# Genomic epidemiology of Rift Valley fever in East Africa: A data driven intervention for effective control and prevention of the disease.

John Juma[1], Samuel Oyola[1], Bernard Bett[1], and Rosemary Sang[2]

[1]*International Livestock Research Institute (ILRI), Nairobi, Kenya*
[2]*Kenya Medical Research Institute (KEMRI), Nairobi, Kenya*

## Introduction

Rift Valley fever (RVF) virus is a re-emerging zoonotic disease of arboviral origin, and belonging to the *Bunyaviridae* family [1]. The disease is responsible for deaths in human and animals. It leads to major losses in livestock production, thus negatively affecting livelihoods in Sub-saharan Africa. Phylogenetic analysis on the virus have reported that it's first emergence was in the mid 19 th century, and was first reported in 1930s in the Rift Valley region in Kenya [3]. The RVF virus shows a simple but temporally and geographically stable genome. However, in spite of this attribute, the virus has continued to ravage new territories as exemplified by outbreaks in Egypt (1977), Western Africa (1988) and the Arabian Peninsula (2000) [1]. The recent re-emergence of the disease in Kenya and South Africa has indeed displayed it's real capacity to enter into new territories.RVF is one of the several diseases identified by the World Health Organization, (WHO) as a likely cause of future epidemic in a new emergency plan developed after the Ebola epidemic, and classified for urgent research and development toward new diagnostic tests, vaccines and medicines [4].

## Purpose

To understand the epidemiology of RVF virus in East Africa, using biobanked human and animal samples, we aim to:

1. Genetically characterize the current RVF strain(s) circulating in Kenya and Uganda.
2. Assess potential co-infection with Ngari virus (NRIV)
3. Undertake transmission dynamics by integrating genomic and epidemiologal data to ascertain spread and persistence.

## Workflow

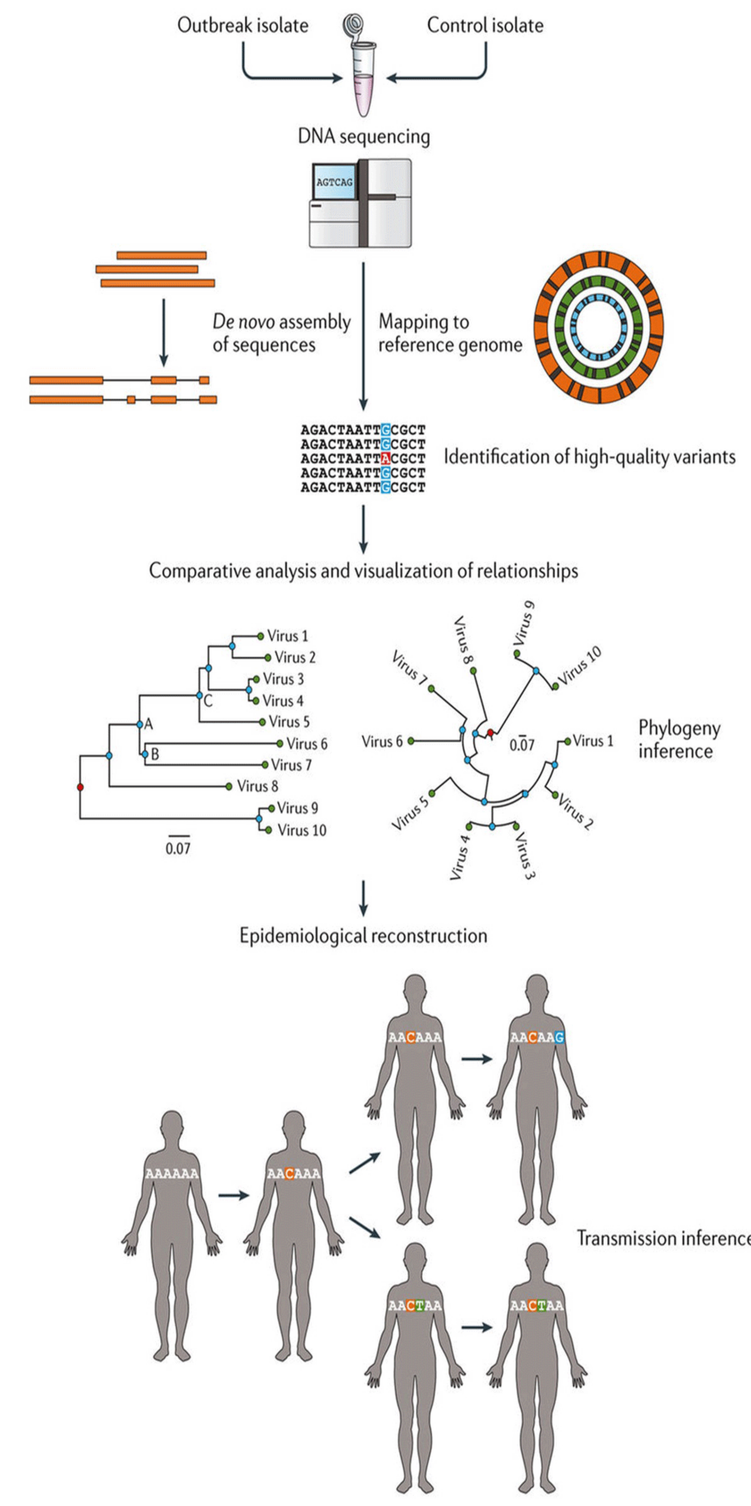


Figure 1: Process and utility of genomic epidemiology [2].

## Methods

1. Virus culture and isolation of nucleic acid - RNA
2. Confirmatory tests using serology (IgM) and Real Time quantitative polymerase chain reaction (RT-qPCR)
3. Next generation sequencing: Illumina MiSeq and Oxford Nanopore (MinION)
4. Genome assembly to characterize genetic diversity and viral mutations
5. Multiple sequence alignment (MAFFT) and Maximum Likelihood tree inference using RAxML under a GTR + Γ 4 nucleotide substitution model
6. Reconstruction of time-scaled phylogenetic trees using the Bayesian phylogenetic inference framework (BEAST).

## Expected results

Preliminary data are expected to be analyzed in March, 2020. Results of the viral genomes will be a valuable source of information for epidemic dynamics which will be used to examine specific RVF outbreaks indepth. By combining genomic, epidemiological and spatial data, we will be able to offer insightful knowledge about the transmission of RVF. Such surveillance approach is very crucial for early detection and rapid prevention of RVF transmission.

### References

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