

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

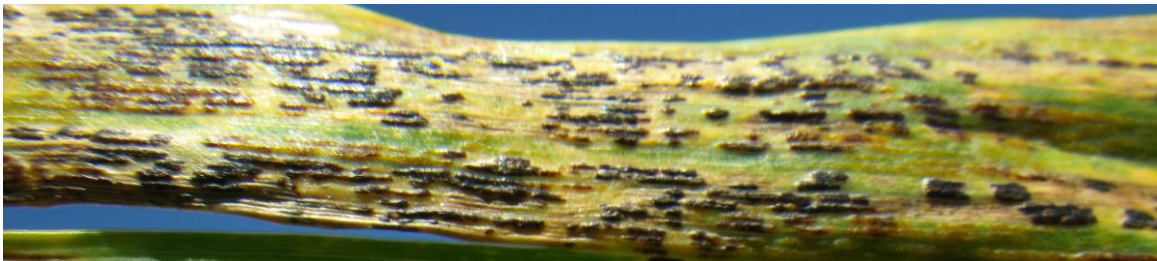


Soils & Crops -2015

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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'

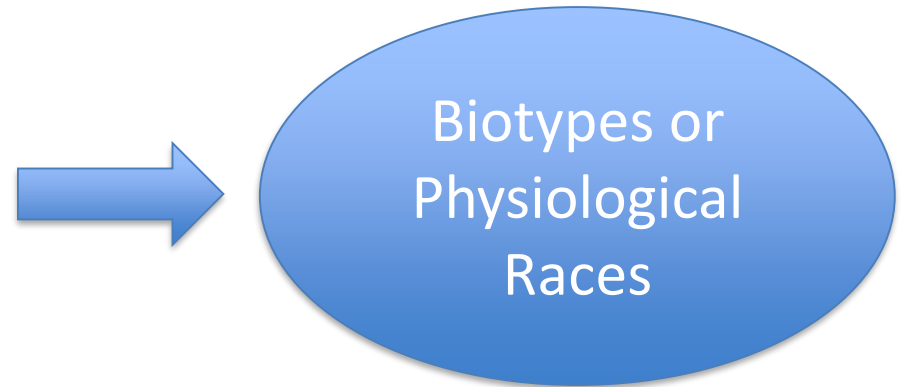


Photos Credit: Gurcharn Brar



Variation in the pathogen population

- Mutation
- Selection
- Somatic recombination
- Sexual recombination



Hypothesis 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

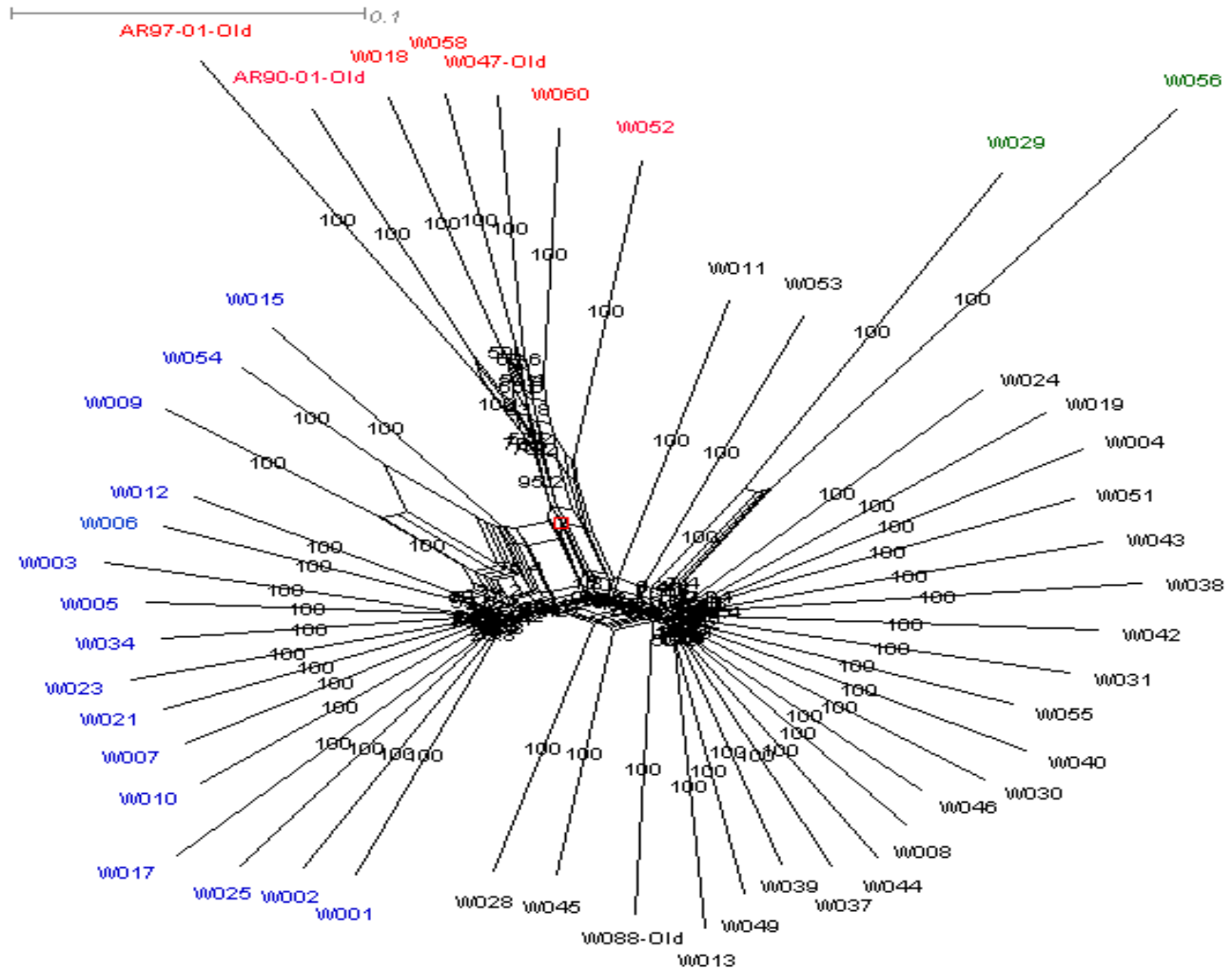
- **Recombination analyses:** Various methods implemented in RDP4 and; PHI-test implemented in SplitTree4



Results

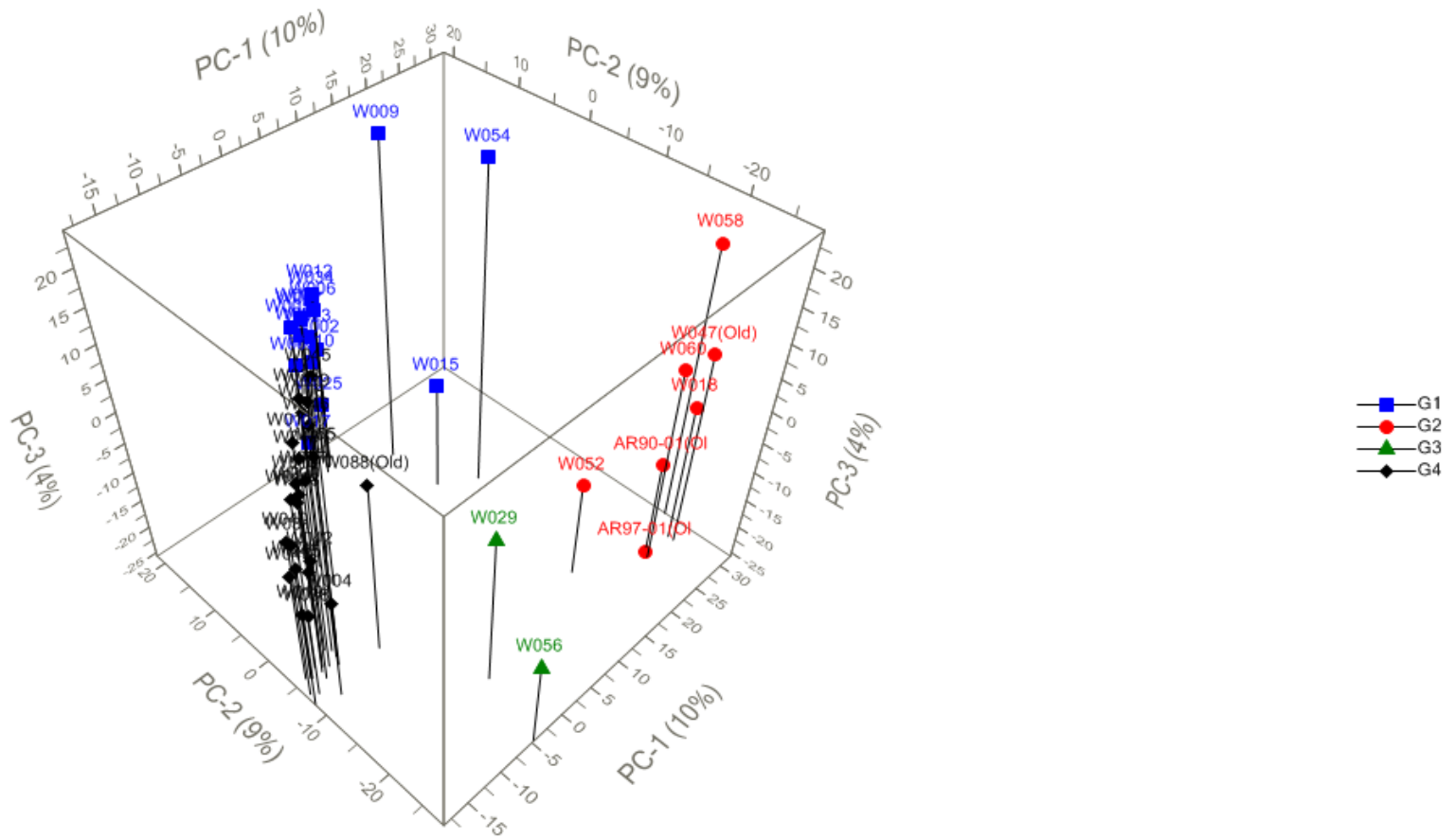
Diversity analyses

Neighbor-net
obtained from
SplitTree4
software

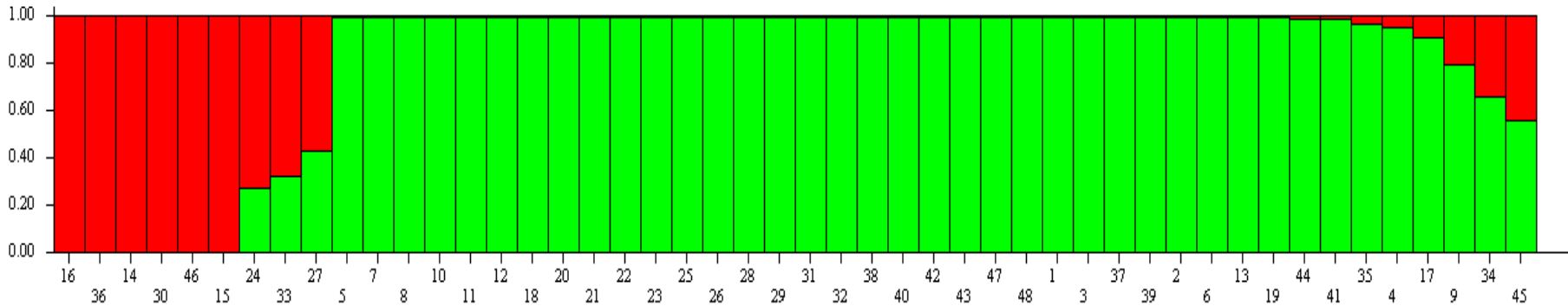
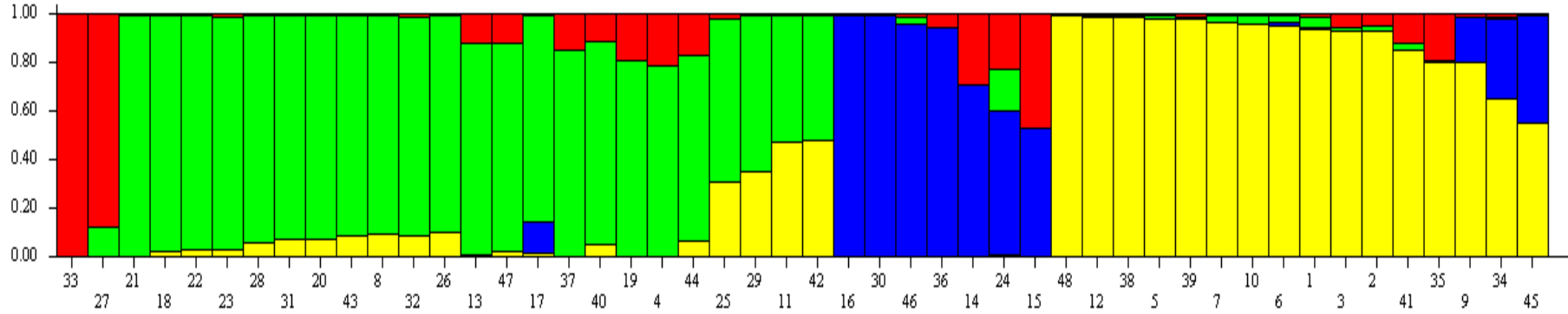


Results

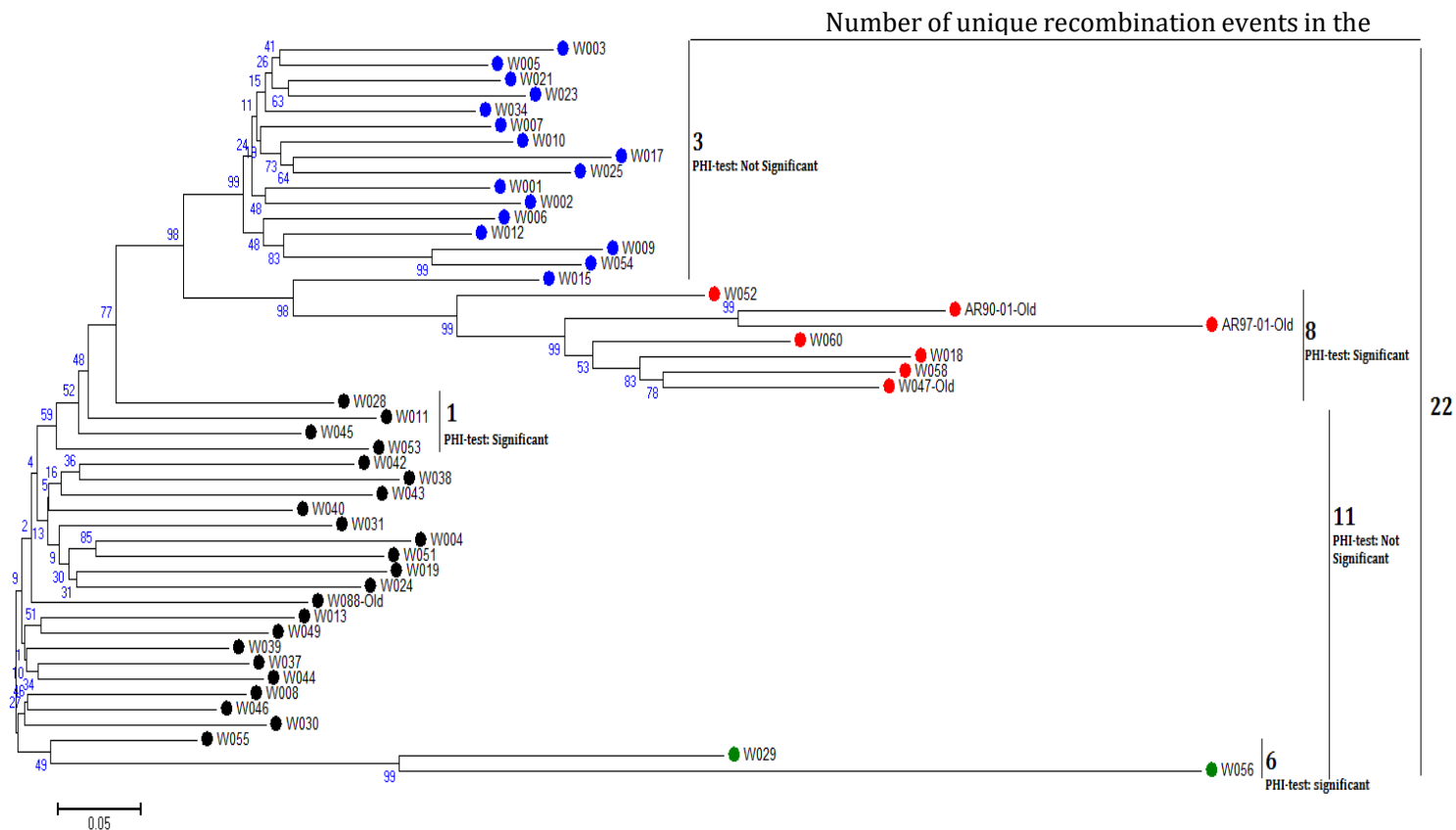
3-D PCA plot for 48 *Pst* isolates



Results from STRUCTURE software



Results



Clade	Number of individuals in clade	Number of recombination events detected ^a	PHI-test (p-value)
1	15	3	0.1257
2	8	8	6.437x 10 ⁻⁵
3 & 4	23	11	0.2657
4	2	6 ^b	2.139x 10 ⁻⁷



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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