

# NEWS RELEASE

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## Mitochondrial Genome of Irish Potato Famine Pathogen Sequenced

### FOR IMMEDIATE RELEASE

In a classic case of “chicken or egg” detective work, scientists at North Carolina State University and The Institute for Genomic Research have concluded that previous hypotheses about the evolution of one of the world’s worst pathogens – *Phytophthora infestans*, the pathogen that caused the Irish potato famine in the 1840s – are wrong.

By sequencing the set of all genes, or genome, inside the cellular power plants, the mitochondria, of the different strains of the pathogen, Dr. Jean Beagle Ristaino, professor of plant pathology at NC State, and a team of researchers discovered that type II strains did not evolve from the type I strains, as was previously hypothesized. Instead, Ristaino and her colleagues say that the strains evolved from a common ancestor and that the type II strains diverged earlier than the type I strains.

The research is published in the January 2006 edition of *Current Genetics*.

There are four different strains, or haplotypes, of *P. infestans* – types Ia, Ib, IIa and IIb. The fungus-like pathogen causes severe lesions on leaves of potato and tomato plants. Ristaino called into question prevailing theories that the Ib strain of the pathogen caused the Irish potato famine in a paper published in the journal *Nature* in 2001, and published findings that pointed the finger instead at the Ia haplotype in 2004.

“We wanted to know how the four strains evolved and how they are related to each other,” Ristaino said. “This will help us learn how mutations, or changes in the genome, are leading to sensitivity to fungicide, for example.”

The Ib strain has been termed the ancestral strain by other researchers. Ristaino and her team discovered that while the Ib strain is most closely related to the common ancestor – it has the fewest mutations of the four strains – evidence suggests that it diverged from the common ancestor later in time than the divergence of the type II strains.

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Type Ia and IIa still affect potato plants around the world; in fact, more fungicide is sprayed for potato late-blight, which is caused by *P. infestans*, than any other potato disease, Ristaino said. Type IIb has a large number of mutations, which could explain why it is so rare and why it most often affects tomato plants instead of potato plants, she added.

Ristaino's lab is currently investigating the center of origin of *P. infestans*. She hypothesizes that the pathogen originated in South America and perhaps made its way to Europe and the United States via exports of potato seed on steamships.

The late-blight pathogen led to the Irish potato famine, which killed or displaced millions of Irish people, and other epidemics across the world.

The research is funded by the National Geographic Society, the USDA National Research Initiatives Cooperative Grants Program, the North Carolina State Agricultural Research Service and NC State's International Programs Office.

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**Note to editors:** An abstract of the paper follows.

## “Mitochondrial Genome Sequences and Molecular Evolution of the Irish Potato Famine Pathogen, *Phytophthora infestans*”

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**Abstract:** The mitochondrial genomes of haplotypes of the Irish potato famine pathogen, *Phytophthora infestans*, were sequenced. The genome sizes were 37,922, 39,870 and 39,840 bp for the type Ia, IIa and Iib mitochondrial DNA (mtDNA) haplotypes, respectively. The mitochondrial genome size for the type Ib haplotype, previously sequenced by others, was 37,957 bp. More than 90% of the genome contained coding regions. The GC content was 22.3%. A total of 18 genes involved in electron transport, 2 RNA encoding genes, 16 ribosomal protein genes and 25 transfer RNA genes were coded on both strands with a conserved arrangement among the haplotypes. The type I haplotypes contained six unique open reading frames (ORFs) of unknown function while the type II haplotypes contained 13 ORFs of unknown function. Polymorphisms were observed in both coding and noncoding regions although the highest variation was in non-coding regions. The type I haplotypes (Ia and Ib) differed by only 14 polymorphic sites, whereas the type II haplotypes (IIa and IIb) differed by 50 polymorphic sites. The largest number (152) of polymorphic sites was found between the type IIb and Ia haplotypes. A large spacer flanked by the genes coding for tRNA-Tyr (trnY) and the small subunit RNA (rns) contained the largest number of polymorphic sites and corresponds to the region where a large indel that differentiates type II from type I haplotypes is located. The size of this region was 785, 2,666 and 2,670 bp in type Ia, IIa and IIb haplotypes, respectively.

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Among the four haplotypes, 81 mutations were identified. Phylogenetic and coalescent analysis revealed that although the type I and II haplotypes shared a common ancestor, they clearly formed two independent lineages that evolved independently. The type II haplotypes diverged earlier than the type I haplotypes. Thus our data do not support the previous hypothesis that the type II lineages evolved from the type I lineages. The type I haplotypes diverged more recently and the mutations associated with the evolution of the Ia and Ib types were identified.