



# Incidence, severity and spatial patterns of distribution of citrus greening in Kenya and Tanzania

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## INTRODUCTION

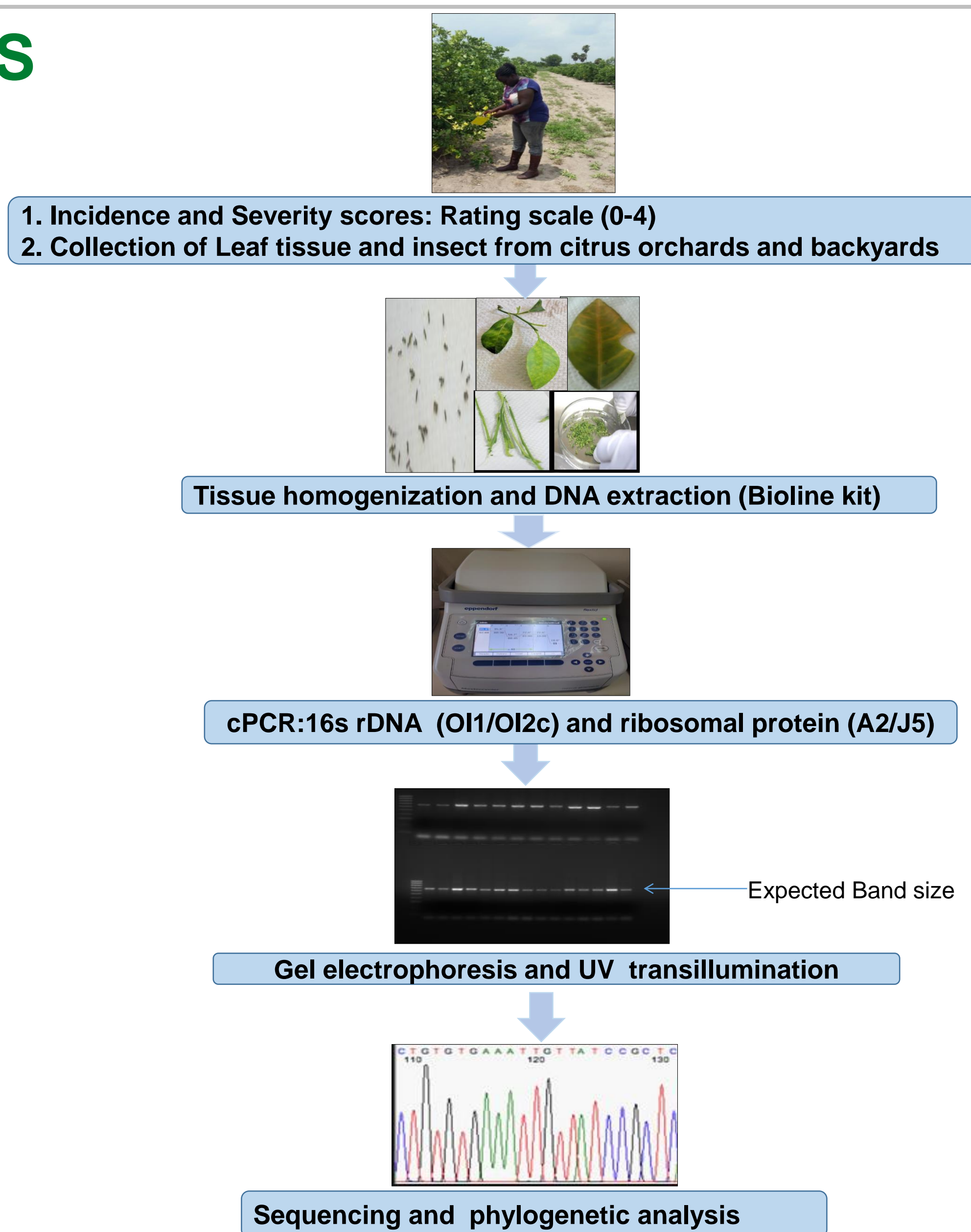
- Citrus greening disease has hindered citrus production both in Kenya and Tanzania<sup>1,2</sup>.
- Greening disease is caused by a phloem limited bacterium *Candidatus Liberibacter* species and African Citrus Triozid : *Trioza erytrae* and *Diaphorina citri* are the natural vectors<sup>3</sup>.
- In the two target countries, the disease is believed to be restricted to the highlands, since *Candidatus Liberibacter africanus* (CLaf), the causal agent, is heat sensitive<sup>4</sup>.
- A thorough and innovative strategic research covering aspects of the incidence, severity, distribution and molecular phylogeny of the pest and bacterium is the prerequisite for successful and sustainable management of ACT and the associated greening problems on citrus.



## RESEARCH AIMS

- To determine the incidence and severity of citrus greening disease in Kenya and Tanzania
- To characterize circulating *Liberibacter* strains associated with citrus greening in Kenya and Tanzania
- To map the distribution patterns of citrus greening in the two countries

## METHODS



## RESULTS

### Greening Incidence across different locations in Kenya and Tanzania

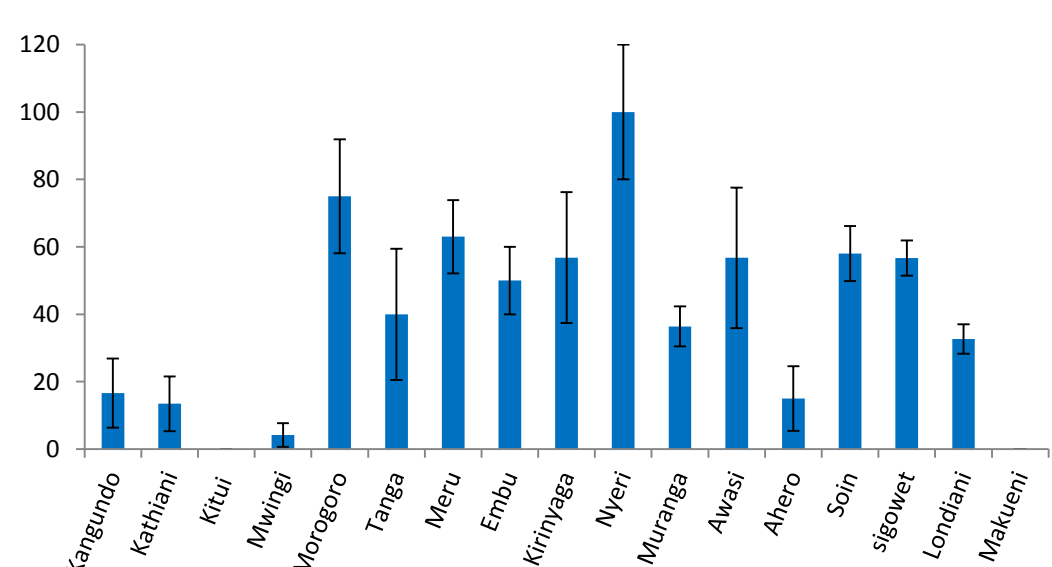


Figure 1: Incidence of greening disease in Kenya and Tanzania

### Disease severity scores across surveyed locations

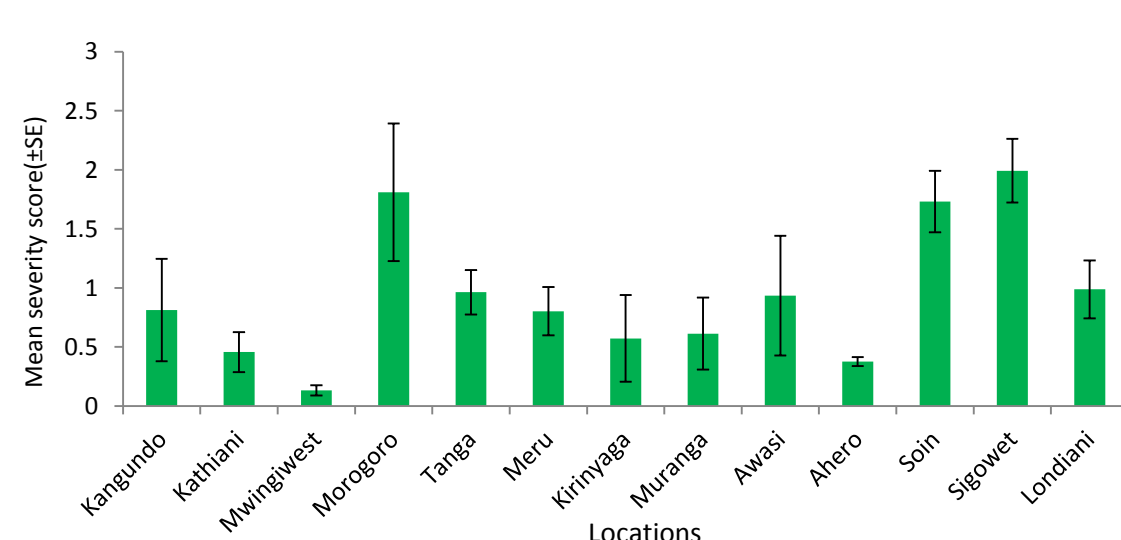


Figure 2: Percentage severity scores of citrus greening

- Highest percentage mean incidence recorded in Nyeri (100%) and Morogoro (75%).
- No disease presence observed in Makueni and Kitui
- Maximum mean severity observed in Soin, Sigowet and Morogoro
- Minimum severity in Mwingi west

## RESULTS

### Maximum-likelihood Phylogeny based on rplJ gene sequences

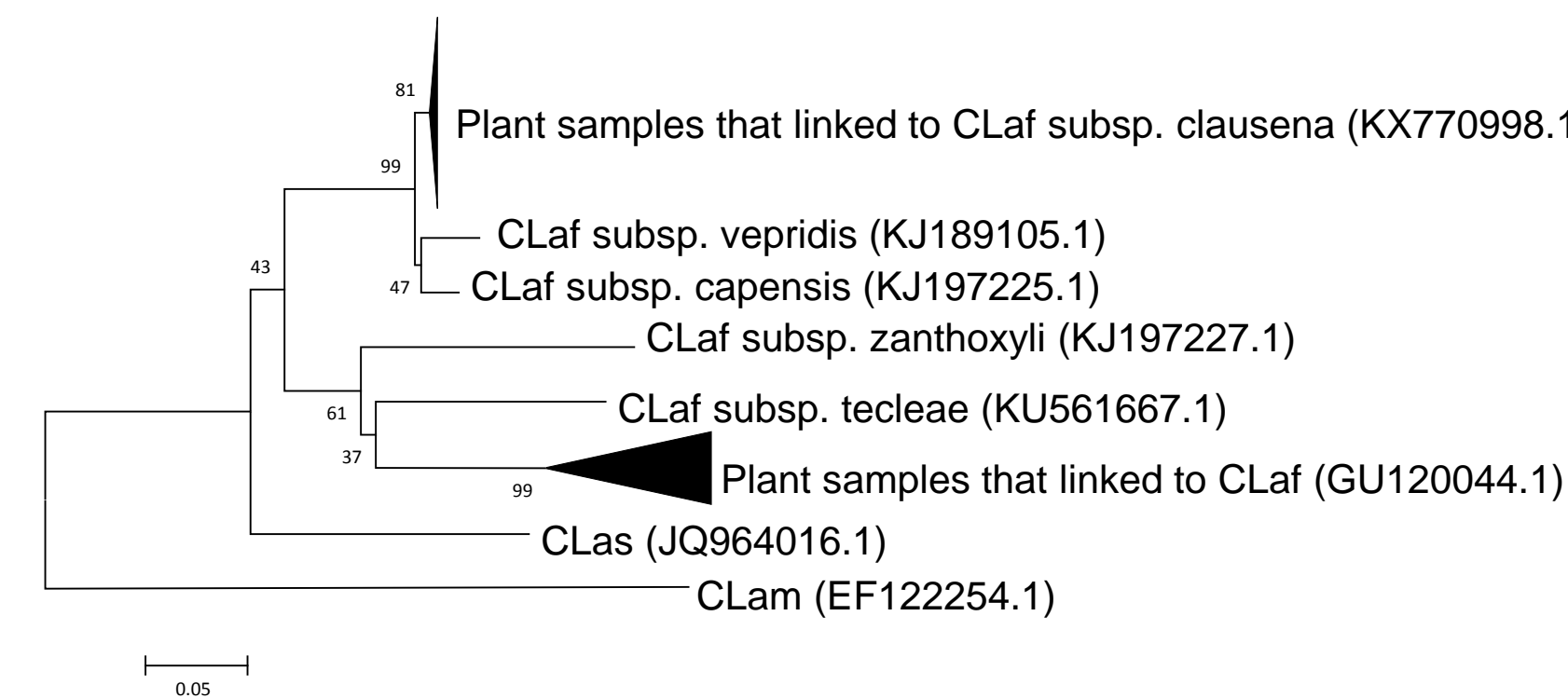


Figure 3: Phylogeny of CLaf from plant samples collected in Kenya and Tanzania

### Maximum-likelihood phylogeny based on 16S rDNA gene sequence from insect samples

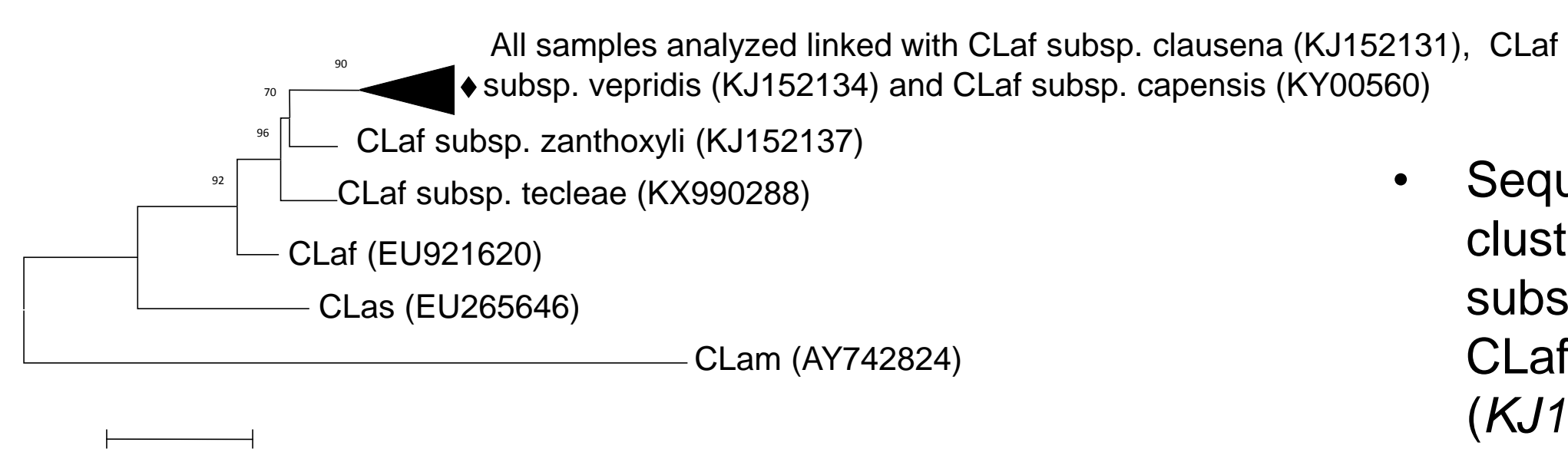


Figure 4: Phylogeny of CLaf from insect samples

### Plots of the principal component analysis (PCA) for symptomatic citrus samples and other *Candidatus Liberibacter* species

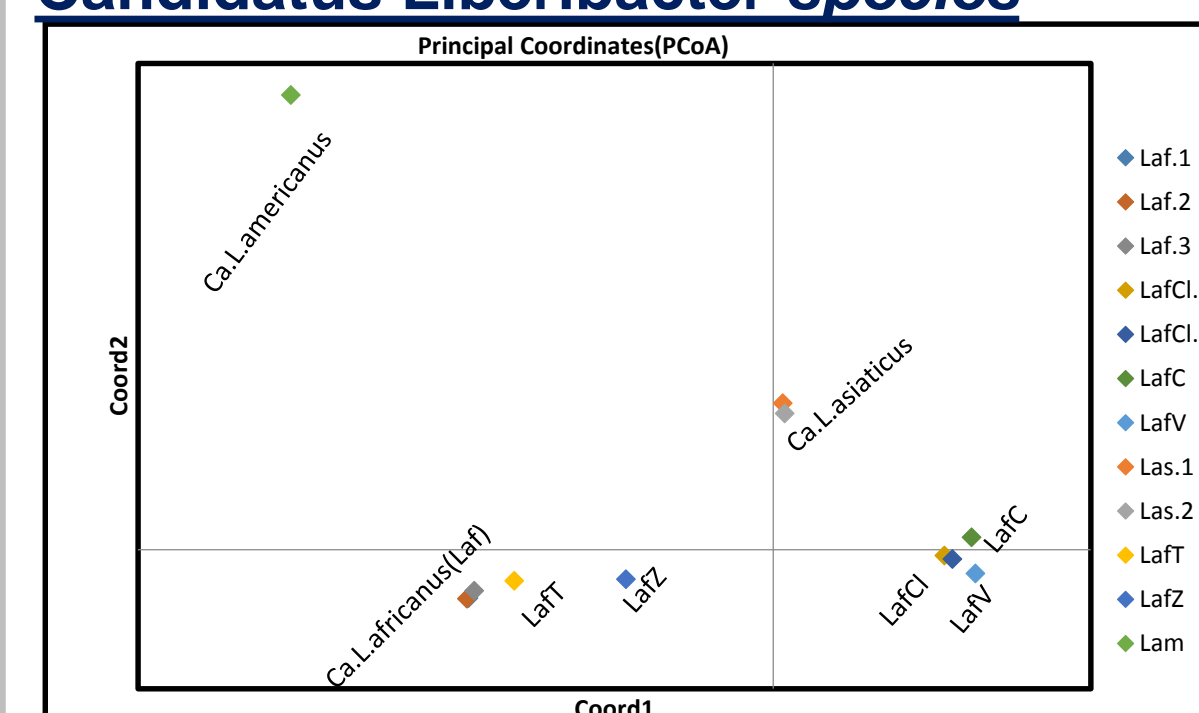


Figure 5: Principal component analysis plot of CLaf species

### Distribution of citrus greening Disease in Kenya and Tanzania

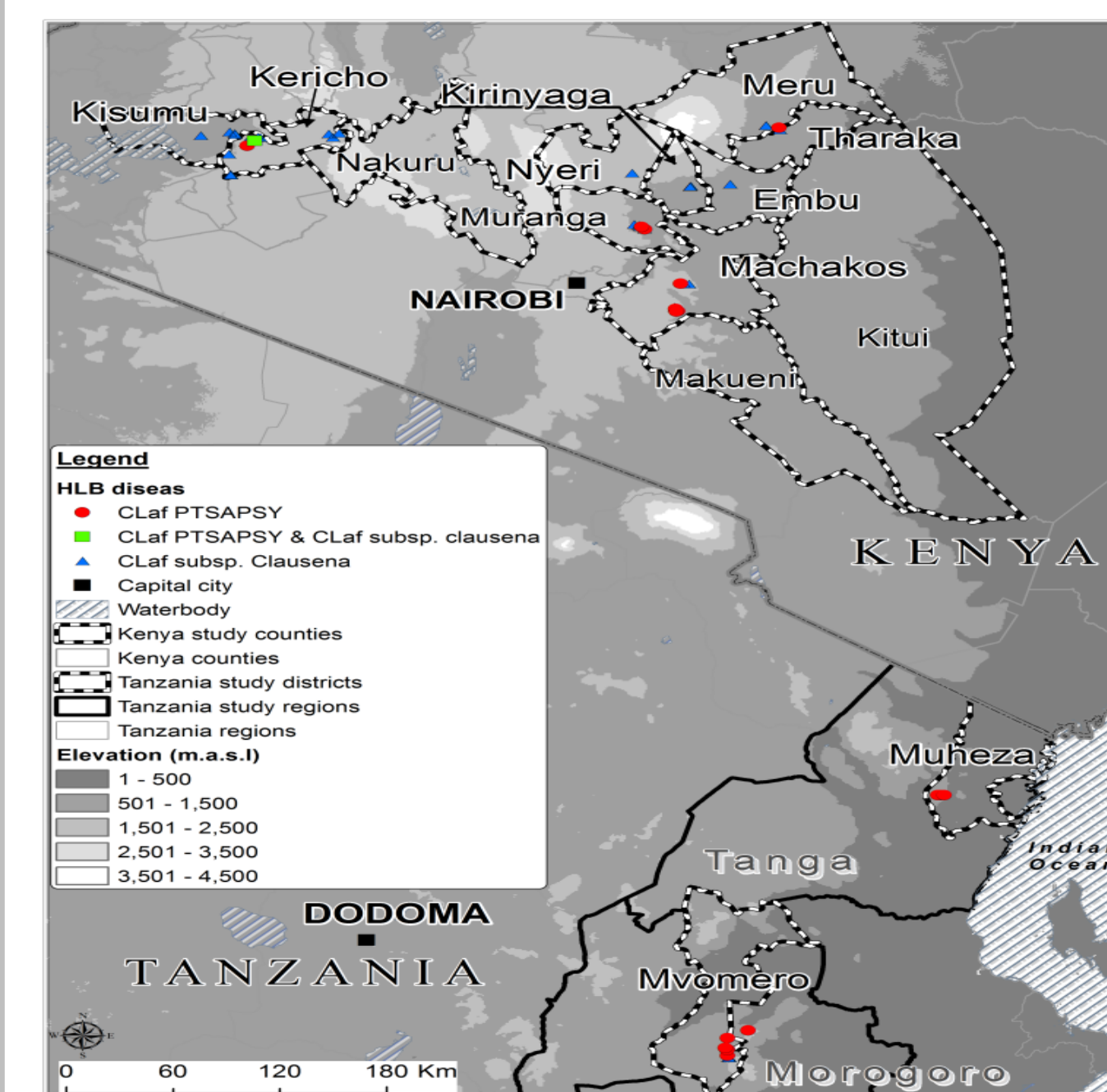


Figure 6: Distribution patterns of citrus greening disease in Kenya and Tanzania

- CLaf and CLaf subsp. clausena sequences from this study clustered with their respective GenBank accessions GU120044.1 and KX770998.1
- CLam and CLas clustered on different axis
- CLaf subsp. tecleae and CLaf subsp. zanthoxyli were closely associated with CLaf
- Widespread distribution of citrus greening across highlands and midland regions of western (Kisumu and Nakuru) central (Murang'a, Nyeri, Kirinyaga) and Eastern (Meru, Embu, Machakos) parts of Kenya and Tanzania

## CONCLUSION

- The pathogen CLaf subsp. clausena played a major role in the spread of citrus greening disease.
- The association of CLaf subsp. clausena with citrus stresses the potential importance of *Clausena anisata* trees as reservoirs for CLaf.
- Both *T. erytrae* and *D. citri* vectors were found to coexist at high altitudes, illustrating that *D. citri* is quickly adapting to new geographical areas and ecologies.
- No CLaf pathogen was detected in *D. citri* specimens sampled

## REFERENCES

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