

# The 2nd International Electronic Conference on Entomology



19-21 May 2025 | Online

# Preliminary genetic characterization of Spodoptera frugiperda from maize fields in Cabo Verde

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# **INTRODUCTION & AIM**



Accurate pest identification are crucial for developing effective management strategies. This study aims to:

## Species identification

All analyzed samples were confirmed as S. frugiperda

**RESULTS & DISCUSSION** 



Spodopterafrugiperda(Lepidoptera:Noctuidae), aninvasivepestin WestAfricathreating agricultural production

 Characterize S. frugiperda population, identifying it's strains diversity in maize fields across Cabo Verde

 Study potential migration routes within the archipelago



**Figure 1.** Sampled *S. frugiperda* in West Africa countries: Cabo Verde islands (39), Burkina Faso (2), Ghana (2), Gambia (2), Guinea (2), Guinea Bissau (2), Mauritania (2), Senegal (2) and São Tomé & Principe (3).

Genomic DNA extraction

### □ Sequence and phylogeny analysis

Three distinct groups identified (Fig. 2):



**Figure 2**. Phylogenetic tree of 74 S. *frugiperda sequences* by ML (100 bootstraps). Bootstrap values  $\geq$ 50 are indicated.

## Distinct *S. frugiperda* haplotypes detected in Cabo Verde within islands and agroecological zones

- Genetic/strain variability in S. frugiperda populations across Cabo Verde islands and within agro-ecological zones -Arid/semiarid (A) & Humid/subhumid (H) in Santiago island
- Evidence of strain overlap in maize: presence of Corn-strain dominant, but Rice-strain detected in Santiago (ST03) and São Vicente (SV02)
- Distinct group was detected, its should be the hybrids or third lineage, samples from Santiago (CV ST16 & CV ST23) similar to São Tomé (STP01, STP02 & STP 03)

# Evidence of multiple migration events within the arquipelago

Evidence of early migration in Cabo Verde from São Tomé and Príncipe (1st African record of *S. frugiperda* in 2016), and followed with regional diversity and

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Ciência LP



DNA Barcoding



PCR amplification with universal primers targeted to *COI* gene

Sanger sequencing, sequence editing by BioEdit and alignment with reference data from NCBI and BOLD System databases

### □ Sequence & Phylogenetic Analysis

From the total 86 sequences (including 3 *Spodoptera exigua* outgroups and 27 *S. frugiperda* from nucleotide databases), about 74 were analyzed by Maximum Likelihood (*ML*) in MEGA software with 100 bootstrap replicates to determine evolutionary relationships and strain identification.

#### expansion

## **CONCLUSION / FUTURE WORK**

- ✓ Genetic data indicate multiple migrations, strain coexistence, and regional dispersal of S. frugiperda in Cabo Verde, highlighting the need for genetic monitoring in pest management
- ✓ Future work will use genome-wide markers to refine strain identification and analyze hybridization and migration dynamics

## ACKNOWLEDGMENTS

This work was funded by national funds through FCT – Foundation for Science and Technology, I.P., to UID/04129 LEAF-Linking Landscape, Environment, Agriculture and Food Research Center, UIDB/00239 CEF – Forest Research Center, the PhD grant PRT/BD/154281/2022 to Carla Tavares within the Consortium of Schools of Agricultural Sciences (CECA), and by the Scientific Employment Stimulus 2022.00392.CEECIND to Filipa Monteiro.



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