PUBLISHABLE SUMMARY

The oomycete *Phytophthora infestans* causes late blight, a re-emerging and ravaging disease of potato and tomato. It is renowned for its "high evolutionary potential" that allows to rapidly overcoming sources of resistance introduced in crop varieties. In recent years, the regular emergence of new *P. infestans* genotypes caused destructive epidemics in Europe and North America. Pathogens in *Phytophthora infestans* lineage, like many plant pathogens, evolve by host jumps followed by specialization, processes that play a critical role in the emergence of new *P. infestans* epidemics. However, how host jumps impact genome evolution remains largely unknown. An improved understanding of the genomic basis of adaptation to host plants will lead to conceptual advances in plant pathology and renewed opportunities for durable management of disease resistance in crop plants.

The long-term objective of our work is to understand the mechanisms underlying the emergence of pathogenicity and virulence in filamentous plant pathogens. We revised the initial proposal focused on the detailed characterization of one effector protein to adopt a large scale approach based on next generation sequencing. The overall objective of this project was to characterize genome evolution in *P. infestans* lineage in order to understand how this pathogen adapted to new hosts. Questions we expected to address, include how polymorphisms distribute across *P. infestans* genome, how do effector genes evolve, can we use *P. infestans* genomic data to propose new strategies for the management of resistance in crops?

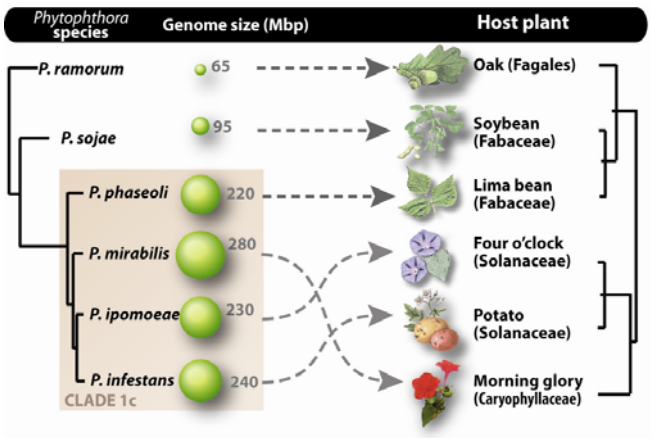

Figure 1. Phylogeny of sequenced *Phytophthora* species compared to the phylogeny of their hosts. Host jumps in clade 1c are revealed by non congruence of the phylogenies.

To determine the patterns of sequence variation and selective forces that shape sequence variation in the *P. infestans* lineage, we re-sequenced eight representative genomes of covering four sister species and four *P. infestans* strains using Illumina technology (**Figure 1**). We aligned re-sequenced genomes to *P. infestans* reference genome (Haas *et al.*, Nature 2009) to identify presence/absence polymorphisms, estimate copy number variation and identify single nucleotide polymorphisms. Haas *et al.* reported that the *P. infestans* genome experienced a repeat-driven expansion relative to distantly related Phytophthora spp. (74% repeats versus <40%) and shows an unusual discontinuous distribution of gene density. Disease effector genes, such as members of the RXLR and CRN families, localize to expanded, repeat-rich and gene-sparse regions of the genome, in sharp contrast to core ortholog genes, which occupy repeat-poor and gene-dense regions. We demonstrated that highly dynamic genome compartments enriched in non-coding sequences underpin accelerated gene evolution following host jumps (**Figure 2**). Gene-sparse regions that drive the extremely uneven architecture of the *P. infestans* genome are highly enriched in plant-induced genes, particularly effectors, therefore implicating host adaptation as a driving force of genome evolution in this lineage. In addition, we unexpectedly identified several genes involved in epigenetic processes, notably histone methyltransferases, as rapidly evolving residents of the gene-sparse regions (Raffaele *et al*. Science 2010).

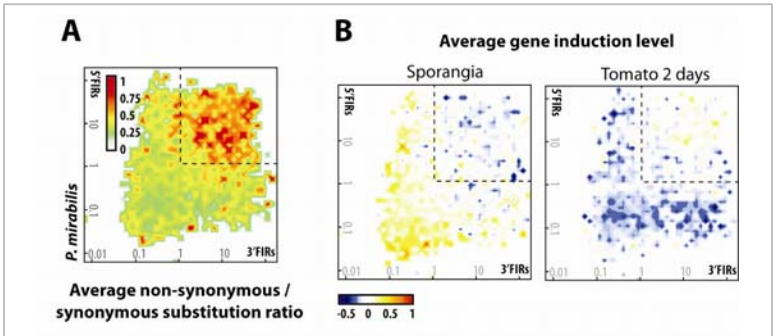

Figure 2. *P. infestans* two-speed genome. The distribution of the ratio of non-synonymous / synonymous substitutions (A) and of gene expression levels (B) relative to genome environment (length of flanking intergenic regions, FIRs) reveal two genome compartments with different evolution and expression patterns.

Next, we combined genome architecture analysis, transcriptomics and prediction of secreted proteins to identify novel proteins potentially involved in pathogenicity in *P. infestans* (Raffaele *et al*. BMC Genomics 2010). We have also exploited our expertise in genomics and *in silico* analysis to develop a new methodology for the classification of effector gene candidates and to identify promising candidates in the genome of rust fungi (Saunders *et al.*, Plos One 2012).

Our data, and other recent reports, point to an unexpected role of repeat-driven genome expansion in the adaptability of several lineages of filamentous plant pathogens. This trend is opposite to the well documented view that specialized parasites and symbionts evolve by genome reduction. This suggests that the cost of maintaining large genomes is counterbalanced by the benefits of adaptability conferred by repeat-rich genome regions in these lineages. In a recent review (Raffaele and Kamoun, Nat Rev Microbiol. 2012) we propose a model in which large adaptable genomes confer a macro-evolutionary advantage by reducing the likelihood of pathogen lineage extinction due to the depletion of host plants in the biota (**Figure 3**).

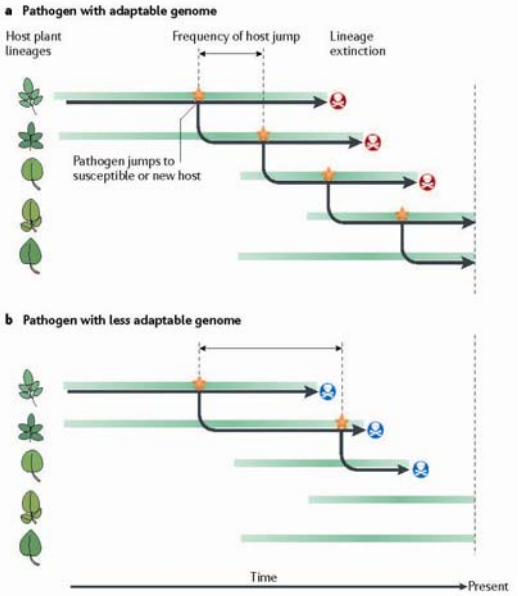

Figure 3. Jump or die: a model to account for the macroevolutionary persistence of host-specialized filamentous plant pathogens. The model illustrates the evolutionary fate of pathogens with (a) highly adaptable genomes and (b) less adaptable genomes.

The perspective to develop strategies for durable management of resistance in crop plants is central to the pathogenomics approaches we performed in frame of this proposal. With an aim to propose such management strategies, we analyzed the genome sequence and transcriptome of several *P. infestans* emerging aggressive strains that caused Blight epidemics in recent years. We identified sequence and expression polymorphism affecting effector genes and could identify polymorphisms explaining the virulence of theses strains on various resistant plants. We could also reveal "core effectors" that are expressed in all *P. infestans* strains analyzed so far. These effectors are recognized by their cognate R genes, the deployment of which could provide a mean for the durable management of Blight resistance.

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