

Rift Valley fever virus lineages from selected sites in Kenya, 1997-2020

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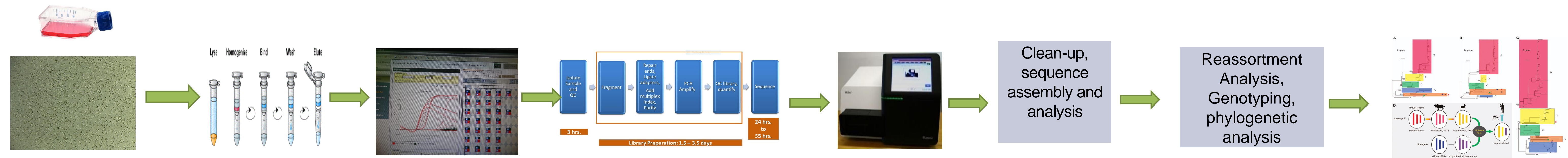


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Introduction

- Zoonotic disease emergence and reemergence in on the rise, prompt pathogen detection and characterization are critical.
- The geographical range of RVF is expanding but factors associated with the trend are not fully understood.
- There is need to monitor epidemic and interepidemic virus strains to inform epidemiological analyses including basis of clinical severity.

Methods



Findings

- Whole genome RVF sequences from human samples representing various years and geographical zones generated
- Majority of the sequences belong to lineage C with close relationships to RVF isolates obtained in the East African region between 2007 and 2017
- Potential genetic reassortment of different viral lineages C and A detected in two samples (2007 & 2018) detected in the M and L segments (Fig 2&3)

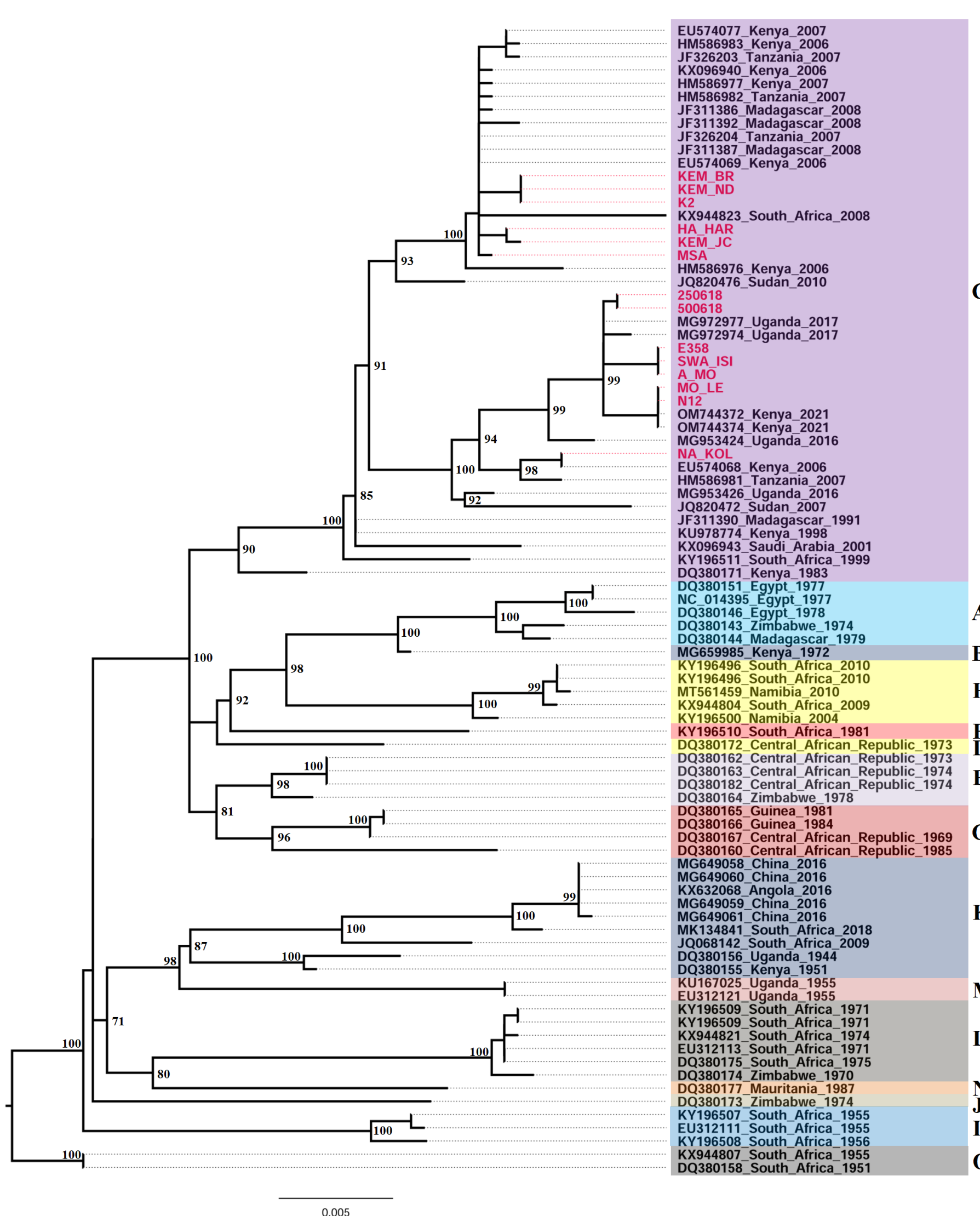


Fig 1: Phylogenetic tree based on the S segment sequences

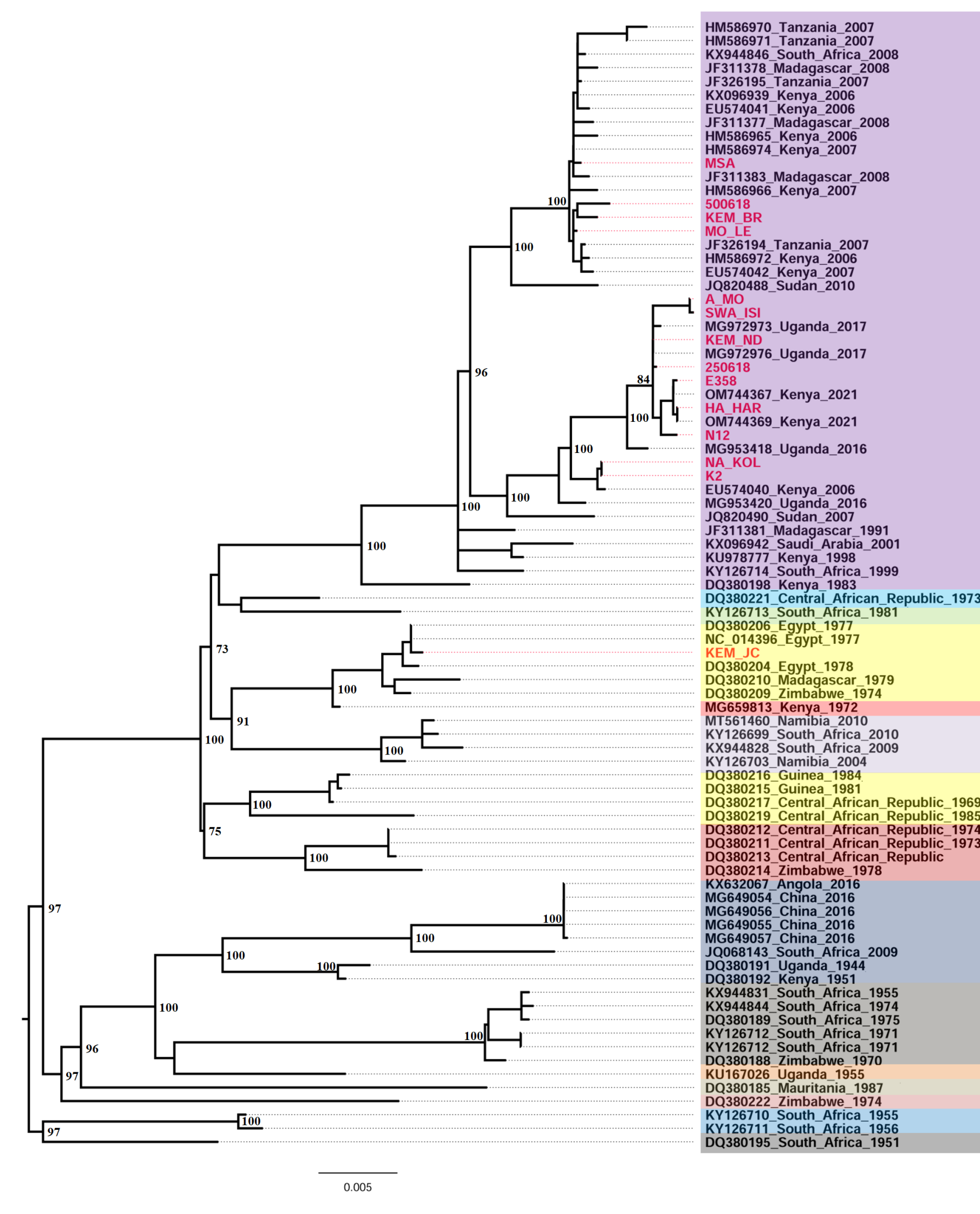


Fig 2: Phylogenetic tree based on the M segment sequences



Fig 3: Phylogenetic tree based on the L segment sequences

Conclusions and limitations

- The findings suggest that lineage C is associated with multiple RVF outbreaks in Kenya in line with previous reports that it's the most predominant lineage in Africa caused by virus strains maintained in local enzootic cycles.
- Genetic reassortment has potential to alter viral biological properties as the segments encode for various viral functions that can alter occurrence of outbreaks posing serious threats to global public health and the livestock industry.

Contribution to Uganda's livestock development agenda

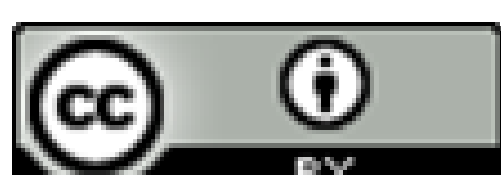
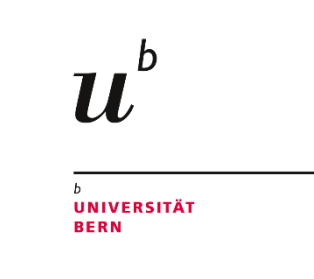
- Provision of baseline data on circulating lineages, identify molecular drivers of clinical disease outcome and increased geographical occurrence and spread of Rift Valley fever.

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