices, we will examine the sensitivity of our results to changes in potato prices, potato yields, tuber quality, and fungicide costs.

Factors influencing U.S. consumer support for genetic modification to prevent crop disease.

J. Steinhardt, K. McComas; Department of Communication, Cornell University, Ithaca, NY, USA

This study examines support for the genetic modification (GM) of crops in the context of preventing “late blight,” a devastating potato and tomato disease that caused the Irish Potato Famine in the 1850s and results in substantial crop loss today. We surveyed U.S. adults who do the primary grocery shopping in their household (n = 859). Half of the respondents were randomly assigned to read a vignette describing late blight before responding to questions about GM, whereas the other half read a vignette about generic crop disease before responding to questions. We also examine how the perceived fairness of decision makers relates to GM support and the perceived legitimacy of GM decision making. We found that disease specificity mattered less to support and legitimacy than the perceived fairness of decision makers. The perceived risks of GM to human and environmental health negatively related to GM support and legitimacy, whereas the perceived benefits (e.g. reduced threats to crops and a more secure food supply) positively related to support and legitimacy. Objective knowledge about GM had a small, negative relationship with legitimacy whereas self-assessed familiarity with GM had a positive relationship. Overall, the results offer additional confirmation of past findings from more localized settings that perceived fairness of decision makers matters to support for GM and underscore the importance of considering how risk managers’ behaviors and actions are perceived alongside individuals’ perceptions about the risks and benefits.

Session 6: Chemical Control

DuPont™ Zorvec™ (“DPX-QGU42”, “oxathiapiprolin”): The first member of a novel class of Oomycete fungicides.

*C. Shepherd*¹, *W. Summers*²; ¹*DuPont Crop Protection, Newark, DE*, ²*E.I. Dupont Canada Company, Mississauga, ON, Canada, USA*

DuPont™ Zorvec™ is the global branded name for oxathiapiprolin (approved ISO common name), a novel fungicide recently discovered by DuPont and the first member of a new class of “piperidinyl-thiazole- isoxazoline” fungicides. It acts at a unique site of action in Oomycete pathogens. At use rates 5-100 times lower than current commercial fungicides, oxathiapiprolin is highly effective for the control of *Phytophthora infestans*, causal agent of late blight in potato and tomato. High intrinsic efficacy, an effect on all stages of *Phytophthora infestans* development and systemic movement within the host plant allow oxathiapiprolin to provide robust and reliable late blight disease control even under the most severe conditions. Product development is focused on potato as well as other crops where Oomycete pathogens limit agricultural productivity and profitability including grapes, cucurbits, tomato and other vegetable crops. Its new mode of action makes oxathiapiprolin a valuable option for fungicide resistance management strategies, while safety to key beneficial organisms confer a strong fit within integrated pest management programs. A remarkably favorable toxicological and environmental profile, combined with low use rates, provides large margins of safety for consumers, agricultural workers and the environment.

Fungicide sensitivity of US genotypes of *Phytophthora infestans* (Mont.) de Bary to six oomycete-targeted compounds.

*J. Ristaino*¹, *A. Saville*¹, *K. Graham*², *N. Grünwald*², *K. Myers*³, *W.E. Fry*³; ¹*Department of Plant Pathology, North Carolina State University, Raleigh, NC, USA*, ²*Horticultural Crops Research Laboratory, US Department of Agriculture Agricultural Research Service, Corvallis, OR, USA*, ³*Department of Plant Pathology and Plant-Microbe Biology, Cornell University, Ithaca, NY, USA*

Phytophthora infestans (Mont.) de Bary causes potato late blight, an important and costly disease of potato and tomato crops. The baseline sensitivity of recent clonal lineages of *P. infestans* for six oomycete-targeted compounds was tested. Forty-five isolates collected between 2004 and 2012 were tested in vitro on media amended with a range of concentrations of either azoxystrobin, cyazofamid, cymoxanil, fluopicolide, mandipropamid, or mefenoxam. Measurements of radial growth were used to generate dose-response curves and calculate EC50 values for each isolate. The US-8, and US-11 clonal lineages were insensitive to mefenoxam while the US-20, US-21, US-23 and US-24 clonal lineages were sensitive to mefenoxam. Insensitivity to azoxystrobin, cyazofamid, cymoxanil, fluopicolide, or mandipropamid was not detected among any lineage. Examination of disease outbreaks documented in USAblight revealed a rapid change in clonal lineages over time in the US and the displacement of the US-22 lineage by US-23, both of which are sensitive to mefenoxam. Neither the introduction nor development of insensitivity to mefenoxam in current US populations during the displacement of lineages was observed.

Determinants of mefenoxam insensitivity are heterogeneous in *Phytophthora infestans*.

M. Matson, H.S. Judelson; Department of Plant Pathology and Microbiology, University of California, Riverside, CA, USA

The fungicide mefenoxam has been used to control many oomycete pathogens, including *P. infestans*. The utility of the compound decreased in past decades due to the appearance of insensitive strains, which dominated populations of *P. infestans* in the United States and Canada in the 1990s. Due to shifts in pathogen populations, many strains causing late blight in the United States are once again sensitive. The availability of a rapid diagnostic test for insensitivity would help inform growers about the best strategy for disease management. Recently, Whisson *et al.* demonstrated that an altered sequence of RNA polymerase I subunit I (RPA1) was responsible for insensitivity in most strains, and we have developed a PCR-based high resolution melt (HRM) assay that can rapidly diagnose genotypes at that locus. By HRM analysis and DNA sequencing, we identified resistant isolates that lack that change (SNP T1145A, Y382F). In such cases, which include some isolates from North America, resistance is not associated with SNPs elsewhere in RPA1 or genes encoding other subunits of RNA polymerase 1. The T1145A SNP also does not cosegregate with resistance in the sexual progeny of such isolates. It thus appears that the basis of insensitivity is complex and assays for diagnosing the response of isolates to mefenoxam may not be trivial.

Poster Directory

Posters will be in "bus stop" format. Participants will be divided up into groups, which will rotate between posters every 5 minutes. At each "bus stop", each group will have the opportunity to hear the presenter discuss their work and answer questions.

Abstracts for Poster Session 1:

1. Lineages of *Phytophthora infestans* detected in the USA (2009-2013). **Kevin Myers**
3. *Phytophthora infestans* isolates collected by Ken Deahl are looking for a new home. **Leslie Wanner**
5. Genotypic diversity in Estonian populations of *Phytophthora infestans*. **Riinu Kiiker**
7. Characterization of genetic structure in Mexico populations of *Phytophthora infestans* using simple sequence repeats. **Jianan Wang**
9. Susceptibility of immature and mature potato tubers to different genotypes of *Phytophthora infestans*. **Sandesh Dangi**
11. Differential susceptibility of thirty-nine tomato varieties to *Phytophthora infestans* clonal lineage US-23. **Zachariah Hansen**
13. Frequency of resistance to *Phytophthora infestans* in potato seedling families from dedicated late blight parental crossing blocks. **Gary Secor**
15. Transforming potato late blight point forecasts for use with the National Digital Forecast Database. **William Kirk**
17. A coalescence analysis of *Phytophthora infestans* in Scandinavia reveals population structuring. **Lina Sjöholm**
19. Investigating potential of tomato fruit with late blight to serve as a source of inoculum for seedlings growing out of these fruit. **Margaret McGrath**

Abstracts for Poster Session 2:

2. Phytophthora-ID 2.0: Novel open source tools for *Phytophthora* species and genotype identification. **Nicklaus Grünwald**
4. Virus mediated RNA silencing in *Phytophthora*. **Sean Patev**
6. Comparison of tuber inoculation techniques with *Phytophthora infestans*. **Sandesh Dangi**
8. Seed treatments, in furrow and early foliar treatments for control of seed-borne *Phytophthora infestans*. **William Kirk**

10. Analysis of late blight outbreak trends using multiple diverse data types. **Carla Thomas**
12. Antimicrobial peptides from seeds of wild plants suppress *Phytophthora infestans*, the causative agent of late blight disease in tomato and potato. **Eugene Rogozhin**
14. Small plot research for testing *Phytophthora infestans* control by multiple products for fresh market Brandywine tomatoes grown on the central coast of California. **Frank Sances**
16. Assessment of bacterial populations obtained from native Chilean potatoes with activity on *Phytophthora infestans* cell wall glucans. **Ernesto Moya-Elizondo**
18. Sensitivity to eight systemic fungicides in *Phytophthora infestans* and fungicides efficacy in controlling potato late blight in North of China. **Wenqiao Wang**

Poster Abstracts

Session 1: odd numbers
Session 2: even numbers

1. Lineages of *Phytophthora infestans* detected in the USA (2009-2013).

K. Myers¹, G. Danies¹, K. Everts², W.E. Fry¹, A. Gevens³, N. Grünwald⁴, B. Gugino⁵, S. Johnson⁶, H. Judelson⁷, M. McGrath⁸, J. Ristaino⁹, P. Roberts¹⁰, A. Seaman¹, G. Secor¹¹, K. Seebold¹², I. Small¹, C. Smart¹³; ¹Department of Plant Pathology and Plant-Microbe Biology, Cornell University, Ithaca, NY, ²University of Maryland, Lower Eastern Shore Research and Education Center, Salisbury, MD, ³Department of Plant Pathology, University of Wisconsin-Madison, Madison, WI, ⁴USDA-ARS Horticultural Crops Research Unit, Corvallis, OR, ⁵Department of Plant Pathology & Environmental Microbiology, The Pennsylvania State University, University Park, PA, ⁶University of Maine Cooperative Extension, Presque Isle, ME, ⁷Department of Plant Pathology & Microbiology, University of California, Riverside, CA, ⁸Department of Plant Pathology, Cornell University, Long Island Horticultural Research and Extension Center, Riverhead, NY, ⁹Department of Plant Pathology, North Carolina State University, Raleigh, NC, ¹⁰Carolina State University, ¹⁰University of Florida, SWFREC, Immokalee, FL, ¹¹Department of Plant Pathology, North Dakota State University, Fargo, ND, ¹²Department of Plant Pathology, University of Kentucky, Lexington, KY, ¹³ Cornell University, New York State Agricultural Experiment Station, Geneva, NY, USA

Beginning in 2011 and continuing through the present time (spring 2014), the authors have been participants in a project to report the occurrence of late blight when it occurs in the United States. Many of the authors have participated informally since 2009. Since 2011, reports have been posted on <http://USAblight.org>. In addition to the reports of occurrence, samples have been collected and shipped via courier to be assessed with microsatellite markers for a rapid determination of genotype. Data concerning the results of the analysis were typically returned to the submitter within 48 hr. From 2009 through 2013 more than 800 samples were assessed, with data obtained on more than 780 of these. The numbers of samples assessed were: 80 (2009); 51 (2010); 137 (2011); 237 (2012); and 274 (2013). The microsatellite analyses were confirmed on a subset of samples by isolating the pathogen into pure culture and determining DNA fingerprint with RG57, Gpi genotype, and mating type. The predominant lineages of *Phytophthora infestans* have changed during the course of this study. In 2009, the predominant lineage was US22 (>90%), and US8 accounting for most of the remainder. In 2010, the predominant lineage was still US22 (~50%), with US8, US24 and US23 accounting for > 30%. In 2011, US23 (~30%) and US24 (~30%) were both more abundant than US22 (~10%). However, in 2012 US23 was predominant (>70%) with US11 being regionally important (~25%) and in 2013, US23 retained its predominance accounting for about 95% of samples.

2. Phytophthora-ID 2.0: Novel open source tools for *Phytophthora* species and genotype identification.

N. Grünwald¹, J. Tabima², S. Everhart², M. Larsen¹, Z. Kamvar²; ¹USDA-ARS Horticultural Crops Research Unit, Corvallis, OR, ²Department of Botany and Plant Pathology, Oregon State University, OR, USA

Identification of *Phytophthora* strains is critical yet challenging, especially when morphological traits are limited and only molecular data can identify certain species. We created *Phytophthora*-ID 2.0, a website that allows rapid identification of species and strains using previously described genetic markers. For identification, *Phytophthora*-ID 2.0 has two modules, Sequence-ID and Genotype-ID.

Sequence-ID allows users to identify *Phytophthora* species using the carefully curated database of *Phytophthora* species identified with two commonly used barcodes, the internal transcribed spacer (ITS) and the cytochrome oxidase (COX) spacer regions. The Sequence-ID component has been improved from version 1 of the website to be faster and improve uptime. Genotype-ID is new in version 2 and implements the ability to place individuals into clonal lineages based on simple sequence repeat (SSR) identification for the two species *P. infestans* and *P. ramorum* using graphical tools such as UPGMA/NJ dendrograms and minimum spanning networks. All code is open source and available via github and CRAN providing the ability for other groups to develop web-based, interactive genotyping capabilities with minimal technical expertise on any server running R shiny and R.

3. *Phytophthora infestans* isolates collected by Ken Deahl are looking for a new home.

L. Wanner, F. Perez, B. Moravec, K. Deahl; USDA-ARS, Beltsville, MD, USA

A collection of >1300 *Phytophthora infestans* isolates was established by Dr. Kenneth Deahl, USDA-ARS, Beltsville, Maryland, now retired. This collection contains unique and valuable genetic material. Isolates were collected from 21 countries and 18 USA states between 1999 and 2010 (plus 1 from 1995- still viable). They came from potato or tomato leaves or tubers/fruits with late blight symptoms. They were isolated on Rye B media and maintained on sterile rye kernels in water at 20C for up to 19 years, with infrequent transfers. There are also small amounts of dry DNA (for 1016 of the isolates) and freeze-dried mycelia (from 995 isolates) available, both maintained frozen at -20C. The collection is partially characterized, with information on geographic origin, year of isolation, plant host (tomato or potato), mitochondrial haplotype, mating type, GPI isozyme pattern, PEP isozyme pattern, metalaxyl resistance phenotype and RG 57 genotype. Isolates are available to anyone who is interested, but will require a Materials Transfer Agreement and a valid APHIS permit for receiving materials in your lab. Requests for <50 isolates will be plated from rye kernels onto PDB, and sent (if growing) after 3 weeks. For requests for larger numbers of isolates, a few rye kernels containing the isolate will be transferred to vials of sterile water and shipped. The isolates come 'as is' –no guarantee that all are viable, pure and uncontaminated, or that they will be pathogenic. Some isolates may have lost pathogenicity during years of storage. We sub-cultured a subset of isolates from two rye kernels to check viability; 112 were viable, and 122 did not grow. Six (out of a total of 240 isolates checked) were contaminated. It is possible some isolates of special interest could be resuscitated from different kernels if someone wants to try this. Contact: Leslie.Wanner@ars.usda.gov

4. Virus mediated RNA silencing in *Phytophthora*.

S. Patev, W.E. Fry; Department of Plant Pathology and Plant-Microbe Biology, Cornell University, Ithaca, NY, USA

Gene knockdown and transient gene expression are valuable tools utilized in functional genomic experiments that have until now been largely absent from the study of *P. infestans* and other *Phytophthora* species. Gene knockout mutants or individuals expressing transgenes haven been difficult and costly to produce, and because of this are rarely utilized. It has recently been demonstrated that Tobacco Mosaic Virus can infect and reproduce in a number of Oomycetes including *Phytophthora* species. Once persistent and reproducing in a host, genes included in TMV viral constructs for ectopic expression are able to be stably transiently expressed. It has been shown in other systems that if gene constructs are included that are incomplete or without the necessary upstream elements to ensure transient expression, transcription induces RNA silencing

of corresponding native genes. Since TMV infection and persistence has been achieved in *Phytophthora*, this virus mediated silencing is now feasible. TMV constructs containing large segments of GFP or RFP genes were introduced into previously transformed *Phytophthora capsici* isolates each containing a functioning copy of the respective fluorescence gene. Through assessment of resulting fluorescence, TMV constructs were assessed as a viable vector for gene silencing in *Phytophthora*.

5. Genotypic diversity in Estonian populations of *Phytophthora infestans*.

R. Kiiiker, A. Aav, M. Hansen, E. Runno-Paurson; Estonian University of Life Sciences, Tartu, Estonia, USA

The main aim of the study was to determine the genetic variation in *Phytophthora infestans* populations in Estonia using microsatellite SSR markers. Isolates were collected from potato late blight outbreaks during the period of 2010-2012 from 30 potato fields in 7 regions of Estonia. 183 isolates average of 6 isolates per field were chosen for genotyping with SSR marker 12-plex. 128 multilocus genotypes (MLG) were identified, of which 98 (77 %) were present only once. Isolates with the same genotype mainly appeared on the same field. Except for the 6 MLGs (all isolates collected in 2012) which were identified from the other fields nearby. No dominating clonal lineages were detected between the years. At the 12 SSR loci used, up to 56 alleles were found. The number of alleles ranged from 2 in loci Pi70 and SSR2 to 10 in loci D13. During the three years the most frequent alleles for 10 SSR loci were the same, greater differences in allele frequencies appeared in loci Pi4B and G11. In conclusion, genotypic diversity of the late blight pathogen in Estonia is extremely high in almost every sampled field and no dominating clonal lineages appear. Our study indicates that sexual recombination is common in the *P. infestans* populations in Estonia.

6. Comparison of tuber inoculation techniques with *Phytophthora infestans*.

S. Dangj, W. Kirk, P. Somohano; Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, MI, USA

Potato tubers differ in susceptibility to *Phytophthora infestans* and different techniques have been used in various studies to determine the effect of different variables such as temperature, relative humidity, growing season fungicide application and cultivar on the degree of tuber susceptibility. The inoculation techniques were 1) direct injection of a zoospore/sporangial suspension by syringe into the flesh of the tuber; 2) the insertion of colonized agar plugs into wounded tubers; 3) placing inoculum-saturated filter paper onto the eyes of tubers; 4) spraying the tuber surface with a zoospore/sporangial suspension; and 5) direct immersion of tubers into a zoospore/sporangial suspension. The inoculation techniques 1) and 2) involved skin injury of the tubers and the other techniques involved no skin injury. Four genotypes of *P. infestans* (US-8, US-22, US-23 and US-24) and three cultivars of potato (Dark Red Norland, Russet Norkotah and Snowden) were tested. Direct injection of zoospore/sporangial suspension and insertion of colonized agar plugs into tubers caused significantly higher disease incidence and severity compared to all other inoculation techniques. Among the techniques with no skin injury, the immersion method produced consistent disease incidence and severity followed by inoculum-saturated filter paper technique. Spraying the tuber surface with a zoospore/sporangial suspension produced the least infection. Overall, results indicated that the direct injection of zoospore/sporangial suspension and use of colonized agar plugs outperformed all other inoculation techniques; Russet Norkotah was the most susceptible cultivar and US-8 and US-22 were the most aggressive genotypes.

7. Characterization of genetic structure in Mexico populations of *Phytophthora infestans* using simple sequence repeats.

*J. Wang*¹, *M. Larsen*², *R. Gregorio-Cipriano*³, *G. Rodríguez-Alvarado*³, *N. Grünwald*², *S. Fernandez-Pavia*³, *E. Goss*¹; ¹Department of Plant Pathology and Emerging Pathogens Institute, University of Florida, Gainesville, FL, ²USDA-ARS Horticultural Crops Research Unit, Corvallis, OR, ³Laboratorio de Patología Vegetal, Universidad Michoacana de San Nicolás de Hidalgo, Michoacán, México

Phytophthora infestans, the causal agent of late blight in potato and tomato, is a devastating plant pathogen around the world. In the central highlands of Mexico, *P. infestans* undergoes regular sexual reproduction. The biology of these populations together with multilocus genetic data points to Central Mexico as its center of origin. The diversity and population structure of *P. infestans* in the Toluca Valley has been previously described. However, other populations in Central Mexico have not received as much attention and have not been characterized using the simple sequence repeat (SSR) markers currently being used to monitor *P. infestans* in the United States, Europe, and elsewhere. Given that Mexico may be a source of past introductions of new genotypes in the U.S., an understanding the diversity and structure of *P. infestans* in Mexico can contribute to ongoing management of late blight in North America. We genotyped *P. infestans* isolates sampled from eight states in Mexico using a 12-plex SSR assay. First, we used the full eight-population data set to examine genetic structure using Bayesian clustering and discriminant analysis of principal components. We found substantial genetic structure among states. Due to small sample sizes from five states, we utilized samples from Michoacán, Tlaxcala, and Toluca to further investigate genetic diversity. We found significant genetic variation both within and between the three states. Allelic diversity was slightly higher in the Toluca sample than the Michoacán and Tlaxcala samples. Notably, the Michoacán population was genetically distinct from the Toluca population. Characterization of the genetic structure and diversity of *P. infestans* in Mexico, using the same set of hypervariable markers as used to study *P. infestans* in other countries, will contribute to our understanding of the contemporary global diversity and migration of this problematic pathogen.

8. Seed treatments, in furrow and early foliar treatments for control of seed-borne *Phytophthora infestans*.

S. Dangi, *W. Kirk*, *P. Somohano*, *R. Schafer*; Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, MI, USA

The efficacy of nine commercially available fungicides against potato seed-borne late blight caused by different genotypes of *Phytophthora infestans* (US-8, US-22, US-23 and US-24) was evaluated in controlled environment (CE) chambers and in the field. After inoculation of cut seed pieces (immersion in zoospore/sporangium inoculum suspension for 30 min) and application of fungicides plant stand (%) was recorded over a 6-week period after planting and the Relative Area Under the Emergence Progress Curve (RAUEPC) was determined. In CE experiments, all treatments were significantly different from the inoculated check in both years at the final plant stand evaluation. Mandipropamid (single and double rates), flutoloniil + mancozeb, fludioxonil + mancozeb and mandipropamid + mancozeb were not significantly different from the not-inoculated check in terms of plant stand and RAUEPC. There were no significant differences among genotypes of *P. infestans* on plant stand and RAUEPC in 2012 but in 2013 US-22 inoculated seed treatments had a lower plant stand relative to the other genotypes. All the treatments had lower disease incidence compared to the inoculated check. In the field experiment, all the treatments except the foliar application of mefenoxam + chlorothalonil (applied at 95% emergence) had significantly greater plant stand and RAUEPC in comparison to the inoculated check. Responses of some treatments, relative to the not-inoculated not-treated check, indicated that some treatments enhanced

emergence rate in 2012. The period between inoculation and seed piece treatment was increased in 2013 by 12 h, resulting in higher disease severity and lower plant stand compared to 2012. No treatments except mandipropamid + mancozeb (single and double rates), fludioxonil + mancozeb and mancozeb were significantly different in plant stand and RAUEPC in comparison to the inoculated check in 2013. These results demonstrated the efficacy of some commercial fungicides to manage seed borne late blight.

9. Susceptibility of immature and mature potato tubers to different genotypes of *Phytophthora infestans*.

S. Dangj, W. Kirk, P. Somohano; Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, MI, USA

Potato tuber periderm is a significant morphological barrier that prevents infection by various pathogens. The importance of the tuber periderm to infection by *Phytophthora infestans* was determined. Three different cultivars of potato (Dark Red Norland, Russet Norkotah and Snowden) and four genotypes of *P. infestans* (US-8, US-22, US-23 and US-24) were used in the study. The tubers were immersed in the suspension of inoculum for 24 h to determine the susceptibility of potato tubers at different maturity stages. Periderm resistance to physical injury was determined using a skin set measuring device (Halderson Periderm shear tester). The device measured the amount of torsional force [mNm (milliNewton meters)] required to produce skinning injury. Immature and mature Russet Norkotah required the highest torque (273.5 and 450.7 mNm in 2012 and 298.3 and 398.7 mNm 2013, respectively) in comparison to Dark Red Norland (223.3 and 304.1 mNm in 2012 and 212.0 and 296.1 in 2013 mNm, respectively) and Snowden (208.0 and 316.4 mNm in 2012 and 235.5 and 299.5 mNm) in 2013, respectively. Russet Norkotah had thicker periderm and more phellem cells in the periderm than Dark Red Norland and Snowden. Immature cultivars were most susceptible to infection in both years. Immature Dark Red Norland and Russet Norkotah in 2012 and immature Dark Red Norland in 2013 were most susceptible to infection by *P. infestans*. Genotypes US-22 and US-8 were the most aggressive genotypes of *P. infestans*. These results indicated that the immature potato tubers were more susceptible than mature potato tubers.

10. Analysis of late blight outbreak trends using multiple diverse data types.

C. Thomas¹, H. Scherm², J. Olsen³, D. DeBrito⁴, L. Coop⁴; ¹Department of Plant Pathology, University of California, Davis, CA, ²Department of Plant Pathology, University of Georgia, Athens, GA, USA, ³Skoll Global Threats Fund, Palo Alto, CA, USA, ⁴Integrated Plant Protection Center, Oregon State University, Corvallis, OR, USA

The www.uspest.org/wea weather-based IPM Pest and Plant Disease Models and Forecasting System for Agricultural, Pest Management and Plant Biosecurity Decision Support is hosted by the Oregon State University Integrated Plant Protection Center. It provides national quality-controlled infrastructure for real-time weather data, weather forecasts, disease, pest and phenology model outputs including late blight disease model outputs for over 16,000 locations in the 48 contiguous United States, Alaska, and the pacific islands. Virtual weather stations (interpolated weather data for a specific location), forecasts and model outputs also are available on request. The information is public, provided by funding from competitive grants, and other public programs including the National Plant Diagnostic Network, The Western IPM Center and IPM PIPE. Several examples of its use during the past 8 years to monitor late blight outbreaks will be discussed. The relationship between weather-based disease model outputs, cooperative extension reports, laboratory results and internet communications trends will be discussed.

11. Differential susceptibility of thirty-nine tomato varieties to *Phytophthora infestans* clonal lineage US-23.

*Z. Hansen*¹, *I. Small*², *M. Mutschler*³, *W.E. Fry*², *C. Smart*¹; Cornell University, New York State Agricultural Experiment Station, Geneva, NY, USA, ²Department of Plant Pathology and Plant-Microbe Biology, Cornell University, Ithaca, NY, USA, ³Department of Plant Breeding & Genetics, Cornell University, Ithaca, NY, USA

During the summers of 2012 and 2013 thirty-nine tomato (*Solanum lycopersicum* L.) lines or varieties were evaluated for resistance to late blight in three separate field trials. In each trial, late blight was caused by field isolates of *Phytophthora infestans* (Mont.) de Bary clonal lineage US-23. Varieties with the late blight resistance genes Ph-1, Ph-2, Ph-3, and Ph-2 + Ph-3 were included, along with several heirloom varieties with grower-reported resistance and varieties with no known resistance. All six varieties with Ph-2 + Ph-3, along with 'NC25P', which is homozygous for Ph-3 only, showed a high level of resistance. 'Plum Regal F1', which is heterozygous for Ph-3 only, showed moderate resistance. 'Legend', the only variety with Ph-2 alone, also showed moderate resistance. Three heirloom varieties, 'Matt's Wild Cherry', 'Lemon Drop', and 'Mr. Stripey', showed a high level of resistance comparable to that of varieties with Ph-2 + Ph-3. 'New Yorker', possessing Ph-1 only, showed no resistance. Indeterminate varieties had significantly less disease than determinate varieties in two of the three trials. Overall, this study suggests that tomato varieties with both Ph-2 and Ph-3 can be used to effectively manage late blight caused by *P. infestans* clonal lineage US-23. Varieties possessing only Ph-2, or heterozygous for Ph-3, were better protected than those without any late blight resistance, but might still require supplemental fungicide applications, while the variety that was homozygous for Ph-3 was highly resistant. Several heirloom varieties were also highly resistant, and the unknown mechanism of their resistance warrants further research. Finally, the plasticity observed in United States *P. infestans* populations over the past several decades necessitates continued monitoring for genetic changes to the pathogen that could lead to the breakdown of resistance reported here.

12. Antimicrobial peptides from seeds of wild plants suppress *Phytophthora infestans*, the causative agent of late blight disease in tomato and potato.

*E. Rogozhin*¹, *A. Smirnov*²; ¹Shemyakin and Ovchinnikov Institute of Bioorganic Chemistry, Russian Academy of Sciences, Moscow, Russia, ²Timiryazev Russian State Agrarian University, Moscow, Russia

Among diverse defense mechanisms exploited by plants to protect themselves from invaders and activated upon their recognition, chemical defenses play a crucial role. Secondary metabolites and polypeptide-based molecules comprise a vast arsenal of defensive compounds that prevent pathogen-induced colonization and destruction of plant tissues, with antimicrobial peptides (AMPs) supposed to be of prime importance. AMPs are ubiquitous throughout plant and animal kingdoms. In this study, we determined the functional activity of peptides from the seeds of certain wild plants: barnyard grass, common chickweed, dandelion, and black seed, and found that more than 20 isolated peptides belonged to one of five AMP families and 2 families of plant protease inhibitors, and possessed an ability to suppress *P. infestans* (Odintsova et al., 2008, 2010; Rogozhin et al., 2009, 2011, 2012; Nolde et al., 2011; Slavokhotova et al., 2011, 2014). It was accomplished through inhibition of zoospore out coming, lessening of mycelium growth, and significant reduction of oomycete development inside plant tissues (potato tuber discs and leaves). Our data show that peptides isolated from plants belonged to various botanical families that are not attacked by late blight, can participate in inhibition of its development, and eventually may play a role in forming resistance to this disease. The peptides studied are prospective candidates for genetic engineering to create genetically modified breeds resistant to late blight.

13. Frequency of resistance to *Phytophthora infestans* in potato seedling families from dedicated late blight parental crossing blocks.

G. Secor, V. Rivera, S. Thompson, J. Rodriguez; Department of Plant Pathology, North Dakota State University, Fargo, ND, USA

Dedicated crossing blocks consisting of parents with resistance to *Phytophthora infestans* were used to develop seedling populations of potato during the five year period from 2009-2013. A sub sample (n=100) of each family were screened by a detached leaf assay to estimate the incidence of resistance in each family. The goal of this work was to determine if this procedure could identify families with increased levels of late blight prior to field selection based on agronomic traits. The parents used for crossing were similar each year. The US8 A2 genotype was used for screening in 2009-2011, and US24 A1 used in 2012-2013. A total of 29,186 seedlings in 379 families were screened during the five year period. Late blight on detached leaves was scored on a scale from 0-3, with zero hypersensitive and three with large sporulating lesions after incubation for five days at 18-20°C. The percentage of scores in each category from 0-3 ranged from 0.1-2.9 %, 0.9-11.4 %, 1.9-10.6 % and 75.5-97.1 % respectively. The incidence of resistance to *P. infestans* in the seedling families did not change appreciably during this five year period with resistance categories remaining low. This extensive study shows that traditional breeding alone may not be sufficient to develop populations of potato with high frequencies of late blight for subsequent agronomic selection, and other techniques such as gene transfer and cisgenic stacking of R genes may be necessary to increase the frequency of resistance. However, the resistance identified may be durable because of the complexity of the Pi genotypes used for screening and the possibility of natural gene stacking.

14. Small plot research for testing *Phytophthora infestans* control by multiple products for fresh market Brandywine tomatoes grown on the central coast of California.

F. Sances¹; V. Shinde¹, M. LeBlanc¹, K. Coons¹, E. Flora¹, S. Ockey²; ¹Pacific Ag Research, San Luis Obispo, CA, ²Certis USA, L.L.C, Columbia, MD, USA

Late season tomato growers on the central coast of California face an ideal climate for late blight (*Phytophthora infestans*) development, with mild temperatures and humidity from marine fog. The fresh market tomato industry in this region depends on multiple applications of conventional and/or biological fungicides. Here we present data from two trials which compare efficacy of multiple products, alone or in rotation, in a small plot research format between August and November of 2013. Severity ratings were statistically lower for plants treated with all tested fungicides (Bravo Weather Stik, Inspire, Revus, BmJ WG, Ridomil Gold, Topguard, Koverall and Quadris) compared to the untreated check, until a rapid increase in disease inoculum in late October. AUDPC calculations between severity ratings which included or excluded November assessments showed disease control for Quadris (0.0975 lb ai/a, applied weekly) and Ridomil Gold (2 pt/a, applied bi-weekly) were most impacted and had greatest loss of control. These data also showed an organic fungicide, BmJ WG at 4.5 fl oz/100gal applied alone at weekly intervals, was more effective in late blight control than conventional standards. Our service, using small plot systems, analysis of diverse data sets and the truncation of high pressure disease ratings, is ideal for comparing multiple products and interpreting novel trends.

15. Transforming potato late blight point forecasts for use with the National Digital Forecast Database.

W. Kirk¹, K. Baker², P. Roehsner²; ¹Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, MI, USA, ²Western Michigan University, Kalamazoo, MI, USA

As publicly available weather forecasting datasets advance in accuracy and spatial and temporal resolution, it is relatively simple to apply these established models to new datasets but the results may deviate from what users of decision support systems have come to expect. Potato late blight risk models were some of the earliest weather-based models. This analysis compares two types of potato late blight risk models that were originally trained on location specific (point) data in Michigan. A unique system using NoSQL was developed to train, validate and implement potato late blight risk modeling using a grid data format. Each model was tested two ways; it was first deployed directly with gridded weather forecasting data as a replacement for point data, and then retrained on the gridded data. Despite consistently lower overall accuracy, the grid trained artificial neural network model was deemed of better quality for use by stakeholders because of its accuracy on days with potato late blight risk. However, the success of the model was dependent upon its retraining using the newly available data source. In the direct implementation scenario without retraining, a simpler modified-Wallin model achieved better results than the neural network model.

16. Assessment of bacterial populations obtained from native Chilean potatoes with activity on *Phytophthora infestans* cell wall glucans.

E. Moya-Elizondo¹, P. Tejada-Tribeño²; ¹Universidad de Concepción, Biobío, Chile, ²Universidad Austral de Chile, Los Ríos, Chile

Late blight disease caused by *Phytophthora infestans* (Mont.) De Bary is considered the most devastating disease of potato crops in Chile and worldwide. In Chile, during the last two decades, this disease has become more severe and metalaxyl resistance isolates of the pathogen have been detected. This situation is forcing to develop new strategies for managing this disease. In this study, bacterial populations isolated from the phyllosphere and endosphere of four native Chilean *Solanum tuberosum* L. cultivars (Bruja, Cabra, Cabrita y Chona negra) and the commercial potato cultivar Desireé were assessed in their abilities to growth on agar mycelium of *P. infestans*. Sixty-one bacterial isolates were able to grow on agar mycelium and their 1, 3 β -glucanase activity was determined by measuring their degradation haloes in a plate assay based in laminarin and carboxymethyl pachyman as carbon sources. From the total bacterial isolates obtained from the agar mycelium, 41% were obtained from the endosphere and 59% from the phyllosphere. Cultivars Cabrita and Chona had the highest number of isolates obtained from agar mycelium with 17 and 22 isolates, respectively. Degradation halo for the isolates averaged 2.8 mm and ranged between 10.8 mm to 0.0 mm with 90.2% of the bacterial isolated showing some 1, 3 β -glucanolityc activity. From those isolates, 24 were chosen for subsequent test on potato plants. We expect to assess the ability of these isolates to induce plant resistance or to control directly late blight disease on potato plants. Project DID-UACH S-2011-03.

17. A coalescence analysis of *Phytophthora infestans* in Scandinavia reveals population structuring.

L. Sjöholm, B. Andersson, J. Yuen; Sveriges lantbruksuniversitet, Uppsala, Sweden

The genotypic diversity and the migration patterns of *Phytophthora infestans* in the Nordic countries is consistent with sexual reproduction and limited migration. Isolates of *P. infestans* from outbreaks in 43 fields sampled in 2008 were collected using stratified sampling with country, field, and disease

foci as the different strata. Microsatellites were used as markers to determine the genotypic variation in the sampled material. The results show a high genotypic variation of *P. infestans* in the Nordic countries. Most of the genotypes found only once among the collected isolates, and for most cases where a genotype occurred twice, it was in the same field. The major part of the genotypic variation was observed within the fields, with low differentiation between the fields. The observed low association of alleles among loci is consistent with frequent sexual reproduction of *P. infestans* in the Nordic countries. Coalescence analyses with the program 'Migrate' was used to examine if there was differentiation between the countries. Several models were compared using Bayes factors. These analyses did not support a single common population for the four countries, thus indicating some degree of geographic differentiation. Analyses of migration patterns showed differing levels of gene flow among the Nordic countries. No correlation between migration rates and geographical distance could be seen. This could be explained by different degrees of genetic similarity between the pathogen populations in the different countries.

18. Sensitivity to eight systemic fungicides in *Phytophthora infestans* and fungicides efficacy in controlling potato late blight in North of China.

W. Wang, R. Meng, J. Zhao; Plant Protection Institute, Hebei Academy of Agricultural and Forestry Sciences, Hebei, China

Foliar spray of fungicides play an important role in the integrated management of potato late blight, which often causes destructive losses potato tubers in one-cropping areas of North of China. [Objectives] to clarify the sensitivity shift of *P. infestans* to the common fungicides and select the effective fungicides, sensitivity to eight fungicides was tested by mycelial growth rate assay in 266 isolates collected in 2011-2013 from potato fields of Hebei, Liaoning, Jilin and Inner Mongolia. And the field trials on controlling efficacy of fungicides against potato late blight were conducted at Dunhua, Jilin and Weichang, Hebei in 2012-2013. [Results] The populations of *P. infestans* tend to be less sensitive to metalaxyl, mefenoxam, cymoxanil, azoxystrobin and fluopicolide, but no obvious variation occurred in sensitivity to dimethomorph and mandipropamid. EC₅₀ of all the isolates to metalaxyl and mefenoxam ranged from 10 ug/ml to 100 ug/ml, and below 1 ug/ml to the other six fungicides. In the field trials, 400 g/L SC, 5% WG, and 250 g/L EW of the synergistic combination (1:4) of fluopicolide + pyraclostrobin (288-480 g a.i./hm²) gave about 90% control efficacy to late blight. Applied at the recommended rates, dimethomorph 50% WG (300 g a.i./hm²), pyraclostrobin 250 g/L EC (150 g a.i./hm²), mandipropamid 250 g/L (150 g a.i./hm²), mefenoxam + mancozeb 68% WG (1024 g a.i./hm²), fluopicolide + propamocarb 687.5 g/L SC (1031g a.i./hm²), mancozeb 80% WP (2400 g a.i./hm²), fluazinam 500 g/L SC (200 g a.i./hm²), cymoxanil + mancozeb 72% WP (1400 g a.i./hm²) and azoxystrobin 250 g/L SC (150 g a.i./hm²) gave control efficacy of 86.4%, 83.9%, 85.9%, 80.5%, 93.6%, 78.0%, 78.9% 80.0% and 80.3%, respectively. [Conclusion] *P. infestans* populations from the four provinces widely developed resistance to metalaxyl and mefenoxam, but remained sensitive to azoxystrobin, cymoxanil, dimethomorph, mandipropamid, pyraclostrobin and fluopicolide. Fungicides containing dimethomorph, mandipropamid, pyraclostrobin, fluopicolide, or cymoxanil can effectively control potato late blight in areas where metalaxyl- or mefenoxam-resistant isolates predominate.

19. Investigating potential of tomato fruit with late blight to serve as a source of inoculum for seedlings growing out of these fruit.

M. McGrath, V. Kramer, A. Gardner; Department of Plant Pathology, Cornell University, Long Island Horticultural Research and Extension Center, Riverhead, NY, USA

The impetus for this project was an outbreak of late blight in a greenhouse for which volunteer tomatoes appeared to be a possible source of the pathogen (*Phytophthora infestans*). Fruit of 13 tomato cultivars that were naturally infected with genotype US-23 were obtained from a garden and research plantings in fall 2011 and 2013. Fruit were put on a thin layer of potting mix in seeding trays then covered with potting mix on 7 Sep 2011 and 17 Oct 2013. Trays were kept in a greenhouse and watered as needed. Seedlings began emerging within 7 days. Seedlings were moved in groups to pots. Late blight symptoms appeared on lower stems starting 13 days after set up. The last affected seedlings were observed 56 and 79 days after experiments were set up in 2011 and 2013, respectively. Lower stems turned dark brown on affected seedlings. Diagnostic sporulation was observed, typically at a very low level until incubated in a moist environment. Cultivars with affected seedlings were Black Cherry (58% of seedlings in 2013), Juliet, Sakura Honey (100%), SunGold (13%), Sweet Treats, and Wapsipinicon Peach (32%). No symptoms developed on any of the 40 seedlings that emerged from asymptomatic mature fruit of SunGold, thus these fruit were not latently infected. No symptoms developed on any seedlings of Orange Banana (45 seedlings) or Black Zebra (13). Additionally, symptoms developed on seedlings growing from commercial seed put inside affected fruit in place of the seeds there, but not from seed removed from affected fruit. In conclusion, *P. infestans* can survive for several weeks in affected tomato fruit tissue that is covered by soil mix and can infect volunteer seedlings emerging from this fruit. Only one genotype was found on Long Island both years, thus it is highly unlikely oospores had formed in affected fruit.

List of participants

Sidrat Abdullah
South Dakota State Univ.

Audrey Ah-Fong
Univ. of California, Riverside

Sandra Alcaraz
Gowan Company

Khalil Al-Mughrabi
Government of New
Brunswick

Monica Alvarado-Hernandez
Gowan Company

Bjorn Andersson
Swedish Univ. of Agric.
Sciences

Mitchell Bauske
North Dakota State Univ.

Jaime Blair
Franklin & Marshall College

Susan Boyetchko
Agric. & Agri-Food Canada

Kristen Brown
Univ. of Maine

Odille Carisse
Agri. & Agri-Food Canada

Claudia Caro
Gowan Company

Nicolas Champouret
J.R. Simplot Company

Brady Code
Syngenta Canada

Fouad Daayf
Univ. of Manitoba

Sandesh Dangi
Michigan State Univ.

Giovanna Danies
Cornell Univ.

Patricia de Sa Snow
USDA APHIS

Claudia Diaz
Oklahoma State Univ.

Kathryne Everts
Univ. of Maryland
College Park

Mamadou Fall
Univ. of Sherbrooke

Dimitri Fonseka
North Dakota State Univ.

William Fry
Cornell Univ.

Kenneth Frost
Univ. of Wisconsin, Madison

Carla Garzon
Oklahoma State Univ.

Amanda Gevens
Univ. of Wisconsin, Madison

Erica Goss
Univ. of Florida

Niklaus Grünwald
Oregon State Univ.

Beth Gugino
Penn. State Univ.

Emily Haga
Johnnys Selected Seeds

Zachariah Hansen
Cornell Univ.

Jianjun Hao
Univ. of Maine

Michael Harding
Alberta Agric. &
Rural Development

Shafiqul Islam
Michigan State Univ.

He Jiang
Univ. of Maine

Dennis Johnson
Washington State Univ.

Steven Johnson
Univ. of Maine Coop Ext.

Howard Judelson
Univ. of California, Riverside

Geert Kessel
Plant Research International

Riinu Kiiker
Estonian Univ. of Life
Sciences

William Kirk
Michigan State Univ.

Brian Knaus
USDA-ARS

Paul Kuhn
Syngenta Crop Protection

Michael Langemeier
Purdue Univ.

Yangxuan Liu
Purdue Univ.

Hector Lozoya-Saldana
Autonomous Univ. of
Chapingo

Saltanat Mambetova
Michigan State Univ.

Nayara Marangoni
Univ. of Maine

Michael Matson
Univ. of California Riverside

Margaret McGrath
Cornell Univ.

Charles Mellinger
Glades Crop Care Inc.

Ernesto Moya
Universidad de Concepcion

Kevin Myers
Cornell Univ.

Gilberto Olaya
Syngenta Crop Protection

Aidee Orozco
McCain Foods Limited

Sean Patev
Cornell Univ.

Sarah Pethybridge
Cornell Univ.

Anette Phibbs
Wisconsin Dept. of Agric.
Trade & Consumer
Protection

Kate Rappaport
USDA Aphis BRS

Silvia Restrepo
Universidad De Los Andes

Pele Rich
North Hennepin Community
College

Diana Rios
Gowan Company

Jean Ristaino
North Carolina State Univ.

Viviana Rivera
North Dakota State Univ.

Pamela Roberts
Univ. of Florida

Eugene Rogozhin
Shemyakin and Ovchinnikov
Institute of Bioorganic
Chemistry

Frank Sances
Pacific Ag Research

Gary Secor
North Dakota State Univ.

Reza Shekasteband
Univ. of Florida

Christopher Shepherd
Dupont Crop Protection

Taiki Shiobara
ISK Bioscience

Lina Sjöholm
Swedish Univ. of Agric.
Science

Ian Small
Cornell Univ.

Christine Smart
Cornell Univ.

F.D. Smith
Bayer Crop Science

Joseph Steinhardt
Cornell Univ.

Walter Stevenson
Univ. of Wisconsin, Madison

Martha Sudermann
St. Olaf College

Allison Tally
Syngenta Crop Protection

Connie Tande
South Dakota State Univ.

Carla Thomas
Univ. of California, Davis

James Tucker
Paul Smith's College

Brett Tyler
Oregon State Univ.

Benjamin Valiente
Anasac Chile S.A.

Leon Van Eck
Univ. of Minnesota

Karen Walker
USDA APHIS

Wenqioa Wang
Hebei Academy of Agric. &
Forestry Sciences

Jianan Wang
Univ. of Florida

Leslie Wanner
USDA ARS

Eugene Wisakowsky
Proptera LLS

Xiaoyu Zhang
Agric. Univ. of
Inner Mongolia

Notes