

# Mitochondrial COI-based Genetic Diversity of *Thrips tabaci*

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## Abstract

*Thrips tabaci* is a globally important crop pest and vector of Iris yellow spot virus (IYSV), an important virus of *Allium* species. *T. tabaci* is a key pest of *Allium cepa*. The genetic variation within and among *T. tabaci* populations on *A. cepa* in selected onion-growing states of the USA was investigated. Eighty four *T. tabaci* specimens were collected from *A. cepa* from 15 different locations in four states. A total of 93 COI gene sequences including nine accessions from GenBank were analyzed to determine the genetic diversity and structure of *T. tabaci*. Twelve distinct haplotypes of *T. tabaci* were identified. Based on the phylogenetic analysis, all the populations collected were thelytokous. While nine *T. tabaci* sequences retrieved from GenBank comprised of four haplotypes and two of those corresponded to leek-associated arrhenotokous populations. The highest genetic variation was found in populations from Raleigh and Elba with seven haplotypes identified in each. Results demonstrate that haplotype 2 and 4 are more prevailing haplotypes in the northwestern USA. The eastern part of the US has a more diverse group of haplotypes and haplotype 4 is predominant. The geographical distribution of these haplotypes in other regions of the country and their relative efficiency in transmitting IYSV remain to be seen.

## BACKGROUND

- Thrips tabaci* (Thysanoptera; onion thrips) is a serious pest, and is a virus vector of economically important crops including *Allium cepa*.
- COI has been recognized as a particularly suitable marker for molecular characterization and genetic variation studies of thrips.
- The use of COI-5' (DNA barcode) region (Hebert *et al.* 2003) to discriminate cryptic species of insects has been validated (Ashfaq *et al.* 2014) including *T. tabaci* (Khan *et al.* 2022).
- There is limited information on the genetic variation and haplotypes of *t. tabaci* infesting *A. cepa* in onion growing regions of the pacific northwestern USA.

## OBJECTIVES

- Determine DNA barcode-based genetic variation and haplotypes of *T. tabaci* infesting *A. cepa*
- Analysis of *T. tabaci* biotypes with relation to different plant hosts

## METHODOLOGY

- T. tabaci* specimens were collected from *A. cepa* from several localities of USA and identified using morphological keys (Fig. 1)
- Amplification of COI-5' (DNA barcode) region
- Molecular analysis of *T. tabaci* by MEGA-X, DnaSP and Arlequin 3.5
- Haplotype analysis of *T. tabaci* using minimum spanning tree constructed in PopART (<http://popart.otago.ac.nz>)
- Phylogenetic analysis of *T. tabaci* biotypes in relation to different host plants

## RESULTS

- 12 haplotypes of *T. tabaci* specimens were found with haplotype diversity Hd: 0.3893 of which two haplotypes are more prevalent (Fig. 2)
- Haplotype 4 was recorded in 70 *T. tabaci* specimens which are predominant in the northwest and eastern US
- AMOVA results indicated that the major portion of the molecular genetic variation was found within locations (99%), rather among the locations (0.11%) (Table 1)
- All the eight haplotypes of *T. tabaci* collected from *A. cepa* clustered within L2 clade of *T. tabaci* that corresponds to leek-associated thelytokous populations (Fig. 3)
- Two haplotypes in the present study were grouped in clade L1 that corresponds to leek-associated arrhenotokous populations (Fig. 3)
- L1 and L2 lineages of *T. tabaci* recorded in the current study have a wide host range and share many host plants while the T lineage of *T. tabaci* has narrow host range and adapted to solanaceous plants (Fig. 4)

Table 1: Comparisons between different haplotypes of *Thrips tabaci* collected from USA by AMOVA based on COI-5' sequences

Model	Hierarchical levels	Degree of freedom	Sum of square	Variance components	Percentage of variation
Thrips species	Among populations	1	4.383	0.00447	0.11
	Within populations	89	372.068	4.18054	99.89
	Total	90	376.451	4.18501	

Fixation indices  $F_{ST} = 0.00107$ ,  $P$ -value 0.31672  
Significance tests (1023 permutations)

## RESULTS

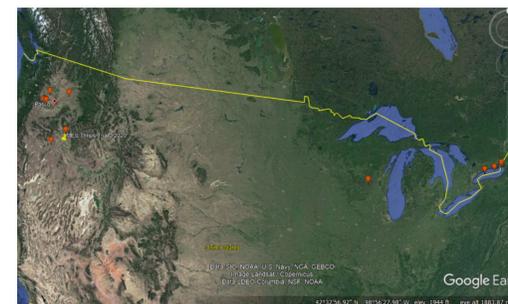


Figure 1: Physical map of some of the collection sites for *Thrips tabaci*

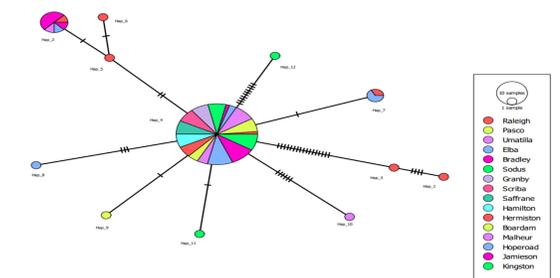


Figure 2: Haplotype network analysis for *Thrips tabaci* based on COI-5' sequences including presumptive conspecifics from GenBank

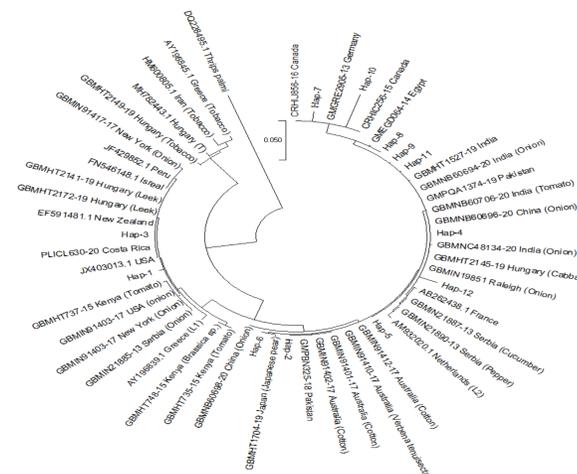


Figure 3: Maximum likelihood method-based phylogenetic tree of different haplotypes of *Thrips tabaci* collected from onion. *Thrips palmi* was included as the outgroup.

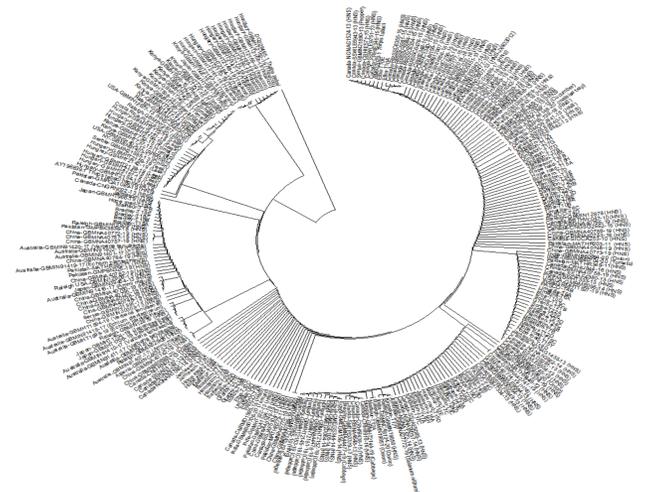


Figure 4: Phylogenetic tree of *Thrips tabaci* from all plant hosts including onion. *Thrips palmi* was included as the outgroup.

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