Phenotypic variation within a clonal lineage of *Phytophthora infestans* from Nicaragua

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Introduction

Late blight caused by the fungus-like oomycete *Phytophthora infestans* (Mont.) De Bary is one of the main constraints affecting both potato and tomato crops in the northern highlands of Nicaragua (Figure 1). The main objective of this study was to assess comparatively the genotypic and phenotypic variation of *Phytophthora infestans* isolates collected in potato and tomato growing areas.

Figure 1. Potato experimental plot planted with the susceptible cultivar CalWhite apparently healthy (A) and two weeks later under favourable conditions for potato late blight development (B)

Materials and Methods

Sampling of *Phytophthora infestans* (Figure 2).

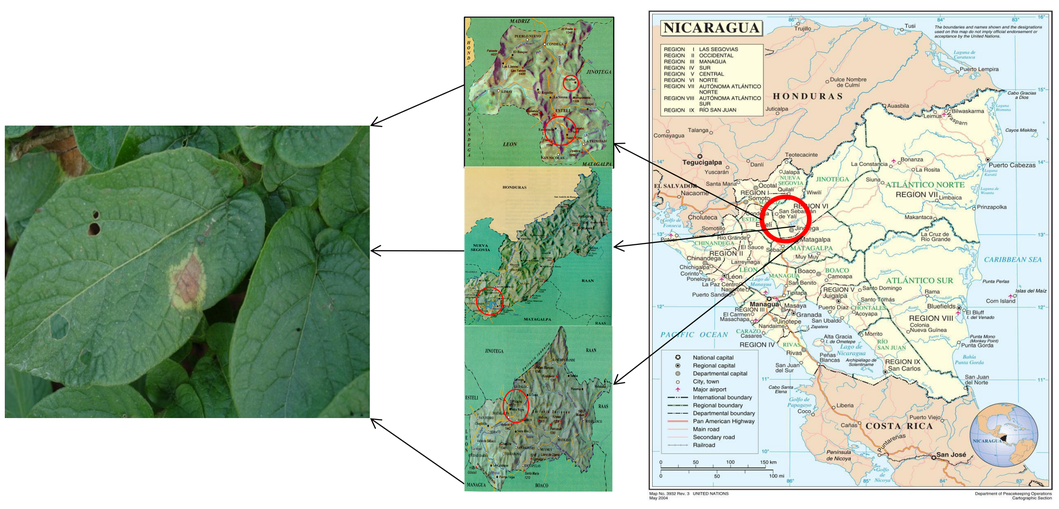

Figure 2. Single lesion isolates were collected in three northern departments of Nicaragua from 2007 to 2010. In each department many sites were sampled.

Genotypic analysis

- Simple sequence repeats (SSR) markers: Pi4B, PiG11, Pi16, Pi70, PiD13, Pi63 and Pi04 (Knapova and Gisi, 2002; Lees et al., 2006).
- Mitochondrial DNA (mtDNA) haplotyping (Griffith and Shaw, 1998).

Phenotypic analysis

- Mating type determination (conventional pairing)
- Virulence testing and fungicide sensitivity were done as described by Lehtinen et al., 2008. Mean number of virulence factors per isolate (*Ci*) and pathotype (*Cp*) were calculated as described by Andrivon (1994).

Results

From 2007 to 2010, 248 isolates of *P. infestans* were collected. All of them were tested for mating type, 132 isolates were used for genotypic analysis and 98 were used for virulence and fungicide testing. SSR genotyping revealed no polymorphism among tested isolates of *P. infestans*. Mitochondrial DNA haplotyping detected the Ia haplotype (Table 1).

Table 1. Alleles detected by 7 SSR markers and mtDNA haplotype of *Phytophthora infestans* isolates collected in Nicaragua.

	SSR markers							mtDNA
Loci	4B	G11	Pi16	Pi70	D13	Pi63	Pi04	Ia
Alleles	205	132	176	192	98	148	166	
	213	156	176	192	107	157	170	

Ninety-eight percent of the isolates were resistant to metalaxyl, 1% intermediate and 1% sensitive, while 82% sporulated in propamocarb-HCl at 10 mg.l^{-1}, 28% sporulated in propamocarb-HCl at 100 mg.l^{-1} and no isolate sporulated at 1000 mg.l^{-1} (Figure 3).

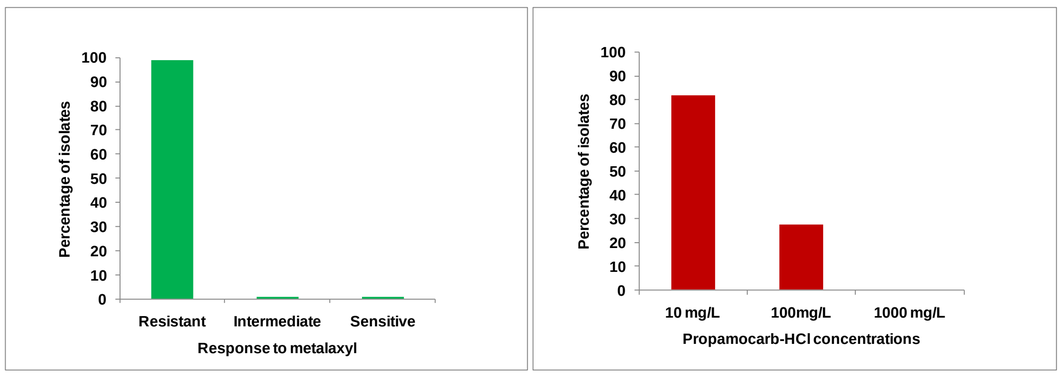

Figure 3. Response of *Phytophthora infestans* isolates from Nicaragua to metalaxyl and propamocarb-HCl.

The virulence testing showed a high variation among isolates. A total of 37 different races were identified. The percentage of isolates overcoming R-genes varied. Only one isolate overcame R9 and no one overcame R8 (Figure 4). The *Ci* and *Cp* were 6.2 and 5.4 respectively.

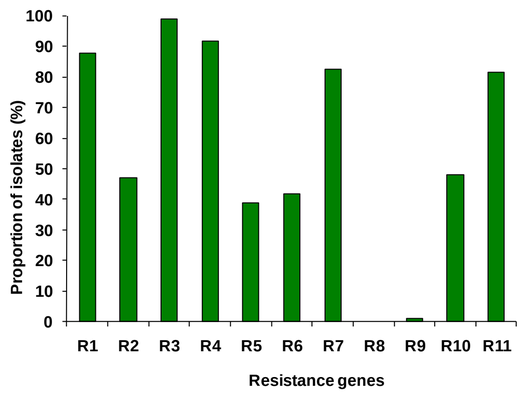

Figure 4. Percentages of *P. infestans* isolates overcoming R-genes

References

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Conclusions

- Nicaraguan population of *P. infestans* is dominated by a clonal lineage (based on 7 SSR markers) that has the A2 mating type and the Ia haplotype
- The virulence spectrum within this clonal lineage is highly variable.