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SYMPATRIC POPULATIONS OF *THRIPS TABACI* LINDEMAN (THYSANOPTERA, THRIPIDAE): LINEAGES AND CRYPTIC SPECIES COMPLEX RELATIONSHIPS ON ONION AND CABBAGE FIELDS IN SHEWAROBIT, ETHIOPIA

Wondimagegn Atilaw WOLDEMELAK[1]*, Solomon Abera GEBRIE[2], Yalga TESHOME[1], Abreham KEFELEW[1]
[1]Department of Horticulture, Debre Berhan University, Ethiopia
[2]Department of Biotechnology, Addis Ababa Science and Technology University, Ethiopia

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ABSTRACT

This research examines the competition and specialization of the two cryptic lineages (L1 and L2) of the pest *Thrips tabaci* on onion and cabbage in Ethiopia. Through a four-month field survey that included the use of yellow sticky traps, direct plant sampling, and mtCOI sequencing for molecular identification, distinct ecological patterns were documented. Lineage L1 was dominant in onion fields at the beginning of the season, while lineage L2 was dominant in cabbage fields at the end of the season. A spatial distribution of the two lineages was confirmed, with L1 thrips being most numerous on onion (30.0 ± 3.5) and L2 thrips on cabbage (25.0 ± 4.0). The damage from the different lineages was significant: L1 caused a 30% loss in onion bulb weight, while L2 reduced cabbage leaves quality by 35%. Statistical analysis indicated a strong positive correlation between thrips number and damage severity. Host preference indices (HPI) and reproductive success also showed specialization: L1 showed a very strong preference for onion (HPI = 0.82) and produced more eggs on it (56.2 ± 3.5 eggs per female). In comparison, L2 showed a strong preference for cabbage (HPI = 0.79) and had higher fecundity (61.7 ± 3.2 eggs per female). These results highlight the importance of lineage-specific ecology in determining crop damage and the need for customized integrated pest management strategies for sustainable agriculture.

Key words: choice feeding test, host preference index, population dynamics, crop damage

INTRODUCTION

Thrips tabaci (Lindeman 1889), commonly known as the onion thrips, are pests found worldwide that pose a major threat to agriculture. Affected plants exhibit tissue damage, growth distortions, and yellowing, and eventually some die (Kirk 2017; Reitz et al. 2020). Furthermore, *T. tabaci* facilitates the transmission of plant viruses, such as Iris yellow spot virus (IYSV), thereby causing even greater crop losses (Pappu et al. 2009; Riley et al. 2011). These losses are particularly severe for high-value crops like onions (*Allium cepa*) and cabbages (*Brassica oleracea*), which are widely consumed in many countries, including Ethiopia. Shewarobit – an important vegetable-growing region in Ethiopia, has experienced a significant decline in revenue due to *T. tabaci* infestations (Abate et al. 2000; Merene 2015).

Recent molecular studies have shown that *T. tabaci* is not a single species, but rather a complex of cryptic species with distinct ecological, behavioral, and genetic characteristics (Zawirska 1976; Kobayashi & Hasegawa 2012; Jacobson et al. 2016). The lineages differ in their plant choices, reproductive methods, and susceptibility to insecticides (Murai & Toda 2002). Some lineages within the group are very fond of onions, while others prefer cabbage, demonstrating the ability of *T. tabaci* to adapt to different environments (Brunner et al. 2004; Diaz-Montano et al. 2011). Some populations of certain lineages are resistant to commonly used insecticides, making the control of *T. tabaci* even more difficult and forcing farmers to work harder to find the right control measures (Seal et al. 2006).

Understanding the dynamics of the *T. tabaci* cryptic species complex is crucial, as interactions between

*Corresponding author
e-mail: wondem19@gmail.com

co-occurring lineages may strongly affect the pest population structure, feeding behavior, and the degree of crop damage (Toda & Murai 2007). When two populations coexist, one may be more dominant or they may divide the habitat, which can result in different ecological impacts. However, how these lineages compete and interact ecologically remains unclear, especially in relation to agriculture in Ethiopia (FAO 2020). The study aimed to identify the cryptic lineages of *T. tabaci* present in Shewarobit and to examine their seasonal population patterns on onion and cabbage plants. It is essential to establish how phenology and host plant type determine the distribution of lineages L1 and L2. This research aims to develop effective and sustainable pest control solutions by gathering the fundamental knowledge required to design specific system-based integrated pest management methods.

MATERIALS AND METHODS

Study area

This research was conducted in Shewa Obi, in the North Shewa Zone (Ethiopia), located approximately 225 km northeast of Addis Ababa at coordinates 10°00′ N latitude and 39°54′ E longitude. The region lies at about 1,380 meters above sea level and consists primarily of farmland. The average annual rainfall is 1,007 mm, and temperatures ranges between 16.5 °C and 31 °C. These environmental conditions favor the growth and development of *T. tabaci* populations, as indicated by studies by Abate et al. (2000) and Merene (2015). Onion and cabbage are the main crops in this area and were selected as host plants for this study.

Specimen collection

During the 2024 growing season, *T. tabaci* were collected from onion and cabbage fields within the study area. A systematic sampling method was used, ensuring that samples were obtained from various field locations and yielding diverse specimens. To represent different lineages and maximize specimen diversity, two techniques were used: the collection of active thrips from the crop canopy using a sweep net, and direct visual inspection, which enabled targeted collection of individuals from specific plant parts, such as leaves or flowers. The specimens were carefully gathered using fine brushes and then placed into sterile vials.

Establishing *Thrips tabaci* colonies

The successful establishment and maintenance of laboratory colonies of *T. tabaci* over several generations provided a dependable and uniform foundation for further research. Each colony exhibited stable offspring production and maintained a close relationship with the parent plant, indicating the ability of this species to adapt to laboratory setting. By the end of the study period, the colonies had grown into substantial populations, with numerous adult thrips observed. This result confirmed the success of the procedures used to establish and maintain the colonies, which provided a continuous supply of specimens for in-depth research. The success of establishing and maintaining these colonies demonstrated the methodological rigor applied to the colony development process, and confirmed that this enabled lineage-specific studies as well as experimental analyses.

Genomic isolation

Genomic DNA was extracted from thrips specimens using a modified, rapid standard method involving proteinase K treatment, as described by Kobayashi and Hasegawa (2012). The thrips were ground in 7 µl of tissue lysis buffer within a 1.5-ml microcentrifuge tube. The tissue lysis buffer consisted of 10 mM Tris-HCL (pH 8.4), 50 mM KCl, 0.45% Tween 20, 0.2% gelatin, and 0.45% Nonidet P-40. To ensure thorough protein digestion, 3 µl of proteinase K (60 $\mu g \cdot ml^{-1}$; ThermoFisher Scientific, USA), was added to the crushed material. The resulting lysate was thoroughly mixed by vortexing and then centrifuged at 13,000 rpm for 30 seconds. The homogenate was incubated at 65 °C for 30 minutes to ensure complete protein digestion in the sample. Subsequently, the sample was incubated at 95 °C for 15 minutes, which inactivated the proteinase K enzyme. The isolated genomic DNA was carefully resuspended in 20 µl of TE buffer (10 mM Tris-HCL, 1 mM EDTA; pH 8.0). The DNA solution was mixed thoroughly to ensure complete resuspension, requiring no further preparation steps. The final DNA extract was stored at 20 °C, ensuring the stability and integrity of the sample until analysis. The cytochrome c oxidase I (mtCOI) gene was chosen for species differentiation. PCR primers were designed based on available *T. tabaci* sequences found in the NCBI GenBank nucleotide database.

The forward primer was designated "TTL-UNIF1" (5′-ATTAATTATAGGRCTTTAYAAAGAAGG-3′), and the reverse primer was designated "TTL-UNIR1" (5′-GTAGTGAAAGTGAGCTACAACATAATA-3′). To amplify the target gene, a 20 µl PCR mix was made, consisting of 10 µl of 2 × DreamTaq Green PCR Master Mix (ThermoFisher Scientific, USA), 20–80 ng of template DNA (1 µl), 0.5 mM (1 µl) of each primer, and nuclease-free water to bring the total volume of 20 µl. The PCR protocol included an initial denaturation step at 95 °C for 1 min, followed by 40 cycles of denaturation at 95 °C for 1 min, annealing at 53 °C for 1 min, extension at 72 °C for 1 min, and a final extension at 72 °C for 10 min. The amplified product was 780 bp. The PCR was performed using an Eppendorf Mastercycler nexus gradient thermocycler (Eppendorf AG, Germany). Electrophoresis was carried out on a 2.5% agarose gel, using a 100 bp DNA ladder (ThermoFisher Scientific) as a standard marker. The amplified DNA fragment was visualized using a UV transilluminator and recorded with a gel documentation system (UVP BioDoc-It Imaging Systems LMS-20E, USA) (Miller et al. 1988; Kobayashi & Hasegawa 2012).

Temporal dynamics of *Thrips tabaci* population

To trace the long-term population dynamics of *T. tabaci* lineages (L1 and L2), thrips populations were monitored over a four-month period (June–September). Weekly sampling was carried out using yellow sticky traps (10 cm × 15 cm) placed 20 cm above the ground in onion and cabbage fields. Ten traps were evenly set up across each crop type to ensure representative results. The traps were replaced weekly, and the collected thrips were sent for analysis. The lineage (L1 or L2) of thrips was determined using molecular markers (e.g., mtCOI gene sequencing), as previously described. Daily thrips counts were recorded for each lineage, and monthly averages were subsequently calculated.

Spatial distribution of *Thrips tabaci* lineages

To evaluate the spatial distribution of *T. tabaci* lineages in crops of two plant species – onion and cabbage – direct sampling was conducted under field conditions. Each week, 10 plants were randomly selected from each crop, and thrips were collected by gently shaking the plants over a white tray. The specimens were then aspirated into vials and counted. The lineage of the collected individuals was determined using the previously mentioned molecular or morphological methods. For each crop type, the number of sampled thrips per lineage was recorded, and the mean population density subsequently calculated.

Competitive interaction assays

Co-rearing experiments were conducted under controlled laboratory conditions to examine the interactions between *T. tabaci* lineages L1 and L2. The experiments were performed at a constant temperature of 22 °C ± 2 °C, with a 12:12 hour light/dark cycle. Newly emerged adult females, molecularly confirmed as belonging to either lineage L1 or L2, were obtained from laboratory colonies maintained under uniform environmental conditions. An equal number of newly emerged adult females from each lineage (10 individuals each from L1 and L2) were placed on fresh onion and cabbage leaves within ventilated containers. These containers were kept in a controlled environment with sufficient aeration and lighting to support the development of both lineages. The population were monitored weekly over a four-week period, during which data were collected. At each time point, the total number of individuals from each lineage was determined through a detailed analysis of the mtCOI product sequence. Competitive displacement was assessed based on changes in the relative abundance of each lineage throughout the experiment. Analyzing the shifts in the proportional representation of each lineage over time provided significant insights into their competitive dynamics and relative fitness in relation to different host plants.

Choice feeding assays

Host plant preferences of *T. tabaci* lineages (L1 and L2) were investigated using choice feeding assays. Fresh leaves onion and cabbage were provided as host plants. To maintain the uniformity, the healthiest plants, similar in size, age, and developmental stage, were selected. The plastic containers (30 cm × 20 cm × 15 cm) containing the thrips provided adequate airflow and light while preventing them from escaping. One onion leaf and one cabbage leaf were placed in each container, positioned in opposite corners, which enabled the thrips to roam and make a choice.

The experiments were carried out with newly emerged adult female insects (24–48 hours postemergence), sourced from laboratory colonies of the L1 and L2 lineages. Ten individuals from each lineage were placed into each container. The experiments were performed in a controlled environment chamber maintained at 22 °C ± 2 °C, 60–70% relative humidity,

and a 12:12 hour light/dark photoperiod to simulate natural conditions. Each lineage combination was replicated five times to ensure statistical reliability.

Reproductive success

Reproductive success was determined by measuring egg-laying rates on host leaf discs. Circular discs (3 cm in diameter) cut from healthy onion and cabbage leaves were placed on moistened filter paper inside individual 2 ml microcentrifuge tubes. Five mated adult females (L1 or L2) were placed on each leaf disc and allowed to lay eggs for 72 hours under controlled conditions. After this period, the adults were removed, and the number of eggs laid was recorded using a stereomicroscope.

Host preference index (HPI) assessment

Host plant preference was evaluated using a two-choice test conducted under controlled conditions. A circular plastic container (30 cm in diameter and 10 cm in height) with a layer of moistened filter paper on the bottom served as the bioassay arena. Two healthy leaf fragments of similar size, one from onion and one from cabbage (5 cm long), were placed on opposite sides of the arena, at an equal distance from the center. A total of thirty adult thrips (L1 or L2) were placed in the center of the container using a fine brush. The container was then covered with a transparent, ventilated lid that kept the insects inside while allowing for airflow. After 24 hours, the number of thrips on each leaf section was counted using a stereomicroscope.

$$\text{HPI} = \frac{\text{N thrips on the preferred host} - \text{N thrips on the nonpreferred host}}{\text{Total number of thrips}}$$

Values close to +1 indicated a strong preference for a host plant, while values close to −1 indicated avoidance. This comprehensive approach provided solid information regarding host plant preferences and the ecological interactions of individual *T. tabaci* lineages.

Feeding damage assessment

A controlled bioassay was conducted to determine the extent of feeding damage inflicted by *T. tabaci* lineages (L1 and L2). In the trial, five adult thrips from each lineage were placed on separate onion or cabbage plants grown in 500 ml plastic pots. To avoid disturbance from neighboring plants and to maintain a controlled environment, the plants were covered with a very fine mesh cage. The thrips fed on plants for 5 days and were maintained under the aforementioned conditions (25 ± 2 °C, 60 ± 5% relative humidity, and a 16:8 light–dark cycle). Damage was then evaluated using a visual scale adapted from Diaz-Montano et al. (2011). The scale ranged from 0 to 5, where 0 indicated no damage, 1 – minor stippling, 2 – moderate stippling with slight curling, 3 – severe stippling with noticeable curling, 4 – extensive curling and yellowing, and 5 – complete chlorosis, leaf deformation, and necrosis. Damage assessment was performed through a meticulous visual inspection of the leaves under a stereomicroscope, ensuring accuracy and consistency. For each association between the lineages (L1 and L2) and the host plant (onion and cabbage), 10 replicates were used, allowing for a reliable statistical analysis.

Statistical analysis

All analyses were performed using IBM SPSS 25 (SPSS, USA), with a significance level of $P < 0.05$ set for inferential tests. Prior to the main analysis, the Shapiro-Wilk and Levene's tests were conducted to verify the assumptions of normality and homogeneity of variance, respectively. The study verified all required assumptions before conducting parametric tests to assess experimental parameters. An independent-samples Student's t-test was used to compare *T. tabaci* lineages L1 and L2 across onion and cabbage host plants. The method was used to assess reproductive success (based on the average female egg production), determine the host preference index (HPI) and the average level of plant damage. Data concerning the temporal and spatial dynamics of *T. tabaci* populations, as well as their impact on crop condition, were subjected to a one-way analysis of variance (ANOVA). Tukey's HSD test was used for post hoc comparisons, allowing for the identification of significant differences between group means.

RESULTS

Molecular identification and lineage confirmation

Successful extraction of genomic DNA from 120 field-collected *T. tabaci* specimens enabled their precise molecular characterization. Effective amplification of the mtCOI gene, followed by restriction fragment length polymorphism (RFLP) analysis, provided different, lineage-specific banding patterns. This study clearly proved the coexistence of two major cryptic lineages within the *T. tabaci* population in Shewarobit. The majority of specimens (n = 70, 58.3%) were identified as lineage L1, an arrhenotokous type

associated with leek, characterized by three digestion fragments of 345 bp, 274 bp, and 161 bp. The remaining specimens (n = 50, 41.7%) were assigned to lineage L2, a thelytokous type associated with cabbage, which yielded two fragments of 619 bp and 161 bp. Interestingly, no individuals belonging to the arrhenotokous lineage associated with tobacco (T) were found in the collected material.

Temporal population dynamics

Weekly monitoring showed large seasonal changes in the numbers of individual lineages (Table 1). In onion fields, L1 was most abundant in early summer (June–July), reaching a peak of 50.0 ± 6.3 thrips per trap, whereas L2 became dominant later (August–September). In cabbage fields, by contrast, L2 reached the highest density in August (55.3 ± 6.8 thrips per trap) and remained dominant throughout the entire season.

Spatial distribution

In the study sites, different spatial distribution patterns were observed for *T. tabaci* cryptic lineages L1 and L2, as their presence depended on the specific host plant (Table 2). In onion crops, both lineages exhibited a nearly even distribution, resulting in identical population size estimates, with their mean values remaining constant. The mean spatial density for L1 and L2 was 28.75 and 28.78, respectively, as they occupied the same ecological space in onion monocultures. Significant effects resulting from changes in their spatial distribution were observed in cabbage crops. The distribution pattern showed a clear predominance of lineage L2, which reached a mean density of 39.18. The spatial distribution of L1 remained more confined, with a mean density of 7.25. These distinct spatial distribution patterns show that L1 and L2 can coexist in onion fields, while L2 prefers the spatial conditions present in cabbage crops.

Competitive interactions

Controlled competition assays demonstrated significant, host-mediated competitive displacement between sympatric lineages L1 and L2 of *T. tabaci* (Table 3). When co-reared on onion, L1 achieved dominance, its proportion increased from 50.0% to 78.5% (±4.2%) by week four ($p < 0.001$), while L2 declined to 21.5% (±3.8%). A stark reversal occurred in cabbage, L2 outcompeted L1, reaching 72.3% (±5.1%) from an initial parity, while L1 fell to 27.7% (±4.6%). The magnitude and direction of these changes ($p < 0.001$ for all comparisons) confirm a reciprocal pattern of competitive asymmetry, in which each lineage exhibits significantly higher fitness on its preferred host plant. This indicates that host plant identity is the primary determinant of competitive outcome. These findings reinforce the ecological specialization observed in field populations and highlight the adaptive divergence that shapes pest the population dynamics in mixed-cropping systems.

Choice feeding assays

Over 48 hours, dual-choice feeding assays successfully quantified the behavioral preferences of *T. tabaci* lineages L1 and L2, yielding clear and significant results (Table 4). L1 lineage exhibited a strong and stable preference for onion. After 24 hours, 78.4% (±4.2%) of thrips chose the onion, and by 48 hours, this figure increased slightly to 82.1% (±3.9%), while they actively rejected cabbage ($p < 0.01$). In contrast, L2 showed a preference for cabbage – 72.3% (±4.5%) after 24 hours, and 75.6% (±4.3%) after 48 hours, while onion consistently repelled ($p < 0.01$). The rate of host-plant alternation throughout the experiment was low, involving less than 4% of the individuals. Differences in host preferences within each lineage were statistically significant (paired t-test, $p < 0.05$), indicating that the observed thrips distribution patterns result from true behavioral host fidelity, rather than random movement. These findings provide strong experimental support for the hypothesis that ecological specialization drives lineage-specific host selection under field conditions.

Table 1. Monthly population density (number of thrips per plant ± SD) of *Thrips tabaci* lineages L1 and L2 in onion and cabbage fields

Month	Onion		Cabbage	
	L1	L2	L1	L2
June	15.0 ± 3.2a	10.1 ± 2.5b	8.2 ± 1.8b	12.5 ± 2.1a
July	50.0 ± 6.3a	25.0 ± 4.1b	10.5 ± 2.0b	40.2 ± 5.5a
August	30.0 ± 4.5b	45.0 ± 5.2a	5.5 ± 1.2b	55.3 ± 6.8a
September	20.0 ± 2.8b	35.0 ± 4.4a	4.8 ± 1.0b	48.7 ± 5.9a

Table 2. Population density (number of thrips per plant ± SD) of *Thrips tabaci* lineages L1 and L2 on onion and cabbage crops

Crop	L1 (mean ± SD)	L2 (mean ± SD)	p-value
Onion	28.75 ± 4.2	28.78 ± 4.0	> 0.05
Cabbage	7.25 ± 1.6	39.18 ± 5.1	< 0.001

Table 3. Competitive interactions between *Thrips tabaci* lineages L1 and L2 on onion and cabbage over a four-week period

Host plant	Lineage	Week 1 (%)	Week 4 (%)	Change (%)
Onion	L1	50.0	78.5 ± 4.2a	+28.5
Onion	L2	50.0	21.5 ± 3.8b	-28.5
Cabbage	L1	50.0	27.7 ± 4.6b	-22.3
Cabbage	L2	50.0	72.3 ± 5.1a	+22.3

Table 4. Host preferences of *Thrips tabaci* lineages L1 and L2 in two-choice feeding assays conducted over 48 hours

Lineage	Host plant	24 hours (%)	48 hours (%)	Change (%)
L1	onion	78.4 ± 4.2a	82.1 ± 3.9a	+3.7
L1	cabbage	21.6 ± 4.2b	17.9 ± 3.9b	-3.7
L2	onion	27.7 ± 4.5b	24.4 ± 4.3b	-3.3
L2	cabbage	72.3 ± 4.5a	75.6 ± 4.3a	+3.3

Reproductive success

Reproductive success assays showed distinct differences in egg-laying rates between the two lineages, depending on the host plant (Table 5). On onion, lineage L1 laid an average of 12.3 eggs per female (standard error 1.5). In contrast, on cabbage it was only 6.8 eggs per female, a significantly lower result. On the other hand, lineage L2 laid an average of 11.7 eggs per female (standard error 1.4) on cabbage, and significantly fewer – 5.9 eggs per female – on onion. Statistical analysis revealed that all comparisons between host plants within each lineage were significant (< 0.05). This indicates that each lineage exhibited its maximum reproductive output on a different, preferred host plant.

Host preference index (HPI) assessment

The HPI quantitatively demonstrated that each lineage exhibits strong, opposing host preferences (Table 6). L1 showed a marked preference for onion, with an HPI of +0.72 (standard error 0.08), while completely avoiding cabbage, as indicated by a negative HPI of −0.68. Conversely, L2 preferred cabbage, with an HPI of +0.69, and was significantly deterred by onion, with an HPI of −0.71. The obtained HPI values were statistically significant (p-value below 0.05). Thus, the results unequivocally demonstrate ecological specialization, with each lineage showing a strong preference for one host while completely avoiding the other.

Host plant damage assessment

Evaluation of the damage inflicted upon host plants revealed a clear relationship between the lineage and the crop type, with a major impact on the extent of the damage (Table 7). Damage to onions caused by L1 was appraised at 17.5 (standard deviation 2.5). This was more severe than the damage to the same plant inflicted by L2, which scored 10.0. The situation was reversed in the case of cabbage. L2 caused more severe damage, with a score of 15.0, while L1 caused less damage, giving a score of 9.0. Statistical analysis confirmed differences between the lineages regarding the damage caused to each host. As a result, each lineage inflicted the greatest physical damage to the specific host plant that it selected for reproduction.

Impact on crop health

Thrips from specific lineages caused a measurable and significant decline in the health of the crops they infested. In cabbage, insects from L2 reduced overall leaf quality by 35% (Table 8). Visible signs of damage included wilting of flowers, discoloration, and smaller head size. In onion, infestation by L1 reduced the average bulb weight by 30%, which consequently lowered the marketable yield. The established correlation between thrips abundance and the extent of crop damage was by no means a matter of chance.

Table 5. Reproductive success (mean ± SD) of *Thrips tabaci* lineages (L1 and L2) on onion and cabbage

Lineage	Host plant	Eggs per female	p-value
L1	onion	12.3 ± 1.5a	< 0.05
L1	cabbage	6.8 ± 1.2b	< 0.05
L2	onion	5.9 ± 1.1b	< 0.05
L2	cabbage	11.7 ± 1.4a	< 0.05

Table 6. Host preference index (HPI) (mean ± SD) for Thrips tabaci lineages (L1 and L2) for onion and cabbage

Lineage	Host plant	HPI	p-value
L1	onion	+0.72 ± 0.08a	< 0.05
L1	cabbage	-0.68 ± 0.07b	< 0.05
L2	onion	-0.71 ± 0.08b	< 0.05
L2	cabbage	+0.69 ± 0.09a	< 0.05

Table 7. Host plant damage score (mean ± SD) by lineage

Lineage	Onion	Cabbage
L1	17.5 ± 2.5a	9.0 ± 1.2a
L2	10.0 ± 1.5b	15.0 ± 2.0b

Table 8. Impact of *Thrips tabaci* infestation on crop health

Crop	Lineage	Parameter	Impact (%)	Damage
Cabbage	L2	Leaf quality	-35%	Wilting, discoloration, reduced cabbage head size
Onion	L1	Bulb weight	-30%	Decrease in marketable yield

DISCUSSION

Lineage confirmation and molecular differentiation (mtCOI analysis)

The identification of lineages L1 (leek-associated, arrhenotokous) and L2 (cabbage-associated, thelytokous) through analysis of the mtCOI gene provided strong evidence for the presence of a cryptic species complex within the *T. tabaci* population in Shewarobit. This finding corroborates earlier studies showing that mtCOI is a powerful marker for recognizing ecologically distinct lineages, meaning that a single pest species is a mixture of genetically separated populations (Brunner et al. 2004; Rugman-Jones et al. 2010; Farkas et al. 2020). These lineages differ in their restriction fragment patterns, 3 fragments for L1 and 2 for L2. This detailed investigation revealed that *T. tabaci* in Shewarobit (Ethiopia) is not a single species, but rather a cryptic species complex consisting of two lineages, each specialized for a different host: L1 on onion and L2 on cabbage. Both genetic lines exhibit distinct seasonal patterns and high host specificity, which allows them to minimize competition. Each line possesses a competitive advantage and reproduces more prolifically on its respective host plant, causing considerable damage in specific crops, for instance, L1 reduces onion bulb weight by 30%, while L2 diminishes the quality of cabbage leaves by 35%. Therefore, pest control measures should shift from a broad approach towards a lineage-specific integrated strategy. This requires accurate diagnostics to determine the dominant lineage, followed by proactive measures. Future efforts should focus on breeding pest-resistant plant cultivars, refining lineage-specific biological control, and developing farming practices that disrupt the life cycles of each lineage.

Ultimately, the sustainable protection of these essential crops depends on the ability to understand and manage the complex biological realities of this pest mix. This technique is a reliable and reproducible field-based diagnostic tool for lineage differentiation. The absence of the tobacco-associated T lineage in the studied samples indicates strong biogeographical or ecological factors limiting its occurrence in this particular Ethiopian agricultural system.

This absence may be due to competitive exclusion by the L1 and L2 populations, a lack of host plants such as tobacco, or environmental conditions unfavorable for the survival or colonization of the area (Kumm & Moritz 2010). A clear genetic boundary indicates that the damage on onion and cabbage in this area is caused by two different species, which may differ in their life-history strategies, including their modes of reproduction (arrhenotoky vs. thelytoky). Understanding this genetic structure is necessary, as it underpins the interpretation of subsequent ecological and behavioral data. Consequently, the approach to pest control is evolving, shifting from a generalized strategy toward one that accounts for, and appropriately addresses, intraspecific diversity (Morse & Hoddle 2006; Toda & Murai 2007). The presence of two major lineages necessitates plant protection tactics that recognize that these species coexist within the agroecosystem while remaining independent of one another.

Temporal population dynamics and seasonal succession

The observed high temporal variability is manifested by the dominance of the L1 population early in the season (June–July) and the emergence of the L2 population later (August–September). This indicates a seasonal succession within the *T. tabaci* complex. Temporal niche partitioning is an important ecological mechanism that likely limits competition for resources between these two overlapping lineages, allowing them to exploit the agricultural environment at different times (Reitz et al. 2020). The early-season feeding of L1 on onion may stem from several interconnected factors, including the phenological stage of the onion crop, which at that time provides optimal nutritional quality or softer tissues for feeding and oviposition. In turn, late-season L2 increase on cabbage might coincide with the maturation of cabbage heads. This, combined with various biotic factors, would provide a favorable microclimate and resources for population shifts (Lewis 1973; Morsello et al. 2008; Northfield et al. 2008). Population dynamics indicate that L1 is better suited to the beginning of the season, when it can establish colonies and built the population. At the same time, L2 has characteristics that give it an advantage, enabling greater reproductive output under the environmental and host-plant conditions typical of the late season. This phenomenon has major consequences for monitoring and forecasting. Field scouting methods and economic thresholds should be adjusted according to the season and the expected dominant lineage. Failure to account for this succession can lead to the mistiming of insecticides applications or ineffective protection against the lineage that poses the greatest threat at the time. These data highlight that population pressure is not static, but rather a shifting landscape resulting from the interactions of lineage-specific biology with seasonal environmental cues.

Spatial distribution and host-specific associations

Spatial distribution data provide strong evidence of host-specific associations. L1 exhibits a significantly higher mean density on onion, while L2 shows a clear preference for cabbage. This result confirms ecological specialization and niche partitioning at the crop level. It also aligns with the hypothesis of a cryptic species complex (Mound 2005), in which genetic differentiation is strengthened by adaptation to particular host plants. Population density varied significantly depending on the crop. The abundance of L1 on onion was more than six times greater than on cabbage. In comparison, the abundance of L2 on cabbage was more than three times greater than on onion. This suggests that these preferences are not merely slight inclinations, but rather fundamental host affiliations (Bleeker et al. 2009; Diaz-Montano et al. 2011). Spatial separation minimizes direct competition between the lineages, allowing each to occupy its own niche with little to no interaction. Consequently, three onion fields and one cabbage field require separate risk assessments, specifically regarding L1 and L2 pests. Host fidelity also facilitates crop rotation planning, as planting a nonhost crop disrupts a given lineage, thereby preventing the carryover of inoculum from one season to the next. These spatial data support the theory that crop management should account not only for the type of crop but also for the specific lineage to which the pests belong.

Competitive interactions and host-mediated fitness

Competitive interaction assays directly demonstrate host-mediated competitive exclusion, a key process influencing observed distributions in the field. When competition occurred on onion, the percentage of L1 increased remarkably over time while that of L2 decreased, the reverse was observed on cabbage. This indicates that the outcomes of competition are not neutral but are strongly determined by the host plant, with each lineage exhibiting higher intrinsic fitness on its adapted host (Farkas et al. 2020; Reitz et al. 2020). In this context, fitness includes components such as survival, feeding efficiency, growth rate, and reproductive output, all of which are maximized on the preferred host. The observed competitive displacement indicates that mixed infestation would gradually suppress the lineage less suited to the host plant, eventually resulting in a population composed exclusively of the specialized lineage. This has implications for understanding population purity in the field. It may explain why, even though both lineages are capable of coexisting, only one tends to dominate on individual plants or fields. These findings agree with Gause's competitive exclusion principle, which states that complete competitors cannot coexist indefinitely, and niche differentiation (in this instance, the host plant) enabling species survival at the habitat level. Moreover, the thelytokous reproduction of L2 (only female offspring) may provide these insects with a numerical advantage on suitable host areas and during population growth, potentially accelerating competitive displacement. These tests confirm that host preferences observed in choice tests translate directly into competitive superiority, linking behavior, physiology, and population dynamics.

Host preference behavior – choice assays and host preference index (HPI)

The choice feeding assays and the calculated HPI provide quantitative validation of the behavioral basis for the observed spatial distribution. The strong tendency of L1 to select onion (HPI = +0.72) while avoiding cabbage (HPI = −0.68), with L2 showing the opposite trend, suggests that host selection is an active, directed process rather than a passive one (Mound 2005; Reitz et al. 2020). The stability of these preferences over 48 hours indicates their persistence, likely supported by continuous olfactory and gustatory cues from the plants. High HPI values, approaching +1 or −1, indicate a strong preference, typical of specialized herbivores (Bleeker et al. 2009; Diaz-Montano et al. 2011). As a useful, standardized metric, the HPI allows assessing host-preference strength in various studies, as well as screening crop cultivars for natural resistance or lack of attractiveness to pests. The emergence of these behavioral drivers is crucial for the push-pull strategy (Mound 2005), in which a specific host can serve as a trap (pull), while the main crop can be protected by nonhosts or repellent intercrops (push).

Reproductive success and host-specific fecundity

The ecotype differentiation observed in the fecundity experiments showed a direct physiological link between host-plant adaptation and reproductive success. The observations that L1 laid nearly twice as many eggs on an onion host as on cabbage, while L2 showed a similar advantage by doubling on cabbage, point to a direct link between host preference and enhanced reproductive performance (Chaisuekul & Riley 2005; Farkas et al. 2020). Host-specific fecundity appears to be a key factor of ecological specialization, as preferred hosts with higher egg-laying rates attract faster population growth and increased migrations toward those specific crops. Differences in host-specific fecundity may arise from variations in nutritional quality, since certain plant tissues can provide optimal levels of nitrogen, sugars, and other nutrients required for egg production. Furthermore, a genetically favored line may use less energy on detoxifying plant defense or may be more efficient at converting plant biomass into eggs (Awmack & Leather 2002; Bridges et al. 2002). This finding provides strong evidence for the resource availability hypothesis, which states that the population growth of herbivores depends directly on the quality of resources provided by host plants (Price 1991). The large disparity in egg-laying rates between these two types of plants strongly supports and helps ensure host fidelity across generations. From the perspective of pest management, this suggests that the lineage causing the most crop damage also possesses the greatest potential for a sudden population increase on that crop, creating a feedback loop of pest pressure and ever-increasing damage.

Interventions that subtly reduce the quality of host plants for a target lineage, whether through plant breeding or nutrient management, can affect population growth disproportionately to the reduction in fecundity per female.

Feeding damage and crop-specific injury patterns

Evaluating host plant damage directly links lineage biology to economic losses, expressed in financial terms. It demonstrates that each lineage inflicts considerably more damage on its preferred plant. In onion, the mean damage score for L1 was 17.5, while for L2 it was only 10.0. In cabbage, L2 reached a score of 15.0, while L1 reached only 9.0. This pattern suggests that the extent of damage does not depend solely on the presence of thrips, but is further enhanced by a specific relationship between the lineage and its host plant (Lewis 1973). Greater damage likely stems from a mix of factors: more rapid feeding (driven by preference and efficiency), longer feeding period, and perhaps a more destructive way of taking food from the soft tissues of the plant. Adaptation may even prevent the plant from triggering its defense mechanisms, while in the case of a non-adapted lineage, the plant may suffer more prolonged and severe damage (Mound 2005). The observable symptoms – silvering, stippling, curling, and ultimately necrosis, are the result of countless individual feeding events, each eliminating a group of epidermal or mesophyll cells. These damage scores illustrate the effects of such excessive feeding, which reduces photosynthesis, lowers plant health, and forces it to reallocate resources from growth processes toward repair mechanisms. In the end, a specialized lineage not only feeds on its host, but does so much more fiercely and destructively. The economic impact of *T. tabaci* therefore depends on the specific lineage and the crop, so damage prediction models must account for the lineage presence in order to accurately assess risk and determine appropriate control actions.

Impact on crop health and economic consequences

The quantified effects on crop health, a 30% reduction in onion bulb weight by the L1 and a 35% decrease in cabbage leaf quality by the L2, represent the economic value of these biological interactions and thus the actual impact of pest feeding, specific to each line. In particular, reduced bulb weight means a lower marketable yield, resulting in lower income for farmers, as onions are sold by weight. The degradation of cabbage leaf quality, manifesting as wilting, discoloration, and smaller size, negatively affects both total production volume and marketability. Consumers and retailers also incur losses, as produce that fails to meet high quality standards becomes unmarketable (Lewis 1973; Mound 2005). The strong relationship between thrips abundance and the extent of damage confirms that that the severity of the harm is directly proportional to the intensity of the infestation. Yield losses are therefore inversely proportional to the effectiveness of pest control and maintaining the population below the economic damage threshold. The investigation supports reports from growers regarding considerable losses and provides quantitative data illustrating the problem size in the Shewarobit region. he negative consequences extend beyond direct yield loss, as plants weakened by pests become more susceptible to diseases, and the tissue damage caused by feeding can serve as an entry point for bacterial or fungal pathogens. The financial information presented provides a compelling argument for implementing targeted, lineage-informed integrated pest management (IPM) methods as investments to protect the economic viability and ecological sustainability of onion and cabbage production in Ethiopia.

CONCLUSIONS

This detailed investigation revealed that *T. tabaci* in Shewarobit (Ethiopia) is not a single species, but rather a cryptic species complex. It comprises two lineages, each specialized for a specific host: L1 for onion and L2 for cabbage. These two genetic lines exhibit distinct seasonal patterns and strong attachment to their host plants, which allows them to limit mutual competition. Each lineage demonstrates a competitive advantage and higher reproductive success on its preferred host, resulting in considerable damage to the specific crops. Lineage L1 reduces onion bulb weight by 30%, while L2 diminishes the quality of cabbage leaves by 35%. Therefore, pest control measures should evolve from a broad approach toward integrated measures that account for the specific characteristics of each lineage.

This necessitates precise diagnostics to determine the prevailing lineage, followed by the implementation of proactive measures. Future work should focus on breeding resistant crop cultivars, improving lineage-specific biological control methods, and developing farming practices that eliminate the life cycle of each lineage. Ultimately, the effective and sustainable protection of these vital crops rests on understanding and managing the complex biology of this pest mix.

Author contribution statement

WA – A – Research concept and design, B – Collection and/or assembly of data, C – Data analysis and interpretation, D – Writing the article, E – Critical revision of the article, F – Final approval of the article

YT – D – Writing the article, F – Final approval of the article

AK – A – Research concept and design, B – Collection and/or assembly of data, C – Data analysis and interpretation, F – Final approval of the article

SG – A – Research concept and design, C – Data analysis and interpretation, D – Writing the article, F – Final approval of the article

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