Genetic diversity of aphid (Hemiptera: Aphididae) species attacking amaranth and nightshades in six agroecological zones of Kenya and Tanzania

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INTRODUCTION

Aphids invade both food and non-food crops, causing over 70% loss in yield worldwide. They destroy crops by sucking the sap resulting in discoloration, wilting and early senescence (Aslam *et al.,* 2007). Indirectly, aphids transmit over 50% of plant potyviruses (Gray and Banerjee, 1999). No documented information exists on the exact species and genetic characterisation of the various aphid species infesting amaranth and nightshades in Kenya and Tanzania, an important factor in pest management strategies. We used PCR of a mitochondrial cytochrome *c* oxidase subunit I (*COI*) variable region, which is the standard DNA barcode for almost all animal groups including insects, in this study.

OBJECTIVES

1. To describe and assess the genetic diversity of aphid species attacking amaranth and nightshades in Kenya and Tanzania using mitochondrial DNA *COI* gene region.
2. To determine the relationship between environmental variation and the genetic diversity of aphid species of amaranth and nightshades in Kenya and Tanzania.

METHODS

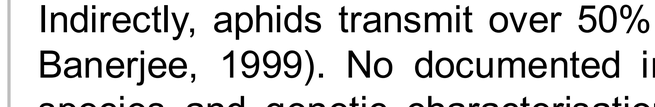

Fig.1. A: *Myzus persicae,* B: *Aphis craccivora*, **C**: *Aphis fabae.*

- Aphids (Fig. 1) were collected in two localities of the sites indicated in Fig. 2.
- DNA was isolated using Genomic DNA Kit (Bioline).
- COI gene was PCR amplified using LCO-1490 and HCO-2148 primers.
- Five samples per site per host crop were bi-directionally sequenced.
- Sequences were edited in Chromas Lite 2.0, aligned in ClustalX and analysed using Mega 6.0 and BLAST.

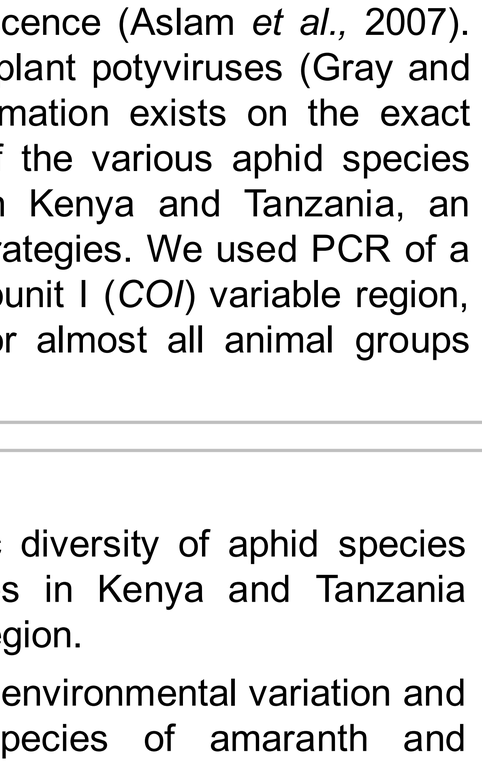

Fig. 2. Map of Kenya (top) and Tanzania (bottom), showing the sampled localities.

RESULTS

- The Basic Local Alignment Search Tool (BLAST) identified three major aphid species attacking amaranth and nightshades in both countries as *Aphis craccivora* Koch, *Aphis fabae* Scopoli and *Myzus persicae* Sulzer (each with ≥96% identity).
- The intra-specific divergence for *A. fabae*, *A. craccivora,* and *M. persicae* was 0.057, 0.009 and 0.020, respectively.
- The inter-specific divergence (Table 1), shows that *A. craccivora* and *A. fabae* have a lower interspecies divergence compared to *M. persicae.*
- The phylogenetic tree in Fig. 3, built under K-2-P model and 1000 pseudo replicates shows that similar species clustered together in distinct clades irrespective of where collected or host crop.
- The principal coordinate analysis (PCA) plot derived from the distance divergence matrix (Table 1) is as shown in Fig. 4. The first and second axes account for 60.97 and 39.03 variations, respectively.

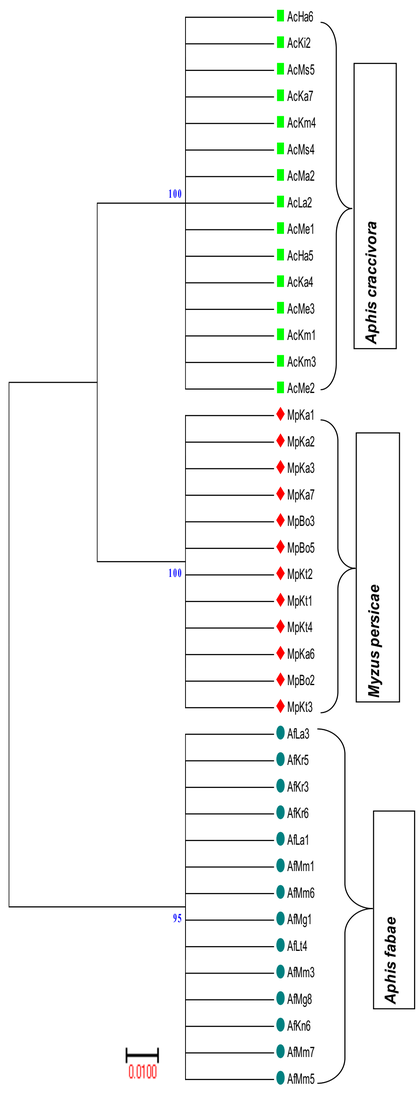

Fig. 3. Neighbour-joining tree showing evolutionary relationships between 41 aphid samples collected in Kenya and Tanzania.

Table 1. Estimates of Intra-species divergence between three aphid species collected in Kenya and Tanzania.

	A. craccivora	*A. fabae*	*M. persicae*
A.craccivora	0		
A.fabae	0.085	0	
M. persicae	0.118	0.123	0

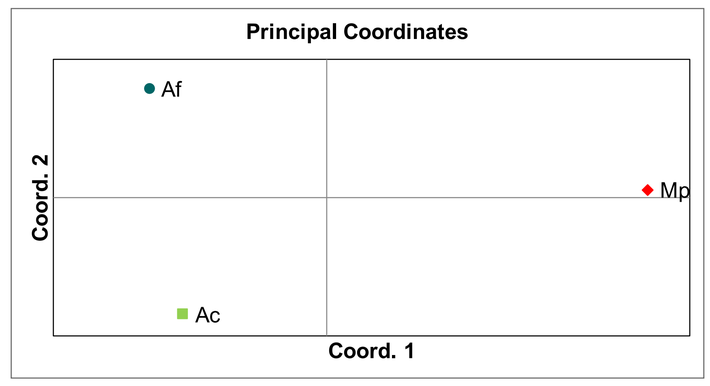

Fig. 4. PCA plot generated from the inter-specific distance matrix for the three aphid species collected in Kenya and Tanzania.

CONCLUSIONS

- The ability of the mitochondrial *COI* region to separate species of aphids irrespective of the agro-ecological zone or geographical location makes it a suitable tool for species identification.
- The study created a reference barcode library to help identify new and invasive aphid species.
- It is evident that the three major aphid species attacking nightshade and amaranth in Kenya and Tanzania are *A. craccivora, A. fabae* and *M. persicae.*
- We infer that because of low intra- and inter-species diversity among these aphid species, similar strategies can be used during pest management practices across the two countries.

REFERENCES

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