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Genome evolution in the Irish potato famine pathogen lineage

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Eukaryotic plant pathogens, such as oomycetes and fungi, cause highly destructive diseases that negatively impact commercial and subsistence agriculture worldwide. Many plant pathogen species, including those in the lineage of the Irish potato famine organism *Phytophthora infestans*, evolve by host jumps followed by adaptation and specialization on distinct hosts. However, the extent to which host jumps and host specialization impact genome evolution remains largely unknown. This talk will provide an update on our work on genome evolution in the *P. infestans* clade 1c lineage. To determine the patterns and selective forces that shape sequence variation in this cluster of closely related plant pathogens, we and our collaborators resequenced several representative genomes of four sister species of *P. infestans*. This work revealed extremely uneven evolutionary rates across different parts of these pathogen genomes (a two-speed genome). Genes in low density and repeat-rich regions show markedly higher rates of copy number variation, presence/absence polymorphisms, and positive selection. These loci are also highly enriched in genes induced *in planta*, such as disease effectors, implicating host adaptation in genome evolution. These results demonstrate that highly dynamic genome compartments enriched in non-coding sequences underpin rapid gene evolution following host jumps.

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