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Roche NimbleGen Arrays Help Unveil the Secrets of Insidious Potato Blight

A large international team of researchers recently published the 240-megabase DNA sequence of *Phytophthora infestans*, a robust parasitic water mold responsible for the Irish potato famine of the 1840s, in *Nature* (1). Breeders have not been able to produce potato cultivars that remain resistant to this insidious blight, aptly named as the plant (phyto) destroyer (phthora). This fungal-like pathogen is an oomycete, an eukaryote related to algae and diatoms that is transferred by wind-borne spores that spread rapidly and germinate on wet leaves, killing entire fields of potatoes, tomatoes, and other plants within a few weeks. Conservative estimates of potato crop losses attributed to late blight are about 16% (US\$ 7.7 billion) of the global potato crop (US\$ 47.2 billion) each year (2). The sequencing of this mold and subsequent genomic analyses will now help reveal details of its biologic and pathogenic processes, allowing more rapid development of reliable, environmentally benign, and economically feasible management tactics as well as insight into new breeding strategies.

Yearly potato production (300 Mt) substantially contributes to worldwide food security, surpassed only by wheat (630 Mt) and rice (608 Mt)(2). While it is important to identify the problem genes responsible for infection, it is equally important to identify the genes that develop resistance.

Brian J. Haas, a primary contributor from the Broad Institute of MIT and Harvard, noted that “NimbleGen services generated the data that made it possible for us to identify key genes in pathogenesis, as described in our recent *Nature* publication on the potato blight genome. In particular we identified a large number of so-called effector genes that are critical to pathogenesis that had been previously unknown and are extremely challenging to predict because of their small size and unusual structure.”

Senior author Chad Nusbaum, co-director of the Broad Institute’s Genome Sequencing and Analysis Program, added that “NimbleGen services generated data that made it possible for us to identify these genes in a timely and cost-competitive manner.”

The authors capitalized on Roche NimbleGen's flexible array design capability to use the data from the newly sequenced genome to build a custom gene expression microarray, which helped measure gene level changes between the vegetative stage and infection stage. Nearly 3% of approximately 18,000 genes analyzed on the NimbleGen Gene Expression microarray are induced at least twofold during infection. Some of the induced genes belong to gene families with functions previously known to be involved in infection, such as RXLR genes, which may maintain virulence by suppressing host cell death. Understanding the *P. infestans* genes responsible for potato blight, and having unraveled its genetic code, will lead to methods for controlling the infection to improve food production and reduce the impact on worldwide crop losses.

- (1) BJ Haas, S Kamoun, et al., *Nature* 2009 September 17; 241: 393–398; doi: 10.1038/nature08358
(2) AJ Haverkort, PC Struik, et al., *Potato Res* 2009 August 8; 52:249-264; doi: 10.1007/s11540-009-9136-3

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