



Coffee berries. iStockphoto / Thinkstock

Genomics of emerging plant pathogens: too little, too late

We need to rapidly sequence and release the genomes of emerging plant pathogens. Food security and environmental preservation hang in the balance.

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LAST YEAR during a visit to Colombia's Zona Cafetera, my host singled out one coffee farm amid the enchanting rolling hills. That farm's owner may have looked like the iconic Juan Valdez, but he is far from being cherished by his 'cafeteros' colleagues. He is infamous for having brought into Colombia a few coffee plants from Brazil. Unbeknown to him, a few leaves bore small orange spots, the telltale sign of the terrible coffee rust fungus, *Hemileia vastatrix*. Ever since that fateful introduction in 1983, Colombian cafeteros have struggled with managing this formidable foe. In recent years, after a brief lull, coffee rust came back with a vengeance casting a shadow on a critical Colombian agroindustry just as the country was emerging from years of social instability.

The history of agriculture is replete with sorry tales like the one of 'la roya del café'. From the upheaval caused by the Irish potato famine pathogen to recent epidemics such as wheat yellow rust, sudden oak death and horse chestnut canker, the British Isles have seen their share of plant pathogen introductions. Elsewhere, emerging infectious plant diseases cause havoc to world agriculture and threaten to slow laudable efforts to launch a second green revolution to meet the food security needs of a booming world population.

When faced with opponents like these, we need to know our adversary. The genome sequence of a plant pathogen is a deep look into its soul. From important and often unexpected insights into the biology of the pathogen to the tools needed to develop surveillance and diagnostic DNA markers, the genome is an invaluable resource that accelerates research and output delivery. With the cost of gene sequencing decreasing even faster than Moore's law, the cost-benefit calculation is evident. For instance, countless time and money are spent in developing DNA markers, investigating population structures, debating the pathogen origin, etc. – activities that can be greatly hastened by the genome sequence.

Many of the plant pathologists that sit on the front line of the epidemics are not properly trained to fully exploit the genome data and may not be inclined to lobby for sequencing funds. We simply cannot afford to wait. Genomes of emerging plant pathogens need to be immediately sequenced and released into the public domain as is routinely done with human pathogens.

A few months ago, I watched in awe as my bacteriologist colleagues accessed within days of the first reports the genome sequence of the *Escherichia coli* O104:H4 strain that killed about 50 people in Germany. The following 'crowdsourcing' of the genome analysis, during which scientists around the world pored over the freely available data to mine it and openly share their results on the internet, is a sure sign of things to come. A similar exercise is yet to happen in plant pathology.

Meanwhile, back in Colombia, scientists continue to scrape together enough funds to sequence and analyse the genome of the coffee rust fungus. I wholeheartedly support Bill Gates' recent call to arms for innovation in agricultural research, a philosophy we have fully embraced at The Sainsbury Laboratory over our 23-year history. But first things first – let's get the basics in place and develop lists of emerging and important plant pathogens. We have enough genome sequencing capacity, but progress so far has been piecemeal. We need to accelerate efforts to sequence and analyse the genomes of multiple races of the world's most important plant pathogens. Otherwise, you may have to start worrying about the cost of your lunch, and of your espresso!

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