The potato blight population in Northern Ireland

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Late blight has challenged potato growers in Ireland since 1845

- 1845: late blight arrives in Ireland
- 1845-48: Irish Potato Famine
For much of the 20th century, global populations were dominated by a single clonal A1 lineage, US-1.

From the mid-1970s, migration events spread new strains of both mating types worldwide, displacing US-1.

This triggered ongoing population changes.

Some regions now have recombinant populations, others have remained largely clonal.
Northern Ireland

- A2 mating type identified 1987
- By mid-1990s: population highly clonal, no US-1, one major A1 genotype, other A1 genotypes, A2 at low frequency
- 1996-2004: A2 not detected, clonal A1 population, 2 major genotypes, NI-1 = 8_A1, NI-2 = 5_A1

* number of isolates tested
21\textsuperscript{st} century genotypes in Europe

- Marked changes in \textit{P. infestans} populations in Europe in the last 10 years
- New genotypes identified since 2005, notably Blue 13 (13\_A2)
- May have originated as sexual recombinants in mainland Europe
- Some more aggressive and harder to control, but reasons for dominance not fully explained
Northern Ireland

- 2005: first A2s detected since 1995
- 2007: Blue 13 identified
- 2008-present: population studies as part of all-Ireland projects funded by DAFM and led by Teagasc
- Currently the DAFM-funded MonPESC project:
  - Monitoring Pathogen Evolution for Sustainable Cropping led by Teagasc Oak Park
Northern Ireland

- 2008-2014: population studies
- Phenotypic characterisation
  - mating type
  - phenylamide resistance
- Genotypic characterisation
  - SSR
  - RG57 (sub-set up to 2011)
  - mtDNA (up to 2009)
  - Pep allozymes (sub-set)
- SSR genotyping 2008-2013 from isolates, 2014 direct from FTA cards
Phenotypic and genotypic characterisation

- Close association between markers indicative of a highly clonal population

- Within genotypes (clonal lineages) find:
  - similar SSR patterns
  - same RG57 fingerprint
  - same Pep allozyme
  - same mtDNA haplotype
  - (sometimes) same phenylamide resistance status
Mating type

- Steady increase in A2 2007-2010 in NI, similar trend in GB 2003-2008
- Due to increasing incidence of Blue 13 in both cases
Phenylamide resistance

- Has shown similar trend to A2 mating type since 2005 – hitch-hiking selection
**A1 genotypes identified in NI**

**Major A1 genotype 8_A1:**
- SSR pattern 8_A1
- RG57 fingerprint NI-1, commonest in 1990s
- mtDNA IIa
- Pep 100/100
- phenylamide-sensitive (mainly) or –resistant

**Minor A1 genotypes 5_A1, 12_A1, 6_A1:**
- 5_A1 (NI-2), 12_A1 both present in UK in 1990s
- 6_A1 (Pink 6) not found in NI before 2009
  - characteristic SSR pattern, RG57 fingerprint
  - mtDNA Ib
  - Pep 96/96
  - phenylamide-sensitive
• A2 genotypes identified in NI

Only one A2 genotype: Blue 13 (13_A2) from 2007

• SSR pattern 13_A2
• common RG57 fingerprint
• mtDNA Ia
• Pep 96/96
• phenylamide-resistant

Green 33 not detected

A2 genotypes present in 1990s not found
Genotype/mating type frequencies 2014

- 80 isolates from 30 crops: 6 A2 isolates - 7% A2

- SSR analysis of 75 FTA samples
  25 samples 13_A2 - 33% A2
Genotype frequencies 2014

FTA cards detected 13_A2 at higher frequency than isolations (33% c.f. 7%)

13_A2 detected at 11 sites
  - 3 sites FTA only
  - 3 sites A2 isolated
  - 5 sites only A1 isolated, but at these locations FTAs detected both 13_A2 and A1 genotypes, phenylamide-resistant strains were identified

Difficulty in isolating 13_A2

Influences detected genotype frequencies?
Genotypes identified in Northern Ireland

Northern Ireland *Phytophthora infestans* genotypes, 2008-2014

<table>
<thead>
<tr>
<th>Year</th>
<th>13_A2</th>
<th>12_A1</th>
<th>8_A1</th>
<th>6_A1</th>
<th>5_A1</th>
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<td>2013</td>
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<td>53</td>
</tr>
<tr>
<td>2014</td>
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<td></td>
<td></td>
<td></td>
<td>75</td>
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</table>
2008-2014: GB population dominated by 6_A1, 13_A2
NI population dominated by 8_A1, 13_A2
In years with less 13_A2, its place is taken by 6_A1 in GB, but 8_A1 in NI
More 6_A1 and 13_A2 detected in NI in 2014, 13_A2: GB 28%, NI 33%
N. Ireland Phytophthora infestans population

- EuroBlight Late Blight Tool Box - Northern Ireland data
N. Ireland Phytophthora infestans population

- EuroBlight Late Blight Tool Box - Northern Ireland data
N. Ireland Phytophthora infestans population

- How can the EuroBlight Late Blight Tool Box help us to compare the Northern Ireland population with that in GB and elsewhere in Europe?

<table>
<thead>
<tr>
<th>Pop</th>
<th>2013</th>
<th>2014</th>
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<td>9</td>
</tr>
<tr>
<td>SE</td>
<td>28</td>
<td>26</td>
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<tr>
<td>ND</td>
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<tr>
<td>EN</td>
<td>130</td>
<td>30</td>
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<tr>
<td>SC</td>
<td>36</td>
<td>6</td>
</tr>
<tr>
<td>WA</td>
<td>31</td>
<td>11</td>
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N. Ireland Phytophthora infestans population

- How can the EuroBlight Late Blight Tool Box help us to compare the Northern Ireland population with that in GB and elsewhere in Europe?

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<tr>
<th>Pop</th>
<th>2013 N</th>
<th>MLG</th>
<th>N/MLG</th>
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<tbody>
<tr>
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<tr>
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<tr>
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<td>15</td>
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<td>EN</td>
<td>130</td>
<td>30</td>
<td>4.3</td>
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<tr>
<td>SC</td>
<td>36</td>
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<tr>
<td>WA</td>
<td>31</td>
<td>11</td>
<td>2.8</td>
</tr>
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</table>

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<tr>
<th>Pop</th>
<th>2014 N</th>
<th>MLG</th>
<th>N/MLG</th>
</tr>
</thead>
<tbody>
<tr>
<td>BY</td>
<td>24</td>
<td>24</td>
<td>1.0</td>
</tr>
<tr>
<td>SE</td>
<td>22</td>
<td>22</td>
<td>1.0</td>
</tr>
<tr>
<td>ND</td>
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<td>21</td>
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<tr>
<td>EN</td>
<td>377</td>
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<tr>
<td>SC</td>
<td>235</td>
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<tr>
<td>WA</td>
<td>89</td>
<td>15</td>
<td>5.9</td>
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</table>
Late Blight Tool Box comparing 2013 NI data with GB (EN, SC, WA), Belarus (BY) and Sweden (SE)

Countries
ND red
EN blue
WA green
SC orange
SE yellow
BY purple

PCA with bruvo distance as input
Late Blight Tool Box comparing 2013 NI data with GB (EN, SC, WA), Belarus (BY) and Sweden (SE)

Genotypes
13_A2 blue
6_A1 pink
8_A1 yellow
other grey

PCA with bruvo distance as input
Late Blight Tool Box comparing 2014 NI data with GB (EN, SC, WA), Belarus (BY) and Sweden (SE)

Countries
ND orange
EN red
WA blue
SC green
SE yellow
BY purple

PCA with bruvo distance as input
Late Blight Tool Box comparing 2014 NI data with GB (EN, SC, WA), Belarus (BY) and Sweden (SE)

Genotypes
13_A2 blue
35_A2 purple
2_A1 red
5_A1 green
6_A1 pink
8_A1 yellow
12_A1 brown
other grey

PCA with bruvo distance as input
Late Blight Tool Box 2014 NI data only

Genotypes
13_A2 blue
35_A2 purple
2_A1 red
5_A1 green
6_A1 pink
8_A1 yellow
12_A1 brown
other grey

PCA with bruvo distance as input
• Late Blight Tool Box 2013 NI data only

MSN tree
Late Blight Tool Box 2014 NI data only

MSN tree
Late Blight Tool Box comparing 2013 NI data with GB (EN, SC, WA), Belarus (BY) and Sweden (SE)

- MSN tree
- Countries
- ND green
- EN blue
- WA beige
- SC yellow
- SE yellow
- BY purple
Late Blight Tool Box comparing 2013 NI data with GB (EN, SC, WA) and Sweden (SE)

MSN tree
Genotypes
13_A2 blue
5_A1 green
6_A1 pink
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12_A1 brown
other grey
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MSN tree
Genotypes
13_A2 blue
5_A1 green
6_A1 pink
8_A1 yellow
12_A1 brown
other grey
Can these tools help us to understand:

- Why genotype frequencies in clonal populations fluctuate markedly from year to year?
- Why frequencies in NI differ from those in GB?
  - Fungicide usage?
  - Cultivars?
  - Environmental conditions?
- Why some European countries have recombinant *P. infestans* populations while others remain highly clonal?
• **Environmental interactions?**

• **Need to consider:**
  • tuber infection
  • overwinter survival
  • initial outbreaks

<table>
<thead>
<tr>
<th>Year</th>
<th>1st blight outbreak</th>
</tr>
</thead>
<tbody>
<tr>
<td>2008</td>
<td>2 July</td>
</tr>
<tr>
<td>2009</td>
<td>8 June</td>
</tr>
<tr>
<td>2010</td>
<td>19 July</td>
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<td>2011</td>
<td>18 June</td>
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<td>2012</td>
<td>22 June</td>
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<tr>
<td>2013</td>
<td>17 July</td>
</tr>
<tr>
<td>2014</td>
<td>9 June</td>
</tr>
<tr>
<td><strong>mean 1981-2014</strong></td>
<td><strong>17 June</strong></td>
</tr>
</tbody>
</table>

• **Interact with conditions during summer foliar epidemic phase**
• Clonal populations subject to fluctuations between seasons
• Major impact of bottlenecks (tuber infection, transmission)
• Polycyclic disease
• Magnifies stochastic effects
• Is prediction of future population changes possible?
• ????????????
Many thanks to:

- David Cooke, JHI for SSR, interpretation and analyses
- Agri-food Inspection Branch, DARD for blight samples
- DAFM and DARD for funding
- Teagasc Carlow colleagues, particularly Steven Kildea
- Ken Deahl for RG57 analyses
- Michael Clelland and Amy Mornin for P. infestans isolation and characterisation