

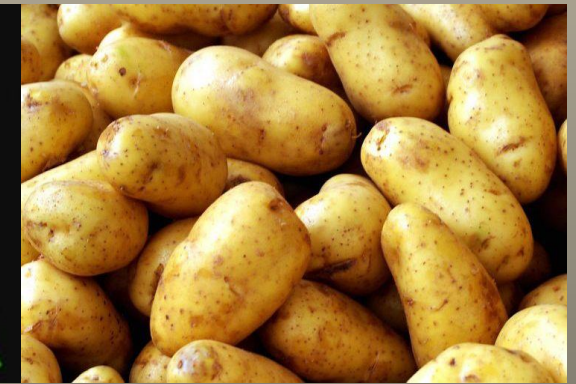
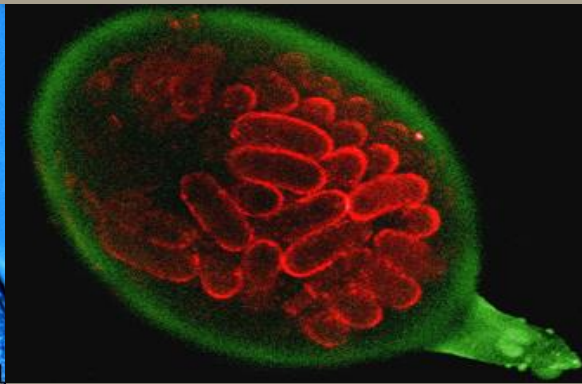
Chapter 3



Sulochana Wasala
03/11/2019

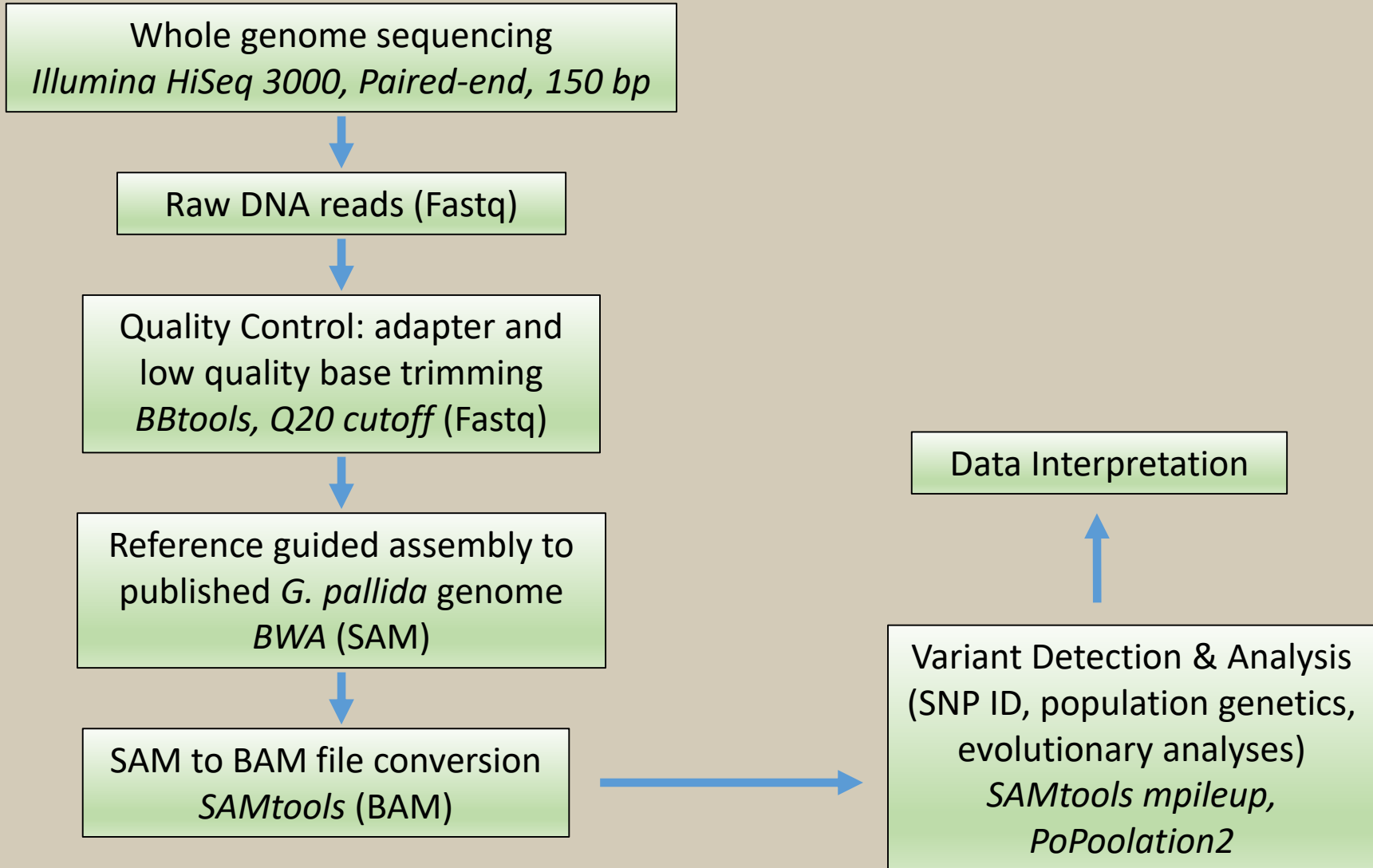
Spatial and temporal genetic diversity of a recent *Globodera pallida* infestation in Idaho.

- Genome-wide spatial patterns of genetic variation.
- Temporal patterns of genome-wide polymorphisms



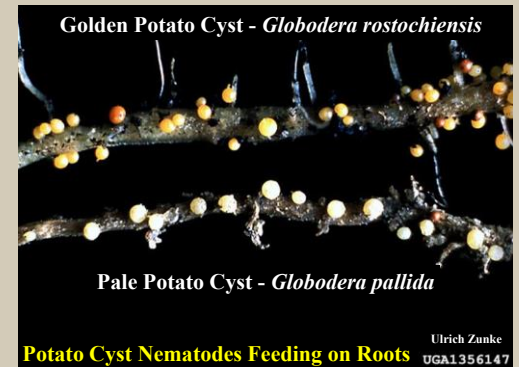
Infected Field	Time point	Date of cyst collection	# Replicates
BIN 25	pre-fumigation	May 2007	4
	post-fumigation-1	Aug 2007	4
	post-fumigation-3	Jun 2008	4
	post-fumigation-7	Apr 2010	4
	post-fumigation-10	Oct 2012	4
BIN 26	pre-fumigation	May 2007	4
BIN 32	pre-fumigation	Sep 2015	1 (42 cysts)
BIN 54	pre-fumigation	Apr 2007	4
	post-fumigation-1	Jul 2007	4
	post-fumigation-11	Oct 2012	4
BON 64	pre-fumigation	May 2007	4
BIN 258	pre-fumigation	May 2014	4
	post-fumigation-1	Aug 2015	4
Green house	Control	Jan 2017	4
<i>Luffness</i>	European sample		1 (5 cysts)
			54

Bioinformatics pipeline for the analysis of Illumina data

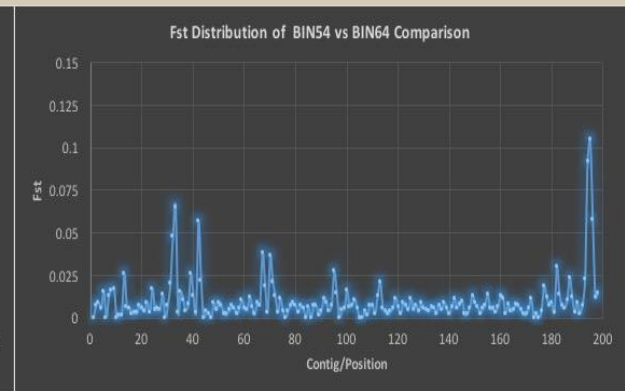
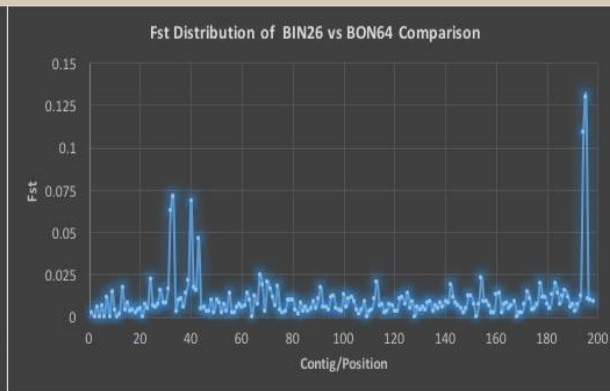
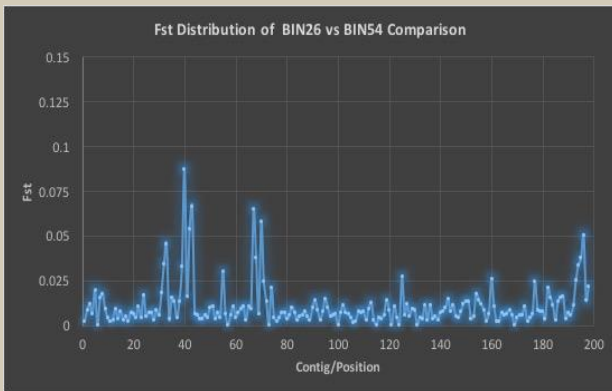
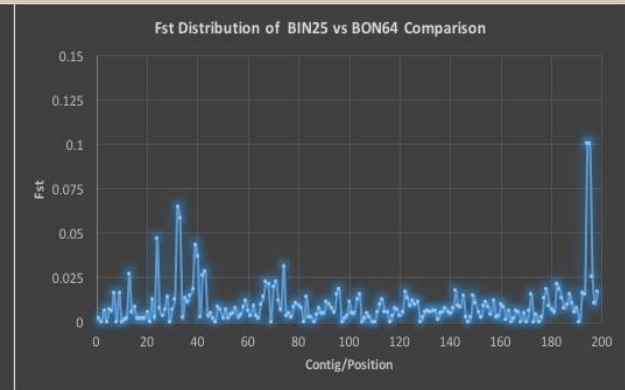
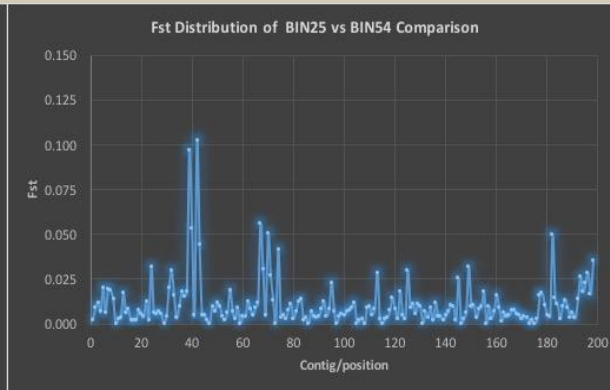
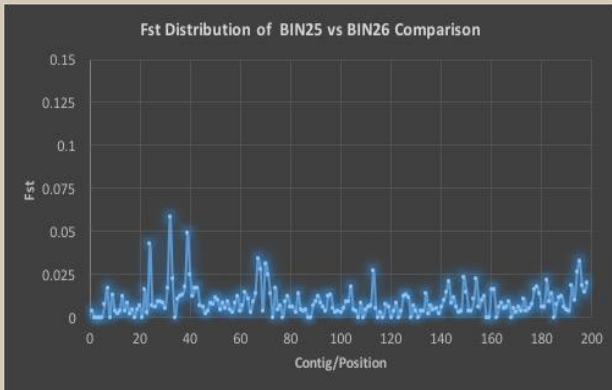


Spatial and temporal genetic diversity of a recent *Globodera pallida* infestation in Idaho.

- According to the genome wide Fst analysis across space, most of the genetic variation was shared between pre-fumigation samples indicating the infestation might have resulted from a single introduction.

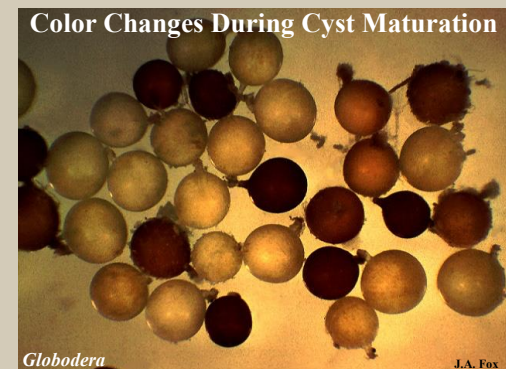
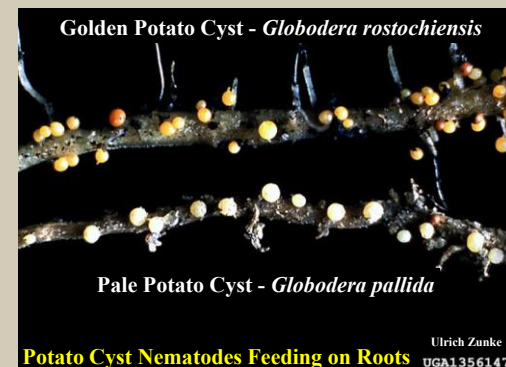


Genome wide Fst analysis: Spatial diversity



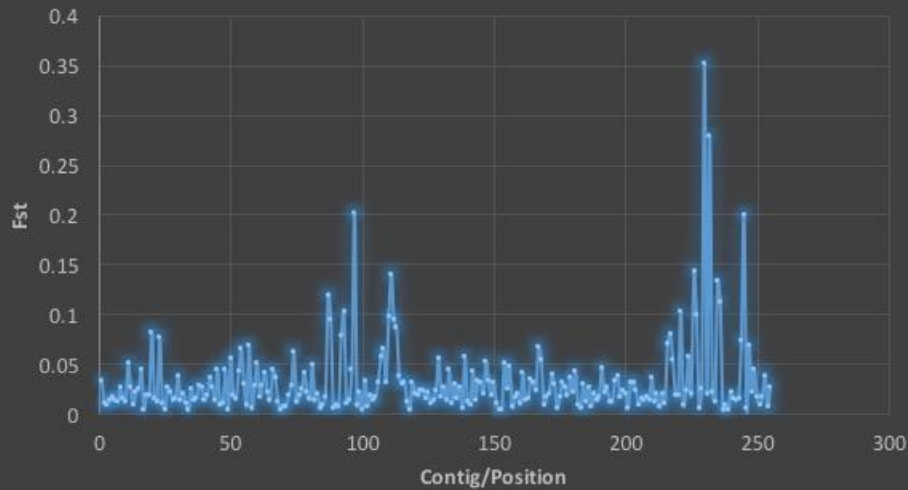
Spatial and temporal genetic diversity of a recent *Globodera pallida* infestation in Idaho.

- Based on allele frequency data and F_{st} analysis across time, some outlier loci were identified in comparing pre-fumigation and post-fumigation samples, indicating the presence of genomic regions putatively involved in nematode adaptation.

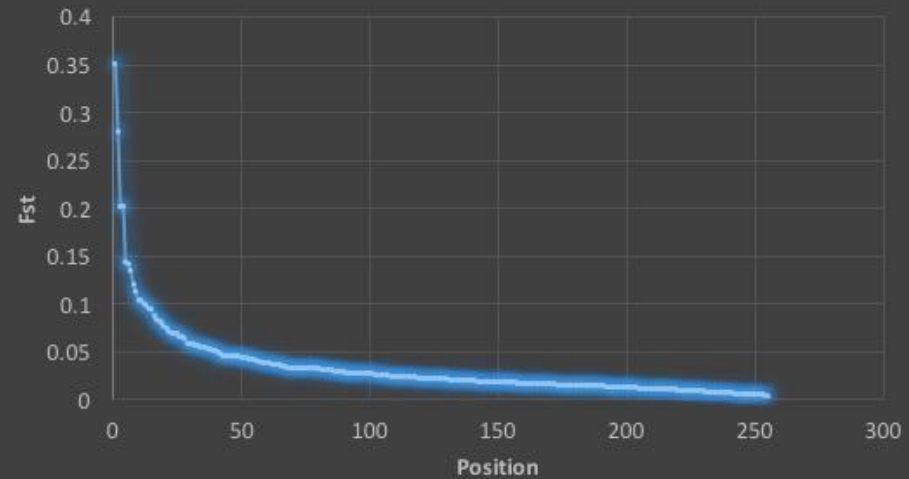


Genome wide Fst analysis: Temporal diversity

Fst Distribution of 25-0 vs 25-1: cov_30



Fst Distribution of 25-0 vs 25-1: cov_30



Q5B: BIN25-0- all vs BIN25-1- all
min_cov_30
Average Fst = 0.032

Thank you!