

effector genes and Solanum host R genes. We leveraged the targeted sequencing approach to generate high coverage of genes responsible for pathogen virulence and host resistance. Many modern well-characterized effector genes have historically been present in *P. infestans*. Both R genes and effectors showed signatures of selection. However, variant calling analysis revealed alternative alleles including avirulent forms compared to the reference genome for many effectors that likely impacted function. The effector *Avr3b* was the only well-described effector not present in Famine era samples but did appear in the mid-1900s. Interestingly, the resistance breaking allele of *Avr1* was present during the famine before the *Solanum R1* gene was deployed by plant breeders. Detailed ploidy analysis of 19 high coverage genomes showed that US-1 lineages appearing in the early 1940s were triploid, in contrast to the FAM-1 lineages from 1845 and thereafter that were diploid. This exploration of historic plant and pathogen genomes will shed light on the past host-pathogen evolutionary relationships of a globally important plant pathogen and could provide insight for future deployment of Solanum R genes.

## F2.3-2

### HERBARIA IN NATURAL HISTORY COLLECTIONS ILLUMINATE THE EVOLUTIONARY HISTORY AND EMERGENCE OF CITRUS BACTERIAL CANKER

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#### Text

The field of ancient genomics has triggered considerable progress in the study of pathogens, including those affecting crops. Herbarium collections have been an important source of dated, identified and preserved DNA, whose use in comparative genomics and phylogeography may shed light into the emergence and evolutionary history of plant pathogens. I will present the reconstruction of 13 historical genomes of the bacterial crop pathogen *Xanthomonas citri* pv. *citri* (*Xci*) from infected citrus herbarium specimens using a shotgun-based deep sequencing strategy. After authentication of the historical genomes based on DNA damage patterns, we compared them to modern genomes to reconstruct their phylogenetic relationships, pathogeny-associated genes content and estimate several evolutionary parameters, using Bayesian tip-dating calibration and phylogeography inferences. Despite a challenging analysis of data, requiring adapted treatment before being compared to modern samples, our results reveal that *Xci* originated in Southern Asia ~11,500 years ago and diversified during the beginning of the 13th century, after Citrus diversification and before spreading to the rest of the world. This updated scenario links *Xci* specialization to Neolithic climatic change and the development of agriculture, and its diversification to the human-driven expansion of citriculture through the early East-West trade and later colonization.

## P2.3-001