High genotypic diversity in Estonian populations of *Phytophthora infestans*

Riinu Kiiker, Eve Runno-Paurson

Brasov, Romania
2015
Potato growing and late blight in Estonia
Sampling of Estonian *P. infestans* populations

- 141 isolates
- 23 potato fields
- 2-15 isolates from one field
- Potato fields
  - Conventional (large and small)
  - Organic
  - Field trials
Characterisation of Estonian *P. infestans* populations

- Mating type determination using A1 and A2 tester isolates

- Genotyping with 12 SSR markers (Li et al. 2013) performed in The James Hutton Institute in Scotland, UK
Mating type

Percentage of *P. infestans* isolates (%)

- **2010 (n=41)**: A1 51.2%, A2 48.8%
- **2011 (n=51)**: A1 45.1%, A2 54.9%
- **2012 (n=49)**: A1 40.8%, A2 59.2%

**Overall (n=141)**: A1 51.8%, A2 48.2%

p=0.55
Mating type incidence on Estonian potato fields

- A1
- A2
- A1 & A2

87% of sampling fields

p<0.001
Genotyping results

- 52 alleles over 12 SSR loci
- All loci polymorphic
- 2-9 alleles per locus
- Highest diversity in loci G11 and SSR4
- Lowest diversity in locus Pi70
- Loci are not linked
  - The standardized index of association (Agapow & Burt, 2001) $r_{d}^{-}=0.003$
  - High level of sexual recombination
Allele frequencies for SSR loci with the highest diversity (H)

Locus diversity:
H = 1 - \( \sum x_j^2 \)

where \( x_j \) is the frequency of the j-th allele at the locus (Nei 1978).
Multilocus genotypes (MLGs) and genotypic diversity

- 96 MLGs from a total of 141 isolates
- 69 (72%) unique MLGs
- High genotypic diversity ($H_s=0.89$)

Normalized Shannon’s diversity index:
$H_s= -\sum P_i \ln P_i / \ln N$

Pi is the frequency of the ith MLG
N is the population size

<table>
<thead>
<tr>
<th>Year</th>
<th>Isolates</th>
<th>MLGs</th>
<th>$H_s$</th>
</tr>
</thead>
<tbody>
<tr>
<td>2010</td>
<td>41</td>
<td>32</td>
<td>0.898</td>
</tr>
<tr>
<td>2011</td>
<td>51</td>
<td>32</td>
<td>0.837</td>
</tr>
<tr>
<td>2012</td>
<td>49</td>
<td>32</td>
<td>0.858</td>
</tr>
<tr>
<td>Overall</td>
<td>141</td>
<td>96</td>
<td>0.892</td>
</tr>
</tbody>
</table>
Minimum spanning network of MLGs based on Bruvo’s distance

- Each node represents a different MLG
- Maximum of 6 isolates with the same MLG
- Isolates with the same MLG from the nearby fields
- None of the MLGs appeared on consecutive years
Principal coordinate analysis of MLGs based on Bruvo’s distance

Populations from different years are not genetically differentiated:
• Fst values 0.007-0.020
• Nei’s genetic distance 0.021-0.035
Conclusions

• Nearly equal proportion of A1 and A2 mating type isolates
• Coexistence of A1 and A2 mating type isolates on the majority of studied fields
• High genotypic diversity
• No dominating MLGs
• Determinant role of sexual reproduction on *P. infestans* populations in Estonia
Acknowledgements

• Dr David Cooke
• Dr Eva Randall
• Alice Aav
• Merili Hansen
• Helina Nassar
• Kätlin Jõgi

• Estonian Science Foundation grant no 9432
• Target Financing Project SF170057s09
• Institutional Research Funding Project IUT36-2
• Archimedes Foundation Project RESIST 3.2.0701.11–0003.
Thank you for your attention!