Genotypic diversity in *Puccinia striiformis* f. sp. *tritici*, the cause of wheat stripe rust, in western Canada

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Wheat stripe rust

• Disease of worldwide importance

• Caused by obligate biotrophic fungus *Puccinia striiformis* f. sp. *tritici* (*Pst*)

• Also called ‘yellow rust’
Variation in the pathogen population

- Mutation
- Selection
- Somatic recombination
- Sexual recombination

Biotypes or Physiological Races
Hyopthesis and objective

• **Hypothesis:** Molecular genetic variation exists in the *Pst* population in western Canada

• **Objective:** To analyze genetic diversity of *Pst* in western Canada Next-Generation Sequencing (NGS) technology
Materials & methods

- *Pst* isolates: 48 *Pst* isolates (25 from SK, 15 from AB, and 5 from MB, 1 from BC and, 2 from the USA)

- Modified cetyltrimethylammonium bromide (CTAB) procedure for DNA extraction

- The Illumina HiSeq2500 (Illumina®) DNA sequencing platform

- Variant calling by mapping reads against reference genome ‘PST-78’

- Single nucleotide polymorphism (SNP) variants
Materials & methods

• Diversity analyses
  ✓ Neighbor-net using SplitTree4
  ✓ Neighbor-joining tree using MEGA6.06
  ✓ Principal Component Analysis (PCA) using Unscrambler X ver.10.3
  ✓ Population structure analyses using STRUCTURE ver. 2.3.4

• Recombination analyses: Various methods implemented in RDP4 and; PHI-test implemented in SplitTree4
Results

Diversity analyses

Neighbor-net obtained from SplitTree4 software
Results

3-D PCA plot for 48 *Pst* isolates
Results

Number of unique recombination events in the clades

<table>
<thead>
<tr>
<th>Clade</th>
<th>Number of individuals in clade</th>
<th>Number of recombination events detected(a)</th>
<th>PHI-test (p-value)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>15</td>
<td>3</td>
<td>0.1257</td>
</tr>
<tr>
<td>2</td>
<td>8</td>
<td>8</td>
<td>6.437 \times 10^{-5}</td>
</tr>
<tr>
<td>3 &amp; 4</td>
<td>23</td>
<td>11</td>
<td>0.2657</td>
</tr>
<tr>
<td>4</td>
<td>2</td>
<td>6(^b)</td>
<td>2.139 \times 10^{-7}</td>
</tr>
</tbody>
</table>
Results

• Highly polymorphic (0.85%) and heterozygous genome (58.8%)

• Average genome coverage: 11X (12,711,460 reads)

• 4 sub-populations

• Old isolates are different from new isolates

• Largely clonal population with signs of recombination
Conclusions

• Somatic hybridization: need more insights as a possible source of variation in *Pst* population

• Pathogen has high evolutionary potential

• Population structure should be known for successful management of disease
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