RTB Workshop Report

Third AsiaBlight Meeting

Beijing, China

25-27 October 2019

Christelle Lasserre, Alberto Maurer,
Min Li, Philip Kear, Xiaoping Lu,
Jorge Andrade-Piedra

J U L Y 2 0 2 0

CGIAR Research Program on Roots, Tubers and Bananas

Led by CIP International Potato Center

Alliance Bioversity International CIAT International Center for Tropical Agriculture Since 1967 Science to cultivate change

cirad Agricultural Research for Development

IITA Transforming African Agriculture

RTB Workshop Report

Correct citation: Lasserre, C., Maurer, A., Li, M., Kear, P., Lu, X, and Andrade-Piedra, J. 2020. Third AsiaBlight Meeting. Beijing, China. 25-27 October 2019. Lima (Peru). CGIAR Research Program on Roots, Tubers and Bananas (RTB). RTB Workshop Report. Available online at www.rtb.cgiar.org

Published by the CGIAR Research Program on Roots, Tubers and Bananas

The CGIAR Research Program on Roots, Tubers and Bananas (RTB) is a partnership collaboration led by the International Potato Center implemented jointly with the Alliance of Bioversity International and CIAT (International Center for Tropical Agriculture), the International Institute of Tropical Agriculture (IITA), and the Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD), that includes a growing number of research and development partners. RTB brings together research on its mandate crops: bananas and plantains, cassava, potato, sweetpotato, yams, and minor roots and tubers, to improve nutrition and food security and foster greater gender equity especially among some of the world's poorest and most vulnerable populations.

www.rtb.cgiar.org

Contact:

RTB Program Management Unit

International Potato Center (CIP)

Apartado 1558, Lima 12, Peru

rtb@cgiar.org • www.rtb.cgiar.org


3rd AsiaBlight International meeting
第三届亚太马铃薯晚疫病防治协作网国际会议

Contents

Acronyms 5

Preface 6

Acknowledgments 7

AsiaBlight committees and representatives 8

Oral presentations 9

Posters 43

Annexes 46

Annex 1. Program 46

Annex 2. Participants 50

Acronyms

AFBI	Agri-Food & Biosciences Institute
ALAP	Latin American Potato Association
BSU	Benguet State University
CAU	China Agricultural University
CCCAP	CIP-China Center for Asia-Pacific
CIP	*Centro Internacional de la Papa* (International Potato Center)
DSS	Decision support system
HEBAU	Hebei Agricultural University
HEBSPP	Hebei Society of Plant Pathology
INIA	*Instituto de Investigaciones Agropecuarias* (Institute of Agricultural Research)
JSPS	Society for the Promotion of Science
NPRCRTC	Northern Philippines Root Crops Research and Training Center
PASS	Pakistan Agricultural Scientific Society
RDA	Rural Development Administration
RTB	CGIAR Research Program on Roots, Tubers and Bananas
SAYS	Scientific Association of Young Scholars
TSAU	Tashkent State Agrarian University
YAAS	Yunnan Academy of Agricultural Sciences

Preface

AsiaBlight is an inclusive network of scientists, government officials, businesspersons, farmers, extensionists, and other stakeholders working towards improving the management of potato late blight caused by *Phytophthora infestans*. Together, the AsiaBlight network aims to build knowledge and capacity, share information, promote collaboration, and perform research on populations of *P. infestans* and management of late blight in Asia.

The AsiaBlight network started in Nepal in 2014. This meeting was followed by a second meeting in parallel to the World Potato Congress held in Beijing in 2015. Chinese scientists joined the AsiaBlight network in 2018, at the Wuxi Late Blight workshop organized by the University of Chongqing. At that meeting, the International Potato Center's (CIP) China Center for Asia Pacific (CCCAP) accepted to host and support the AsiaBlight network. More information about AsiaBlight can be found on the web site https://www.asiablight.org/.

The 3rd. AsiaBlight meeting was hosted by CCCAP and the College of Plant Protection at the China Agricultural University (CAU) in Beijing in October 2019. The meeting included sessions on the following topics: (1) potato late blight in Asia and beyond; (2) late blight biology, genetics, and population dynamics in Asia; (3) plant-pathogen interactions and potato resistance; and (4) late blight management, fungicides, and decision support systems. The program included 33 oral presentations (7 of them presented as posters as well), and three posters (Annex 1). The meeting was attended by 111 participants (Annex 2) from 17 countries: Bangladesh, Belgium, Chile, China, Georgia, India, Japan, Nepal, the Netherlands, Pakistan, Peru, the Philippines, the Republic of Korea, the United Kingdom, the United States, Uzbekistan, and Vietnam.

Acknowledgments

This research was undertaken as part of, and funded by, the CGIAR Research Program on Roots, Tubers and Bananas (RTB) and supported by CGIAR Trust Fund contributors. Funding support for this work was provided by the following companies and organizations: Farmneed, HSJD, Sinochem Crop Care, ShuangJihuagong, Wageningen University & Research, YedaYinong.

AsiaBlight committees and representatives

Coordination Committee

Oscar Ortiz	International Potato Center (CIP), Peru
Xiaoping Lu	CIP, China
Alberto Maurer	CIP, China (until February 2020)
Christelle Lasserre	CIP, China (until February 2020)
Philip Kear	CIP, China
Jorge Andrade-Piedra	CIP, Peru

Scientific Committee

Pham Thi Thu Huong	Field Crops Research Institute, Vietnam
Sanjoy Guha Roy	West Bengal State University, India
Tongle Hu Plant	Hebei Agricultural University, China
Seishi Akino	Hokkaido University, Japan
Mohammad Rashidul Islam	Bangladesh Agricultural University, Bangladesh

Country Representatives

Kwang-Soo Cho Senior	Rural Development Administration, Korea
Zurab Khidesheli	Scientific-Research Center of Agriculture, Republic of Georgia
Sanjoy Guha Roy	West Bengal State University, India
Alexey Vasilievich Zagursky	Kyrgyz National Agrarian University, Kyrgyzstan
Waqas Raza	University of Sargodha, Pakistan
Xingbi Che	Chongqing Plant Protection Institute, China
Buddhi Prakash Sharma Adhikari	Nepal Agricultural Research, Nepal
Pham Thi Thu Huong	Field Crops Research Institute, Vietnam

Advisor

Louise Cooke	Queen's University, Belfast, UK

Oral presentations

Presentation 1. How does the EuroBlight network help to control the aggressive potato late blight pathogen?

Huub Schepers[1], Jens Grønbech Hansen[2], and Alison Lees[3]

[1]Wageningen University and Research, the Netherlands; [2]Aarhus University, Denmark; [3]The James Hutton Institute, UK

Presentation in pdf format: here

EuroBlight, a European network of scientists, advisors and representatives from agrochemical and potato breeding companies, meets every 2nd year (www.euroblight.net) to coordinate and discuss late blight research. During the workshops, research results are shared, and current challenges and opportunities for late blight control are identified. EuroBlight is organized in working groups that are active in between the workshops. Key activities are: i) monitoring of late blight SSR based genotypes across Europe ii) maintenance and updating of the EuroBlight fungicide table based on coordinated fungicide efficacy trials and iii) development of late blight decision support systems. Data and web tools are managed by a Potato Late Blight Toolbox that controls databases and the generation of interactive map tools and charts available on the EuroBlight web site. The recognised success of EuroBlight has inspired the creation of other international late blight networks, notably USABlight (www.usablight.org), Tizón Latino in Latin America (www.tizonlatino.wordpress.com) and AsiaBlight (www.asiablight.org). Collaboration between these networks through joint research and information sharing makes it possible to improve control of late blight on a global scale. One important aspect of collaboration has been the harmonization of protocols for determining the genotype of *Phytophthora infestans* isolates and linking this to phenotype, allowing an improved understanding of the pathogen population worldwide. The network of networks can be used to generate the global genetic landscape of *P. infestans*, understand drivers for spread and evolution and to develop DSSs adapted to regional conditions, including the production of training and extension material for (smallholder) farmers in potato growing regions worldwide.

Presentation 2. Trends in recent late blight scientific publications

Alberto Maurer

CIP-China Center for Asia Pacific, Beijing, China

Presentation in pdf format: here

This presentation will focus on the most novel trends regarding molecular research on *P infestans* and how this research may influence the future of *P infestans* management.

Also, we will focus on the latest developments regarding the management and control of late blight in the field. We will try to address potential future issues regarding late blight under climate change, transgenic research, and other technologies and their effect on small potato farmers in Asia.

Presentation 3. EuroBlight tracking of evolving European populations of *Phytophthora infestans* as an aid to late blight management

Cooke David EL[1], Hansen Jens G[2], Lassen Poul[2], Lees Alison K[1], and Kessel Geert JT[3]

[1]The James Hutton Institute, Dundee, Scotland, UK; [2]Aarhus University, Tjele, Denmark; [3]Wageningen University and Research, Wageningen, the Netherlands

Presentation in pdf format: here

Late blight, caused by *Phytophthora infestans*, causes significant losses to potato and tomato crops on a global scale. The timing and effectiveness of blight management depends on the pathogen's response to the environment, primary inoculum type, virulence to host resistance and sensitivity to active fungicide ingredients. The pathogen population is continually evolving and emerging clonal lineages with new traits highlight the need to tailor management to the local pathogen population. This has prompted the EuroBlight consortium to collect data on the genetic diversity of *P. infestans*, analyzed with simple sequence repeat (SSR) genetic markers. Our surveys of late blight infected crops alongside research institutes and agrochemical companies from 2013–2018 has generated a database of over 8400 geo-tagged European samples. Standardized protocols, SSR allele scoring and a single data format were required to build the database, associated analysis tools and an elegant mapping interface to view the data. A complex population structure is observed with around 70% of the population dominated by a few widely disseminated clonal lineages; see maps at www.euroblight.net. The SSR diversity within lineages has also been tracked over time and highlights the local spread of some sub-clonal variants. In contrast to the clones, 20–30% of the sampled European population comprises genetically diverse pathogen populations consistent with local, ephemeral oospore-derived sexual populations. Integration with the R-based population genetics application *poppr* is providing deeper insights into pathogen diversity at a range of scales in Europe. When combined with phenotypic data on the traits, the EuroBlight approach provides an early warning system that helps mitigate management failures due to the emergence and spread of new clones. The flexible structures, systems and tools developed by EuroBlight partners will be presented to highlight the benefits of such tracking of *P. infestans* in potato and tomato cropping systems in Asia.

Presentation 4. AsiaBlight: The beginnings

Louise Cooke

Queen's University, Belfast, UK

Presentation in pdf format: here

Late blight (LB) is a significant constraint to potato production throughout Asia. Although the region has numerous researchers working on LB, their efforts have not been coordinated, so an overall picture of *Phytophthora infestans* in Asia, including population dynamics, distribution of major genotypes and the most effective control measures, is lacking.

To overcome these problems, AsiaBlight, a pan-Asian Late Blight scientific network, was initiated in 2014-15 under the auspices of the International Potato Center by Dr. Greg Forbes. AsiaBlight initially focused on establishing a coarse-scale map of *P. infestans* in the region with the assistance of Dr. Louise Cooke. FTA cards (funded by Bayer) were distributed by the Inner Mongolia Potato E & T Center, Hohhot, China to contacts across the region, their voluntary assistance and the invaluable help of Dr. David Cooke (James Hutton Institute, UK) with genotyping are gratefully acknowledged.

Challenges highlighted by this project included:

- obtaining LB samples across a vast, politically disparate region
- loss of contacts and consequently of FTA cards
- restrictions owing to biosecurity legislation
- genotyping: lack of continuity, difficulty in standardising allele calling

The project, nonetheless, achieved recognition of AsiaBlight, highlighted the benefits of Public-Private Partnerships and succeeded in achieving voluntary collection of LB samples by many contacts across the region and their SSR genotyping. The aggressive genotype 13_A2 (Blue 13), already reported from China and India, was shown to be widespread across continental Asia and present in Georgia, Nepal, Bangladesh, and Vietnam. In contrast, 13_A2 was not detected in the *P. infestans* populations of those islands of Asia that were sampled; in each case, distinct and disparate populations were found.

This initial, mostly voluntary, network is now being developed by the CIP–China Center for Asia-Pacific, which took on the challenge of implementing a self-sustaining AsiaBlight in 2018.

Presentation 5. AsiaBlight's present and future: Organization, events, a developing network

Christelle Lasserre and Alberto Maurer

CIP-China Center for Asia Pacific, Beijing, China

Presentation in pdf format: here

Starting in 2018, the CIP–China Center for Asia-Pacific (CCCAP) has taken up the challenge of implementing a self-sustaining AsiaBlight network. Since September 2018, CCCAP has had many discussions with LB stakeholders in Asian and previous meeting organizers, to understand better how the new AsiaBlight network can respond to the expectations of the region. CCCAP put together an international scientific committee for AsiaBlight and is gathering country representatives to relay the info. AsiaBlight will focus on training and capacity building, aiming to increase understanding of LB through collaborations and also perform research to establish a pan-Asia community of LB stakeholders.

AsiaBlight held its 3rd International meeting in October 2019 and two training workshops are planned end of 2019. AsiaBlight workshops and training will be in Chinese and English to support communication among experts.
In January 2019, an AsiaBlight WeChat group was launched, a Twitter feed, as well as a Facebook page. AsiaBlight's website was launched in April 2019.

A broader sampling effort through collaboration within eight different provinces of China has also been started as a pilot study. Fungicide efficacy analysis and variety performance studies are currently being established. In parallel, academic researchers are being identified and projects planned for a better understanding of the LB population throughout the region. Thanks to an intensive fundraising effort, CIP-CCCAP hopes AsiaBlight will become financially independent in the next few years.

Presentation 6. Potato late blight in Latin America

Acuña, Ivette[1]; Florencia Lucca[2], Silvia Restrepo[3]; and Jorge Andrade-Piedra[4]

[1]Intituto de Investigaciones Agropecuarias, Chile; [2]Instituto Nacional de Tecnología Agropecuaria, Argentina; [3]Universidad de Los Andes, Colombia; [4]International Potato Center CIP, Peru

Presentation in pdf format: here

Late blight is the most important potato disease in Latin America, causing significant production losses and affecting food security. Therefore, a group of researchers has decided to constitute the Tizonlatino network (https://tizonlatino.wordpress.com/), to share knowledge and protocols about the pathogen, the disease and its management, with the goal to advance its control sustainably. This group is performing studies to monitor and characterize the causal agent of late blight in different countries, disease management and control strategies using predictive systems. Phytophthora associated with Solanaceae in Latin America is diverse; this is the case of *P. andina, S. muricatum, S. betaceum* in Ecuador, Perú, Colombia. On the other hand, the *P. infestans* population shows a clonal population in some countries, such as in Colombia, Ecuador, Costa Rica, Peru and Chile. Also, much work has been done searching variety resistance in Solanaceae diversity. It is expected that there are more unidentified genes or genes interaction enhancing the resistance. Therefore, a new source of resistance is being studied in Peru, Chile, Colombia and Bolivia.

Additionally, combining different cultivar resistance and fungicide strategies, suggested that the use of cultivars with reduced susceptibility to late blight can be managed with reduced fungicide rates and longer application intervals, thus offering more economical control of this disease, saving between 30 to 60% of the fungicide input. Moreover, disease forecasting allows better control of a disease and more efficient use of fungicides. In Argentina, Chile, Perú and Ecuador a decision support system (DSS) have been implemented to develop integrated pest management, with reductions in fungicides sprays of up to 50%. Today, the Tizon Latino network is working in new studies focus on Late blight DSS as a tool for climate change adaptation in Latin America with the finance support of a FONTAGRO grant.

Presentation 7. Worldwide migrations, evolutionary relatedness, and the reemergence of *Phytophthora infestans* in Asia

Jean B. Ristaino

Dept. of Entomology and Plant Pathology, North Carolina State University, Raleigh, NC.

Presentation in pdf format: here

Phytophthora infestans, the causal agent of potato late blight, was responsible for the Irish potato famine and is still a threat to food security globally. We have developed disease surveillance and mapping system called USAblight.org to report disease outbreaks in the USA and alert stakeholders. Recent US populations are dominated by the largely mefenoxan sensitive US-23 clonal lineage. We have also identified and tracked the spread of historic lineages of *P. infestans* using multilocus genotyping and next-generation sequencing, geospatial analytics and data mining methods. The same unique multilocus genotype, named FAM-1, caused both US and European historic outbreaks, shared allelic diversity and grouped with the oldest samples collected in Colombia, and formed a genetic group that was distinct from more recent aggressive lineages. Population genomics data from historic *P. infestans* indicates admixture of ancestral lineages with *P. andina* in the Andes. The FAM-1 lineage was widespread and found in the continents of Africa, Asia and Australia/Oceania including Japan (1901), Russia (1903), The Philippines (1910), India (1913), Latvia (1932), China (1938), Malaysia (1950) and Nepal (1954). The US-1 lineage was found later in China (1950), India (1968), Thailand (1981), Bhutan (1986), and Malaysia (1987). In China, the SIB-1 lineage was widespread between 1998-2004 and now many different aggressive lineages occur, suggesting more recent migration events. There is a need to expand geospatial surveillance in Asia with more rapid pathogen detection sensors and bioinformatics databases to report, contain and limit outbreaks of this important plant disease.

Presentation 8. Screening for late blight resistance in wild species and landraces in Peru, and the strategy and resistant materials from CIP's breeding program

Jorge Andrade-Piedra[1], Willmer Perez[1], Priscilla Rojas[2], Lesly Alarcon[3], Soledad Gamboa[1], Manuel Gastelo[1], Claudio Velasco[1], Anne Njoroge[1], Peter Kromann[1], Hannele Lindqvist-Kreuze[1]

[1]International Potato Center, Peru; [2]Universidad Nacional Agraria La Molina, Peru; [3]Universidad Nacional del Centro del Peru

Presentation in pdf format: here

We describe the strategy that the International Potato Center applies to support farmers to manage potato late blight in developing countries. Clones with genetic resistance are the cornerstone of this strategy and are distributed to countries where late blight is the main biotic constrain for potato production. Screening for resistance in wild species and potato landraces helps to identify sources of resistance to late blight, so that they can be used by breeders or by farmers directly, in the case of potato landraces. Pathogen population studies provide information on the genetic makeup of the pathogen that has a direct effect on disease management. We illustrate this by providing an example from Peru. Information about the pathogen and the host is then integrated with weather information using a decision support tool (DST) adapted for low-scale farmers to help them to decide which fungicide spray and when. We describe the validation process to adapt this DSS to local conditions and new studies that are being conducted to evaluate its impact. Training to farmers on the basics of late blight (symptoms, causal agent, the effect of genetic resistance, fungicide use, etc.) is achieved with the support of training materials and methodologies that had been rigorously tested. We conclude by providing perspectives on disease management in developing countries.

Presentation 9 (also presented as poster). Investigation of *Phytophthora infestans* population structures in China

Zhibin Zhang[1], Jian Wu[1], Sihui Chen[1], David Cooke[2], Louise Cooke[3], Qinghua Sun[1], Zhiwen Feng[1], Ruofang Zhang[1]

[1] Potato Engineering and Technology Research Center, Inner Mongolia University, Hohhot, China

[2] The James Hutton Institute, Dundee, UK

[3] School of Biological Sciences, Queen's University, Belfast, UK

Presentation in pdf format: here

Poster in pdf format: not available

A total of 687 *Phytophthora infestans* isolates were collected from infected potato plants from 2015 to 2017 in 8 provinces in China. We aimed to investigate the population structures of *P. infestans* by characterizing their mating types and polymorphisms at 12 simple sequence repeat (SSR) loci. The data provide new baseline information for of populations of *P. infestans* in China. The results show that the majority of isolates were of A2 mating type (516 isolates), and the rest were of A1 mating type (171 isolates). Out of 687 isolates, 373 isolates that were collected in 2015 and 2016, were further analyzed on their genotypes. Results show that, in general, genotype 13_A2 genotype was dominant in the population with a frequency of 77.2 %. Another clone currently reported as misc_RU made up 20.9% of the population and a mix of other genotypes referred to as 'other' comprised the final 1.9%. One dominant mating type and low diversity of genotypes of *P. infestans* in each province indicate that in 7 provinces in China, sexual reproduction of *P. infestans* is limited. The implications for late blight management will be discussed.

Presentation 10 (also presented as poster). ***Phytophthora infestans*** **mating type and dynamic genetic diversity evolution in Yunnan, China over a 12-year period**

Jingsi Liang[1, 2], Juli Zhu[1, 2], Weiwei Wang[1, 2,] Canhui Li[1, 2], Wei Tang [1, 2]

[1]School of Life Science, Yunnan Normal University, Kunming, China; [2]Joint Academy of Potato Science, Yunnan Normal University, Kunming, China

Presentation in pdf format: not available

Poster in pdf format: not available

Potato late blight caused by *Phytophthora infestans* is the most serious disease problem in Yunnan province. To understand the dynamics population structure of *P. infestans* in Yunnan during the year of 2006-2017, 357 isolates collected from Dali and Kunming were purified and detected to mating type, mtDNA haplotype, metalaxyl resistance, pathotypes and 8 SSR DNA fingerprints. The results showed that A1 mating type was the dominated population before the year 2008 but changed significantly from the year of 2008, with more A2, A1A2 and self-fertile but fewer A1 isolates over the years. Two mtDNA haplotype, with dominated Ia and only two isolates of IIa, were detected among 357 isolates. Pathogenicity assays using containing *R1-R11* genes hosts detected 67 pathotypes among all test isolates, virulent against almost *R* genes as privilege dominant after the year of 2010. SSR analyzing distinguished 242 genotypes in all 357 isolates, PCA analysis indicated that populations in 2006, 2007 and 2008 were looks like dominant asexual life cycle while from the year of 2009 to 2017 were with the limited probability sexual reproduction took place. UPGMA analysis indicated that blue 13_A2 reference lineages, including 5 test isolates collected from Dali and Kunming from 2013 to 2015, but not exist in 2016 and 2017. These results supported the hypothesis that clonal reproduction, combined with host selection and limited sexual reproduction, is responsible for the dynamic genetic diversity of *P. infestans* in Yunnan.

Presentation 11. The changing population structure of late blight pathogen in India necessitates continued surveillance

Sanjoy Guha Roy

Professor & Head, Department of Botany, West Bengal State University, Barasat, Kolkata, India

Presentation in pdf format: here

India is the second-largest producer of potatoes worldwide, with late blight being the single most important limiting factor. Historically, the disease was first reported from India between 1870-1880 from the hills in Southern India and in 1890-1900 from the subtropical plains of West Bengal in Eastern India, which was presumed to be of Ia haplotype. Subsequently, US-1 (A1/1b) was detected around 1968-74, complex races by 1990s, and in addition, various haplotypes, Ia and IIb, occurred during the period 1996-2010. Detection of A2 mating type in 1986 and the Metalaxyl-resistance in 1989 soon after its introduction in India in 1988 were two major events in keeping with similar changes worldwide. Late blight epiphytotics have now become a regular feature almost every alternate year or two after the 1960s and with losses varying between 5% to 90%. In recent years the change in population has, however, been very rapid; the blue_13 lineage first detected in Southern India in 2008-09 was very different from that detected in 2014-15 from Eastern India, which caused a devastating epidemic there. The 24 unique subclonal variations found had host preferences, and all were adapted to higher temperatures having implications for disease development, which would be discussed. Continued surveillance is needed for detection of such rapid changes and the preliminary steps taken to supplement AsiaBlight efforts in India would be shared

Presentation 12. Phenotypic and genotypic analyses of late blight pathogen *Phytophthora infestans* in Bangladesh

Md. Rashidul Islam[1], Md. Huzzatul Islam[2], David E. L. Cooke[3], and William E. Fry[4]

[1, 2] Department of Plant Pathology, Bangladesh Agricultural University, Mymensingh, Bangladesh; [3]The James Hutton Institute, Inver Gowrie, Dundee, UK; [4]Cornel University, Ithaca, New York, USA

Presentation in pdf format: not available

Late blight caused by *Phytophthora infestans* (Mont.) De Bary, an oomycete, limits the production of potato worldwide. Experiments were conducted to determine the phenotypes and genotypes of *P. infestans* isolates in Bangladesh. A total of 42 *P. infestans* isolates were identified from late blight infected potato leaf samples collected from fifteen locations by PCR using *P. infestans* specific (PINF) and ITS5 primers. Phenotypes of *P. infestans* isolates were analyzed using virulence, mating type and metalaxyl sensitivity assay. Virulence assay on detached potato leaf and tuber (cv. Diamant) conceded that the *P. infestans* isolates obtained from different growing areas showed incommensurable levels of virulence. Mating type determination of *P. infestans* isolates revealed the presence of only A2 mating type in Bangladesh. Metalaxyl resistant/sensitivity assay of *P. infestans* isolates obtained from major potato growing areas showed that most *P. infestan*s isolates were found metalaxyl resistant. Genotypes of *P. infestans* isolates were assessed using mitochondrial (mt)-DNA haplotyping, microsatellite and RFLP analyses. Mt-DNA analyses attested that all *P. infestans* isolates obtained from different potato growing areas are Ia haplotype. RFLP analyses using RG57 probe and mating type data (A2) confirmed that all Bangladeshi *P. infestans* isolates seems US-8 genotypes. Simple sequence repeat (SSR) analyses of samples collected on FTA cards corroborated that all *P. infestans* samples are blue 13_A2 genotypes, which are dangerous European genotypes.

Presentation 13. Virulence patterns of *Phytophthora infestans* isolates using R differential set of *Solanum demissum* in the Red River Delta, Vietnam

Nguyen Thi Minh, Do Thi Huong, Nuyen Thi Phuong Nga, Nguyen Thi Mai Huong, Truong Thi Thuy, Pham Thi Thu Huong

Horticulture Department at Field Crops Research Institute, Vietnam

Presentation in pdf format: here

Aims of the project were to determine pathogen virulence of late blight isolates collected in potato production areas in the Red River Delta of Vietnam and to determine which R genes the most resistant. The isolates were collected from four provinces: Hai Phong, Thai Binh, Nam Dinh and Bac Ninh on four varieties: Solaea 1, Atlantic, Maeabel 1 and a Chinese variety. Ten isolates were tested on leaves of a differential set of Solanum demissum with 11 late blight resistance R genes. The ten isolates showed different virulence patterns. Ten races were characterized. Late blight resistance gene R8, R9 resisted to 90%, 80% of the isolates, respectively. One race collected from Hai Phong province on Chinese variety overcame all the Rgenes, except R8. If R8 and R9 can be combined in one variety, that variety can resist to all the races characterized. These R genes can be useful tools for a breeding program on potato late blight resistance.

Presentation 14. Genetic and phenotypic characterization of the *Phytophthora infestans* population in South Korea during 2009-2016

Kwang-Soo Cho[1], Jang-Gyu Choi[2], Jin-Hee Seo[2], Hyun-Jin Park[2], Ji-Hong Cho[2], Ju-Seong Im[2], Young-Eun Park[2], and Su-Young Hong[2]

[1] Upland Crop Breeding Research Division, National Institute of Crop Science, Rural Development Administration, Miryng, Republic of Korea; [2] Highland Agriculture Research Institute, National Institute of Crop Science, Rural Development Administration, Pyeongchang, Republic of Korea

Presentation in pdf format: not available

In order to better understand the *Phytophthora infestans* population structure in South Korea, 172 isolates were collected between 2009 and 2016 from four major potato cultivation areas. Fungicides (Metalaxyl and Dimethomorph) response, mating type, and SSR genetic fingerprint were analyzed to characterize these isolates. Ten isolates collected in Gyeongnam Province, specialized in protected winter cultivation in poly-tunnels, were A2 mating type. All other isolates were the A1 mating type. Overall, 42% of the isolates were resistant to metalaxyl, 43% were sensitive. All isolates were sensitive to Dimethomorph. From the SSR fingerprints, forty-five distinct genotypes were identified, which could be clustered into four clonal lines: KR_1_A1, KR_2_A2, RU_1_A1, and US-11. KR_1_A1 was the predominant *P. infestans* genotype in South Korea. KR_2_A2 was only found in Gyeongnam Province; all isolates were A2 mating type and resistant to metalaxyl. RU_1_A1 was dominant until 2013, but its frequency gradually decreased in more recent years. US-11 was first found in 2014, after which its frequency increased to become co-dominant with KR_1_A1. The calculated standardized index of association (Ia) suggests that the South Korea *P. infestans* population is undergoing clonal reproduction. When compared with the population of *P. infestans* from the Netherlands, it has less genetic diversity, and the dominant Netherlands *P. infestans* genotype, EU_13_A2 (Blue_13), was not found in South Korea. Such monitoring of the pathogen population contributes to a more efficient IPM-based control strategy for potato late blight control in South Korea.

Presentation 15. The current state of potato late blight in Japan

Seishi Akino

Laboratory of Plant Pathology, Graduate School of Agriculture, Japan

Presentation in pdf format: here

Japan grew roughly 2,215,000 tons of potatoes on about 74,000 ha in 2018. Potato late blight was first reported in Japan in 1900. The late blight outbreak area covers 11,000 ha. In Japan, there are few potato varieties resistant to *Phytophthora infestans*, and its control depends mainly on fungicides. The occurrence of *P. infestans* varies annually, depending on the conditions. We identified five genotypes of *P. infestans* in Japan using the RG57 fingerprint: US-1, JP-1, JP-2, JP-3, and JP-4. Of these, US-1, JP-1, JP-2, and JP-4 are thought to have been transferred independently from overseas, while JP-3 resulted from sexual mating between JP-1 and JP-2. The genotypes were subcategorized into 30 genotypes using SSR-PCR analysis with 12 markers, demonstrating the accumulation of asexual variation in *P. infestans*. The US-1 group has not been found in Japan since the 1990s. Recently, the JP-4 group has been dominant in Japan. There are many races, and the viable low-temperature range varies widely. The JP-1 group is the only A2 mating type in Japan. It is isolated from tomatoes and potatoes and dominates in parts of central Japan. The JP-2 group is similar to Chinese and European populations but has rarely been seen in Japan in recent years. The JP-3 group is characterized by its resistance to metalaxyl and high sacrificial ability and is a Japan-specific lineage that dominates in part of Hokkaido. The Japanese populations of *P. infestans* resulted from the migration of the pathogen from other countries, in addition to domestic changes following sexual and asexual propagation.

Presentation 16. Status of potato late blight (*Phytophthora infestans*): Management and genetic diversity in Nepal

Buddhi Prakash Sharma Adhikari

Nepal

Presentation in pdf format: not available

Nepal exhibits a wide range of climatic variation where cultivation of potatoes and tomatoes are diverse and are harvested almost round the year. Both crops heavily suffer from late blight disease *Phytophthora infestans* (Mont) de Bary. Late blight is the devastating disease of potato and tomato, causing substantial economic losses. Mancozeb as a protectant and or metalaxyl, a systemic fungicide sprayed single or alternately 10-15 times per crop season. Two hosts crops growing together or in sequence provides an environment for disease development. In addition, the development of a new strain of *P. infestans* with metalaxyl resistance character is a serious challenge for its management. Old potato varieties have lost their resistance to late blight; all these have made the disease management more complex. Since 2014, fenamidone and dimethomorph have been recommended wherever metalaxyl resistant strain prevailed. Genetic diversity of *P. infestans* studied during 2010 to 2012 revealed that, 39% were of A1 and 61% A2 mating types. The proportion of A1 and A2 mating types varied greatly among the three major environments: the mid hills, terai and high hills. The proportion percentage of A1 and A2 mating type was 88:12 in terai, 28:72 in mid hills and 12:88 in high hills. Regarding efficacy of metalaxyl against *Phytophthora infestans* 31.5% resistant, 38.2% intermediate and 30.3% were found sensitive. The majority of Phytophthora isolates (88%) at high hills were still found sensitive to metalaxyl compared to the isolates of mid hills and terai. Microsatellite analyses of 19 isolates, representing high hills (5), mid hills (5) and terai (9), were compared with the fingerprints of the European genotypes 13_A2. These 19 Nepalese isolates were also found lineage of 13_A2 (Blue_13), which has been considered as the most aggressive strain in some of the European countries. Use of resistant varieties, appropriate fungicide and adoption of DSS would be scientific options for disease management.

Key words: dimethomorph, fenamidone, fungicides, management, metalaxyl, mating types, resistance

Presentation 17. Late blight *Phytophthora infestans* population dynamics (genotyping, phenotyping) in Uzbekistan

Mukhtabar Tashmatova

Department Agrobiotechnology Tashkent State Agrarian University, Uzbekistan

Presentation in pdf format: here

In the Republic of Uzbekistan, the main types of diseases of nightshades (*Solanaceae*) of potato (*Solanum tuberosum*) and tomato (*Solánum lycopérsicum*) are the roots of Fusarium decomposition and Late blight. The presentation gives the highlights and presents the points of key dynamics and phenotype of phytophorosis of potato and tomato in recent years in Uzbekistan.

Tomato plants are also susceptible to late blight, and the foliar symptoms are similar to those on potato. The incidence rate of diseases of potato and tomato fields the degree of infection. Measures against potato and tomato disease pre-planting potatoes with fungicides, the effect of potato crop rotation on the development of the disease. The impact of the use of chemicals against diseases of potato and tomato and the impact on productivity.

Indicators of the Republic of Uzbekistan (by regions) for the implementation of measures to combat diseases and pests of potatoes and tomatoes sown for the 2019 crop.

Theoretical inclusion on *arbuscular mycorrhiza* (AM) on the possibilities of developing a dry form of the biological product AM and its further introduction and application as a control against late blight of potato and tomato on saline and non-saline soils of Uzbekistan.

Presentation 18. Population structure of *Phytophthora infestans* causing late blight in potato growing areas of Pakistan

Waqas Raza and Muhammad Usman Ghazanfar

Department of Plant Pathology, College of Agriculture, University of Sargodha, Pakistan

Presentation in pdf format: not available

Phytophthora infestans (Mont.) de Barry is one of the most destructive pathogen and model organism for the oomycetes studies and has a terrific effect on human history resulting in Irish famine and population displacement. Despite the numerous efforts conducted to alleviate the yield losses, the pathogen's population structure has been a key factor in disease control failures. Continuous monitoring of this pathogen trait is essential for selecting the best disease control measures. Several sexually and asexually reproducing lineages of the pathogen have been identified and new lineages are more virulent as compared to their parental lineages.

The current study was designed to understand the *P. infestans* population structure in the Pakistan. Keeping in mind of my research objectives, a total 149 single-lesion isolates of the pathogen collected from potato growing areas during surveyed in both the years 2017-18. The results revealed highest disease prevalence and diversity was observed and it was increasing from one year to next year while the diversity among the isolates of *P. infestans* was observed in all surveyed potato growing areas of Pakistan. The pathogen aggressiveness and fitness were also showed significant difference across the locations. Mating types (A1 and A2) are distributed throughout surveyed areas while A1 (73%) is more abundant. It has also been observed that A2 mating type increased from 21% to 23 % which is an alarming signal for potato growers due to its oospores viability in soils for more than 4 years even absence of potato crop. Molecular characterization was performed yielded an estimated 300-600 bp product size which showed variations among isolates. The PCR bands were purified with gel purification kit, processed further for sequencing. Based upon the above fact, we would conclude that different control events for the management of *P. infestans* should be done according to prevalence, aggressiveness and mating types present in the field.

Presentation 19. The current studies of potato late blight in Heilongjiang province, China

Mei Guo

Potato Institute of Heilongjiang Academy of Agricultural Sciences

Presentation in pdf format: not available

Potato late blight is the most important disease in Heilongjiang Province, and the control of PLB accounts for more than 60% of the total cost of fungicides invested in potato production. In the past 14 years, the population structure of *P. infestans* has been intensively studied, including genotype, mating type, metalaxyl sensitivity and virulence. Genotypes of local populations of *P. infestans* have been classified as 13_A2, misc, misc_RU and misc_RU_var. A2 mating type was first detected in 2011. Metalaxyl resistant isolates comprised to over 70% of the population. The physiological races tended to be more complicated, and the dominant race was physiological race composition of *Phytophthora infestans* tends to be more complex, and the dominant physiological races are 1,3,4,7,8,10,11 and 1,3,4,7,10,11.

Presentation 20. Pathogen effectors as probes for improving late blight disease resistance in potato

Weixing Shan

College of Agronomy and State Key Laboratory of Crop Stress Biology for Arid Areas, Northwest A&F University, Yangling, Shaanxi, China

Presentation in pdf format: here

Diseases caused by pathogenic microbes are major constraint for sustainable production of many crops. A notable example is the potato late blight caused by the oomycete Phytophthora infestans. It is well documented that small secreted effector proteins encoded by pathogens play vital roles in both susceptibility and genotype-specific resistance. Use of disease resistance is increasingly important in modern crop production. In this presentation, I will show the use of pathogen effectors in understanding disease resistance, identification of new resistance genes, and accelerated classical crop breeding for late blight resistance. Identification of host proteins targeted by effectors crucial for pathogenicity is an important aspect of understanding on host-pathogen interactions and plant susceptibility. I will also show how research in this field offers excellent opportunities for developing knowledge-based novel strategies for improving crop breeding for enhanced and durable late blight disease resistance.

Presentation 21. Sustaining the promotion of late blight resistant locally developed potato varieties in the Philippines: An overview

Teresita Masangcay

Northern Philippines Root Crops Research and Training Center (NPRCRTC), Benguet State University (BSU), Benguet, Philippines

Presentation in pdf format: here

The BSU, NPRCRTC--CIP collaboration paved the way for capacity building of the technical staff in various field of specialization: tissue culture, variety selection and evaluation, rapid multiplication techniques, pest identification and management as well as graduate thesis mentoring and funding. The collaboration developed the Center's strong foundation to do Research Development and Extension (RDE) related to potato. From the numerous germplasms received in the form of clones and true potato seeds, the Center was able to release seven late blight resistant and processing type varieties approved by the National Seed Industry Council (NSIC) namely: Dalisay and Montañosa (1986), Igorota and Solibao (1996), Ganza (2004) and, Gloria and Bengueta (2006). Further, the technical staff became recipients of trainings on serological methods of bacterial wilt and potato viruses indexing, late blight races culture and identification using deferential plant varieties and cryogenic preservation. Knowledge acquired through the years of collaboration had qualified the staff to attend comprehensive trainings abroad and as trainers on potato production and seed propagation in the country.

The simple tissue culture laboratory and greenhouse structures established from CIP funding, today had improved into more serviceable laboratory and series of greenhouses occupying 1000 sq. meters had been established. Participatory field trials with other stakeholders, info-caravans, and continuous propagation of the varieties for walk-in clients and giving seed samples to interested farmers, somehow helped in promoting the LBR-varieties so that their popularity increased and considerable number of clients was served.

Proceeds became the revolving fund of the Seed Production Project and with assistance from outside funded projects from other government agencies, the project was able to sustain itself of what it is today. Realization on the importance of potato in the country as a whole initiated funding from known institutions such as the Philippine Council for Agriculture and Aquatic Research Resources and Development (PCAARRD) and the

Department of Agriculture-Bureau of Agricultural Research (DA-BAR) in the mid 1990' s-early 2000s which led to the improvement of the production technologies and the informal seed system to semi-formal. Increased in demand for potato and urbanization boom the industry in the highland making potato one of the five high value crops. Hence, the regional office of the Department of Agriculture aware of the need for quality seeds funded the commercialization and further promotion of I*gorota* in partnership with legitimate farmers' organizations. These made Igorota the second most grown variety next to Granola.

The variety is now being grown by about 60% of farmers based on 2018 survey. At present, potato is tapped as national commodity, thus, the production of quality seeds is being pushed by the government towards its commercialization through the standardized seed production system, and concurrent to this, the Department of Science and Technology through its niche centers in the Region for R and D program (NICER) also funded the strengthening of the supply of quality seed of the processing potatoes in the Philippines. In addition, the Commission on Higher Education thru the efforts of a private university took part to this holistic potato undertaking. This private--public partnership was geared towards "Elevating Potato as Food Security Crop in the Philippines: Response to Climate Change". Partial result revealed that LBR varieties Ganza, Gloria, and Montañosa are potential potato varieties in addition to Raniag for lowland areas in Luzon and Visayas islands in terms of yield and post-harvest qualities

Presentation 22. Observation for the way of primary infection of *Phytophthora infestans* in potato

Tongle Hu

Plant Pathology in Hebei Agricultural University, China

Presentation in pdf format: here

From 2010 to 2019, the way of the primary infection of *Phytophthora infestans* in potato has been investigated under controlled and outdoor conditions. The results showed that the pathogen in the latent infected tubers could sporulation on the tuber surface and/or growth in to shoots after planting. In the former case, the sporangia/zoospores could infect the tip of young shoots during emergence and/or the lower leaves near ground level. In the later ones, the pathogen could growth with the shoots development and result in stem blight. Nine years farmer filed investigation in Northern China planting areas indicated that the former way is more popular and earlier than the later one.

Presentation 23. Understanding and exploiting late blight resistant and susceptible genes based on the effectors' function

Xiaodan Wang

[1]Plant Protection College of China Agricultural University, Beijing, China,100193; [2]Division of Plant Sciences, College of Life Sciences, University of Dundee at The James Hutton Institute, Invergowrie, Dundee, DD2 5DA, UK; [3]Institute of Plant Virology, Fujian Agriculture and Forestry University, Fuzhou, China

Presentation in pdf format: not available

The oomycete pathogen *Phytophthora infestans* is responsible for causing late blight disease in *Solanaceous* plants. The pathogen secretes essential effectors into plant cells that target critical host cellular mechanisms to promote disease. We will report our recent progress on identifying novel resistance proteins that recognize a specific effector in wild potatoes, and the mechanistic relationship between such recognition and the host target for this effector. Evolutionary and functional dynamics of the effector are also analyzed in order to assess the conservatism of this effector. To our knowledge, plant can facilitate or suppress pathogen penetration, fulfill or inhibit metabolic or structural needs of the pathogen during infection. We will investigate how to understand and exploit late blight resistant and susceptible genes in potato and utilize effectors as a tool to explore new host resistance genes to accelerate disease resistance breeding against late blight in future work.

Presentation 24 (also presented as poster). Genome and transcriptome analysis of Chinese potato late blight field strains provides insight into pathogen aggressiveness and valuable [plant] resistance

Fan Zhang[1], Han Chen[1], Xinjie Zhang[1], Li Lv[1], Chuyun Gao[1], Jie Huang[1], Xiaobo Zheng[1,2], Jack H. Vossen[3], and Suomeng Dong[1,2,]

[1]Department of Plant Pathology, Nanjing Agricultural University, Nanjing 210095, China; [2]Key Laboratory of Integrated Management of Crop Diseases and Pests (Ministry of Education), Nanjing, China; [3]Wageningen University and Research, Wageningen, the Netherlands

Presentation in pdf format: here

Poster in pdf format: here

Phytophthora infestans, the causal agent of potato late blight which sparked Irish Great Famine in the 1840s, is one of the most important crop pathogens that that threaten global food security. Late blight resistance (R) genes were introgressed into cultivated potato (*Solanum tuberosum*). A collection of eleven conventional R potatoes were used to characterize the virulence phenotype of individual *P. infestans* isolates, and as such to monitor the dynamics of *P. infestans* field populations. However, emerging reports suggest that the field strains already breakdown a substantial R gene in different geographic regions, threatening the local potato production. Here we performed genome and transcriptome sequencing analysis on two Chinese field strains. The filed strain HB1501 (from north of China) and HN1602 (from south-west of China) overcome all the eleven conventional potato resistance. Our analysis reveals extensive sequence and expression polymorphisms in these strains. In particular polymorphisms at AVR locus enable these strains to overcome conventional R genes. Although field strains have evolved multiple strategies to evade disease resistance, we experimentally verified that the R genes such as *R8/Rpi-Smira2*, *Rpi-vnt1* are still effective against these strains, and are valuable to potato breeding in the future.

Presentation 25 (also presented as poster). PiCP1, a catalase-peroxidase, is critical for the survival to adverse environment and asexual reproduction of *Phytophthora infestans*

Tu-Hong Wang, Xiao-Wen Wang, Li-Yun Guo

College of Plant Protection, China Agricultural University, Beijing, 100193, P. R. China

Presentation in pdf format: not available

Poster in pdf format: not available

Catalase-peroxidase (CP) is a heme oxidoreductase widely exists in bacteria and lower eukaryotes. Previous studies showed that it plays an important role in antioxidant and pathogenicity and is required for the growth and development of these organisms. However, its role in oomycetes, an important group of fungus-like eukaryotes that produce zoosporangia is unknown. In this study, we identified a catalase-peroxidase in *Phytophthora infestans*. PiCP1 (PITG_05579), which has secretion activity, was highly expressed in asexual stages and could be induced by oxidative and heat stresses. We explore the biological roles of the PiCP1 by analyzing the phenotypes of PiCP1-silenced and -overexpression transformants. Compared with wild type, PiCP1-silenced transformants decreased the catalase activity and antioxidant stress ability and damped the cell wall integrity. Moreover, silencing PiCP1 also reduced the sporangium production, zoospore releasing and appressorium formation, but accelerated the sporangia germination; PiCP1-overexpression transformants also reduced sporangium production, zoospore release and appressorium formation, but increased the tolerance to high temperature. We also found that the pathogenicity of the sporangia, but not the mycelia of PiCP1-overexpression transformants decreased due to the reduction of the appressorium formation ability. These results revealed the important role of PiCP1 in asexual reproduction and abiotic stress resistance in *P. infestans* and showed that a specific PiCP1 level is critical for the formation and normal function of sporangia. Overexpression of PiCP1 improves the adaptability of pathogen to adverse environment but suppress the asexual reproduction and infection. Our findings provide new insights into catalase-peroxidase functions in eukaryotic pathogens.

Presentation 26. Green control technology of potato late blight in Wumeng mountain area

Xia Liu

Yunnan Agriculture University, China

Presentation in pdf format: not available

Yunnan province is one of main potato production area, potato can be planted at four seasons of a year. The unique climate of Yunnan province provides advantage for occurrence and transmission of potato late blight. Owing to residual toxicity and environmental pollution of chemical fungicide and limitation of resistance breeding, exploration of green control technology of potato late blight is top priority. Based on this situation, it has been done on the three parts of work , including drug resistance of potato late blight pathogen in some parts of potato producing area in Yunnan , effect of salicylic acid on resistance for potato late blight of different cultivar potato were preliminarily explored and green control technology of potato late blight was established which fit for Wumeng Mountain Area of Yunnan province.

Presentation 27 (also presented as poster). Quantification of the *Phytophthora infestans* population densities in upland soils in Japan using real-time PCR

Hisashi Osawa[1], Nobuyuki Suzuki[1], Seishi Akino[1], Hiromichi Araki[2], Kotaro Akai[3], Kenji Asano[3] and Norio Kondo[1]

[1]Grad. Sch. Agr. Hokkaido University; [2]Calbee Potato, Inc.; [3]National Agriculture and Food Research Organization

Presentation in pdf format: here

Poster in pdf format: here

Potato tuber rot caused by *Phytophthora infestans* is a serious problem in storage facilities. We have shown that potato tuber rot can be minimized by decreasing harvesting injuries and/or the population density of *P. infestans* in soil at harvest time during commercial potato production (Osawa et al. 2018). However, it is impossible to harvest tubers without injury using existing harvesters. Therefore, we have to manage fields to decrease the population densities of *P. infestans* in soil. To estimate the *P. infestans* population density in soil using real-time PCR, we used a modified CTAB-bead-beating method to extract DNA from upland s s in oil Japan. The quantity data obtained using real-time PCR were compatible with the symptom development in a non-control potato field. Furthermore, there was a correlation between the quantity of *P. infestans* DNA measured by real-time PCR and the inoculum potential in soil. Therefore, the quantification of the population density of *P. infestans* using real-time PCR may be a guide to preventing potato storage rot.

Presentation 28 (also presented as poster). The identification and molecular mechanism of *Streptomyces hygroscopicus* against potato late blight

XiuMei Luo[1], ShuMin Zhang[1], Shun Feng[1], Francois Serneels[2], XingBi Che[1], Bonnave Maxime[2], Pan Dong[1], MaoZhi Ren[1]

[1]The School of Life Science, Chongqing University, Chongqing, China; [2]Centre for Agriculture and Agro-industry of Hainaut Province, Belgium

Presentation in pdf format: not available

Poster in pdf format: here

Pathogenic oomycetes infect a wide variety of organisms ranging from plants, animals to humans. They cause massive economic losses in global agriculture, aquaculture and human health. However, the efficient controlling approaches for pathogenic oomycetes without environmental pollution are still limited. Thus, the effective, safe and eco-friendly alternatives are urgently required for environmental protection and sustainable development. Starting from this point, one actinomyces from the rhizosphere soil of resistant potato varieties had a strong antagonistic effect on potato late blight, which was named as *S. hygroscopicus* CQUSh011 (Accession number: CGMCC NO.15518). Further HPLC-MS analysis confirmed that the strain could synthesize rapamycin and SA, which had direct effects on *Phytophthora infestans*. In conclusion, *S. hygroscopicus* could inhibit the growth of *P. infestans*, including A1, A2, and sterile mating type. Furthermore, the pure metabolites, SA and rapamycin, could inhibit the pathogen growth and decrease the virulence. The *S. hygroscopicus*-mediated biocontrol strategy is efficient on plotato late blight, which could be applied to field trial.

Presentation 29 (also presented as poster). Enhanced biological control of potato late blight with six *Streptomyces* strains combined with biochar and salicylic acid

Shun Feng, ShicaiTang, Liang Jin, Pan Dong, ZhengguoLi, Maozhi Ren

The School of Life Science, Chongqing University, Chongqing, China

Presentation in pdf format: not available

Poster in pdf format: not available

We evaluated new biological control strategies using *Streptomyces* strains with biochar and salicylic acid and compared the disease inhibition capacity of six selected *Streptomyces* strains (A, B, C, D, E, and F), when applied alone or in combination via *in vitro* experiments. Single *Streptomyces* strains exhibited *in vitro* protection against *Phytophthora infestans* (E> F> B> A> C> D). Besides AF, other strains significantly inhibited *P. infestans* growth and sporangial germination; no significant difference was also observed in the inhibition of *P. infestans* growth between the multiple bacterial combinations, indicating that the combination of multiple bacteria has an advantage in inhibiting *P. infestans*. Although combinatorial treatment with single *Streptomyces* strains and biochar inhibited *P. infestans* growth by 1.4%–6.1%, there was no significant effect on the disease index of potato late blight during field application; only strains D and F significantly increased potato tuber biomass, while combinatorial treatment with the six *Streptomyces* strains and biochar significantly reduced the disease index of potato late blight up to 10%. Salicylic acid supplementation with combinatorial bacterial and biochar treatment significantly reduced the disease index of potato late blight up to 13%. The control effect of the combination of *Streptomyces*, biochar, and salicylic acid on potato late blight in the field environment was as follows: six strains mixed + SA > six strains mixed > SA or Single strain > control. Our research highlights the use of combination of multiple strains of *Streptomyces* and biochar or salicylic acid to enhance the biological control of potato late blight in the field environment.

Presentation 30. Late blight in Southwest of China: Pathogen, fungicide evaluation and integrated management

Jifen Cao[1], Chao Huo[1], Lixian Bao[1], Wei Jiang[1], Xianping Li[1], Xingbi Che[2], Qijun Sui[1], Zhijian Zhao[1]

[1]Industrial Crops Institute, Yunnan Academy of Agricultural Sciences, Kunming, China; [2]Plant Protection Station of Chongqing, Chongqing, China

Presentation in pdf format: not available

Potato is one of main crops and planted more than 2.4 million ha in Southwest, which is the biggest potato production region in whole China. However, late blight disease is the first bottleneck in this region and leads to severe losses annually. Since 1998, the population dynamics of *Phytophthora infestans* in Yunnan has been investigated based on phenotypic and genotypic characteristics. Here we showed the pathogen dynamics, potato resistance, fungicide evaluation and late blight integrated managements in Southwest of China. Mating type, physiological race, metalaxyl sensitivity and genotypes of *P. infestans* populations had a dramatic change in Yunnan, Guizhou and Chongqing during 2012 to 2018. The blue13-A2 lineage and sub-lineages replaced and become dominant genotypes in Southwest of China after 2012. Last year, new aggressive isolates with both metalaxyl and fluazinam resistance were found in Yunnan. Potato germplasms introduced from CIP or US and new varieties collected from China were used to evaluate LB resistance level in greenhouse or field-trials. However, most potato materials were susceptible and only few showed high resistance against local pathogen races. Although some resistant varieties possessed *R8* gene were released in China, all of them were rapidly overcome by the new isolates now. Fortunately, *RB* (*Rpi-blb1*) gene still showed wide-spectrum resistance for Chinese *P. infestans* races and could be utilized as an important resistant resource. Fungicides played a crucial role in the integrated control of late blight, therefore, high efficient fungicides, such as mandipropamid·cymoxanil, cymoxanil·mancozeb, propamocarb·fluopicolide, oxathiapiprolin and eugenol·dimethomoph were screened in the fields, meanwhile resistance risks were evaluated. In recent years, new integrated management strategies, including seed tuber dressing, LB prediction and warning systems, resistant varieties, high efficient fungicides, disease diagnosis of artificial intelligence system, were developed and applied to guide famers and potato companies against late blight in the Southwest of China.

Presentation 31. Challenges and strategies against potato late blight in China: How AsiaBlight helps Chinese farmers to control potato late blight

Xingbi Che

Chongqing Plant Protection institute, China

Presentation in pdf format: not available

China is the largest potato producer in the world according to planting area. However, compared to some EU countries, the average yield is very low. Chinese potato experts have concluded that many constraints lead to low yield, such as frequent climate change (especially drought), poor soils and farmers' shortage of knowledge. Despite this, I think one of the constraints is the destruction of potato late blight (*Phytophthora infestans*). In addition, the annual severity of *Phytophthora infestans* causes the price fluctuations in both table potato and seed potato. This report lists the major field issues or challenges items of farmers' potato growing scale in recent years. And analyze the core causes of these problems. For each problem, try to find a tolerable and practical decision support system (DSS) and an efficient management strategy to help Chinese potato producers reduce losses and damage caused by *Phytophthora infestans*. Finally, this report strengthens AsiaBlight should play an important role in capacity building for potato producers by organizing or co-organizing training courses or workshops and ranks the priorities of AsiaBlight activities in China in the future, DSS>Fungicide Evaluation>Resistant Variety>Pathogen Population.

Presentation 32. Late Blight, other major potato diseases in Georgia and integrated protection measures

Zurab Khidesheli

Scientific Research Center of Agriculture, Georgia

Presentation in pdf format: here

In Georgia, potatoes are subject to several serious diseases that are caused by various types of fungi, bacteria, viruses and phytoplasmas. Among other diseases of potato, late blight (*Phytophthora infestans*) ranks first in its scale. It is widespread both in low-lying and high-mountainous regions, both on early and late potatoes, and is characterized by great harmfulness.

In Georgia, control over late blight is carried out by the same methods that are accepted around the world, although it has certain features. Much attention is given to the use of potato varieties resistant to Late Blight. Georgia has been collaborating with the International Potato Center (CIP) for many years. Tested many CIP clones. Comparative resistance to Late Blight and other diseases, as well as high productivity and quality, were shown by the clone CIP "Unika", which was registered under the name "Meskhuri Red".

A more effective way to combat late blight potatoes is through chemical fight. In Georgia, mainly fungicides are used against Late Blight, which contain the following active ingredients: copper hydroxide, copper chloride, fluoxynam, iprovalicarb, mancozeb, famoxadone, mephenoxam, cymoxanil, fenamidone, dimetomorph, fluazinam, metalaxyl, etc. In organic farming, seed treatment and leaf dressing with liquid bio-organic fertilizers are mainly used to enhance immunity. Biological fungicides are also used, such as Timorex gold (etheric oil of *Melaleuca alternifolia*), etc.

In 2016-2018, the IPM department of the Georgian Research Center participated In the AsiaBlight mapping project. Potato leaf samples were collected with late blight symptoms and sent by special FTA Classic Cards to China, at the University of Inner Mongolia for genotyping. Five were classified as miscellaneous, one was a genotype resembling a known Russian type (misk_RU) and two were the aggressive genotype 13_A2 (Blue 13).

Presentation 33. Status of late blight management in India

Sanjeev Sharma

Division of Plant Protection, ICAR-Central Potato Research Institute, Shimla, India

Presentation in pdf format: here

Late blight had been and continues to be the most dreaded disease of potato world over, including India. The disease attacks the potato crop every year in the hilly and plateau regions where potato is grown as a rainfed crop and once in 2-3 years in the plains leading to average crop losses of 15% which comes to loss of 7.95 million tons of potatoes. It is essential to understand the pathogen variability to devise suitable management strategies. Monitoring of *P. infestans* population has revealed a sea change in the population structure which indicates that new strategies are to be developed to tackle this dreaded problem. Management of late blight through host resistance is the most effective strategy and will remain the most environmentally and economically preferred option globally despite the fact that none of the variety could sustain the blight onslaught for more than 5-7 years. Over a dozen of high yielding varieties possessing high degree of resistance have been released and deployed across the country. Management of late blight through judicious use of chemicals aided by the appropriate disease forecasting system(s) and Decision Support System(s) becomes absolute necessity. Indo-Blightcast- a pan India model has been developed and put in use for the prediction of late blight across the agro-ecologies. Both conventional and biotechnological approaches which includes development of late blight transgenics using RB gene construct, RNAi-mediated silencing of *Phytophthora infestans* Avr3a gene, marker assisted breeding, somatic hybridization, and dsRNA technology are being used for managing this dreaded pathogen. The current status of population structure of *P. infestans*, management strategies being followed to tackle this pathogen will be discussed.

Posters

Poster 1. Early warning system provides clues on the chemical control of potato late blight

Xiao Chunfang[1,2], Wang Zhen[1,2], Zhang Denghong[1,2], Gao Jianhua[1,2], Zhang Yuanxue[1,2], Yan Lei[1,2], Yang Guocai[1,2], Shen Yanfen[1,2]

[1]Southern Potato Research Center of China; [2]Enshi Tujia and Miao Autonomous Prefecture Academy of Agricultural Sciences, Enshi, Hubei, China

Poster in pdf format: not available

Potato (*Solanum tuberosum*) late blight (PLB) disease caused by *Phytophthora infestans* is the most destructive disease of potato worldwide and Enshi as well, closely related to meteorological condition. In this study, CARAH forecasting system was used to predict the disease occurrence and guide the fungicide use, that the protectant fungicide in the early stage of potato growth and the curative fungicide in late period. The effectiveness of four different combinations of spray fungicides on the control of late blight and the yield increase of potatoes were investigated. During the growth of potato in 2019, the weather was favorable for the development of PLB. The "Favorita" variety seems to trigger the first symptoms in the fifth generation given by the forecasting model. The first symptoms were observed in the control plots on May 7th, while in the treated region after the heavy rains of May 22nd. In agreement with the observed phenotypes, the results suggested all the chemical groups during the disease epidemic period has a significant effect on disease control and yield increase compared to the untreated control, with more than 99% efficacy of foliar protection, greater than 170% yield of potato, and higher than 17% rate of commercial tuber. Among them, the comprehensive performance of treatment group 4 was the best, that the disease index was only 9.57 after 3 weeks of the last application, and the total harvest reached 79,342.07kg, the average yield was 97,342.07 kg/ha, increased by 279.21%. The rate of commercial tuber was as high as 94.74%, while the rate of diseased tuber was only 1.20%. The contrast test of different fungicides revealed that the preventive efficacy of the agent B was better than that of the agent A, and the agent D showed more excellent curative activity against disease significantly than the agent C. Our results provide further insights into the selection and use of chemicals for controlling late blight that influence potato yield and industrial benefits which could be gradually promoted in potato production.

Poster 2. VigiMAP, a Walloon (Belgium) potato late blight DSS, fruit of Belgo-Chinese cooperation

Bonnave M.[1], Zhang J.[2], Vryghem C.[1], Couvreur B.[1], Mahieu O.[1], Che X.[3], Serneels F[1]

[1]CARAH, Agriculture Research Center of the Hainaut province, Belgium; [2]Beijing Huisi Junda Technology Co., Beijing, China; [3]Chongqing Plant Protection Institute, Chongqing. China

Poster in pdf format: not available

CARAH is the non-profit Agriculture Research Center of the Hainaut province in Belgium. In a region where potato is one of the main crops and is very important economically, the control of potato late blight has always been of priority for CARAH. Since 1987, CARAH late blight model is used to warn the farmers in Hainaut and later the whole Walloon region about the most efficient moment to spray, based on data collected by a weather station network. Since 2000, CARAH has been collaborating with Chinese agronomists and Beijing HSJD company to successfully implement this system in almost all the Chinese provinces where potato is grown, by a combination of technical and organizational achievements: a network of more than 600 weather stations, farmers and agronomists extensive training in China and Belgium and a centralized computing tool running the model. In 2019, this successful collaboration took a new turn with the launch in Belgium of VigiMAP, an interactive DSS platform at the individual plot scale, including CARAH model and the duration of the fungicide protective effect according to actual weather conditions. An instant messaging facilitates the interaction between farmers and experts. Soon, these innovations will also be available for Chinese farmers and agronomists. The potential for the development of this tool in Asia is huge and would certainly benefit from the experience gathered by the collective efforts of Belgian and Chinese teams.

Poster 3. Functional stacking of multiple resistance genes against *Phytophthora infestans* in potato

Xiaoqiang Zhao[1], Jie Huang[1], Chuyun Gao[1], Biying Sun[1], Fan Zhang[1] Liping Xing[3], Xiaobo Zheng[1,2], Suomeng Dong[1,2]

[1]Department of Plant Pathology, Nanjing Agricultural University, Nanjing, China; [2]Key Laboratory of Integrated Management of Crop Diseases and Pests (Ministry of Education), Nanjing, China; [3]National Key Laboratory of Crop Genetics and Germplasm Enhancement, Cytogenetics Institute, Nanjing Agricultural University, Nanjing, China.

Poster in pdf format: not available

Potato late blight caused by the oomycete pathogen *Phytophthora infestans* greatly threatens potato production and food security. We previously analyzed the virulence dynamics of Chinese *P. infestans* population in East and Southwest China and uncovered a few broad-spectrum resistance (*R*) genes are still useful for late blight management. We hypothesize that stacking these *R* genes may potentially enhance the field resistance and provide durable strategy for late blight management. We constituted a Golden Gate Compatible cloning system and a series of modules so that we could assemble *R* genes with flexible combinations upon *P. infestans* field population change in a short time. So far, we had assembled a few *R* genes including *Rpi-vnt1.1* and *R8* into one single binary vector and transformed into the susceptible potato cultivar for further study.

Annexes

Annex 1. Program

Friday, October 25th 2019

09:30 – 11:00 Country correspondents' meeting

17:00 – 20:30 Registration and mounting of posters

Saturday, October 26th 2019

08:00 – 08:30 Official inauguration of the event

08:30 – 08:45 Official picture

08:45 – 09:15 Presentation 1. How does the EuroBlight network help to control the aggressive potato late blight pathogen?
Huub Schepers

Session 1: Potato late blight in Asia and beyond
Chairs: Li-Yun Guo and Alberto Maurer

09:20 – 09:35 Presentation 2. Trends in recent late blight scientific publications
Alberto Maurer

09:35 – 10:05 Presentation 3. EuroBlight tracking of evolving European populations of *Phytophthora infestans* as an aid to late blight management
David Cooke

10:05 – 10:25 Presentation 4. AsiaBlight: The beginnings
Louise Cooke

10:25 – 10:40 Presentation 5. AsiaBlight's present and future: organization, events, a developing network
Christelle Lasserre

10:40 – 11:00 Coffee Break

11:00 – 11:25 Presentation 6. Potato late blight in Latin America
Ivette Acuña

11:25 – 11:50 Presentation 7. Worldwide migrations, evolutionary relatedness, and reemergence of *Phytophthora infestans* in Asia
Jean B. Ristaino

12: 00 – 13:00 Lunch and poster session
Poster 1. Early warning system provides clues on the chemical control of potato late blight
Xiao Chunfang

Poster 2. VigiMAP, a Walloon (Belgium) potato late blight DSS, fruit of Belgo-Chinese cooperation
Maxime Bonnave

Poster 3. Functional stacking of multiple resistance genes against *Phytopthora infestans* in potato

Xiaoqiang Zhao

13:00 – 13:30 Presentation 8. Screening for late blight resistance in wild species and landraces in Peru, and the strategy and resistant materials from CIP's breeding program
Jorge Andrade-Piedra

Session 2a: Late blight biology, genetics, and population dynamics in Asia
Chairs: Jiehua Zhu and Sanjoy Guha Roy

13:30 – 13:50 Presentation 9 (also presented as poster). Investigation of *Phytophthora infestans* population structures in China
Jian Wu

13:50 – 14:10 Presentation 10 (also presented as poster). *Phytophthora infestans* mating type and dynamic genetic diversity evolution in Yunnan, China over a 12-year period
Canhui Li

14:10 – 14:30 Presentation 11. The changing population structure of late blight pathogen in India necessitates continuing surveillance
Sanjoy Guha Roy

14:30 – 14:50 Presentation 12. Phenotypic and genotypic analyses of late blight pathogen *Phytophthora infestans* in Bangladesh
Mohammad Rashidul Islam

14:50 – 15:10 Presentation 13. Virulence patterns of *Phytophthora infestans* isolates using R differential set of *Solanum demissum* in the Red River Delta, Vietnam
Pham Thi Thu Huong

15:10 – 15:30 Presentation 14. Genetic and phenotypic characterization of the *Phytophthora infestans* population in South Korea during 2009-2016
Kwang-Soo Cho

15:30 – 15:50 Coffee Break

Session 2b: Late blight population dynamics (genotyping, phenotyping) in Asia
Chairs: Jorge Andrade-Piedra and Pham Thi Thu Huong

15:50 – 16:10 Presentation 15. The current state of potato late blight in Japan
Seishi Akino

16:10 – 16:30 Presentation 16. Status of potato late blight (*Phytophthora infestans*): Management and genetic diversity in Nepal
Buddhi Prakash Sharma Adhikari

16:30 – 16:50 Presentation 17. Late blight *Phytophthora infestans* population dynamics (genotyping, phenotyping) in Uzbekistan
Mukhtabar Tashmatova (Uzbekistan)

16:50 – 17:10 Presentation 18. Population structure of *Phytophthora infestans* causing late blight in potato growing areas of Pakistan
Waqas Raza

17:10 – 17:30 Presentation 19. The current studies of potato late blight in Heilongjiang province, China
Mei Guo

17:30 – 18:00 Round table – Host: Alberto Maurer

Panelists: Jorge Andrade-Piedra, David Cooke, Huub Schepers, Weixing Shan, Sanjoy Guha Roy, Jane Ristaino, and Tongle Hu

19:00 – 21:00 Gala Dinner at the Friendship Palace
Special Chinese cultural entertainment
AsiaBlight logo prize reward to Buddhi P. Sharma Adhikari
AsiaBlight Special recognition program for our sponsors

Sunday, October 27th 2019

08:00 – 08:30 Presentation 20. Pathogen effectors as probes for improving late blight disease resistance in potato
Weixing Shan

Session 3: Plant-Pathogen interaction and potato resistance
Chairs: Huub Schepers and Weixing Shan

08:30 – 08:50 Presentation 21. Sustaining the promotion of late blight resistant locally developed potato varieties in the Philippines: An overview
Teresita Masangcay

08:50 – 09:10 Presentation 22. Observation for the way of primary infection of *Phytophthora infestans* in potato
Tongle Hu

09:10 – 09:30 Presentation 23. Understanding and exploiting late blight resistant and susceptible genes based on the effectors' function
Xiaodan Wang

09:30 – 09:50 Presentation 24 (also presented as poster). Genome and transcription analysis of Chinese potato late blight field strains provides insight into pathogen aggressiveness and valuable [plant] resistance
Fan Zhang

09:50 – 10:10 Presentation 25 (also presented as poster). PiCP1, a catalase-peroxidase, is critical for the survival to adverse environments and asexual reproduction of *Phytophthora infestans*
Tuhong Wang

10:20 – 11:45 Group work

11:45 – 12:30 Group reports

12:30 – 14:00 Lunch & poster session

Session 4a: Late blight management, fungicides, and decision support systems
Chairs: Zhijian Zhao and Kwang-Soo Cho

14:00 – 14:20 Presentation 26. Green control technology of potato late blight in the Wumeng mountain area
Xia Liu

14:20 – 14:40 Presentation 27 (also presented as poster). Quantification of the *Phytophthora infestans* population densities in upland soils
in Japan using real-time PCR
Hisashi Osawa

14:40 – 15:00 Presentation 28 (also presented as poster). The identification and molecular mechanism of *Streptomyces hygroscopicus* against potato late blight
Xiumei Luo

15:00 – 15:20 Presentation 29 (also presented as poster). Enhanced biological control of potato late blight with six *Streptomyces* strains combined with biochar and salicylic acid
Shun Feng

15:20 – 15:40 Coffee Break

Session 4b: Late blight management, fungicides, and decision support systems
Chairs: Xingbi Che and Tongle Hu

15: 40 – 16:00 Presentation 30. Late blight in Southwest of China: Pathogen, fungicide evaluation and integrated management
Zhijian Zhao

16:00 – 16:20 Presentation 31. Challenges and strategies against potato late blight in China: How AsiaBlight helps Chinese farmers to control potato late blight
Xingbi Che

16:20 – 16:40 Presentation 32. Late blight, other major potato diseases in Georgia and integrated protection measures
Zurab Khidesheli

16:40 – 17:00 Presentation 33. Status of late blight management in India
Sanjeev Sharma

17:00 – 17:20 Poster prize winner announcement and closing remarks

18:30 – 21:00 Buffet Dinner

Annex 2. Participants

No.	LAST, First Name	Organization	Country
1	ACUÑA, Ivette	Institute of Agricultural Research	Chile
2	ADHIKARI, Buddhi	Nepal Agricultural Research Council	Nepal
3	AKINO, Seishi	Hokkaido University	Japan
4	ANDRADE-PIEDRA, Jorge	International Potato Center	Peru
5	BHAIK, Ashutosh	Corteva Agriscience	India
6	BONNAVE, Maxime	CARAH Agro-Food Research and Extension Center	Belgium
7	CHANG, Shiwei	CCCAP	Beijing, China
8	CHE, Xingbin	Chongqing Plant Protection Institute	Chongqing, China
9	CHEN, Qinghe	Fujian Academy of Agricultural Sciences	Fujian, China
10	CHEN, Yawei	Jin Tu Di Potato Research Center	Henan, China
11	CHO, Kwang-Soo	Rural Development Administration	Republic of Korea
12	COOKE, David	James Hutton Institute	United Kingdom
13	COOKE, Louise	Queen’s University Belfast	United Kingdom
14	DUAN, Guohua	Fujian Agriculture and Forestry University	Fujian, China
15	DONG, Jitao	Farming and Animal Husbanfry, Bureau of Yakeshi City	Inner Mongolia, China
16	DONG, Pan	Chongqing University	Chongqing, China
17	DONG, Suomeng	Nanjing Agricultural University	Nanjing, China
18	FAN, Ziyao	Sinochem international Crop Care Limited Company	Shanghai, China
19	FENG, Shun	Chongqing University	Chongqing, China
20	FU, Wei	China Crop Protection Industry Association	Beijing, China
21	GUHA ROY, Sanjoy	West Bengal State University	India
22	GUO, Chengjin	Ningxia Academy of Agriculture and Forestry Sciences	Ningxia, China
23	GUO, Li-Yun	China Agricultural University	Beijing, China
24	GUO, Mei	Heilongjiang Academy of Agricultural Sciences (HAAS)	Harbin, China
25	HE, Lei	CIP-China Center for Asia-Pacific	Beijing, China
26	HU, Baigeng	Xisen Potato Group Limited Company	Shandong, China
27	HU, Tongle	Hebei Agricultural University	Hebei, China

No.	LAST, First Name	Organization	Country
28	HUANG, Chong	National Agriculture Technology Extension	Beijing, China
29	HUANG, Lu	Guizhou Plant Protection Institute	Guizhou, China
30	HUI, Nana	Gansu Academy of Agricultural Sciences	Gansu, China
31	ISLAM, Mohammad	Bangladesh Agricultural University	Bangladesh
32	JIANG, Tao	Hebei Shuangji Chemical Limited Company	Hebei, China
33	JIANG, Wei	Yunnan Academy of Agricultural Sciences	Yunnan, China
34	KEAR Philip	CIP-China Center for Asia-Pacific	Beijing, China
35	KHIDESHELI, Zurab	Scientific Research Center of Agriculture	Georgia
36	LASSERRE, Christelle	CIP-China Center for Asia-Pacific	Beijing, China
37	LI, Canhui	Yunnan Normal University	Yunnan, China
38	LI, Honghao	Sichuan Academy of Agricultural Sciences	Sichuan, China
39	LI, Jianzhong	Bayer Crop Science (China) Limited Company	Beijing, China
40	LI, Jipin	Gansu Academy of Agricultural Sciences	Gansu, China
41	LI, Min	CIP-China Center for Asia-Pacific	Beijing, China
42	LI, Simeng	CIP-China Center for Asia-Pacific	Beijing, China
43	LI, Wanyue	Northwest A&F University	Shaanxi, China
44	LI, Yisen	Yakeshi SenFeng Seed Potato Company	Inner Mongolia, China
45	LIANG Jingsi	Yunnan Normal University	Yunnan, China
46	LIU, Biao	Beijing Shuwang	Beijing, China
47	LIU, Chengtao	Bayer Crop Science (China) Limited Company	Beijing, China
48	LIU Gang	Tianjin Nankai University	Tianjin, China
49	LIU, Si	CIP-China Center for Asia-Pacific	Beijing, China
50	LIU, Xia	Yunnan Agricultural University	Yunnan, China
51	LIU, Yang	CIP-China Center for Asia-Pacific	Beijing, China
52	LIU, Yaping	Yakeshi SenFeng Seed Potato Company	Inner Mongolia, China
53	LU, Jie	CAU	Beijing, China
54	LU, Xiaoping	CIP-China Center for Asia-Pacific	Beijing, China
55	LU, Yao	CIP-China Center for Asia-Pacific	Beijing, China
56	LUAN Hongying	Yunnan Normal University	Yunnan, China

No.	LAST, First Name	Organization	Country
57	LUO, Xiumei	Chongqing University	Chongqing, China
58	LYU, Dianqiu	South West University	Chongqing, China
59	LYU, Jialu	China Agricultural University	Beijing, China
60	MA, Dicheng	China Agricultural University	Beijing, China
61	MA, Yongqiang	Qinghai Academy of Agriculture and Forestry Sciences	Qinghai, China
62	MASANGCAY, Teresita	Benguet State University	Philippines
63	MAURER, Alberto	CIP-China Center for Asia-Pacific	Beijing, China
64	MIN, Fanxiang	Heilongjiang Academy of Agricultural Sciences	Harbin, China
65	OSAWA, Hisashi	Hokkaido University	Japan
66	PARK, Hyunjin	National Institute of Crop Science	Republic of Korea
67	PENG, Youliang	China Agricultural University	Beijing, China
68	PHAM THI THU, Huong	Horticulture Dept of the Field Crops Research Institute	Vietnam
69	QIAN, Hongjie	Yunnan Agricultural University	Yunnan, China
70	QU Chaonan	CIP-China Center for Asia-Pacific	Beijing, China
71	RAZA, Waqas	University of Sarghodha, Punjab	Pakistan
72	REN, Binyuan	National Agriculture Technology Extension	Beijing, China
73	RISTAINO, Jean	North Carolina State University	United States
74	SEO, Jin-Hui	National Institute of Crop Science	Republic of Korea
75	SERNEELS, Francois	CARAH Agro-Food Research and Extension Center	Belgium
76	SHAN, Weixing	Northwest A&F University	Shaanxi, China
77	SHARMA, Sanjeev	ICAR-Central Potato Research Institute, Shimla	India
78	SHEN, Ruiqing	Ningxia Academy of Agriculture and Forestry Sciences	Ningxia, China
79	SHEN, Yanfen	Southern China Potato Research Center	Hubei, China
80	SCHEPERS, Huub	Wageningen University & Research	Netherlands
81	TANG, Wei	Yunnan Normal University	Yunnan, China
82	TASHMATOVA, Mukhtabar	Tashkent State Agrarian University	Uzbekistan
83	WANG, Fengle	National Agriculture Technology Extension	Beijing, China
84	WANG, Guijiang	Heilongjiang Academy of Agricultural Sciences	Harbin, China

No.	LAST, First Name	Organization	Country
85	WANG, Hongyang	Yunnan Normal University	Yunnan, China
86	WANG, Li	Guangdong Academy of Agricultural Sciences	Guangdong, China
87	WANG, Luyao	Agricultural Genomics Institute Shenzen	Guangdong, China
88	WANG, Na	Baoding Yada Yinong Agricultural Technology Limited Company	Hebei, China
89	WANG, Pei	Sinochem international Crop Care Limited Company	Shanghai, China
90	WANG, Shasha	China Crop Protection Industry Association	Beijing, China
91	WANG, Tuhong	China Agricultural University	Beijing, China
92	WANG, Xiaodan	China Agricultural University	Beijing, China
93	WANG, Xigang	Ningxia Academy of Agriculture and Forestry Sciences	Ningxia, China
94	WANG, Xu	Bayer Crop Science Limited Company	Beijing, China
95	WEI, Qi	Heilongjiang Academy of Agricultural Sciences	Harbin, China
96	WEI, Zhouquan	Gansu Academy of Agricultural Sciences	Gansu, China
97	WENG, Ting'en	Yunnan Tumama Bio-Technology Limited Company	Yunnan, China
98	WU, Jian	Inner Mongolia University	Inner Mongolia, China
99	WU, Xuehuong	China Agricultural University	Beijing China
100	XIAO, Chunfang	Southern China Potato Research Center	Hubei, China
101	XU, Zhao	Hebei Shuangji Chemical Limited Company	Hebei, China
102	YUAN, Bo	AVR	Belgium
103	ZHANG, Fan	Nanjing Agricultural University	Nanjing, China
104	ZHANG, Jun	Beijing HuiSiJunDa Limited Company	Beijing, China
105	ZHANG, Zhibin	Inner Mongolia University	Inner Mongolia, China
106	ZHAO, DeYou	Corteva Agriscience	Shanghai, China
107	ZHAO, Donglei	Baoding Yada Yinong Agricultural Technology Limited Company	Hebei, China
108	ZHAO, Xiaoqiang	Nanjing Agricultural University	Nanjing, China
109	ZHAO, Zhijian	Yunnan Academy of Agricultural Sciences	Yunnan, China
110	ZHENG, Jie	Northwest A&F University	Shaanxi, China
111	ZHU, Jiehua	Hebei Agricultural University	Hebei, China

RESEARCH PROGRAM ON
Roots, Tubers and Bananas

The CGIAR Research Program on Roots, Tubers and Bananas (RTB) is a partnership collaboration led by the International Potato Center implemented jointly with the Alliance of Bioversity International and CIAT (International Center for Tropical Agriculture), the International Institute of Tropical Agriculture (IITA), and the Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD), that includes a growing number of research and development partners. RTB brings together research on its mandate crops: bananas and plantains, cassava, potato, sweetpotato, yams, and minor roots and tubers, to improve nutrition and food security and foster greater gender equity especially among some of the world's poorest and most vulnerable populations.

www.rtb.cgiar.org

LED BY
INTERNATIONAL POTATO CENTER
Alliance
Bioversity International
International Center for Tropical Agriculture
Since 1967 Science to cultivate change
cirad AGRICULTURAL RESEARCH FOR DEVELOPMENT
IITA Transforming African Agriculture