

Late Blight in the USA – 2015 and 2016

BILL FRY AND KEVIN MYERS

Section of Plant Pathology and Plant-Microbe Biology, Cornell University, Ithaca NY 14853

Late blight of potato and tomato has been sporadically important in the USA. It is not uncommon to have locally important but widely separated epidemics. Regional or national pandemics have been rare, but in the last several decades there have been two widespread pandemics. The first pandemic was caused by the introduction of the US-8 clonal lineage. US-8 is an especially aggressive lineage that is also largely unaffected by mefenoxam. The pandemic was limited to the eastern half of the USA in 1994, but in 1995 this lineage was found throughout all potato growing regions in the USA and also caused major damage in the western potato growing regions of the USA (Fry and Goodwin 1997; Johnson et al., 1997). The second pandemic was in 2009 when the US-22 clonal lineage was widely transported on infected tomato transplants to many locations in northeastern USA in June of 2009. This pandemic was particularly hard on home owners and organic gardeners throughout northeastern USA (Fry et al., 2013).

The population of *P. infestans* in the USA continues to be dominated by relatively few clonal lineages (Hu et al., 2012; Fry et al., 2013). The most recent dominant strains are US-8, US-11, US-22, US-23 and US-24 (Fry et al., 2015; Figure 1). Individuals within a lineage are very similar to each other in most characteristics. However, there are important differences among lineages (Danieles et al., 2013; Fry et al., 2015; Table 1). For example, the most common lineages differ in terms of their response to mefenoxam, a very effective oomycete fungicide against sensitive strains (Fry et al., 1979). Mefenoxam is ineffective against resistant strains (Goodwin et al., 1996; Matson et al., 2015). From the mid-1990s to 2009, most clonal lineages in the USA were largely resistant to mefenoxam (Fry et al., 2015) so growers in the USA did not use mefenoxam during the mid-1990s to 2009 to manage late blight. We discovered in 2009 that the dominant lineage (US-22) was sensitive to mefenoxam and we've subsequently learned that some lineages dominant since 2009 have also been sensitive to mefenoxam (Hu et al., 2012; Saville et al., 2015). Additionally, lineages in the USA differ in terms of their pathogenicity to tomatoes. US-8 and US-24 are not good pathogens of tomatoes, whereas US-11 and US-23 are very good pathogens of tomatoes as well as potatoes. Thus knowledge of the lineage in a particular area provides crucially important information necessary to select the most effective management strategy.

While immigration of isolates into the USA has been the dominant evolutionary force influencing the *P. infestans* population in the USA there is evidence for the ephemeral existence of at least two sexual recombinant populations there. The first was detected in the 1990s in the Pacific Northwest and this recombinant population contained the US-11 clonal lineage (Gavino et al.,

2000). The second recombinant population was detected in New York State in 2010 and 2011 (Danies et al., 2014), but there has been no evidence that any of the individuals in this population has persisted (Figure 1).

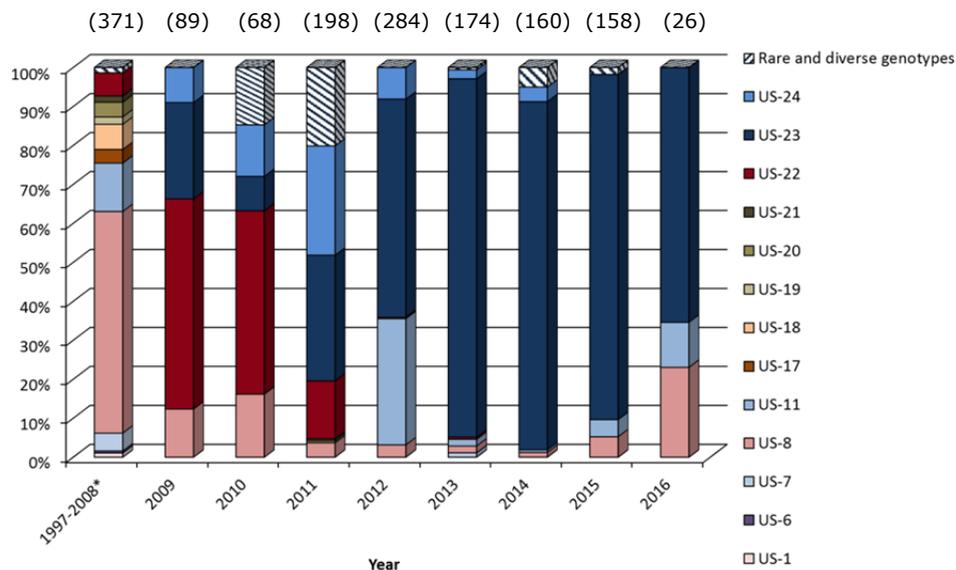


Figure 1. Clonal lineages detected in the USA from 1997 – 2016. The data for 1997-2008 are from the Fry lab; Hu et al., 2012, and (Wangsomboondee et al., 2002); the data for 2009-2016 are from the Fry Lab, the Ristaino lab and the USAblight consortium. The sample size for each year is indicated in parentheses at the top of each column. This figure was prepared by Giovanna Danies.

Table 1. Phenotypic characteristics of the most common clonal lineages of *Phytophthora infestans* detected in the USA 2009-2014. (Data are from Childers et al., 2015; Danies et al., 2013, and Hu et al., 2012)

Lineage	Mating type	Host Preference	Mefenoxam sensitivity
US-8	A2	Potato	moderately resistant
US-11	A1	Potato and Tomato	resistant
US-22	A2	Potato and Tomato	sensitive
US-23	A1	Potato and Tomato	sensitive – moderately sensitive
US-24	A1	Potato	moderately sensitive

Because the populations in the USA has been dominated by so few clonal lineages, and because these lineages have known important different phenotypic characteristics, it is possible and useful to determine the lineage in near real-time. A group of plant pathologists from Florida, North Carolina, Maine, Maryland, New York, Pennsylvania, Washington and Wisconsin have agreed to facilitate the rapid identification of strains causing late blight in the USA. When an outbreak of late blight is discovered, the grower/extension agent, or other personnel send the

sample via overnight courier to Cornell for genotypic (microsatellite) analysis using the system developed by Li et al. (Li Y et al., 2013). The sample is received at Cornell in the morning, processed, sequenced overnight and interpreted the next day. The results can then be sent to the sender the day after receipt of the sample. Thus, the identification of the strain can be learned within 48 hours. Strain identification then informs the management tactics. The reports are also uploaded to the USABlight website (USAblight.org).

The US-23 lineage has dominated the *P. infestans* population in the USA since 2012, including 2015 and 2016 (Figure 1). The weather was quite favorable to late blight in many regions of the USA in 2015, and we received 158 samples from 19 different states, representing all regions of the USA. The vast majority of samples contained only the US-23 clonal lineage. However, US-8 was detected in four states in the Midwest and West. US-11 was detected in the West and US-24 was detected in the East. In 2016, the weather was generally drier over much of the USA, and late blight was much less prevalent, and we received only 26 samples. Again, US-23 was the most prevalent lineage (17 samples from four states). US-8 was again detected in the Midwest and West, and US-11 was detected in the West. (31 samples from the prairies of Canada were all US-23.)

The reasons for the dominance of US-23 over other strains have not been vigorously evaluated. However, two of its phenotypic characteristics could be very important. It is very aggressive on foliage and tubers (Danies et al., 2013), and it is pathogenic on both potatoes and tomatoes (Danies et al., 2013). Chance may also play a role, because this isolate has not been dominant in the Midwest of the USA (but has been prevalent in the prairie provinces of Canada), and it has not been dominant in western USA.

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