

Building a continental picture of *Phytophthora infestans*: population structure and emerging dynamics across Latin America through coordinated genotyping

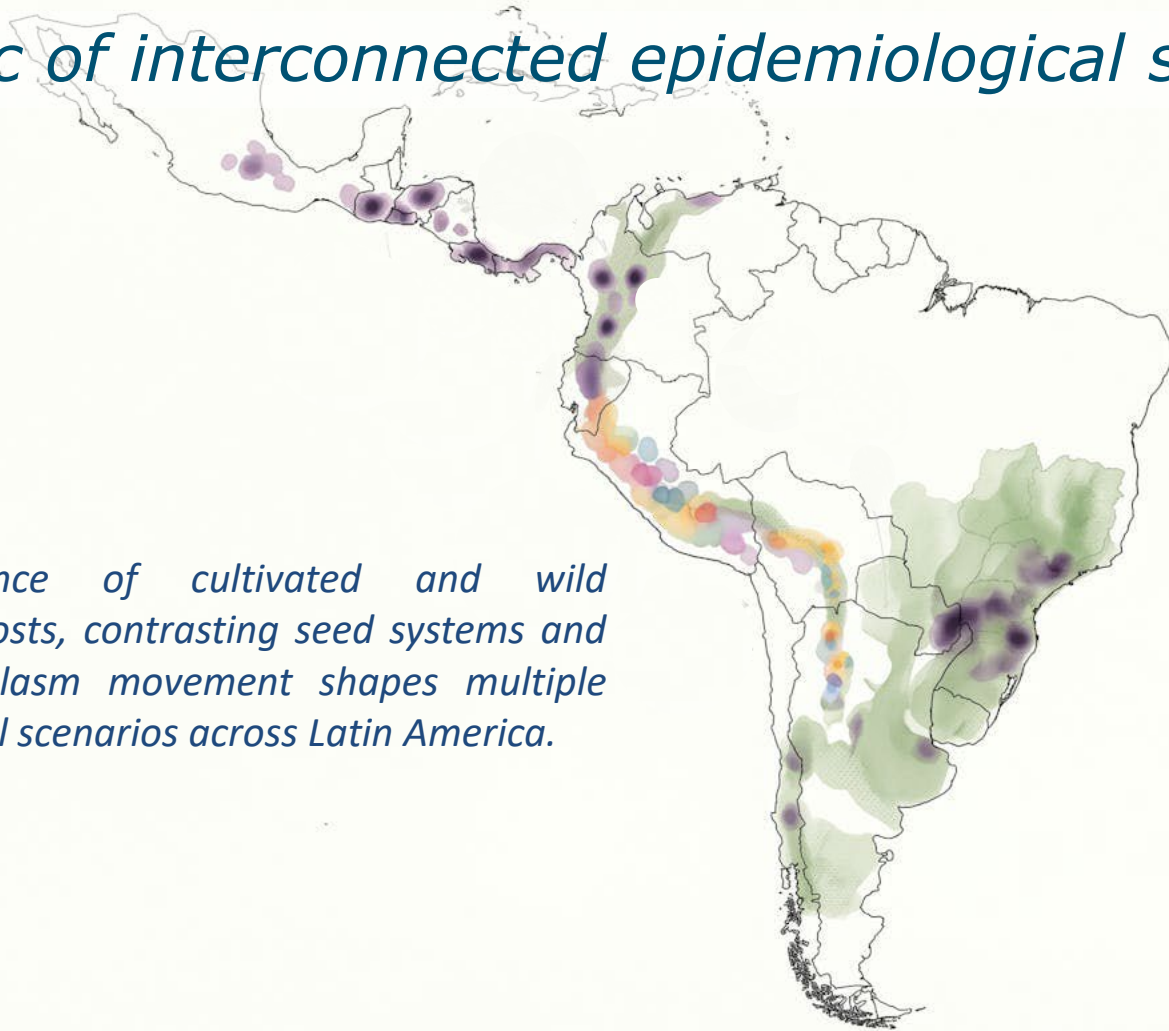
M. Florencia Lucca



Latin America:

a mosaic of interconnected epidemiological scenarios

The coexistence of cultivated and wild Solanaceous hosts, contrasting seed systems and intense germplasm movement shapes multiple epidemiological scenarios across Latin America.



Tizón Latino Network

we built continental surveillance capacity over time



- Established in **2014** during the XXVI Congress of the ALAP (Bogotá, Colombia)
- Harmonized 12-plex SSR protocol aligned with EuroBlight
- FONTAGRO-supported regional initiative (Argentina, Chile, Panama and Ecuador)
- Coordinated by INTA Argentina
- 12 Latin American countries represented
- **>780** harmonized SSR-genotyped isolates, **~1,300** compiled regional isolates



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Harmonized SSR genotyping across Latin America

a coordinated workflow for comparable, high-quality data

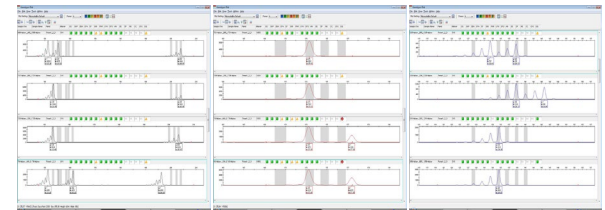
1 *Standardized field sampling*



2 *FTA card DNA preservation*



3 *EuroBlight-aligned 12-plex SSR panel (Li et al., 2013)*



Genotyping supported by the Argentine Consortium for Genomic Technology (INTA)



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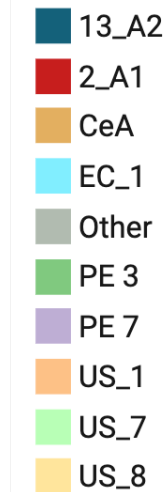
Regional surveillance



Created with Datawrapper

Current Latin American Genotype Map

SSR-genotyped Phytophthora infestans isolates generated through the Tizón Latino network and regional datasets



12

Latin American countries represented



>780

coordinated SSR-genotyped isolates



~1,300

compiled regional isolates

Key population patterns across Latin America

Dominant Southern Cone lineage

EU_2_A1 predominates across the Southern Cone, showing **long-term** regional persistence.

High diversity in Central America

Presence of unique and less frequent lineages including the putative lineage "**Other**", **CeA**, **PE_3**, **PE_7**, **US_8** and **US_7**.

Detection of **13_A2** in Central America.

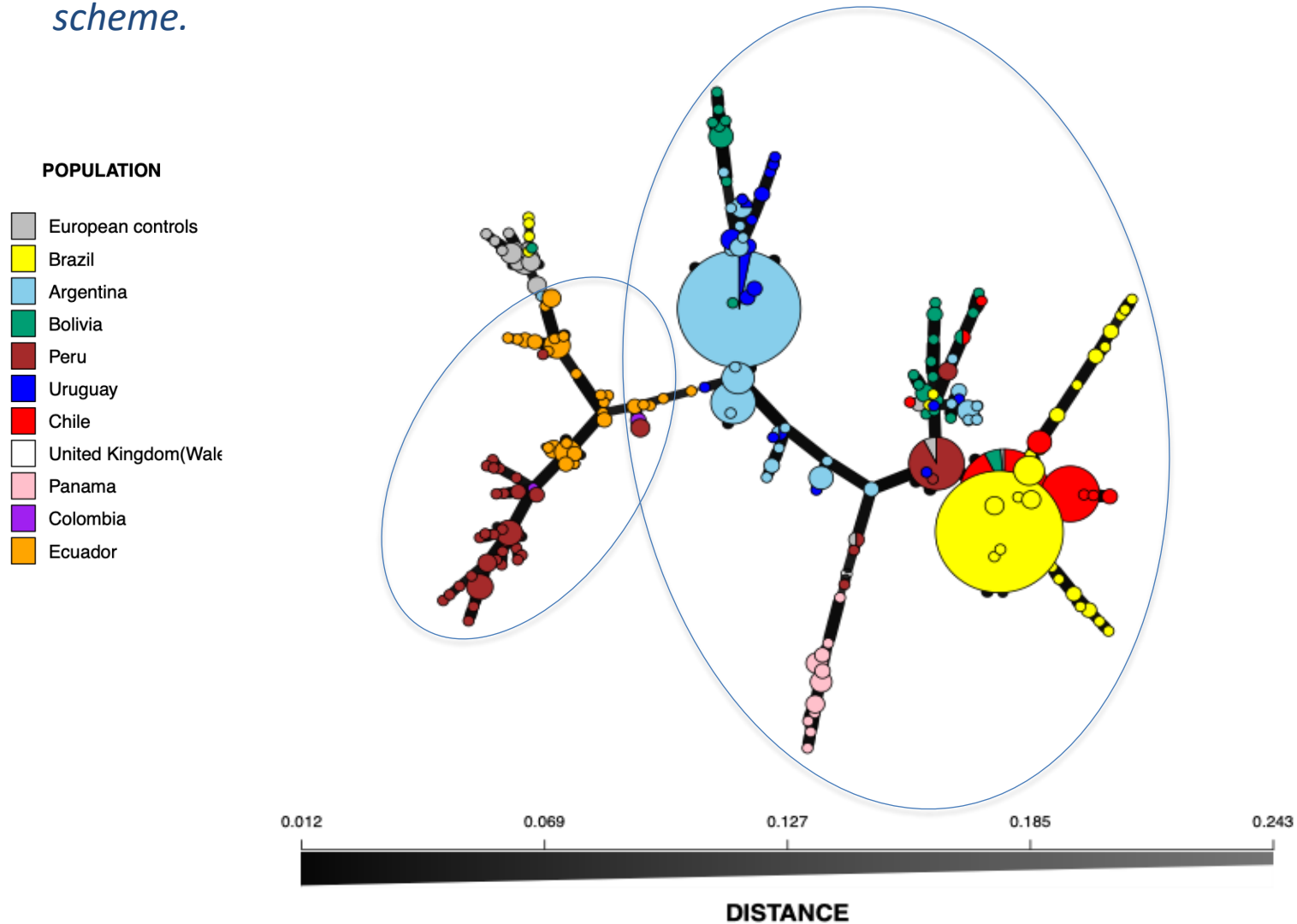
Expanding continental surveillance

Additional isolates from underrepresented regions are currently being incorporated to improve continental representation.



Population structure of *P. infestans* in Latin America

SSR-based minimum spanning network using the EuroBlight 12-plex genotyping scheme.



Linking population surveillance with functional genomics

A representative *EU_2_A1* isolate from Argentina (*PiNSL-19*) was selected for genome, transcriptome and resistance interaction analyses.

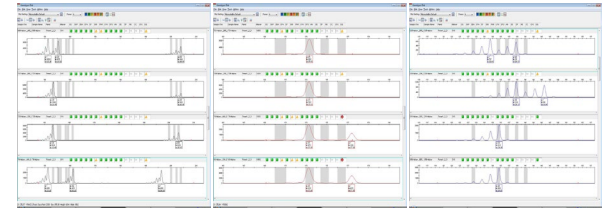
1 Standardized field sampling



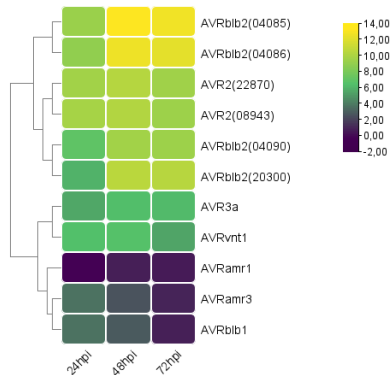
2 FTA card DNA preservation



3 EuroBlight-aligned 12-plex SSR panel (Li et al., 2013)



4 Effector characterization



PiNSL-19

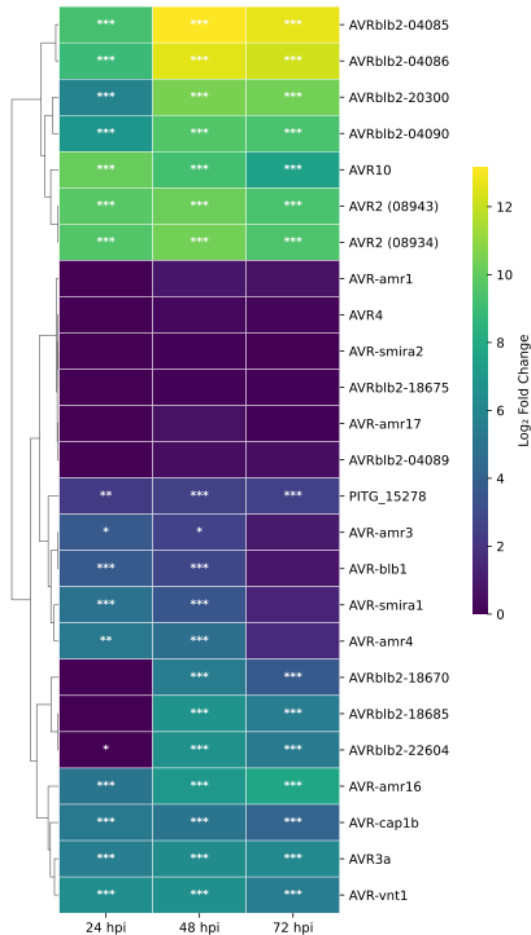
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AVR effector expression during infection of Spunta

Differential expression of AVR effectors during host colonization

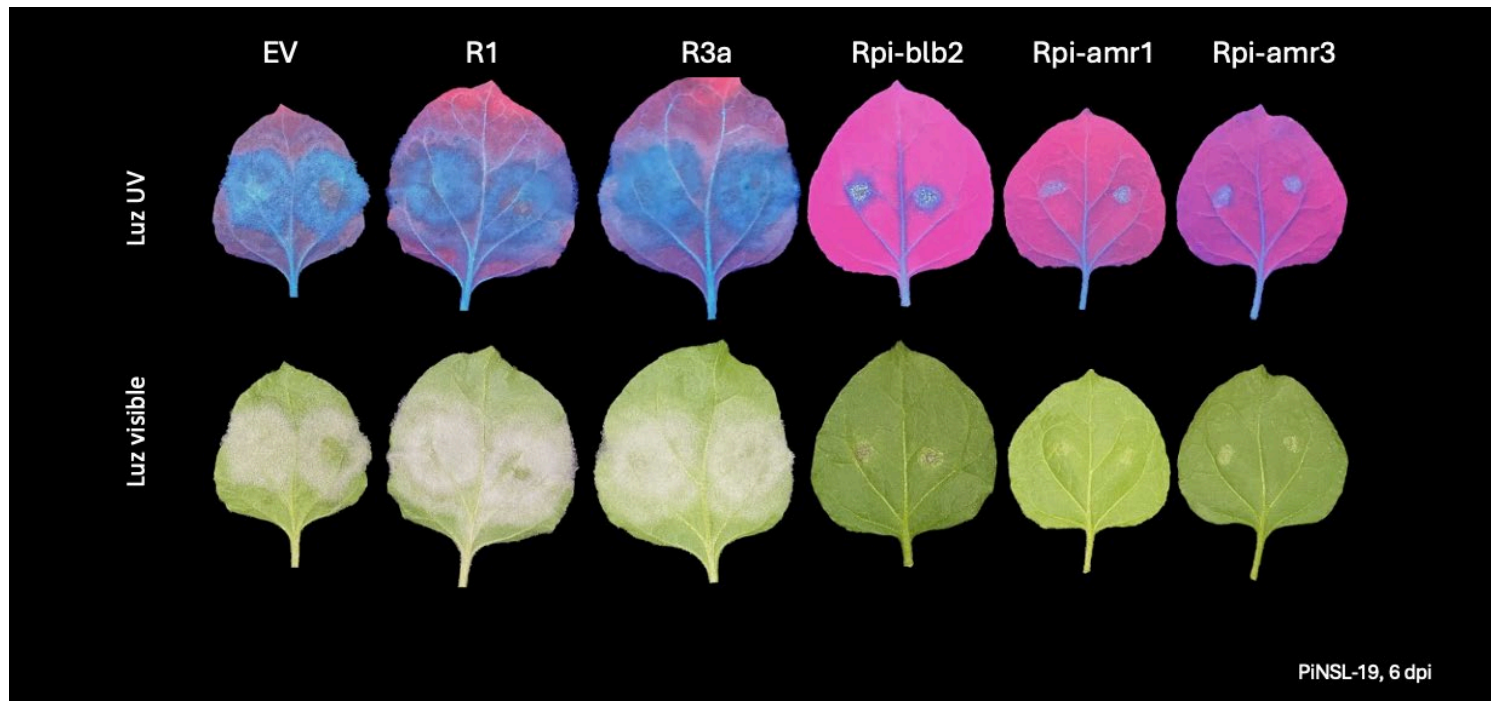


Key findings

- Strong and sustained expression of AVRblb2- and AVRvnt1-associated effectors
- Differential expression patterns among AVRamr-associated effectors
- Potential targets for resistance deployment

Functional validation of AVR-R interactions

Selected resistance genes retained activity against Argentine EU_2_A1 isolates.



- Rpi-blb2, Rpi-amr1 and Rpi-amr3 restricted infection
- R1 and R3a failed to prevent colonization
- Candidate genes for resistance deployment in Latin America

Key take-home messages

- Stable EU_2_A1 clonal populations dominate the Southern Cone
- Greater lineage diversity was detected in Central America and the Andean region
- Effector-informed resistance deployment represents a promising strategy for late blight management in Latin America

Tizón Latino Network – INTA Balcarce – INGEBI-CONICET

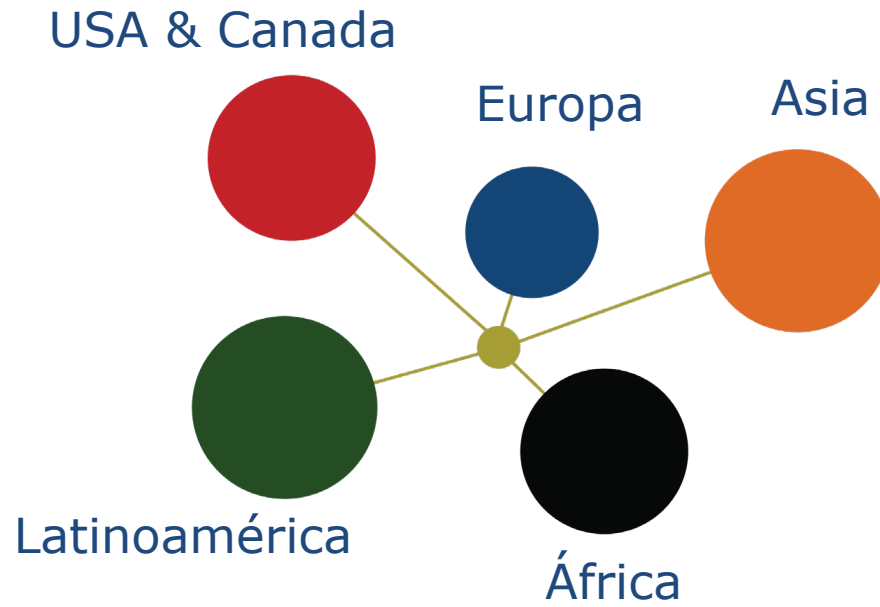
Marcelo Juárez, María Eugenia Segretin, Juan Azcue, Fernando Bravo-Almonacid, Mora Guaglianone, Liliana Cano, Kurt Lamour and collaborators from the Tizón Latino Network.



Thank you



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