WUR - SPECIAL REPORT NO 19 - 2019, 37-44

AsiaBlight: past, present and future

LOUISE R. COOKE1, CHRISTELLE LASSERRE2, ALBERTO MAURER2

- ¹ School of Biological Sciences, Queen's University, Belfast, UK
- ² CIP-China Center for Asia Pacific, Beijing, China

SUMMARY

The formation of a late blight network for Asia, AsiaBlight, first proposed in 2014, initially focussed on generating a coarse-scale map of the Phytophthora infestans population in Asia to underpin future pathogen studies and disease management strategies. This was progressed during 2016-2019 with the assistance of the Inner Mongolia Potato E & T Center, Hohhot and of the James Hutton Institute, Dundee. FTA cards (funded by Bayer) were distributed from Hohhot to contacts in Asian countries who collected late blight samples and returned them to Hohhot. P. infestans DNA was genotyped in Hohhot and at the James Hutton Institute and uploaded to the database hosted by EuroBlight. In addition, other researchers active in Asia also contributed genotyping results to the database. The coarse-scale map shows the aggressive genotype 13_A2 to be widespread across mainland Asia, but the island populations sampled to be distinct and disparate. AsiaBlight began as a network with minimal resources, but has achieved growing recognition, a degree of regional collaboration and limited but successful private-public partnership. Starting in 2018, the CIP-China Center for Asia-Pacific (CCCAP) has taken up the challenge of implementing a self-sustaining AsiaBlight network. A website and workshops have been implemented, and an international meeting has been organized. Progress and future plans for this network are discussed.

KEYWORDS

Phytophthora infestans, potato late blight, China, SSR, population structure

INTRODUCTION

Countries in Asia range from the very wealthy to the very poor. A few have some of the highest malnutrition levels in the world (FAO et al., 2019). Potatoes are highly nutritious, can adapt to marginal conditions and produce more food per unit of water than any other crop, making potatoes a key component of food security. China and India are the two most populous countries in the world and are also the two most important potato producers, generating a third of the world total tonnage (FAOSTAT, 2019). Potato is popular in Asia, with many of its countries ranked within the top 50 potato producers, including Bangladesh (7), Iran (13), Pakistan (20), Kazakhstan (22), Uzbekistan (25), Nepal (26), Japan (31), North Korea (33), Kyrgyzstan (38), Indonesia (43), Azerbaijan (46) and Tajikistan (50) (FAOSTAT, 2019). As in other parts of the

globe, late blight (LB), caused by *Phytophthora infestans*, is the most important disease affecting potato production. An overall picture of *P. infestans* in Asia, including population dynamics, distribution of major genotypes and the most effective control measures, has been lacking. To address this problem, AsiaBlight, an inclusive network of scientists, companies, farmers and other stakeholders working towards reducing the impact of LB in Asia using an integrated approach, was initiated in 2014 under the auspices of the International Potato Center (Forbes, 2015), inspired by the success of EuroBlight and other international late blight networks.

As reported in the 2017 EuroBlight Proceedings (Cooke *et al.*, 2017), AsiaBlight initially focused on establishing a coarse-scale map of *P. infestans* across the region to serve as a baseline for pathogen studies and underpin future endeavours to improve on-farm disease management. Associated objectives of this project were to demonstrate the potential of Public-Private Partnerships (initially between public sector research institutes and agrochemical companies), and to develop a team spirit among Asian partners in order to promote collaboration for future activities. For the mapping project, FTA cards were distributed by the Inner Mongolia Potato E & T Center, Hohhot, China to contacts in many Asian countries. This paper provides an update on progress in the mapping project, which will be reported in more detail in a future peer-reviewed paper, and on plans for AsiaBlight, which are being led by the CIP-China Center for Asia-Pacific (CCCAP).

PROGRESS TO DATE

Organisation of sample collection

Collection of late blight samples followed the EuroBlight model with contacts in Asian countries being asked to collect *P. infestans* DNA from late blight lesions onto FTA cards and provide sample details on standard forms. Purchase of 500 FTA cards was funded by Bayer (Regions APAC 1 and APAC 2) and organised with the assistance of the CIP Office, Beijing. Professor Ruofang Zhang volunteered the assistance of her laboratory and staff in the Inner Mongolia Potato E & T Research Center, Hohhot, China to distribute the cards and to genotype the resultant *P. infestans* DNA samples. For more detail on the process, see Cooke *et al.* (2017).

Country contacts and FTA card distribution

Contacts were identified with the assistance of CIP scientists and other researchers. During 2016-2018, efforts were made to contact researchers in Armenia, Bangladesh, Georgia, India, Indonesia, Japan, Kyrgyzstan, the Republic of Korea, Myanmar, Nepal, Pakistan, the Philippines, Taiwan, Tajikistan, Uzbekistan and Vietnam. The late blight population in China was already being investigated in ongoing projects, so this was excluded from the proposed sampling. Researchers contacted in Armenia responded positively, but had to withdraw owing to changed responsibilities.

FTA cards and sampling instructions and forms were therefore sent to:

- Bangladesh (2016)
- Georgia (2016, 2017)
- India (2016)
- Indonesia (2016, 2017)
- Japan (2016)
- Kyrgyzstan (2017)

- Nepal (2016)
- Pakistan (2017, 2019)
- The Philippines (2017)
- Island of Taiwan (2016)
- Tajikistan (2016, 2017)
- Uzbekistan (2016)
- Vietnam (2016)

After FTA cards had been sent out, organisational changes in Tajikistan and Uzbekistan in 2016 resulted in loss of contacts and consequently of the FTA cards sent there. However, other researchers were identified in Kyrgyzstan and Tajikistan and cards were sent to these in 2017. Although FTA cards were sent to India in 2016, it transpired that Indian biosecurity legislation prohibits pathogen DNA from being sent out of the country, so FTA card samples could not be submitted for genotyping outside India. However, contacts were established with researchers engaged in *P. infestans* population studies within that country.

Contacts between several Asian countries and EuroBlight researchers established that sample collection was also currently ongoing in Bangladesh, Indonesia, Japan, the Republic of Korea, Myanmar and the Philippines with, in some cases, samples being submitted to the James Hutton Institute (JHI) or Wageningen University (WUR) for genotyping and mapping.

Sample collection and submission

For the coarse-scale mapping project, late blight was generally sampled during a single season (although sometimes sampling occurred during the winter over two calendar years), except where initial samples yielded insufficient pathogen DNA or where additional contacts were able to collect samples.

FTA cards with sampled *P. infestans* DNA were returned by the collectors to Hohhot along with completed sampling forms (Cooke *et al.*, 2017). Details of samples collected onto FTA cards during 2016-2019 are shown in Table 1.

DNA Extraction and Genotyping

DNA extraction and genotyping were initially carried out in the Inner Mongolia Potato E & T Center, Hohhot. Despite success in achieving implementation of the 12-plex SSR (Li *et al.*, 2013a), it proved difficult to complete the genotyping there because of staffing issues, which resulted in a lack of continuity. In addition, standardisation of allele calling provided a major challenge, despite provision of DNA standards and of a web workshop in October 2018 by David Cooke (JHI). In November 2018, FTA card samples were therefore divided in two, with half being sent to JHI, while genotyping of the remaining halves continued in Hohhot. Samples from eight countries/regions were successfully genotyped and added to the EuroBlight database (Table 1). Data resulting from samples collected by other researchers in Bangladesh, the Republic of Korea, Malaysia, Myanmar and Sri Lanka were also included in the database. Genotyping results from AsiaBlight samples and from other researchers' samples were uploaded to the map hosted on the EuroBlight website (euroblight.net) and also available from the AsiaBlight website (asiablight.org).

 Table 1.
 AsiaBlight FTA card sampling and genotyping of Phytophthora infestans, 2016-2019

Country/region	Yea	r and cr	ops sam	pled*	Comments on genotyping	Some	Uploaded
	2016	2017	2018	2019	in JHI	samples genotyped	to map
Bangladesh	n/a	25 P	n/a	n/a	24 samples genotyped	- √	√
Georgia	10 P	n/a	10 P	n/a	Insufficient <i>P. infestans</i> DNA in 2016 samples, 8 samples from 2018 genotyped	√	٧
Indonesia	10 P	16 P	n/a	n/a	17 samples genotyped, plus 9 samples genotyped in Hohhot	√	1
Japan	10 P	n/a	n/a	n/a	8 samples genotyped	√	√
Kyrgyzstan	n/a	n/a	n/a	n/a	Cards sent 2018, but no samples collected to date as no late blight in 2018 and 2019	x	x
Nepal	9 P	15 P, 10 T	n/a	n/a	23 samples genotyped	√	1
Pakistan	n/a	n/a	15 P, 5 T		Insufficient <i>P. infestans</i> DNA in 2018 samples, 2019 samples not yet collected.	x	x
The Philippines	n/a	10 P	n/a	n/a	10 samples genotyped	√	√
Taiwan	12 T	n/a	n/a	n/a	Plus 8 T (2014-15); DNA from isolates in culture, 4 samples genotyped	√	x
Tajikistan	n/a	n/a	n/a	n/a	No response from contact since October 2017	x	x
Vietnam	n/a	4 P	3 P, 1 T	4 T	11 genotyped	1	1

^{*} P = potato, T = tomato

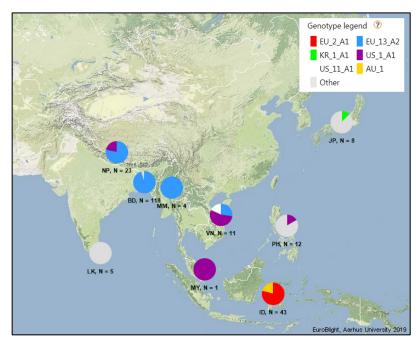


Figure 1. Phytophthora infestans genotype map for late blight samples collected in Asia (excluding India) from 2016-2019 (includes samples collected by researchers in addition to AsiaBlight FTA card sampling)

Genotypes identified in Asia included the old US_1_A1 (on tomato) and the aggressive 13_A2 (Blue 13). In particular, 13_A2, previously reported from Asian countries including China and India (Li *et al.*, 2013b; Chowdappa *et al.*, 2015), was found to be widespread across mainland Asia (Figure 1). However, the *P. infestans* populations on the islands of Asia included in the sampling had distinct and disparate genotypes and 13_A2 was not detected.

It is hoped to obtain additional samples from Japan and Taiwan and to collect samples from Pakistan and Kyrgyzstan in 2019-2020, subject to the occurrence of weather conducive to late blight. Full results of the coarse-scale population study are not detailed here, as it is planned to write them up for a peer-reviewed publication.

CHALLENGES

As noted in 2017, several challenges have been associated with the AsiaBlight coarse-scale mapping project:

- Obtaining pathogen samples across a large, politically diverse region was problematic
- It proved difficult to maintain stable communication channels, leading to consequent loss of the contact and the corresponding FTA cards
- National biosecurity legislation restricted opportunities for participation of some countries
- There were technical issues relating to the genotyping protocol and its standardisation

NEXT STEPS

As noted above, it is planned to write up the coarse-scale mapping project for publication in a peer-reviewed journal. If possible, genotyping of additional samples from Japan, Kyrgyzstan, Pakistan and the island of Taiwan is needed. It is necessary to ascertain from collectors/owners of non-AsiaBlight genotyping data from Asian countries whether their results can be included in the proposed coarse-scale map and publication. Questions remain as to how genotyping can best be progressed in Asia and how genotypic data can be integrated with phenotypic data, such as fungicide sensitivity, to allow appropriate management advice.

Starting in September 2018, CCCAP has taken up the challenge of implementing a self-sustaining AsiaBlight network. Since then, CCCAP has had many discussions with LB stakeholders in different Asian countries, to understand better how the new AsiaBlight network can respond to the expectations of the region. Thanks to these conversations, AsiaBlight will focus on training and capacity building, aiming to increase understanding of LB through research and collaboration, and to establish a pan-Asian community of LB stakeholders.

AsiaBlight will hold its third international meeting in October 2019 and three training workshops were also planned for 2019. All AsiaBlight workshops and training will be in Chinese and English. To support communication within the community, in early 2019, an AsiaBlight WeChat group, a Twitter feed and a Facebook page were launched. AsiaBlight 's website (asiablight.org) went live in May 2019 during the EuroBlight Workshop in York.

A broader sampling effort through collaboration within eight different provinces of China has 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.

ACKNOWLEDGEMENTS

We thank Greg Forbes (CIP) for his vision and leadership in initiating AsiaBlight, David Cooke and Louise Sullivan (JHI) for their invaluable help with the genotyping, Ruofang Zhang and her staff and students (including Lei Wu, Yuanyuan Pu, Sihui Chen, Lan Yu and Zhang Zhibin) for coordinating the FTA card distribution, sample return and implementing genotyping. Many EuroBlight colleagues have provided support to AsiaBlight activities, notably Jonathan Yuen (Swedish University of Agricultural Sciences, SLU), Jens Hansen and Poul Lassen (Aarhus Agricultural University), and Geert Kessel and Huub Schepers (Wageningen University & Research, WUR). We also gratefully acknowledge the assistance of Bayer Regions APAC 1 and APAC 2 who funded the FTA cards and also provided contacts in Indonesia, the Philippines and Pakistan. We thank the following AsiaBlight country contacts for their collaboration: Abdullah-Al-Mahmud, Monower Hossain, Ebna Habib Md. Shofiur Rahaman (Bangladesh); Azamat Azarov, Jalil Chakaev, Zurab Khidesheli, Karbonali Partoev, Rusudan Mdivani (Central Asian Countries); Ineu Sulastrini, Koko Tjintokohadi, Silviya Wiltin (Indonesia); Seishi Akino (Japan); Buddhi Sharma (Nepal); Waqas Raza, Muhammad Taufique Siddiqui (Pakistan); Robert Babaan (the Philippines); Rishi Burlakoti, Lawrence Kenyon, Wallace Chen (Taiwan); Rene van Rensen, Ho Ngoc Anh (Vietnam). We also thank Chris Ursell and Catherine Chatot for providing additional late blight samples from Asia.

REFERENCES

- Chowdappa, P., Nirmal Kumar, B.J., Madhura, S., Mohna Kumar, S.P., Myers, K.L., Fry, W.E., Cooke, D.E.L. (2015). Severe outbreaks of late blight on potato and tomato in South India caused by recent changes in the *Phytophthora infestans* population. Plant Pathology 64, 191-199.
- Cooke, L.R., Zhang, R., Wu, L., Pu, Y., Chen, S-H., Lan, Y., Yuen, J., Cooke, D.E.L., Forbes, G.A. (2017). Recent developments in Asia AsiaBlight. PAGV-Special Report no. 18, 39-44.
- FAO, IFAD, UNICEF, WFP, WHO (2019). The State of Food Security and Nutrition in the World 2019: Safeguarding against economic slowdowns and downturns. Rome, FAO, 239 pp.
- FAOSTAT (2019). Crop production data, potatoes, 2017. Downloaded from www.fao.org/faostat 26 September 2019.
- Forbes, G.A. (2015). Recent developments concerning the population biology and control strategies of *Phytophthora infestans* in Asia and Africa. PPO-Special Report no. 17, 51-56.
- Li, Y., Cooke, D.E.L., Jacobsen, E., van der Lee, T. (2013a). Efficient multiplex simple sequence repeat genotyping of the oomycete plant pathogen *Phytophthora infestans*. Journal of Microbiological Methods 92, 316-322.
- Li, Y., van der Lee, T., Zhu, J.H., Jin, G.H., Lan, C.Z., Zhu, S.X., Zhang, R.F., Liu, B.W., Zhao, Z.J., Kessel, G., Huang, S.W., Jacobsen, E. (2013b). Population structure of *Phytophthora infestans* in China geographic clusters and present of the EU genotype Blue 13. Plant Pathology 62, 932-942.