

Recent developments concerning the population biology and control strategies of *Phytophthora infestans* in Asia and Africa

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INTRODUCTION

This is an overview of the population dynamics of *Phytophthora infestans* in sub-Saharan Africa and Asia. I attempt to give an short review of published historical efforts to study the population dynamics and also more recent developments, particularly related to standardization, data management and collaboration. Being more of a review, the paper does not follow the standard format with sections for methodology, results and discussion but is rather divided by themes.

POTATO IN AFRICA AND ASIA

Prior to looking at the *P. infestans* population in these regions, it is important to understand something of the dynamics of the pathogen's most widely grown host: potato.

Potato is now globally the fourth major crop in terms of total production and the third most important food crop (much of maize is used for feed). Nonetheless, while potato is widely grown, production is concentrated in certain areas, including Asia (Fig. 1). China and India are the first and second producers globally, and for this reason Asia is the region with the greatest potato production (Fig. 2). Potato production is not nearly as important in Africa but it is nonetheless widely grown and plays a very important role in poverty alleviation and food security on the continent (Low *et al.*, 2007).

BRIEF HISTORY OF *P. INFESTANS* POPULATION STUDIES IN ASIA AND AFRICA

There have been a flurry of papers on the population dynamics of *P. infestans* in China in the last few years. A Google Scholar search turns up 14 since 2011. However, only one attempts to make nationwide analysis (Li *et al.*, 2013); this may be due primarily to the fact that China is so big and potato production so extensive. An interesting characteristic of previously-mentioned paper is that it was the first report of the 13_A2 ('Blue_13') clonal lineage in China (discussed more below).

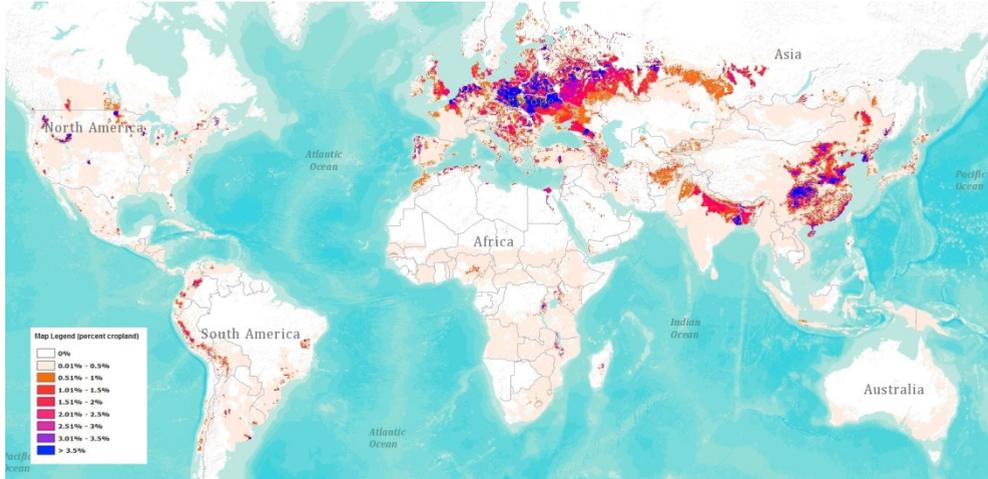


Figure 1. Global potato production, source is RTBMaps (<http://www.rtb.cgiar.org/RTBMaps/>)

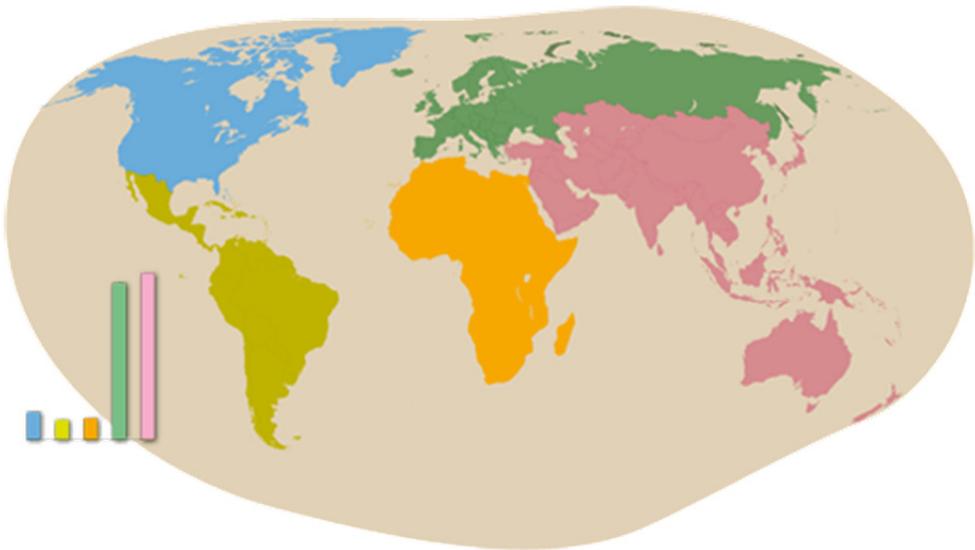


Figure 2. Regional potato production. Source, FAO (<http://www.fao.org/potato-2008/en/world/>)

Much less has been published about the pathogen population in other parts of Asia, with only a few articles looking at the population dynamics using markers that allow comparison across studies. Nonetheless, from these few it is possible to make some interesting observations. For example, while A2 phenotypes were detected relatively soon in China after their appearance in Europe (Zhang *et al.*, 1996), a study published in 2008 (Le *et al.*, 2008) from Vietnam indicated that the pathogen population in that country was still the “old” US-1.

Another important aspect of population studies in Asia is the growing evidence that the lineage A2_13 (blue_13), which has been problematic in Europe, is now relatively widespread in many parts of Asia as it has been reported in India (P. Chowdappa *et al.*, 2015), China (Li *et al.*, 2013) and in Nepal (D. Cooke, personal communication). Thus, it would appear that A2_13 is common through S. China, at least parts of the Himalayas and India. A recent set of studies from NW China indicates that this lineage is not present there (Tian *et al.*, 2015).

What little is known of the *P. infestans* population in E and SE Africa presents at least some enigmas. The earliest reports involving marker data indicated that at least some isolates collected in Rwanda were not US-1 (Forbes *et al.*, 1998). However, since that time and until relatively recently, other reports indicated that the US-1 clonal lineage was dominant in eastern sub-Saharan Africa (Vega-Sanchez *et al.*, 2000; McLeod *et al.*, 2001). In contrast, it would appear that if the US-1 lineage was dominant at one time in Ethiopia, it has been displaced for more than a decade. Schiessendoppler & Molnar (2002) found no US-1 isolates in Ethiopia, but rather a population characterized by the mitochondrial DNA Ia haplotype.

In the last few years it appears that the situation in sub-Saharan Africa has been very dynamic. In collections done in 2007 in eight African countries (Burundi, Kenya, Rwanda, Tanzania, Uganda, Malawi and Mozambique and South Africa), only two fields in Kenya had a new clonal lineage, which the authors labeled KE-1 (Pule *et al.*, 2013); all the other isolates were US-1. Excluding the enigmatic reports about Rwanda noted above, and the one study from Ethiopia, this represented the first indication of a new clonal lineage in sub-Saharan Africa. The presence of a lineage in this region that was not US-1 was also made evident when isolates collected in 2009 were found to belong to an old European lineage known as 2_A1 (Were *et al.*, 2013). In that study, the 2_A1 lineage was found on more farms than was the US-1 lineage, indicating that if it was the same one found by Pule *et al.* (2013), then it appeared to have spread since 2007. Subsequently, Njoroge *et al.* (2015) demonstrated extensive spread of KE-1 (Fig. 3) and also that KE-1 and 2_A1 are identical.

COORDINATION, STANDARDIZATION AND DATA MANAGEMENT

To date there has been little effort to formally coordinate researchers in Africa around the theme of late blight, but there has been an effort to begin implementing data standardization and management. In general, due to a significant number of publications on the theme, and other publicity around Euroblight meetings and Web-based applications (www.euroblight.net), there is a growing understanding among researchers of the utility of using common markers which can allow comparison across studies. Consistent with this, some recent studies have been based on a set (or subsets) of simple sequence repeat (SSR) markers. This has allowed many data from Africa to be included in the Euroblight online database, which means that maps of the isolate locations are publically available.

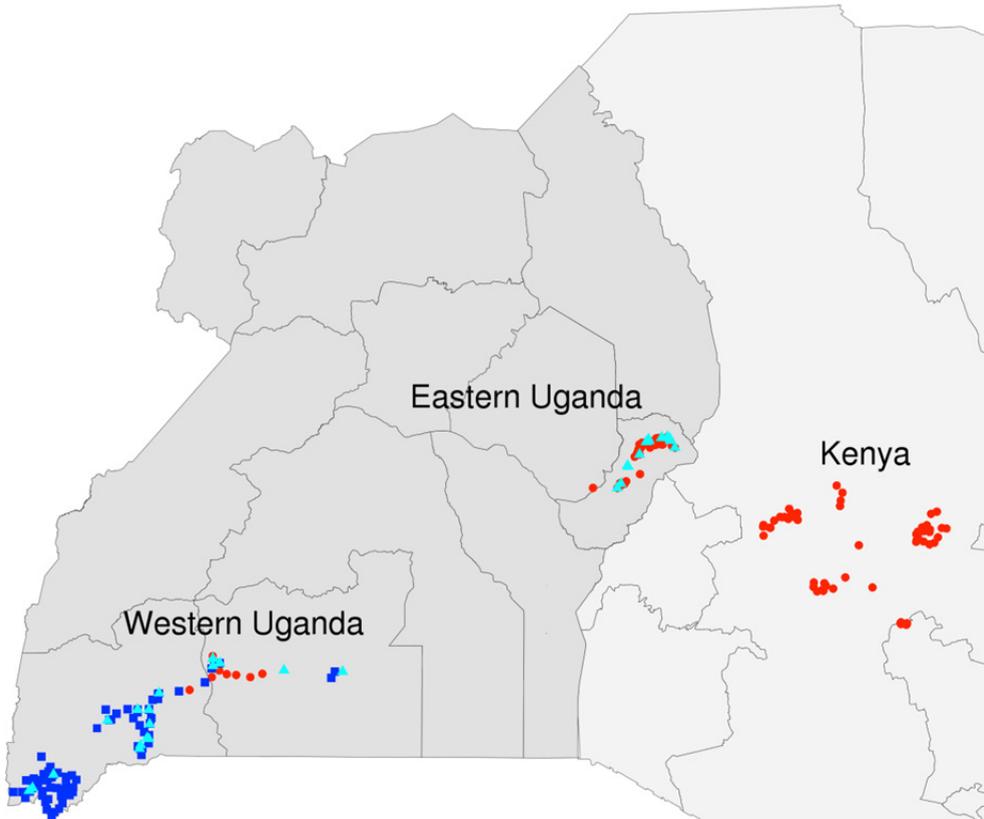


Figure 3. The *Phytophthora infestans* population in Kenya and Uganda showing occurrence and distribution of US-1 and KE-1 lineages. Red circle = KE-1 from potato; blue square = US-1 from potato; cyan triangle = US-1 from tomato. (From Njoroge et al, 2015)

Asia contrasts with Africa in that there has yet to be a standardization of marker approaches and data are not available in the Euroblight database, or any other common database. However, Asia also contrasts with Africa in that there have recently been several efforts to coordinate among researchers. Efforts for coordination in Asia began with a meeting of researchers in Nepal in late 2014. Twenty-five researchers attended this meeting, which was held in Dhulikhel just outside of Kathmandu, Nepal. The workshop was organized by the International Potato Center (CIP) and the National Potato Program of Nepal, and was sponsored by the Rural Development Administration of S. Korea and the CGIAR Research Program on Roots, Tubers and Bananas. Twelve countries were represented. The primary output of the workshop was the development of a roadmap to create a proposal for a region-wide network of collaboration on the subject of potato LB; the network was referred to as Asiabligh.

Subsequent to the Nepal workshop, there was a meeting in Chongching, China, which focused on IPM of potato late blight. In that meeting, the idea of an Asia-wide network for late blight was further discussed and was highly appreciated by the participants.

This was followed by a special session of the 2015 Euroblight meeting in Brasov, Romania, in which regional late blight networks and global coordination were discussed. In that meeting Asiabligh was discussed as well as USAblight and Latinblight (TizónLatino). More about the Brasov meeting is available on the [Euroblight Website](#).

More recently the network got a more formal 'kick-off' at a meeting organized as a satellite to the World Potato Congress (WPC) in Yanqing, China, near Beijing (Fig. 4). About 40 people participated in the meeting, with about half from Chinese potato research groups and the rest from non-Chinese participants at the WPC. The meeting was designed to give participants a better understanding of how well Euroblight has worked, progress in Latinblight and a suggestion for initial activities in Asiabligh. One important aspect of the meeting was the discussion of a project to get a course map for Asia of major genetic groups of *P. infestans*. The consensus was that this is a good activity for Asiabligh because of it's feasibility and because it provides a clear opportunity for public and private sectors to work together.



Figure 4. Asiabligh satellite meeting at World Potato Congress held in Beijing in 2015

COMMENTS

Efforts to 'globalize' the approach of Euroblight have gone on now for more than a decade. Implementing such networks in developing countries is difficult for a number of reasons, not the least of which is funding. One aspect that has led to sustainability in Euroblight is the private sector sees value in the network and thus supports. It would appear that a major challenge for making networks functional and sustainable in developing countries would be to find a model that provides a similar framework, i.e., one that allows both private and public sectors to benefit from the interaction.

One obvious shortcoming of the recent efforts to improve coordination among researchers in the developing world is the lack of emphasis on tomato. Tomato is an important crop in Latin America, Africa and Asia and undoubtedly plays an important role in the dynamics of the overall population of *P. infestans*, and potentially in disease management. Future efforts to develop these networks should include all important hosts of the pathogen.

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