An atlas of the genomes of Phytophthora infestans

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Introduction

Late blight (*Phytophthora infestans*) of potato and tomato causes billions of dollars in mitigation (i.e., fungicide application) and crop loss annually. To date, 26 genomes of this important plant pathogen have been sequenced. Populations occur as assumedly clonal lineages which had been anciently sexually recombinant. Lineages US-8 and US-11 have been characterized as having resistance to the commonly used fungicide metalaxyl. The mode of action for metalaxyl has been reported to include transcription, such that RNA polymerases, and their associated proteins, have been promoted as candidate loci. We present a genome-wide survey of markers which bioinformatically differentiate these fungicide resistant lineages from susceptible lineages and characterize whether these candidate loci contain polymorphisms which segregate in a manner which may infer resistance.

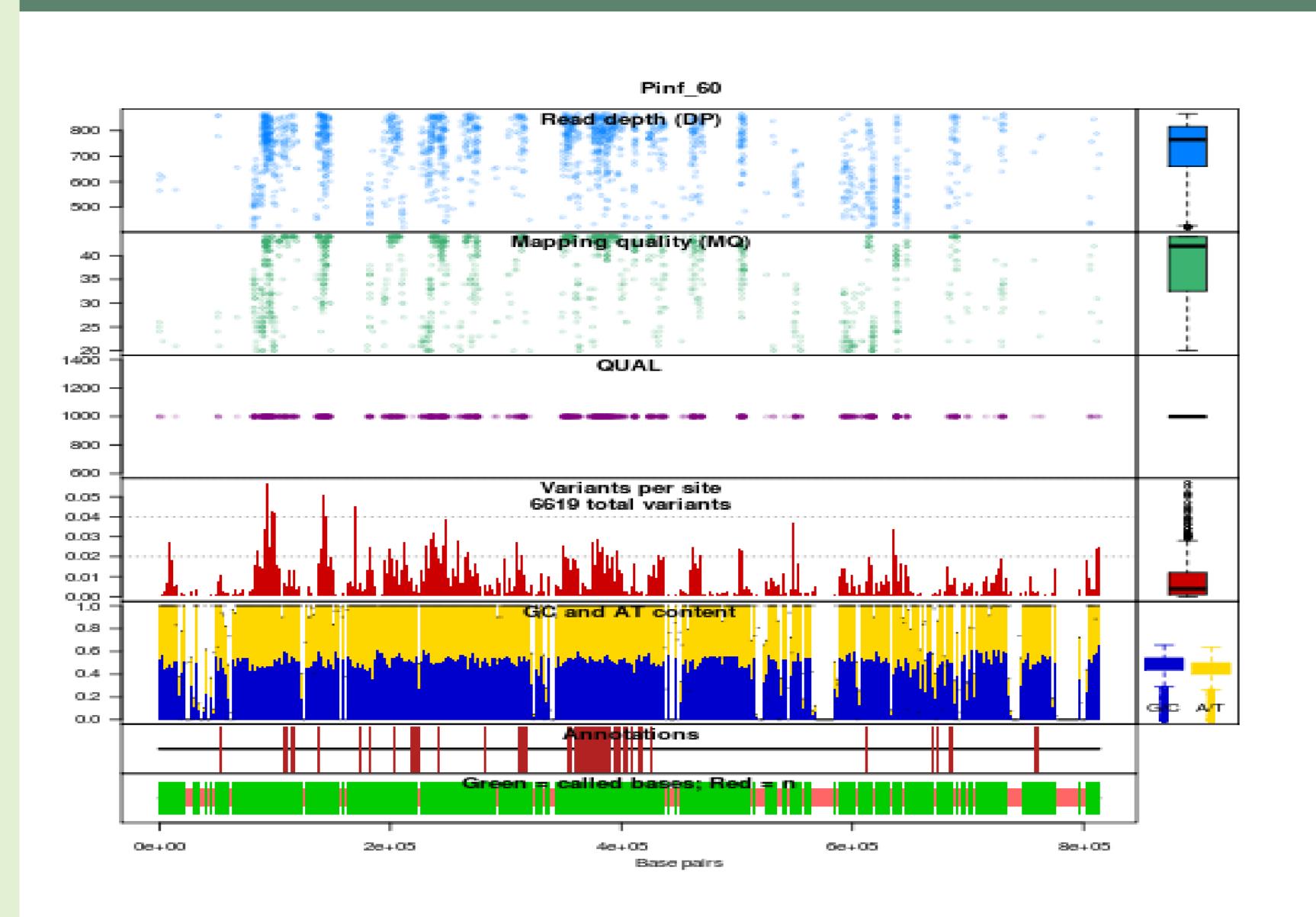
Bioinformatic methods

- Sequence reads were acquired through publicly available archives
- Reads were mapped to the T30-4 reference with bowtie2
- Variants were called using SAMtools
- Varients were post-processed with custom code

Genome summaries

Missip Barplot of RR, RA, AA.

Visualization of Supercontig 60



Describe the plot.

- Filtered on read depth
- Filtered on quality (QUAL)

Variants identifying fungicide resistant lineages (US-8 & US-22)

SupercontigPositionSupercontig_1.NNnnnSupercontig_1.NNnnn

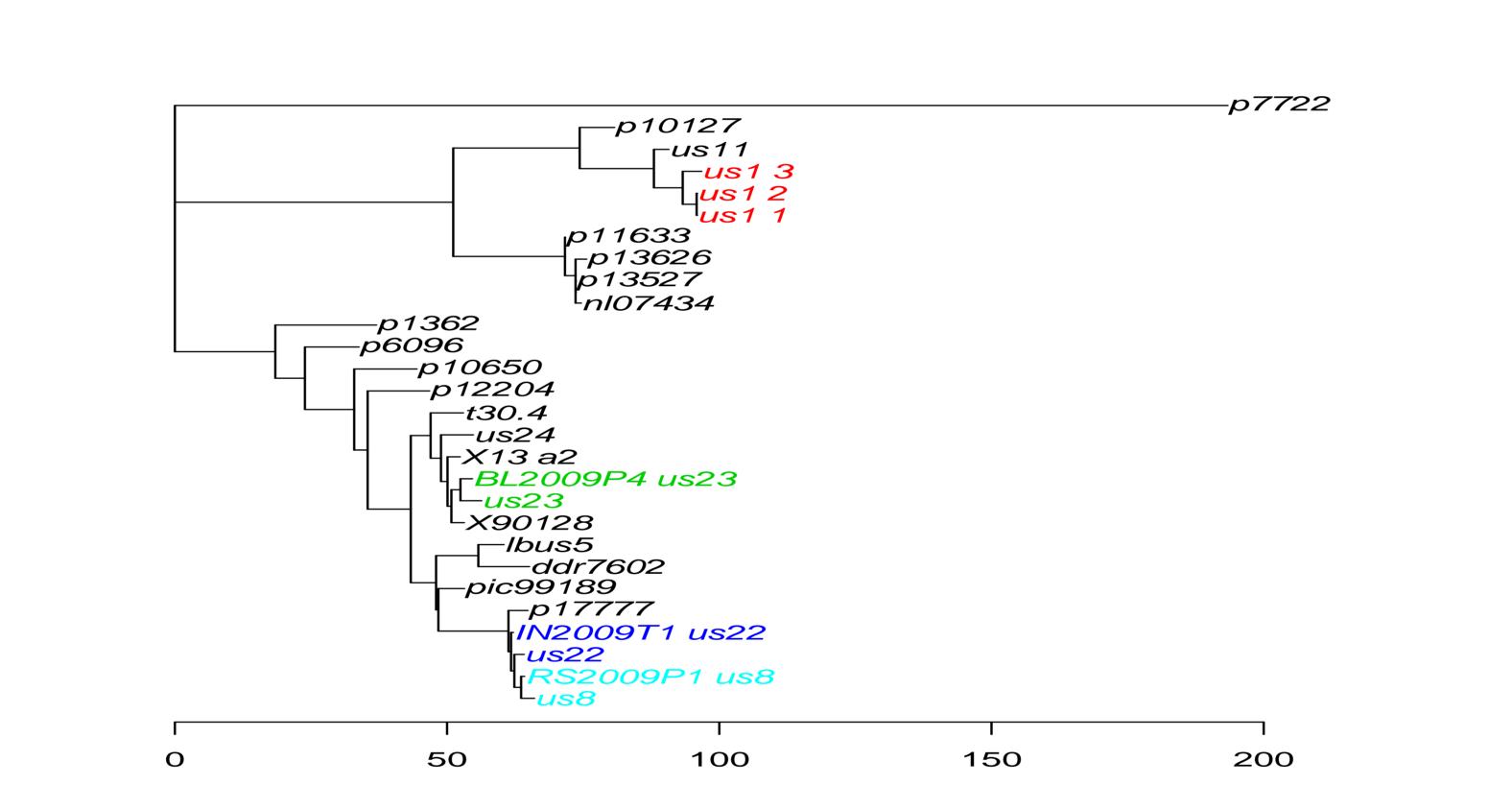
Discussion

Blah, blah and blah.

Conclusions

- Conclusion 1
- Conclusion 2
- Conclusion 3

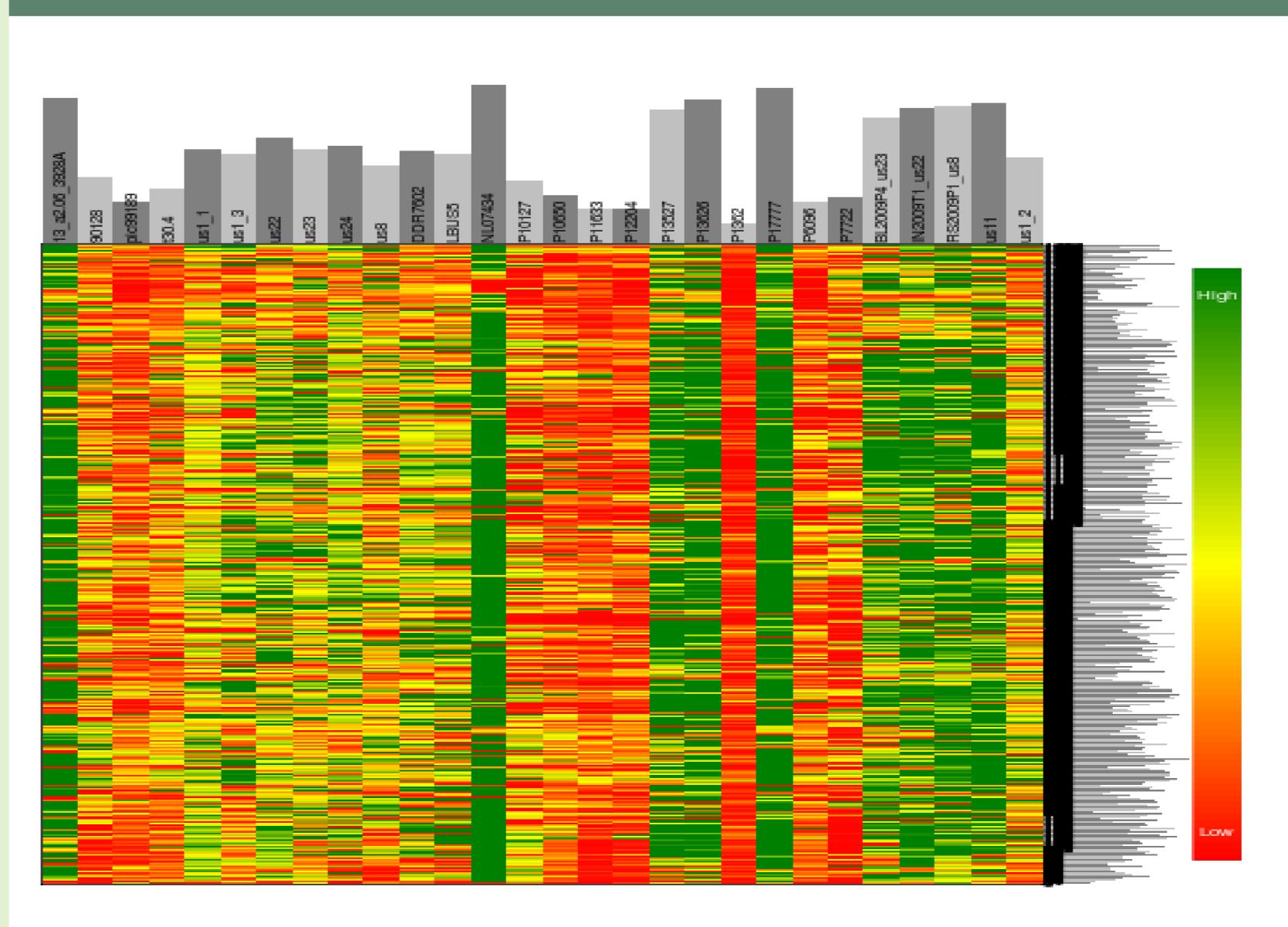
Mitochondrial phylogeny of Phytophthora infestans



Neighbor-joing tree based on Euclidian distances to describe relationships within *Phytophthora infestans*.

- P. mirabilis is outgroup
- Lineage US-1 forms an independant clade
- other stuff

Genotypic quality for Supercontig 60



Summary of genotype qualities

- Green represents a quality of 100
- Red represents a quality of 0
- Most genotypes are of intermediate quality
- ▶ Only genotypes of ≥100X coverage are of high quality (green)
- Most genotypes are of moderate quality