Phenotypic variation within a clonal lineage of Phytophthora infestans from Nicaragua

U. Blandón-Diaz1,2, A-K. Widmark2, A. Hannukkala3, N. Högberg2, J.E. Yuen2

1Universidad Nacional Agraria, Managua, Nicaragua. Apdo 453; 2Swedish University of Agricultural Sciences, Dept of Forest Mycology and Pathology, PO Box 7026, S-750 07 Uppsala, Sweden; 3MTT Agrifood Research Finland, Plant Production Research, FI-31600 Jokioinen, Finland.

Introduction

Late blight caused by the fungus 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.

Materials and Methods

Sampling of Phytophthora infestans (Figure 2).

Genotypic analysis

• Simple sequence repeats (SSR) markers: Pi4B, PiG11, Pi16, Pi70, PiD13, Pi63 and Pi04 (Krapova 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 la haplotype (Table 1).

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

<table>
<thead>
<tr>
<th>Loci</th>
<th>Pi4B</th>
<th>PiG11</th>
<th>Pi16</th>
<th>Pi70</th>
<th>PiD13</th>
<th>Pi63</th>
<th>Pi04</th>
</tr>
</thead>
<tbody>
<tr>
<td>Alleles</td>
<td>205</td>
<td>132</td>
<td>176</td>
<td>192</td>
<td>98</td>
<td>148</td>
<td>166</td>
</tr>
<tr>
<td>213</td>
<td>156</td>
<td>176</td>
<td>192</td>
<td>107</td>
<td>157</td>
<td>170</td>
<td></td>
</tr>
</tbody>
</table>

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.

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 la haplotype
• The virulence spectrum within this clonal lineage is highly variable.

References