POTATO PEST AND DISEASES

TECHNICAL SESSION D

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The potato psyllid *Bactericera cockerelli* (Hemiptera: Triozidae): Does it move between hosts?

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WASHINGTON STATE UNIVERSITY

OVERVIEW

Movement

Bactericera cockerelli
Potato psyllid

https://species.wikimedia.org/wiki/Solanum_dulcamara

Solanum dulcamara
Bittersweet nightshade

http://www.lapureza.com.ar/lapureza/biblioteca/le_hacen_danio_al_perro/plantas_papa_o_patata/plantas_papa_o_patata.htm

Solanum tuberosum
Potato

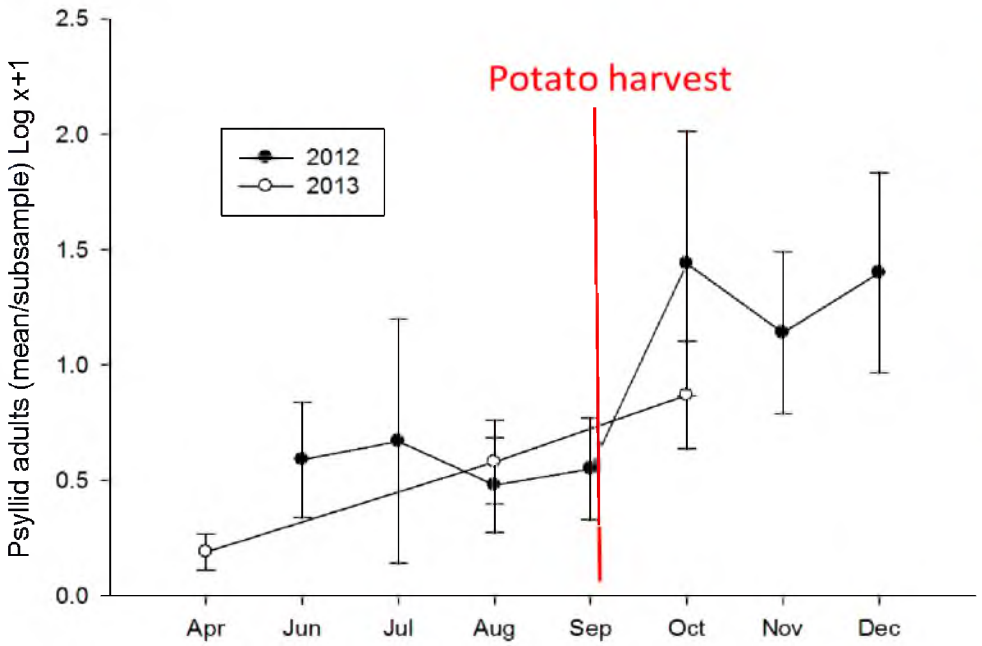
NextRAD sequencing

https://thesoulmatrix.com/transmission/starseed-support-transmission/attachment/dna/

Image source: https://www.agmatters.au/news/news/2018/biosecurity-alert-tomato-potato-psyllid

INTRODUCTION

Potato psyllids density on Nightshades in Washington



Castillo et al 2016, *Env. Ent.*

INTRODUCTION

http://www.nwpotatoresearch.com/insects/potato-psyllid/

Bactericera cockerelli
Potato psyllid

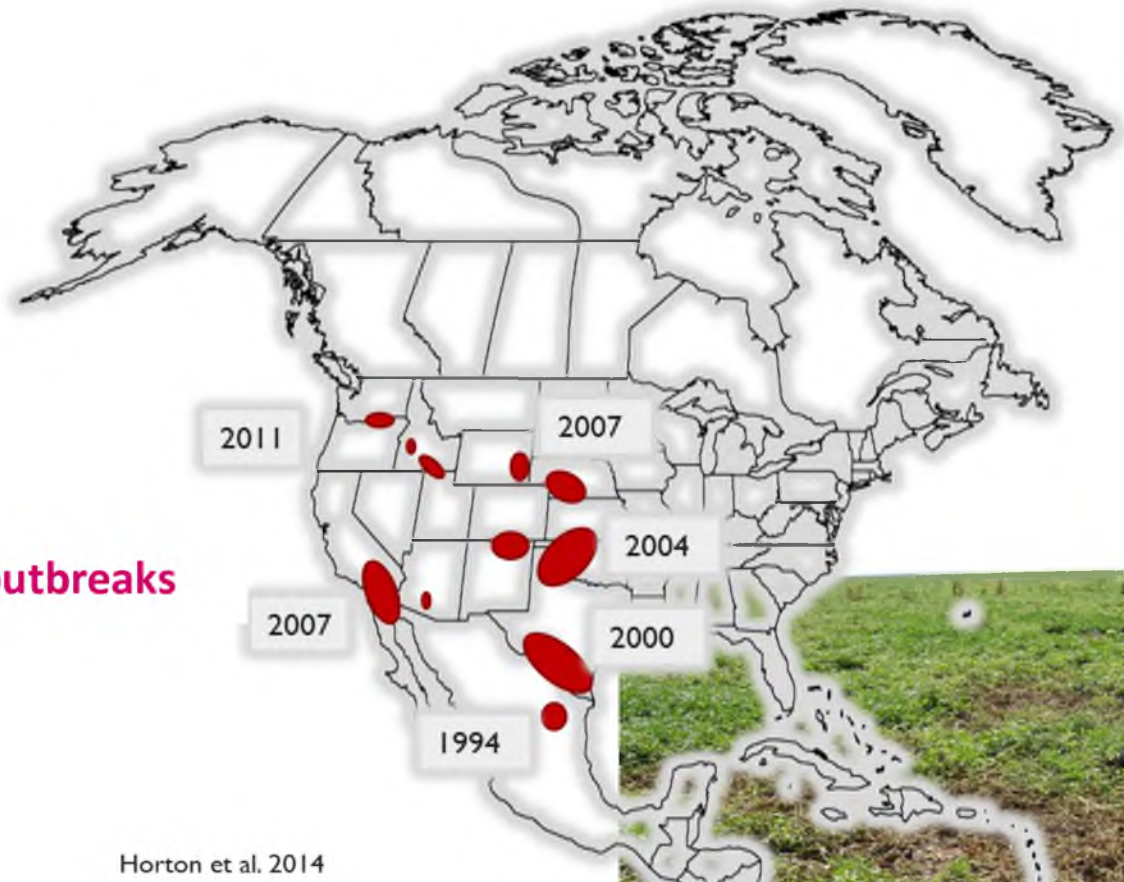
- The potato psyllid *Bactericera cockerelli* vectors the pathogen *Candidatus* Liberibacter solanacearum that causes zebra chip disease in potato (*Solanum tuberosum*)

Candidatus Liberibacter solanacearum
Zebra chip

- Reduced 30% potato acreage (Rosson et al. 2006)
- Losses over 25 million dollars annually (Rosson et al. 2006)
- Between 2000 to 2013, > 20% of the budget in potato production (Greenway et al. 2014)

INTRODUCTION

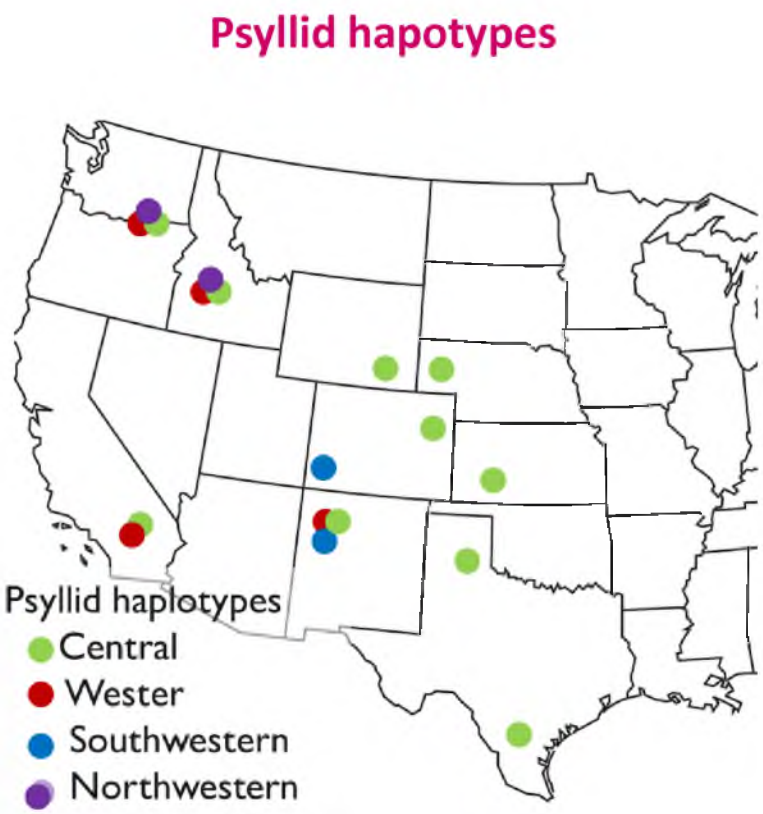
Zebra chip outbreaks

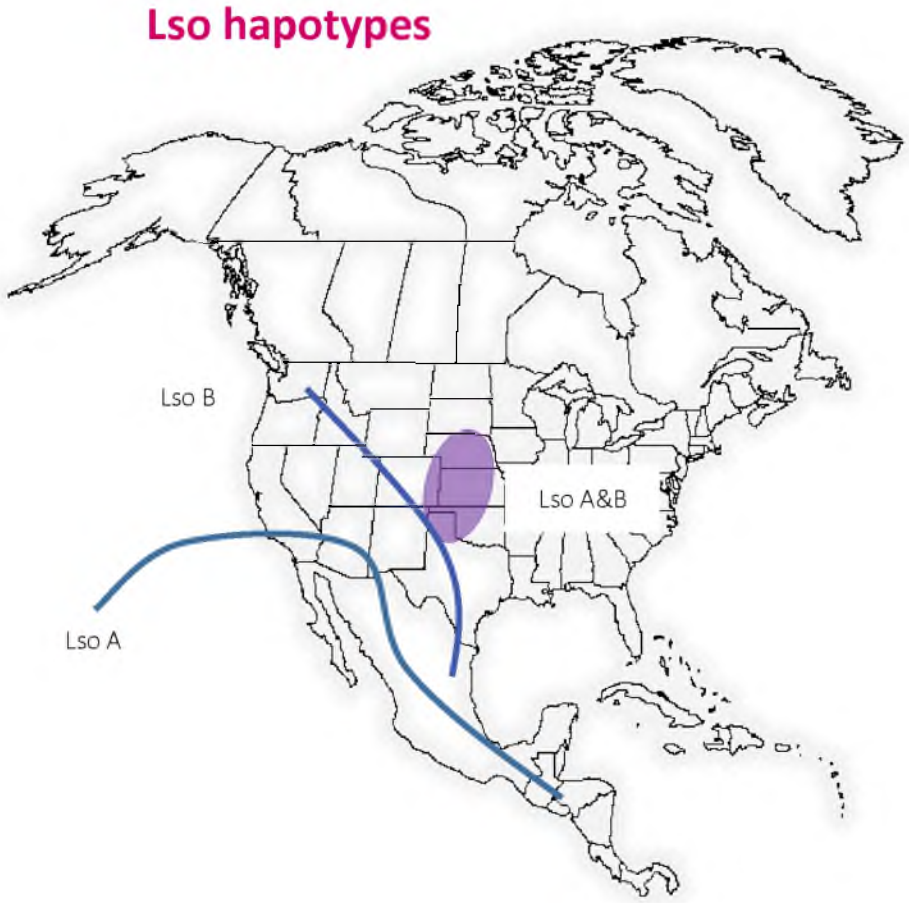


Horton et al. 2014

http://cropwatch.unl.edu/potato/zebra_chip

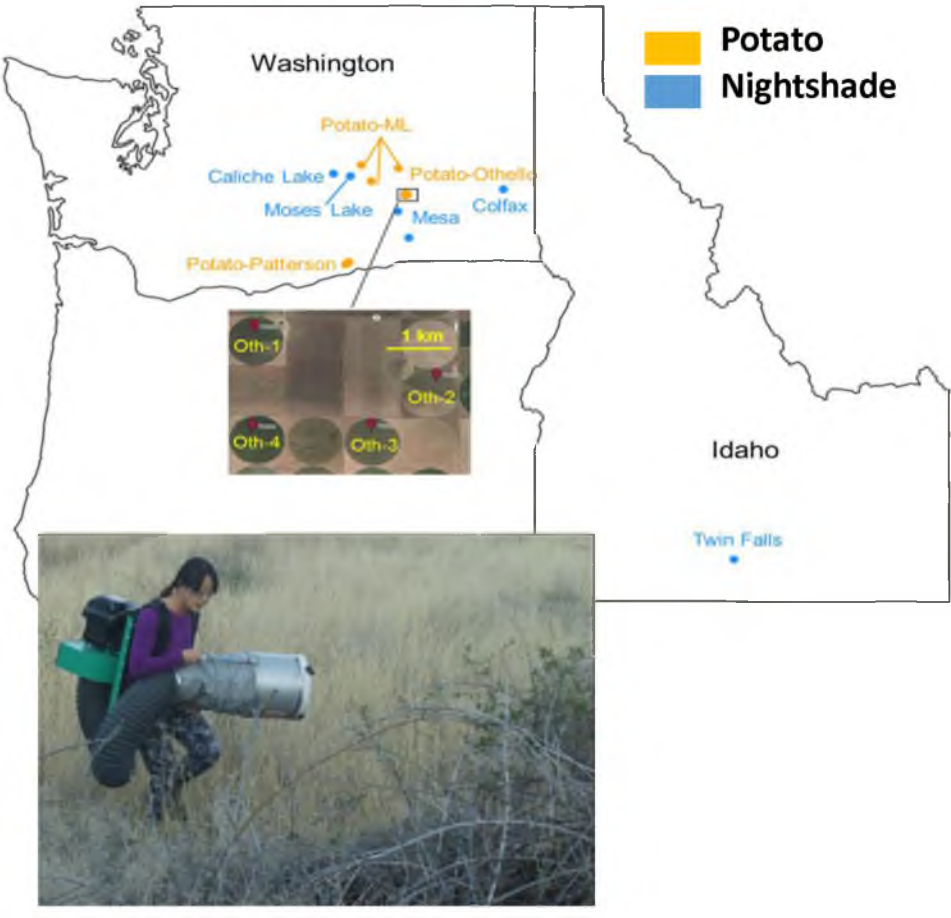
INTRODUCTION





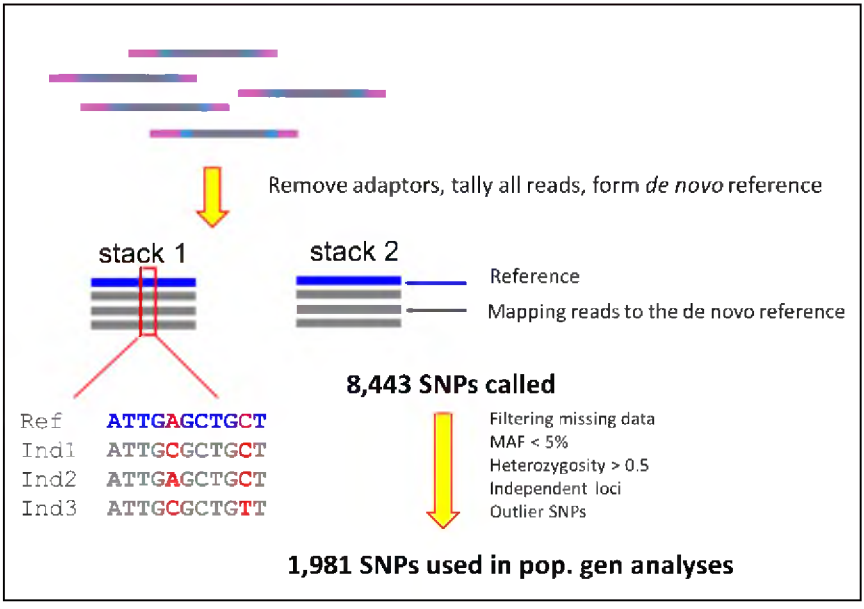
Modified from Horton et al. 2014, Swisher et al. 2012, 2014, Liu et al. 2006, Nelson et al. 2011

Psyllid sampling



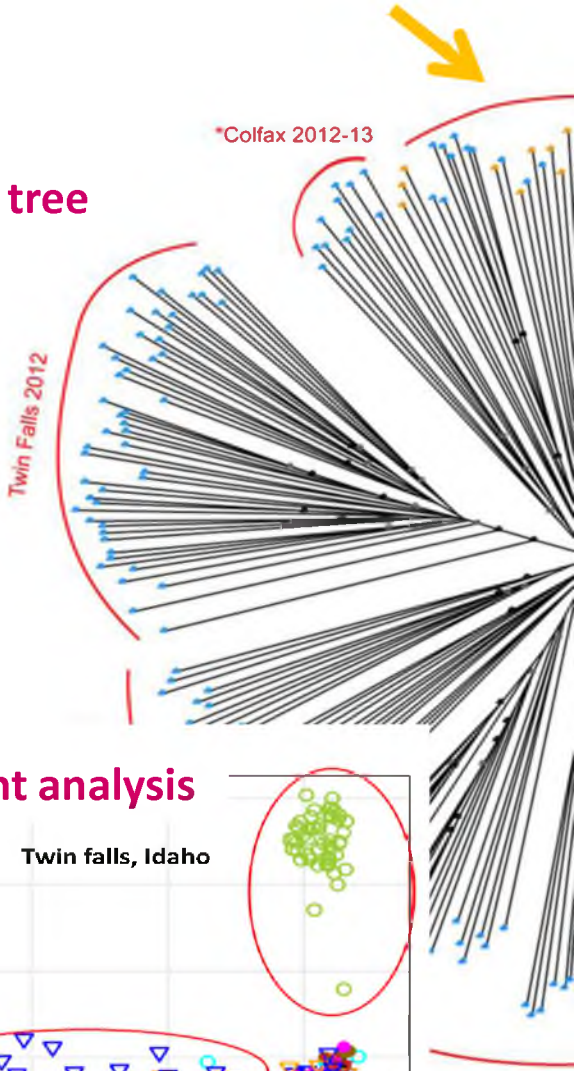
METHODOLOGY

Nextera-tagmented reductively-amplified DNA (NextRAD) sequencing

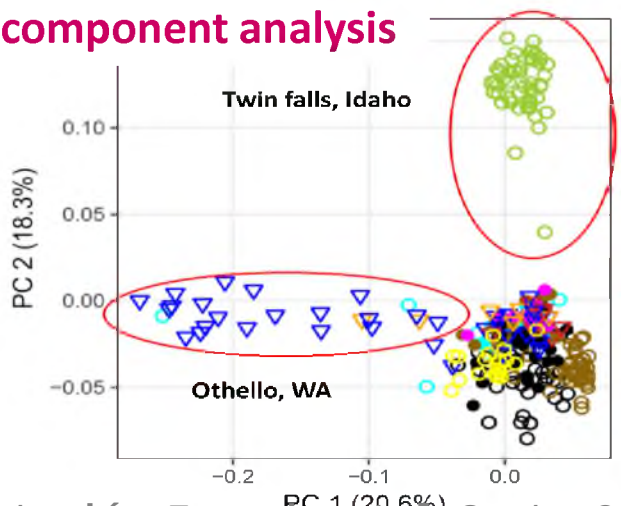


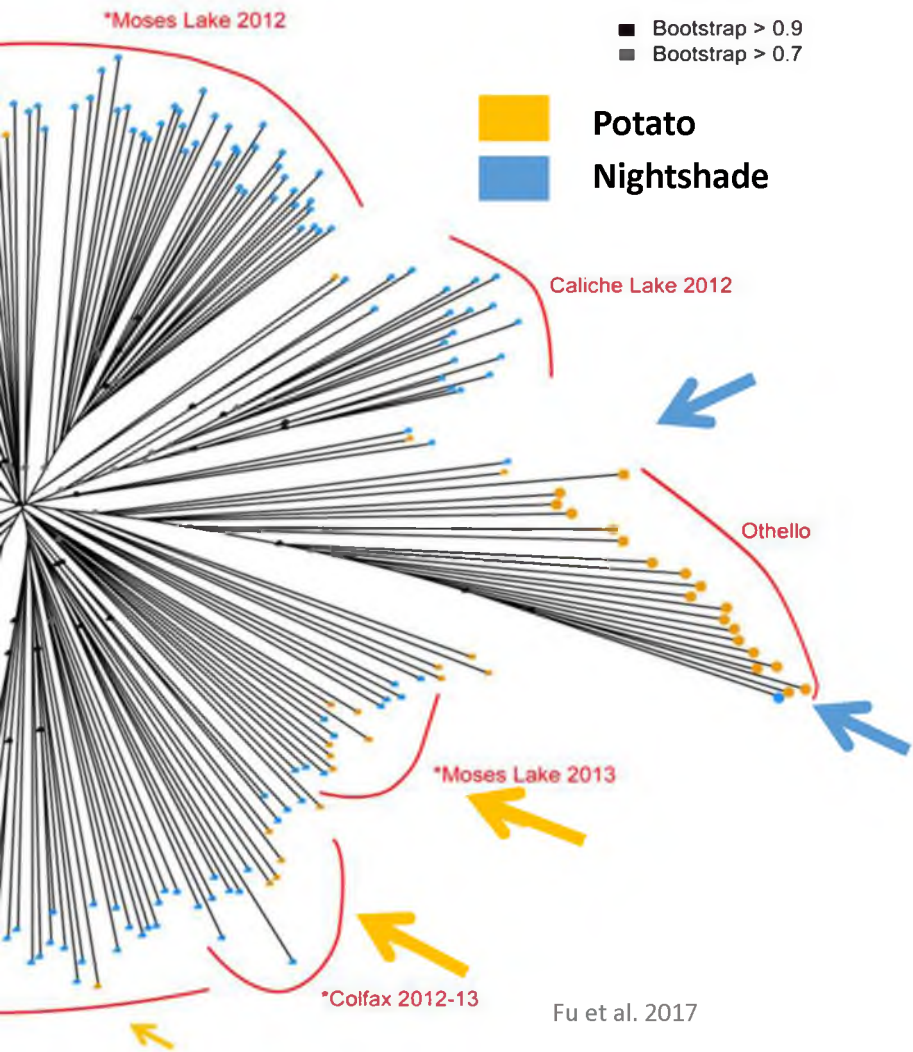
RESULTS

Neighbor-joining tree



Principal component analysis

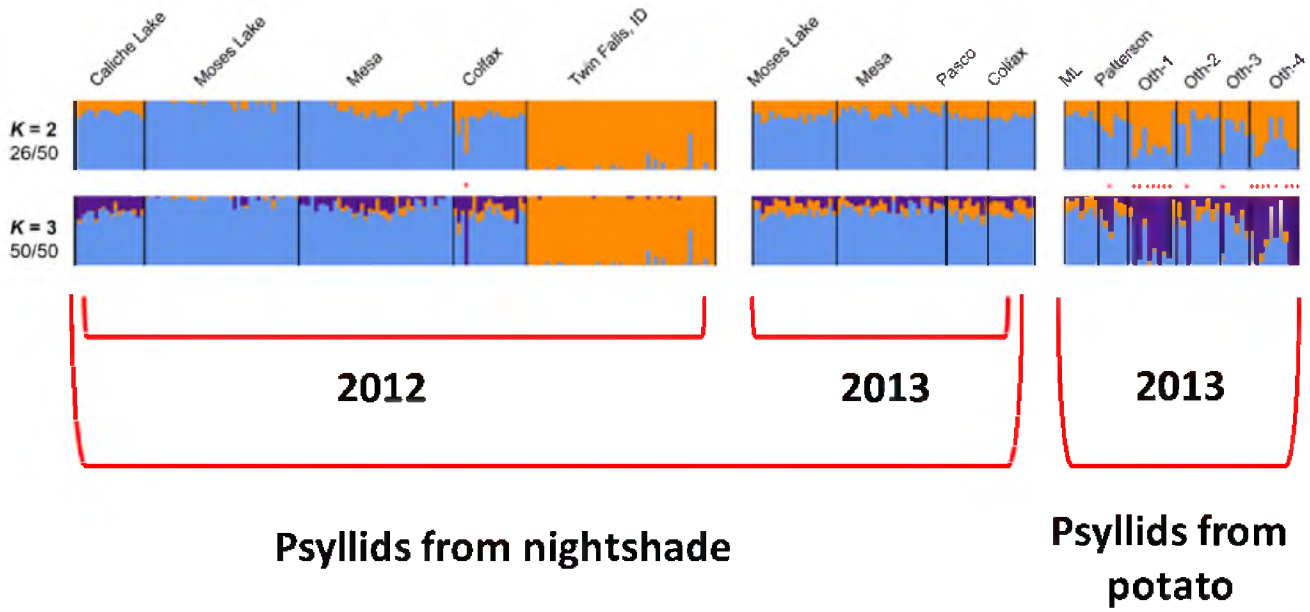



*Moses Lake 2012
Bootstrap > 0.9
Bootstrap > 0.7
Potato
Nightshade
Caliche Lake 2012
Othello
*Moses Lake 2013
*Colfax 2012-13

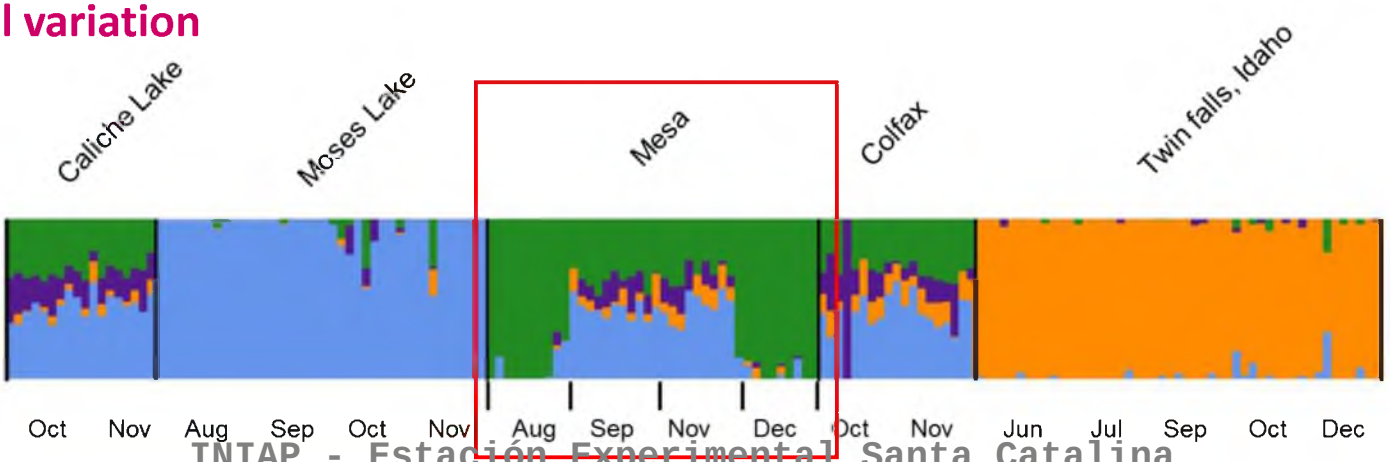
Fu et al. 2017

RESULTS

Genetic admixture



Temporal variation



CONCLUSIONS

- In order to understand, predict, and manage disease spread, dispersal of vectors of pathogens must be tracked at a fine scale
- Emerging sequencing technologies that detect genome-wide SNPs of a vector can be used to infer such localized movement
- Results of multiple population genomic analyses demonstrated a consistent trend that psyllids from *S. dulcamara* and potatoes formed interbreeding populations, suggesting the likely movement between these two host plants
- Meanwhile, a psyllids population collected from potatoes showed distinct genotypes, suggesting another potential host plant serving as host for psyllids invading potato fields

ACKNOWLEDGEMENTS

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THANK YOU