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**Sampling, Distribution, Dispersal**



Sampling, Distribution, Dispersal

# First occurrence records and molecular identification of *Sergentomyia* spp. (Diptera: Psychodidae) sand flies in Praia, Santiago Island, Cabo Verde (2024)

**Hélida Pires[†,1], Fátima Amaro[†,*,2,3], Celivianne Sousa[1], Rita de Sousa[2], and Silvânia da Veiga Leal[1,4]**

[1]Largo do Desastre da Assistência, Instituto Nacional de Saúde Pública de Cabo Verde, Chã de Areia, Praia, Cabo Verde
[2]Centre for Vectors and Infectious Diseases Research, National Institute of Health Doutor Ricardo Jorge, Águas de Moura, Portugal
[3]Environmental Health Institute, Environment and Infectious Diseases Research Group (ISAMB), Lisbon, Portugal
[4]Global Health and Tropical Medicine (GHTM), Associate Laboratory in Translation and Innovation Towards Global Health, LA-REAL, Instituto de Higiene e Medicina Tropical, IHMT, Universidade NOVA de Lisboa, Lisbon, Portugal

*Corresponding author. Fátima Amaro. Centre for Vectors and Infectious Diseases Research, National Institute of Health Doutor Ricardo Jorge, Avenida da Liberdade n.°5, 2965-575 Águas de Moura, Portugal (Email: fatima.amaro@insa.min-saude.pt).

†These authors contributed equally to this work.

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Phlebotomine sand flies are important vectors of pathogens affecting both humans and animals and are widely distributed geographically. In Cabo Verde, research on vector-borne diseases has focused primarily on mosquitoes, leaving other potential vectors understudied. As part of the ONESVEC surveillance project, we conducted a preliminary assessment to determine the presence of sand flies in Cabo Verde. From February to December 2024, entomological surveys using BioGents-Sentinel traps were carried out in five neighborhoods of Praia, Santiago Island: Achada Eugénio de Lima, Ponta de Água, Taiti, Vale do Palmarejo, and Vila Nova. Male specimens were slide-mounted for morphological identification, and randomly selected individuals underwent mitochondrial cytochrome c oxidase subunit I (COI) gene sequencing. Haplotype diversity and species delimitation (*DnaSP*, ASAP) were also assessed. A total of 367 sand flies (184 males, 173 females) were collected, of which 168 males were successfully identified. Most specimens were *Sergentomyia fallax*, found in all neighborhoods, while *S. squamipleuris* was identified in Taiti and Vale do Palmarejo. Phylogenetic analysis showed Cabo Verde *S. fallax* forming a well-supported monophyletic group, distinct from North African and Cyprus–Saudi Arabian lineages. Haplotype analysis revealed high haplotype but low nucleotide diversity, suggesting a genetically diverse yet stable or expanding population. In contrast, *S. squamipleuris* sequences clustered with Kenyan isolates in separate subclades, consistent with higher nucleotide diversity. ASAP species delimitation supported the phylogenetic analysis. This study provides the first confirmed record of phlebotomine sand flies in Cabo Verde and highlights the need for expanded surveillance and pathogen screening across the archipelago.

*Keywords:* phlebotomine sand flies, Cabo Verde, vector surveillance

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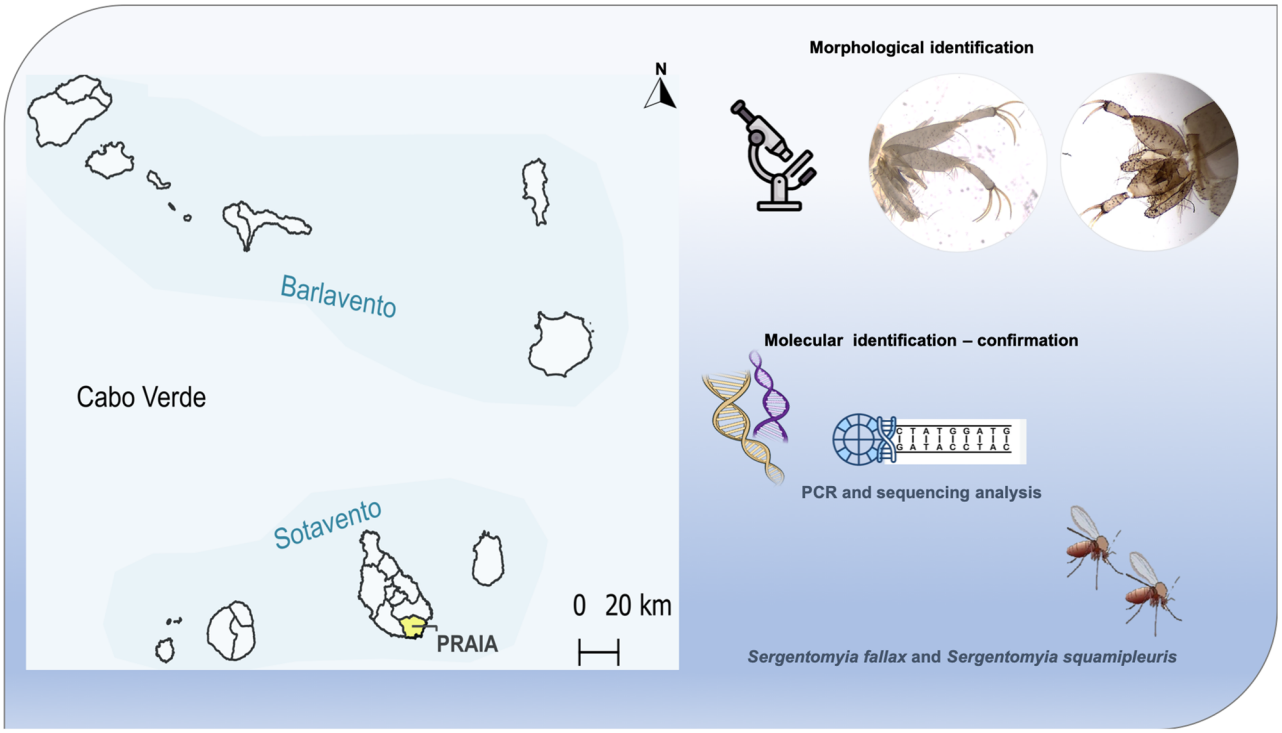
## Graphical abstract




## Introduction

Phlebotomine sand flies are small dipteran insects classified within the subfamily Phlebotominae of the family Psychodidae. They demonstrate extensive ecological adaptability, occupying tropical, subtropical, and temperate habitats across continents such as the Americas, Europe, Africa, and Asia. Globally, over 1,060 species and subspecies of Phlebotominae have been described (Killick-Kendrick 1990, Galati and Rodrigues 2023).

In the Old World, the genera *Phlebotomus* Loew, 1845 and *Sergentomyia* França & Parrot, 1920 are particularly significant as both exhibit hematophagous behavior, feeding on the blood of vertebrates (Service 2014). The genus *Phlebotomus* has a distribution extending across southern Europe, North Africa, the Middle East, and parts of Central and South Asia. Although some members inhabit tropical areas, most species are adapted to arid and semi-arid environments, favoring ecosystems such as savannas and dry plains. Their presence is limited or absent in sub-Saharan Africa, Southeast Asia, and the Pacific Islands (Killick-Kendrick 1999, Service 2012).

From a medical standpoint, *Phlebotomus* species are the primary biological vectors of protozoan parasites from the genus *Leishmania*, which cause leishmaniasis in humans and other vertebrates. In addition, they serve as vectors of several arthropod-borne viruses within the genus *Phlebovirus* (family Phenuiviridae), notably Toscana virus, which has been associated with neuroinvasive manifestations, and sand fly fever viruses, which are implicated in acute febrile syndromes (Charrel et al. 2005, Alkan et al. 2013, European Centre for Disease Prevention and Control 2020).

In Africa, key vector species within *Phlebotomus* genus include *P. ariasi*, *P. duboscqi*, *P. longicuspis*, *P. longipes*, *P. pedifer*, *P. papatasi*, *P. perfiliewi*, *P. perniciosus*, *P. saevus*, and *P. sergenti*. These species have been implicated in the transmission of various *Leishmania* species (e.g., *L. major*, *L. infantum*, *L. tropica*) and phleboviruses of public health importance in that continent (Alkan et al. 2013, Messaoudene et al. 2023, Blaizot et al. 2024).

The genus *Sergentomyia* is distributed widely throughout the Eastern Hemisphere, particularly in the Indian subcontinent, sub-Saharan Africa, and Southeast Asia. Historically, these sand flies have been considered reptile feeders, mainly associated with the transmission of *Leishmania* species in the subgenus *Sauroleishmania* (Remadi et al. 2023). However, recent molecular analysis has detected mammalian host DNA in *Sergentomyia* specimens, suggesting potential interactions with warm-blooded hosts and challenging long-standing assumptions about their host specificity and possible role in disease transmission (Özbel et al. 2016, Abbate et al. 2020, González et al. 2020).

Despite their recognized impact on public health, the geographical distribution, species diversity, and vectorial competence of phlebotomine sand flies remain insufficiently documented in some world regions. Cabo Verde, an African archipelago within the Macaronesian ecoregion, has historically focused entomological surveillance exclusively on mosquitoes (Campos et al. 2020, Da Veiga Leal et al. 2024). In contrast, no comprehensive studies have been conducted to assess the presence of sand flies, their distribution, or potential involvement in pathogen transmission within the archipelago. This lack of data presents a critical gap in vector surveillance, underscoring the need for investigation into sand fly ecology in Cabo Verde. Identifying and understanding the geographic distribution of vectors and their potential association with pathogen transmission are essential for the effective management of vector-borne diseases.

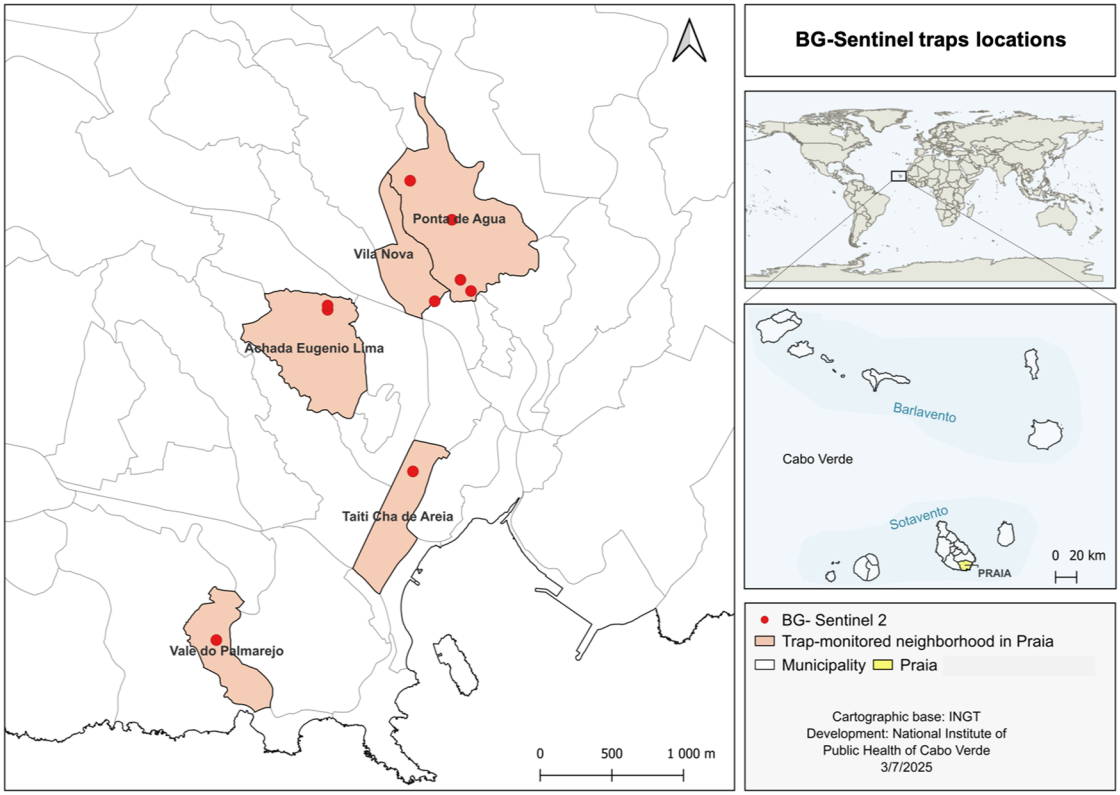



**Fig. 1.** Location of the five neighborhoods where the entomological surveys were conducted in Praia, Santiago, Cabo Verde.

As a part of the ONESVEC project, a One Health project initiative on surveillance of vector-borne diseases in Cabo Verde, entomological surveys were conducted to make a preliminary assessment of the presence of sand fly species. The objective of the present work is to document the occurrence of *Sergentomyia* spp. sand flies in the island of Santiago, in Cabo Verde.

## Materials and Methods

### Study Area and Sand Fly Collections

Located 455 km off the coast of West Africa, Cabo Verde consists of 10 volcanic islands and five islets, which are categorized into two groups—Barlavento and Sotavento—based on their orientation to the prevailing northeastern winds. Cabo Verde's proximity to the Sahel Belt influences its predominantly arid and semi-arid climate, characterized by limited Ocean rainfall and an average annual temperature of around 25°C. The rainy season typically occurs from July to October, featuring brief but intense downpours (Fernández-Alvarez et al. 2022). The capital city of the archipelago, Praia, is located on the largest island, Santiago, included in the Sotavento islands.

Entomological surveys targeting sand flies were conducted in 2024 across five distinct neighborhoods of Praia, Santiago Island, Cabo Verde. The sampling period extended from February to December; however, not all sites were sampled monthly. Site selection was guided by the ecological requirements of sand flies, with preference given to areas characterized by the presence of domestic animals—such as cattle, poultry (chickens and ducks), rabbits, pigeons, dogs, and pigs—which contribute to the accumulation of organic matter and provide potential blood meal sources. A total of nine BioGents-Sentinel (BGS) traps (BioGents AG, Regensburg, Germany) were used to collect specimens at ground level near or in animal shelters. Although Centers for Disease Control and Prevention battery-powered light traps are among the most commonly used tools for sand fly collection in surveillance studies, BGS mosquito traps baited with BG-Lure that operate using mains electricity were selected as an initial approach due to their practical suitability under our field conditions and their demonstrated efficacy in previous research (Hoel et al. 2010). The traps remained in continuous operation throughout the sampling period for each site, and the collection bags from each trap were retrieved every morning and replaced with empty ones. Specimens were transported to the Medical Entomology Laboratory at the National Institute of Public Health for identification and analysis. All trap locations share comparable climatic conditions, with average temperatures ranging from 23 °C to 25 °C. The trap distribution was as follows: two in Achada Eugénio de Lima (14°55′50.00″N 23°30′57.00″W; 14°55′51.00″N 23°30′57.00″W), four in Ponta de Água (14°55′57.00″N 23°30′26.00″W; 14°56′11.00″N 23°30′28.00″W; 14°56′20.10″N 23°30′37.74″W; 14°55′54.38″N 23°30′23.53″W), and one each in Taiti (14°55′12.32″N 23°30′37.09″W), Vale do Palmarejo (14°54′33.00″N 23°31′23.00″W), and Vila Nova (14°55′52.00″N 23°30′32.00″W) (Fig. 1).

### Morphological Identification of Sand Flies

The terminal segments of the male sand fly specimens, including the genitalia, were cleared using Marc André's solution, mounted on spot slides, and examined under a stereomicroscope for species identification based on established genital morphological characteristics (Lane 1986, Benallal et al. 2022).

### DNA Extraction, PCR Amplification, and Sequencing for Molecular Identification

Reliance on morphological traits alone can be inconclusive, particularly when cryptic species or intraspecific morphological variability are involved and/or potential artifacts may be introduced by specimen degradation during collection or handling (Erisoz Kasap et al. 2019, Posada-López et al. 2023). Therefore, to complement the morphological data, molecular characterization was conducted using the cytochrome c oxidase subunit I (COI) gene. This DNA barcoding marker is widely recognized for improving species delimitation and clarifying phylogenetic relationships (Depaquit 2014, Erisoz Kasap et al. 2019). In this way, the remainder of a randomly selected subset of the male sand flies representing each site was used for molecular species identification. Given the greater morphological complexity and potential for misidentification of female specimens, females were not slide-mounted, and a small selection of specimens was also processed for molecular identification. The head, thorax and the first abdominal segments of each male (or the entire female), was homogenized in liquid nitrogen using a mortar and pestle, followed by the addition of 1.5 µl of minimal essential medium supplemented with fetal bovine serum, streptomycin, and amphotericin B. Nucleic acid extraction was carried out from 400 µl aliquots of each sample supernatant as previously described (Amaro et al. 2024). Molecular characterization was performed by PCR targeting a ~650 bp fragment of the COI gene according to Folmer and colleagues (1994). Sequences exhibiting poor quality and/or ambiguous chromatograms were excluded from the study. The nucleotide sequences were edited and aligned using BioEdit version 7.2.5 (Hall 1999) to generate consensus sequences for each sample, with primer regions excluded from the final alignments. The resulting sequences were submitted to GenBank (National Center for Biotechnology Information [NCBI]).

### Phylogenetic and Molecular Analysis

Sequence homology searches were performed using the BLASTN algorithm (Basic Local Alignment Search Tool; NCBI). Reference sequences retrieved from GenBank (NCBI) were aligned with sequences generated in the present study, and a maximum likelihood (ML) phylogenetic tree was constructed using MEGA11 (Tamura et al. 2021). Phylogenetic inference was performed with the ML method under the Tamura model of nucleotide substitution. Evolutionary rate variation among sites was modeled using a discrete Gamma distribution, according to the best-fit model identified by MEGA11 (Tamura et al. 2021). The tree was rooted using *Psychoda alternata* (PP815795) from Mexico to provide clear phylogenetic resolution among the *Sergentomyia* taxa analyzed. The resulting tree file was visualized and edited using the Interactive Tree Of Life (iTOL) platform (https://itol.embl.de) (Letunic and Bork 2023).

### Haplotype Diversity and Species Delimitation

Haplotype diversity of the COI sequences from *S. fallax* specimens collected in Cabo Verde was calculated using *DnaSP* version 6.10.01 with default settings (Rozas et al. 2017). In addition, the *Assemble Species by Automatic Partitioning* (ASAP) method (Puillandre et al. 2021, available at https://itaxotools.org/download.html#hyperlinkDelimit) was also applied to the *S. fallax* sequences to delimit species boundaries within the same sequence dataset as that used for the phylogenetic tree, including specimens from Tunisia, Algeria, Morocco, Cabo Verde, Cyprus, and Saudi Arabia. ASAP partitions were ranked by their ASAP scores, with results reviewed in tabular format, graphical summaries, and the standardized SPART format.

## Results

### Sand Fly Collection and Morphological Identification

From February to December 2024, a total of 367 phlebotomine sand flies (184 males and 173 females) were collected across the five neighborhoods of Praia city, Santiago Island. An overview of the specimen's data, including the number of specimens collected by location, month, sex, number of slide-mounted males, and number of COI sequences retrieved per site, is provided in Table 1.

The slide-mounted males successfully identified were all members of the genus *Sergentomyia*, based on the terminal position of the four spines on the style of their terminalia (Benallal et al. 2022). Following morphological identification, a total of 164 males collected in AEL, PDA, VP, VN, and Taiti presented slender coxites and narrow styles bearing four terminal spines and a short, non-deciduous accessory seta. Additionally, the style was approximately four times longer than wide, and the aedeagus showed a finger-like shape and a round tip, consistent with the morphological traits of *S. fallax* Parrot, 1921 (Fig. 2a–c) (Depaquit et al. 2001). In addition, one male

**Table 1.** Sand flies collected in Praia city in 2024, categorized by neighborhood, collection date, and sex, with counts of slide-mounted and successfully sequenced individuals.

| Collection site | Collection date | Total number of collected sand flies (*n*) (male/female) | Number of slide-mounted males with successful morphological identification (*n*) | Sequences retrieved (*n*) |
|---|---|---|---|---|
| Achada Eugénio de Lima | April–December | 107 (63/44) | 59 *S. fallax* | 2 *S. fallax* (m) |
| Ponta de Água | April–December | 87 (37/50) | 35 *S. fallax* | 6 *S. fallax* (m) |
| Taiti | November–December | 11 (4/7) | 1 *S. fallax*, 3 *S. squamipleuris* | 2 *S. squamipleuris* (m) |
| Vila Nova | December | 5 (3/2) | 3 *S. fallax* | 1 *S. fallax* (m) |
| Vale do Palmarejo | February–November | 157 (77/70) | 66 *S. fallax*, 1 *S. squamipleuris* | 18 *S. fallax* (12 m, 6f) |
| Total | | 367 (184/173) | 164 *S. fallax*, 4 *S. squamipleuris* | 27 *S. fallax* (21 m, 6f), 2 *S. squamipleuris* (m) |

f, female; m, male.


**Fig. 2.** *Sergentomyia fallax* collected in the Vale do Palmarejo neighborhood: (a) genitalia; (b) detail of the terminal part of the coxite, spines, and seta; (c) detail of the aedeagi.

collected in Vale do Palmarejo and three males in Taiti also exhibited four spines (two terminal and two subterminal), but presented broad coxites and short styles—morphological traits consistent with *S. squamipleuris* Newstead, 1912 (Lane 1986; Fig. 3a and b).

## Molecular Identification and Phylogenetic Analysis

A total of 29 COI sequences, ranging from 578 to 659 bp in length, were successfully amplified (GenBank accession numbers PV461191–PV461219). BLASTN analysis of 27 sequences from AEL, PDA, VP, and VN revealed sequence identities ranging from 94.0% to 94.4% with *S. fallax* reference sequences, while one isolate from the Taiti neighborhood (PV461216) showed 100% sequence identity with an unclassified *Sergentomyia* isolate (SP288-KE-2016_C07; accession number: MT644229), and the other isolate (PV461217) exhibited 99.46% identity to *S. squamipleuris* isolate (accession number: OR671499).

Phylogenetic analysis of the 29 *Sergentomyia* COI sequences from Cabo Verde resolved two clades (Fig. 4), consistent with the morphological identification of the specimens as distinct species. A total of 27 sequences clustered into a strongly supported clade corresponding to *S. fallax* (bootstrap = 99). The *S. fallax* sequences from Cabo Verde form a well-supported monophyletic clade, divergent from two other *S. fallax* lineages. One of these comprises sequences from Algeria, Morocco, and Tunisia (bootstrap = 99), while the other includes sequences from Cyprus and Saudi Arabia (bootstrap = 91). The

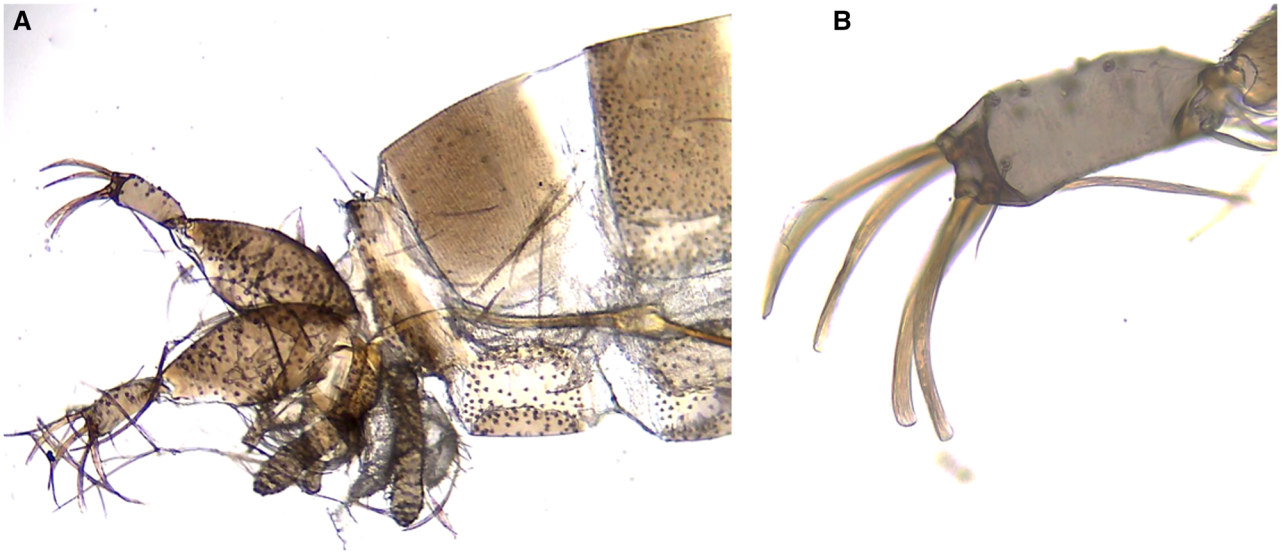



**Fig. 3.** *Sergentomyia squamipleuris* collected in the Taiti neighborhood: (a) genitalia; (b) detail of the terminal part of the coxite, spines, and seta.

major node uniting the Cabo Verdean *S. fallax* clade is supported by a high bootstrap value (=96), indicating strong phylogenetic distinction. Within this clade, several subclades are resolved with varying levels of bootstrap support, suggesting some degree of intraspecific genetic structuring among the Cabo Verdean populations. The two sequences obtained from the Taiti neighborhood were grouped within the *S. squamipleuris* clade, forming a well-supported subclade with sequences from Kenya (bootstrap = 93). The broader *S. squamipleuris* clade, including sequences from Kenya, Cabo Verde, and China, also exhibited strong support for the main grouping (bootstrap = 93).

### Haplotype Diversity and Species Delimitation

Haplotype analysis of the 27 *S. fallax*-like sequences from Santiago Island revealed 11 distinct haplotypes across the 659 bp COI fragment, with 10 polymorphic sites. The haplotype diversity was high (Hd = 0.903 ± 0.028), while nucleotide diversity remained low ($\pi = 0.00396$). Fu and Li's D* (0.88451) and F* (0.67006) tests were not significant ($P > 0.10$). Among the two sequences attributed to the *S. squamipleuris* group, two unique haplotypes were identified, with 4 polymorphic sites, resulting in a high haplotype diversity (Hd = 1.000 ± 0.500) despite the small sample size. The nucleotide diversity ($\pi = 0.00692 \pm 0.00346$) was higher than that observed in *S. fallax* specimens, suggesting relatively greater genetic divergence between the two individuals. ASAP performed on *S. fallax* sequences recovered several alternative species partitions with scores ranging from 1.5 to 5.5. The best-supported partition (ASAP score = 1.5, rank 1) divided the dataset into three distinct groups: (1) Tunisia-Algeria, Morocco, (2) Cabo Verde haplotypes (1–11), and (3) Cyprus + Saudi Arabia. The same 3-group structure was also retrieved in the second-best partition (score = 3.0). Higher-rank solutions produced more fragmented clusters, but the North African samples always clustered together, and the Cabo Verde haplotypes consistently formed a single broader lineage. In contrast, the samples from Cyprus and Saudi Arabia showed lower stability, sometimes splitting or merging with other lineages in alternative partitions (Fig. 5).

## Discussion

This study provides the first evidence of phlebotomine sand flies in the Cabo Verde archipelago, expanding the known geographic distribution of the group and establishing a preliminary entomological baseline for the region. Through morphological identification and molecular analysis, we documented the presence of two *Sergentomyia* species in five neighborhoods of Praia, Santiago Island.

Phylogenetic analysis of the partial COI gene sequences from 27 specimens collected in AEL, PDA, VP, and VN revealed a well-supported clade closely related to *S. fallax* reference sequences. Haplotype diversity analysis indicated high haplotype diversity, reflecting a genetically diverse local population, while low nucleotide diversity suggested limited sequence divergence between haplotypes. This pattern, often observed in demographically stable or expanding populations, aligns with neutral evolution models as supported by non-significant Fu and Li's D* and F* values (Nguyen et al. 2024). According to Grant and Bowen (1998), such results may also be indicative of population growth following a bottleneck.

Interestingly, the genetic identity (~94%) between our sequences and the closest GenBank reference for *S. fallax* exceeded the typical 2% to 3% interspecific divergence threshold in insect barcoding (Cheng et al. 2023), potentially pointing to a divergent lineage or a geographically isolated population. ASAP species delimitation further supported this interpretation, identifying at least three well-supported genetic lineages within *S. fallax*: North Africa, Cabo Verde, and Cyprus, plus Saudi Arabia. The North African and Cabo Verde groups were highly stable across alternative partitions, whereas the Cyprus–Saudi Arabia group was less consistent. Importantly, the Cabo Verde populations of *S. fallax* do not cluster with continental North African populations, instead forming a separate lineage. These findings therefore point to genetic differentiation between the Cabo Verde and continental *S. fallax* populations, which could suggest the presence of a distinct lineage, though further evidence is needed to confirm species-level status. These results are in agreement with the phylogenetic analysis, where *S. fallax* sequences from Cabo Verde form a strongly supported

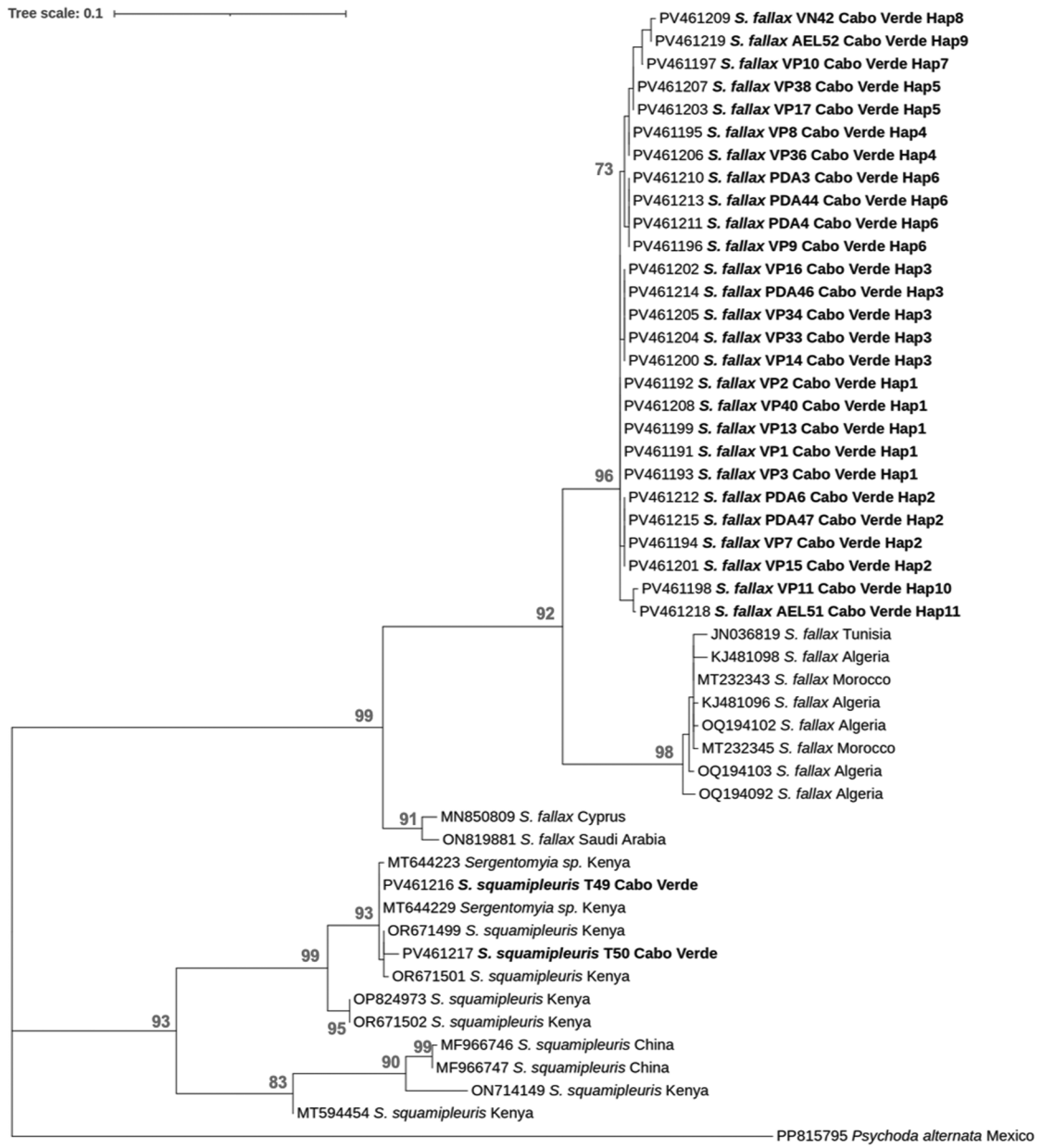



**Fig. 4.** Maximum likelihood phylogenetic tree based on mitochondrial cytochrome c oxidase subunit I (COI) gene sequences. The analysis included 50 *Sergentomyia* (*S.*) specimens, with 549 nucleotide positions in the final dataset. GenBank accession numbers are provided for all sequences; those generated in this study are shown in bold. For *S. fallax* sequences, corresponding haplotypes (Hap 1–11) are indicated. Bootstrap values >70% (based on 1,000 replicates) are shown at the nodes. Phylogenetic reconstruction was performed using MEGA11. *Psychoda alternata* (Diptera: Psychodidae) from Mexico was used as the outgroup. Neighborhood abbreviations: AEL, Achada Eugénio de Lima; PDA, Ponta de Água; T, Taiti; VP, Vale do Palmarejo; VN, Vila Nova.

monophyletic clade distinct from both North African and Cyprus–Saudi Arabian lineages. Minor subdivisions recovered by ASAP within the Cabo Verdean and Algerian samples correspond to shallow clades in the tree and are not strongly supported, illustrating the complementarity of haplotype- and species-level analyses. Similar congruence between ASAP and phylogeny has been observed in other phlebotomine sand fly studies (Soomro et al. 2025). The widespread distribution of *S. fallax* across North Africa, the Middle East, and parts of Asia (Galati et al. 2025) and the limited COI sequence data available in GenBank (only 23 entries from five countries) underscore the need for further molecular characterization to confirm possible subspecific and/or specific distinctions. Lane (1986), for example, has referred to three subspecies—*S. fallax cypriotica* Theodor, 1938; *S. fallax afghanica* Artemiev, 1978, and *S. fallax fallax* Parrot, 1934—but emphasized the uncertainty of their validity due to insufficient taxonomic coverage.

The absence of geographic structuring among the Cape Verdean *S. fallax* sequences may suggest either high dispersal ability or historical connectivity between sampled neighborhoods, possibly facilitated by shared environmental conditions or human-mediated movement. These findings are consistent with Lee and Mitchell-Olds (2011), who proposed that genetic differentiation may be driven more by environmental heterogeneity and spatial isolation than by geographic distance alone. Nonetheless, all these assumptions should be

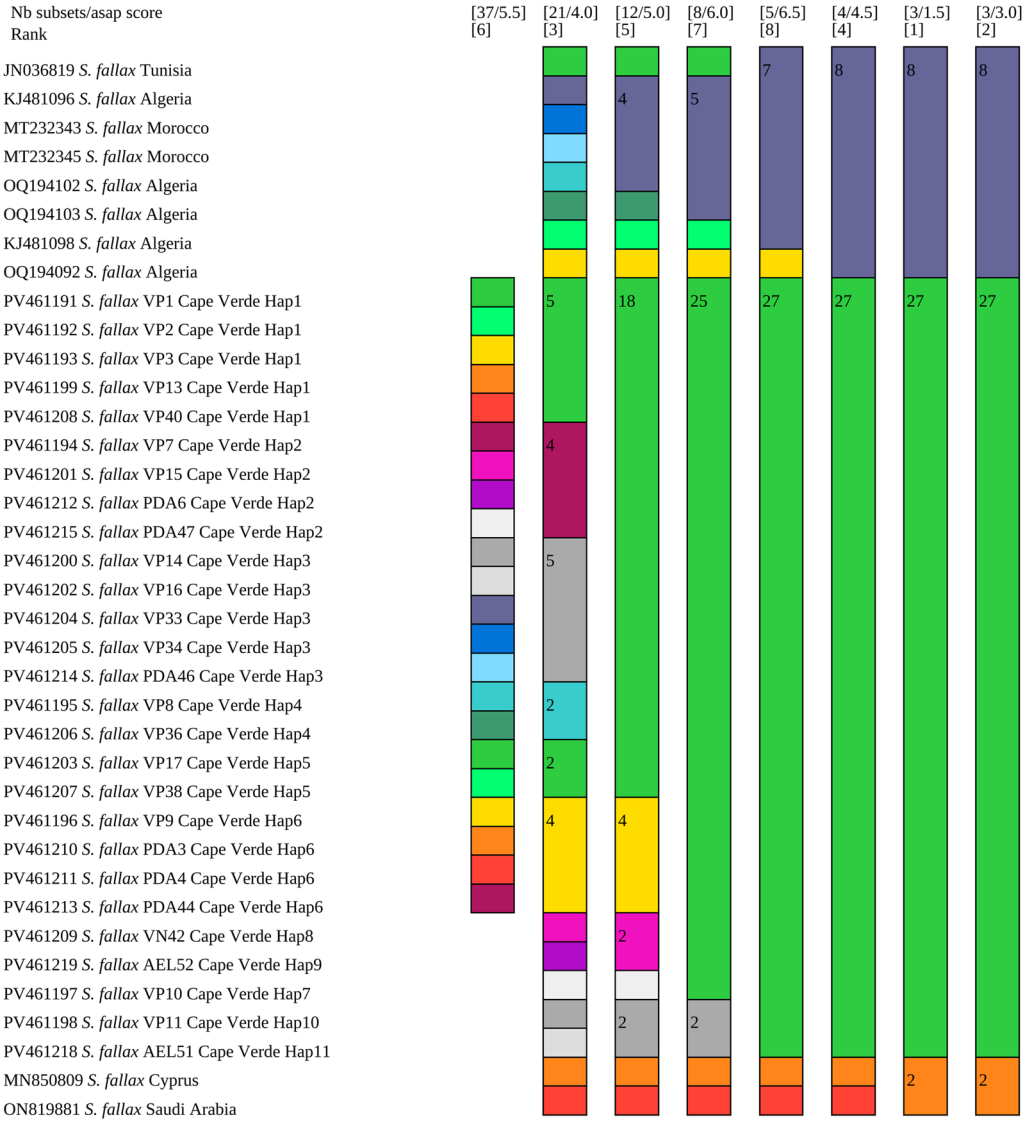



**Fig. 5.** ASAP species delimitation of *Sergentomyia fallax* based on a 549 bp COI fragment. The analysis produced eight candidate partitions. The best-supported solution identified three species-level groups: (1) North Africa (Tunisia, Algeria, Morocco), (2) Cabo Verde haplotypes (1–11), and (3) Cyprus + Saudi Arabia.

interpreted with caution, given the relatively small sample size analyzed.

The two obtained *S. squamipleuris* sequences clustered with Kenyan sequences but were placed in separate subclades, suggesting some level of genetic differentiation. Their comparatively higher nucleotide diversity relative to *S. fallax* may indicate greater intraspecific variation or reflect distinct introduction events. However, and again, due to the limited sample size and geographic representation, these hypotheses remain speculative. The limited number of *S. squamipleuris* COI sequences in GenBank (15 in total, mostly from Kenya) and the known but genetically uncharacterized occurrences of this species across Africa and the Middle East, including countries such as Senegal, Liberia, Sudan, the Democratic Republic of Congo, Saudi Arabia, and Jordan (Morsy and Shoura 1976, Trouillet and Vattier-Bernard 1977, Janini et al. 1995, Ba et al. 1999, Elnaiem et al. 1999, Obenauer et al. 2016) highlight the need for further research into the species' phylogeography.

Traditionally considered non-vectors of human leishmaniasis, *Sergentomyia* species are now receiving increasing attention due to the detection of *Leishmania* spp. DNA in several species, including *S. fallax* and *S. squamipleuris* (Owino et al. 2021, Remadi et al. 2023), as well as the already mentioned evidence of blood meals from warm-blooded hosts. The detection of these two species of phlebotomine sand flies in Cabo Verde provides an important new data point and a basis for future investigations into their potential vector roles.

While our findings are significant, it is important to consider certain limitations. This exploratory study was conducted within a restricted sampling window, covered a limited geographic area, and analyzed a relatively small number of specimens. These constraints may have influenced species detection and limited the ability to draw broader conclusions about sand fly diversity in the region. The scarcity of reference sequences in public databases may have further limited taxonomic resolution.

Future research should involve coordinated, temporally standardized sampling across additional regions of Cabo Verde and

incorporate both molecular and ecological approaches to characterize species distribution, habitat preferences, sand fly density, and seasonal variations. Screening for *Leishmania* spp. and other sand fly-borne pathogens—in both the sand fly populations and through serological surveys in humans and animals—will be critical for assessing the vectorial capacity of local sand flies and their potential role in zoonotic transmission cycles. These studies will be essential to determine the epidemiological significance of sand flies in the region and to inform targeted public health interventions.

## Conclusions

This study presents the first documented occurrence of phlebotomine sand flies in Cabo Verde, marking an important advancement in the entomological mapping of the archipelago. The identification of two species on Santiago Island confirms the establishment of sand fly populations in the region and lays the groundwork for future vector-related research. These findings underscore the urgency of expanding entomological surveillance across Cabo Verde and integrating molecular approaches to clarify species diversity, population structure, and evolutionary patterns.

In light of growing evidence on the potential vectorial capacity of certain *Sergentomyia* species, the presence of these sand flies raises new epidemiological questions that merit further investigation. As such, this work offers a preliminary foundation for further studies on the ecology and potential public health relevance of phlebotomine sand flies in this West African archipelago.

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## Author Contributions

Hélida Pires (Investigation [lead], Methodology [supporting], Writing—review & editing [equal]), Fátima Amaro (Conceptualization [equal], Formal analysis [lead], Methodology [lead], Writing—original draft [lead], Writing—review & editing [lead]), Celivianne Marisia Ramos de Sousa (Investigation [supporting], Methodology [equal], Writing—review & editing [equal]), Rita de Sousa (Conceptualization [equal], Formal analysis [supporting], Funding acquisition [lead], Methodology [supporting], Project administration [lead], Writing—original draft [supporting], Writing—review & editing [equal]), and Silvânia da Veiga Leal (Conceptualization [equal], Funding acquisition [lead], Project administration [lead], Writing—review & editing [equal])

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## Conflicts of Interest

None declared.

## Data Availability

All data supporting the findings of this study are available within the paper. In addition, the partial nucleotide sequences of the sand flies were deposited in the GenBank at the National Center BI with the accession numbers PV461191 to PV461219.

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