# Assessing the microbiome diversity and antibiotic resistance genes of African and Asian *Diaphorina citri* populations using Oxford Nanopore sequencing

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## INTRODUCTION

- *Diaphorina citri* is a key pest of *Citrus* sp. Worldwide, as it acts as a vector for *Candidatus* Liberibacter asiaticus (Las), the bacterial pathogen which causes the destructive Huanglongbing (HLB) disease.
- The study of microbial communities through metagenomics helps to understand their interactions with arthropods, disease transmission, immunity, host resistance and insect host vector competence.
- Recent reports of the presence of *D. citri* in Tanzania and Kenya [1,2] and Las in Ethiopia and Kenya [3,4] highlights the need to profile the microbiota diversity in the insect vector populations.
- The identification of key endosymbionts and other bacteria, as well as antibiotic resistance genes in the microbial community within the insect can inform the diversity between the newly introduced African populations and older populations.

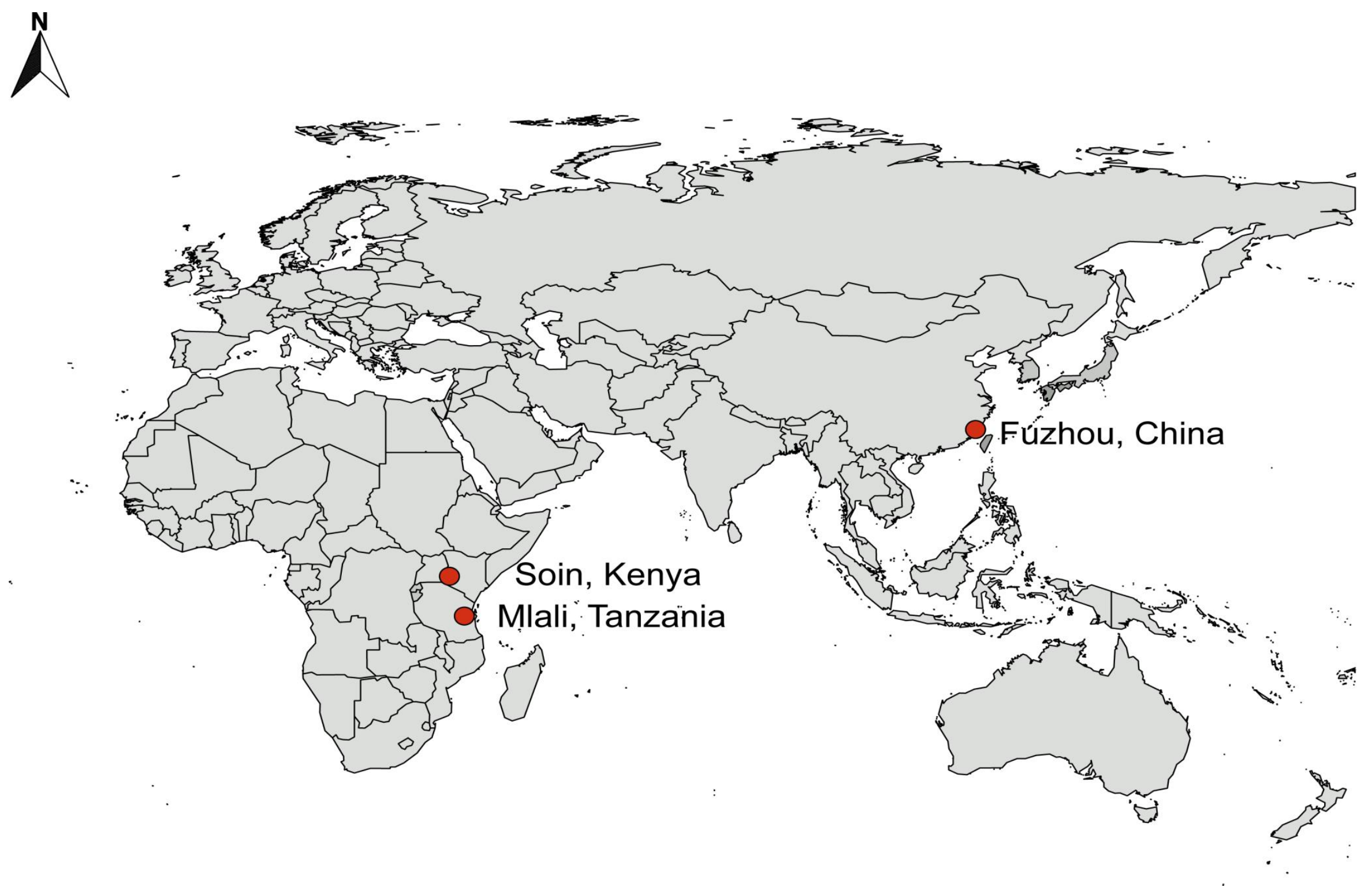
## Aim

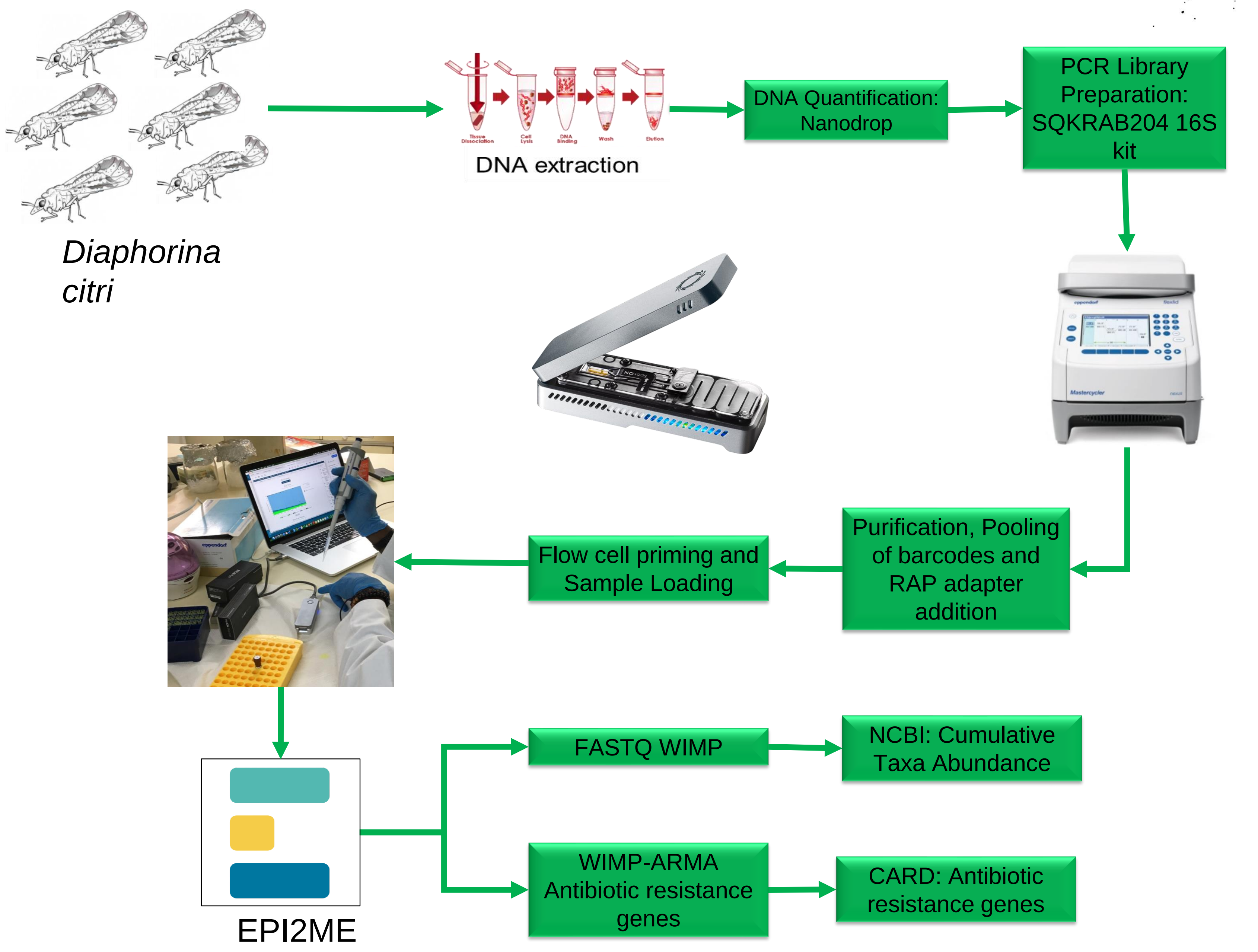
- This study sought to evaluate the bacterial diversity and genes for resistance to antibiotics within the microbiome of *D. citri* populations .

## METHODS

### *Sampling Locations*

- *Fuzhou, China*
- *Soin, Kenya*
- *Mlali, Tanzania*





*Diaphorina citri*

DNA extraction

DNA Quantification: Nanodrop

PCR Library Preparation: SQKRAB204 16S kit

Purification, Pooling of barcodes and RAP adapter addition

Flow cell priming and Sample Loading

EPI2ME

FASTQ WIMP

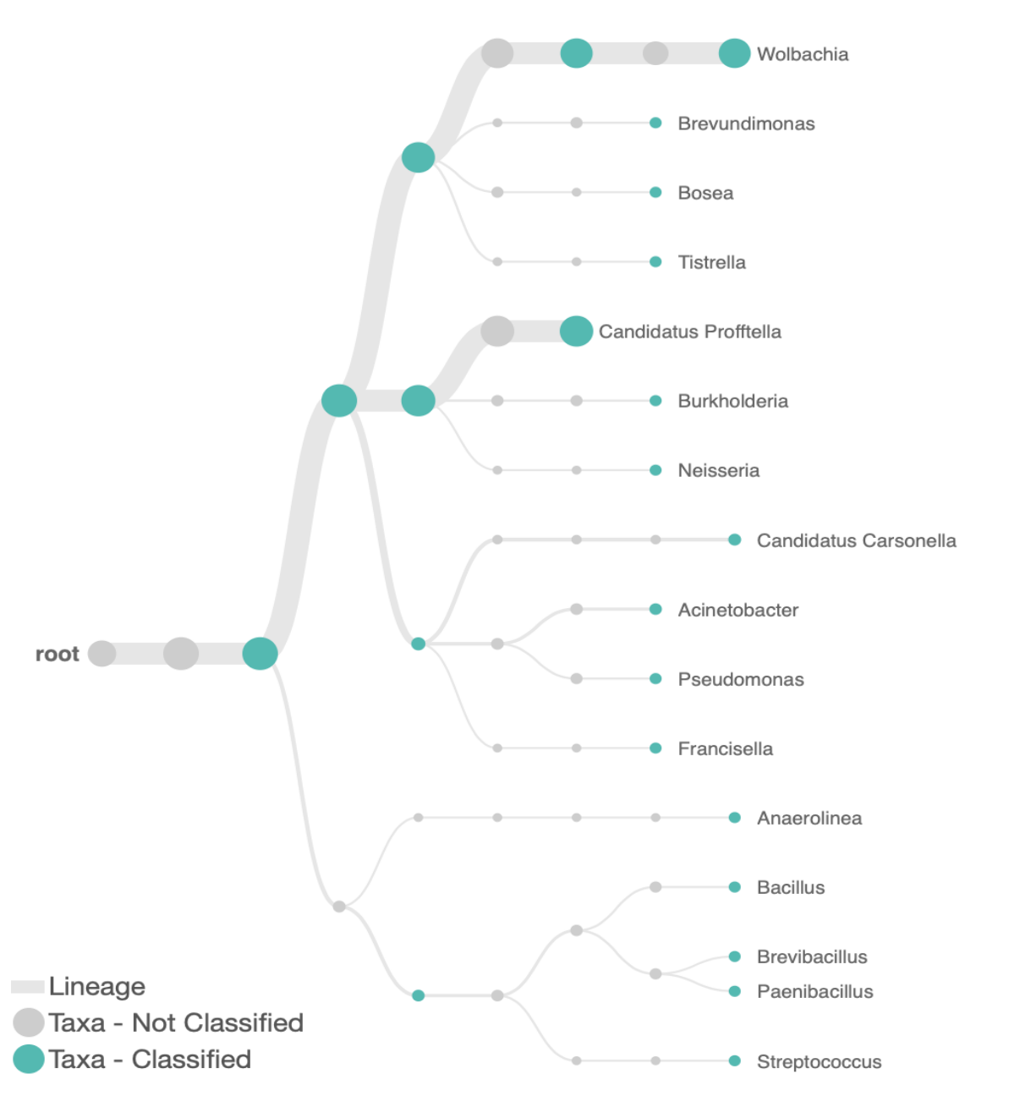
NCBI: Cumulative Taxa Abundance

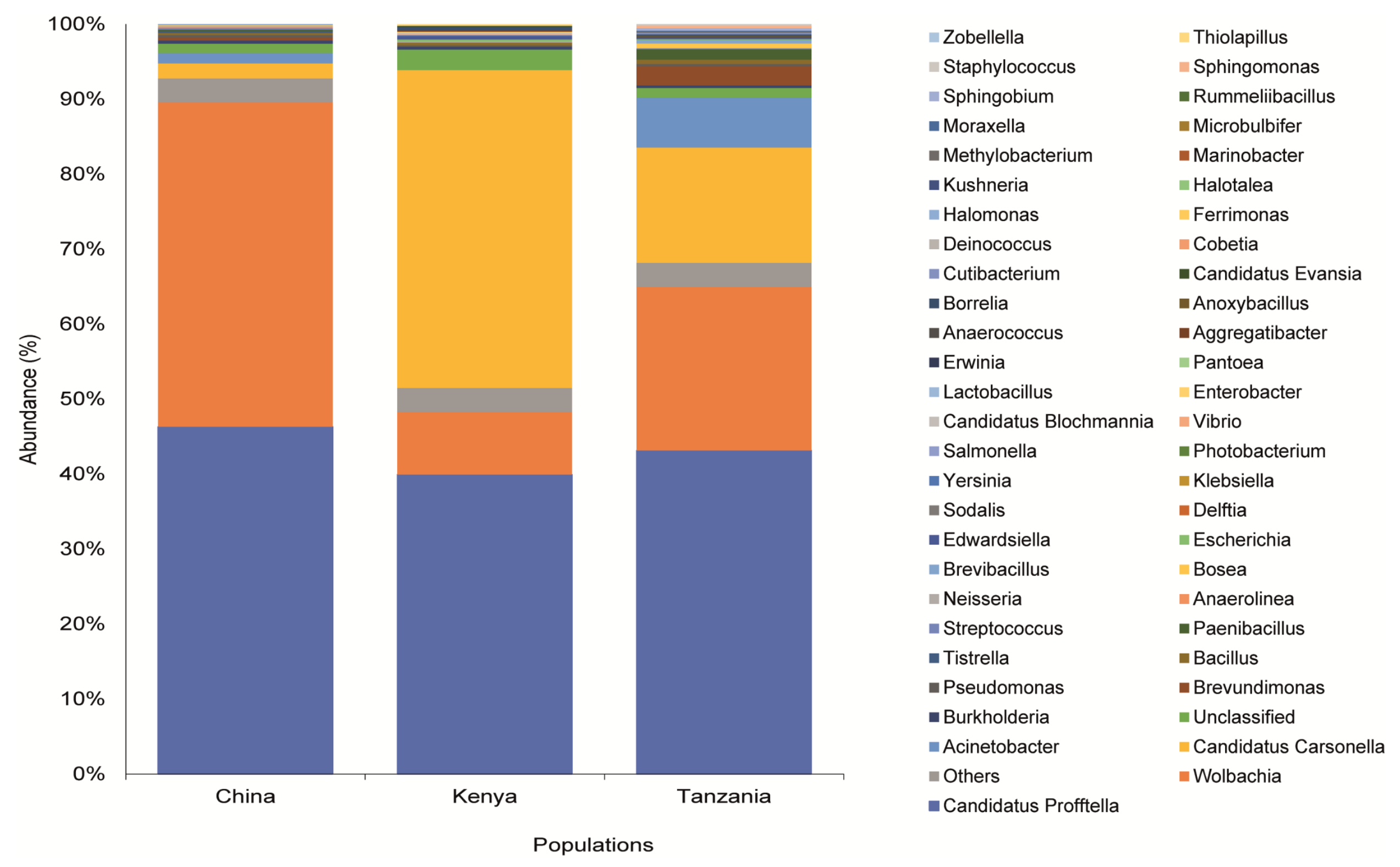
WIMP-ARMA Antibiotic resistance genes

CARD: Antibiotic resistance genes

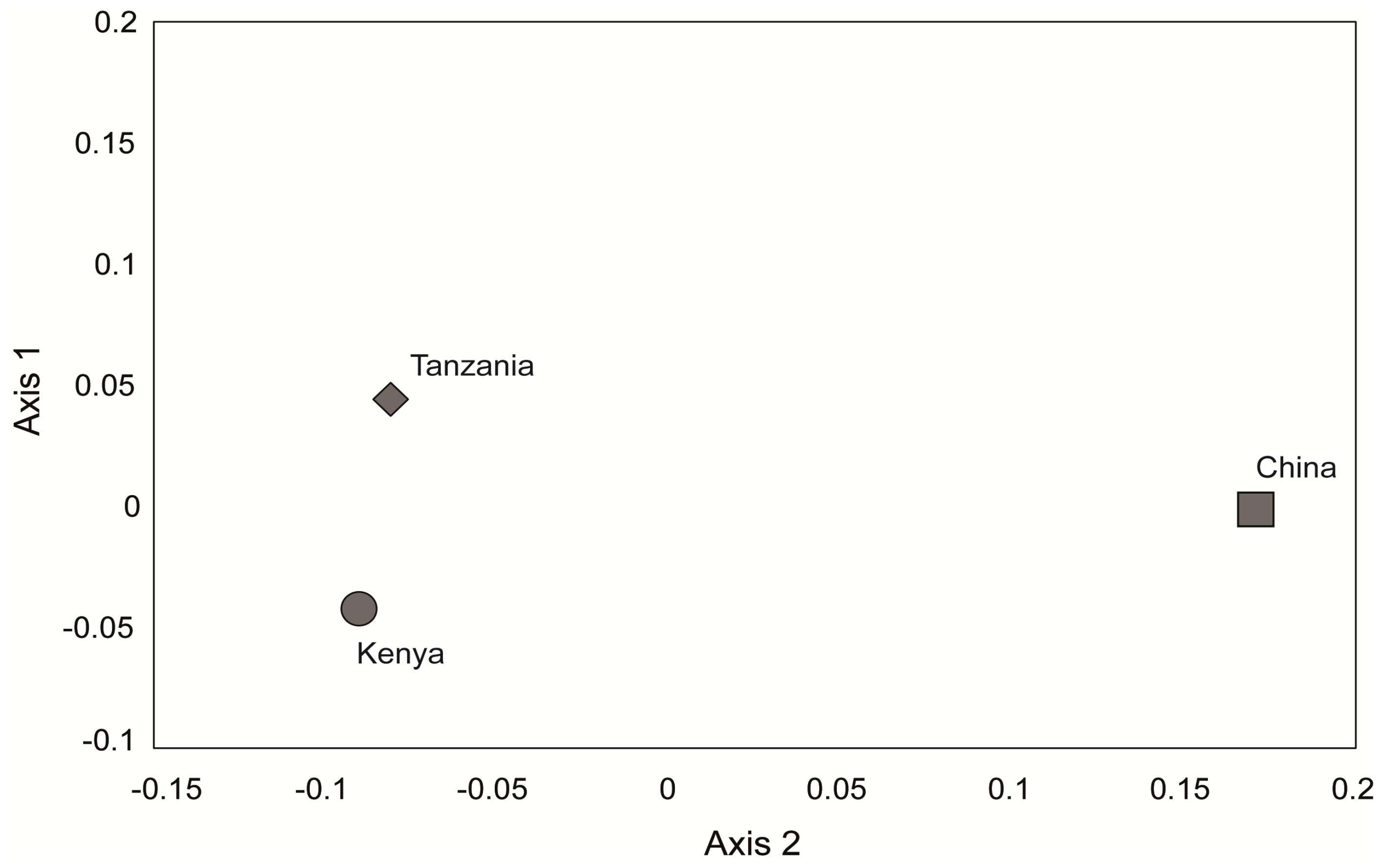
## RESULTS

### *1. Taxonomic assignment and Cumulative abundance of bacterial microbiota in D. citri*

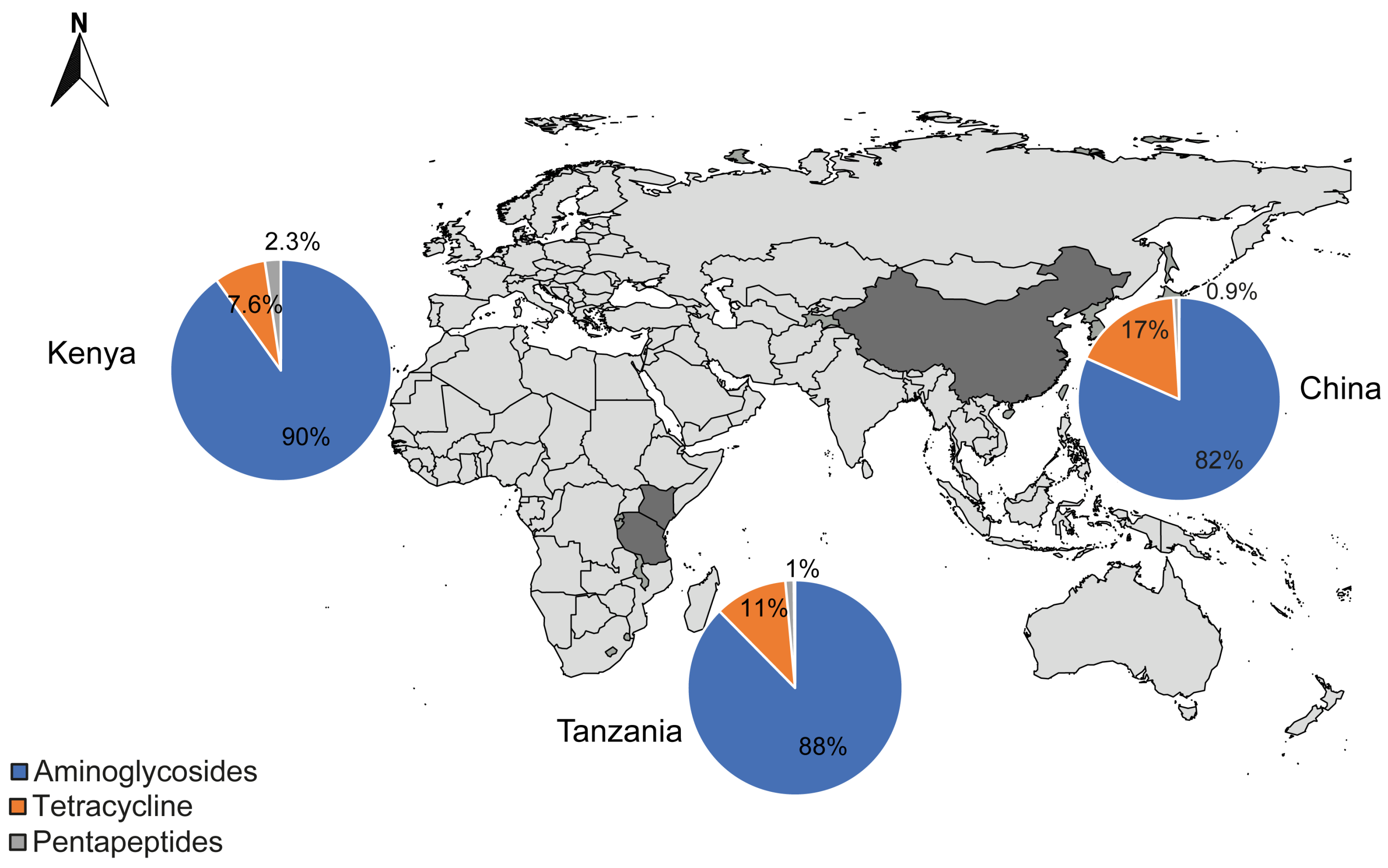




### *2. Inter-Population Diversity (Bray-Curtis index)*



### *3. Abundance of genes for resistance to antibiotic compounds*



## CONCLUSIONS

- The most abundant genera in all populations were the Key endosymbionts of *D. citri* ("Candidatus Profftella", Wolbachia and "Candidatus Carsonella").
- The *D. citri* from Tanzania had the highest bacterial diversity, while Kenya and China were the most diverged populations.
- The most abundant genes for resistance to conferred resistance to aminoglycosides, tetracycline and pentapeptides families of antibiotics.

## IMPACT

- The elucidation of the bacterial microbiota and its ARGs in *D. citri* provide valuable information on potential integrated pest control measures against the psyllid and its ability to transmit diseases. The Exploration of cytoplasmic incompatibility conferred by Wolbachia can be used to interrupt the capacity of the insect to transmit diseases as well as the influence of Wolbachia on the increased susceptibility of the psyllid to parasitoids.

## REFERENCES

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**Acknowledgment:** We gratefully acknowledge the financial and technical support of our core donors: Swiss Agency for Development and Cooperation (SDC), Switzerland; Swedish International Development Cooperation Agency (Sida), Sweden; UK Aid, Government of the United Kingdom; Ministry of Higher Education, Science and Technology, Kenya; and Government of the Federal Democratic Republic of Ethiopia. *The views expressed herein do not necessarily reflect the opinion of the donors.*