



Using DNA Sequences to Determine the Geographic Origins of an Agriculturally Important Invasive Leafmining Fly

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INTRODUCTION

Global movement of people and goods has resulted in the movement of agricultural pests from their native geographic range to new regions where they didn't exist previously. Often, the introduced pests become super-pests in the new location and spread further, becoming "invasive".

It can be difficult to determine the origin and colonization patterns of invasive species. Phylogeography is the study of patterns of geographic variation in genetic markers. This approach can uncover past dispersal patterns of phylogeographic history of movement by invasive species.

Understanding the processes and patterns of colonization by invasive species is crucial in planning interventions and pest management strategies. Knowledge of the natural enemies, pesticide resistance, life cycle, etc., in the native range can provide clues to controlling the population in its new range.

Statement of Problem

Liriomyza huidobrensis is a leafmining fly that damages its host plants by feeding within leaf tissue. It feeds on a wide variety of crops, including potatoes, beans, melon, onions, lettuce, cut flowers and more.

Although native to South America, in recent years highly damaging populations have been inadvertently spread throughout the world causing tremendous damage and crop loss.

GOALS

The primary goals of this study were to:

- 1) Investigate global phylogeographic structure of *L. huidobrensis*.
- 2) Determine the ultimate native origin population(s) of globally invasive *L. huidobrensis*.

MATERIALS AND METHODS

Specimens:

• Obtained DNA sequence data from 50 *L. huidobrensis* specimens from native and invasive populations around the world:

Native: Argentina (5), Columbia (6), Ecuador (6), Guatemala (3), Peru (4)

Invasive: China(2), Israel(4), Italy(1), Java(3), Philippines(2), Sri Lanka(4), South Africa(1)

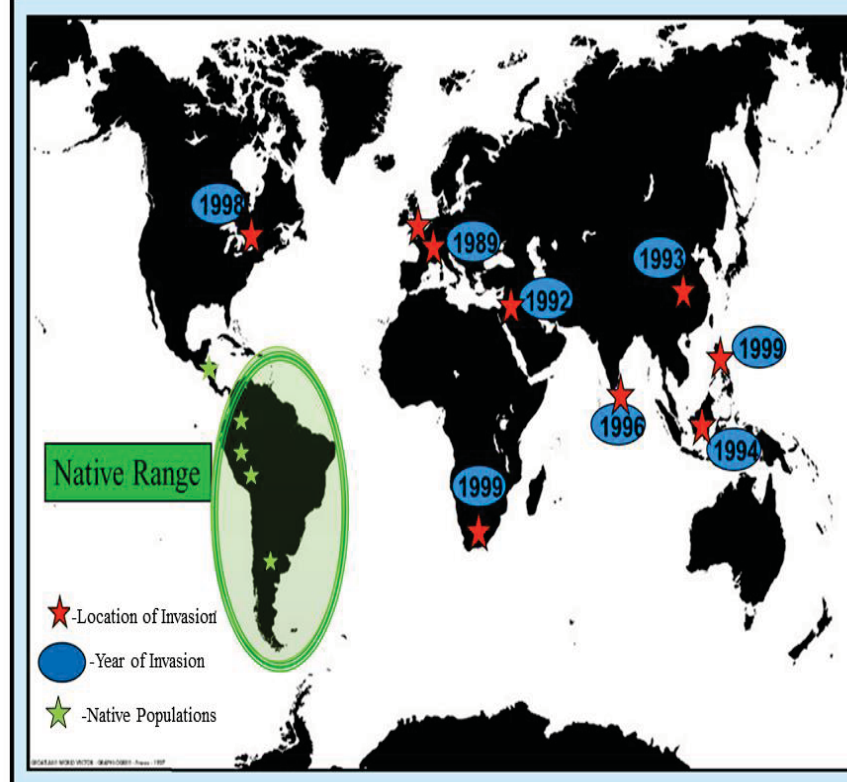
Data Collection:

- Extraction of total genomic DNA from each specimen
- PCR amplification of 2.4 kb of mitochondrial cytochrome oxidase I and II region (COI and COII)
- Sanger sequencing of complimentary strands on ABI-3730XL DNA Analyzer

Analysis:

- Sequencher 5.0.1 used to edit complimentary electropherograms and generate a consensus sequence for each individual.
- All consensus sequences aligned in Sequencher.
- Phylogeographic clustering tree generated using Neighbor-Joining analysis (with 1000 bootstraps) carried out within Geneious R7.

Native and Introduced Ranges



L. huidobrensis Adult flies

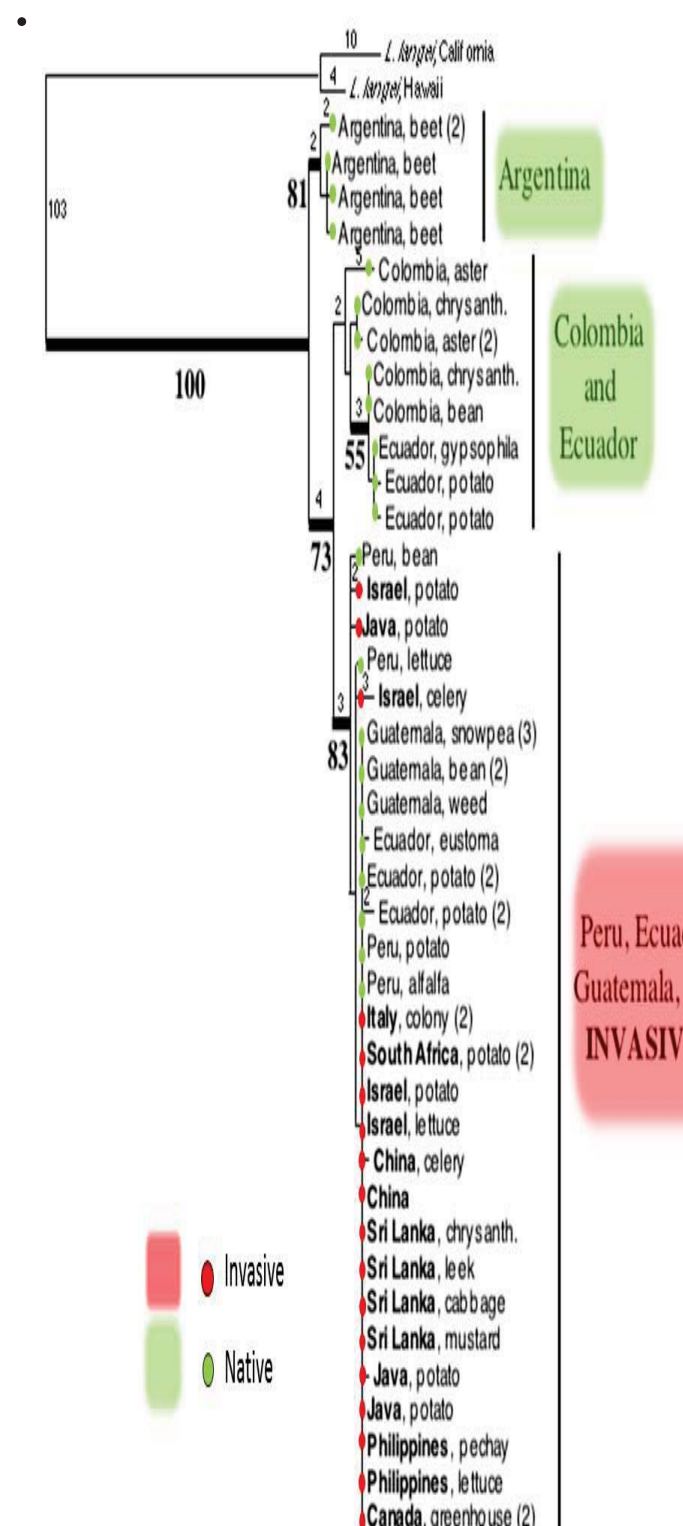


Leafmines of L. huidobrensis



Results

FIGURE 1. Phylogeographic tree of native and invasive *L. huidobrensis*



- Green dots indicate specimens from native populations and red dots indicate those from invasive populations.
- Each country-host label represents one individual except when followed by a number in parentheses, which represents multiple individuals sharing the same sequence.

Results and Discussion

Our data indicate that within *L. huidobrensis* there is phylogeographic structure across South America (Fig 1). Sampled regions of South America form clusters of closely related sequences. For example, all specimens from Argentina cluster together, while those from neighboring regions of Ecuador and Columbia form their own cluster. All specimens from Peru and a few from Ecuador form a third group.

All samples from invasive populations around the world, indicated by red dots, cluster with all the samples from Peru. No samples from invasive populations clustered with other regions of South America (Argentina, Colombia, Ecuador) indicating that these native locations were not the ultimate source of the invasive populations we sampled.

Conclusion and Future Work

Our data clearly show that the ultimate source of global invasive populations of *L. huidobrensis* originated from Peru. However, we cannot currently determine whether the global invasions have resulted from many independent introductions from the Peruvian source or whether initial introductions from Peru have been subsequently followed by localized spread within a particular region.

We plan to use novel markers occurring across the genome to investigate fine scale movements of this invasive species.

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