

**MOLECULAR CHARACTERIZATION OF CHIKUNGUNYA VIRUS.**

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## ABSTRACT

Outbreaks of Chikungunya fever, a viral disease transmitted by *Aedes* spp. Mosquito emerged in a number of islands along the Indian Ocean and India in late 2004. Initially, the disease emerged in Kenya's Lamu islands before occurring in Mombasa, both cases being in late 2004. Early 2005, epidemics of the same virus were experienced in the Comoros islands. The Chikungunya fever has re-emerged as an important health problem, affecting many people and causing increasingly severe symptoms. Mutation of the virus, lack of vector control, and globalization of trade and travel might have contributed to the resurgence of the infection. The study was aimed at characterizing the specific strains of Chikungunya present in the Lamu, Mombasa (KPA) and Comoros outbreaks. ELISA tests were performed to detect presence of the virus in patients' sera. From the positive samples, the virus was cultured by inoculation into vero cells. RNA was then isolated from the cultured virus which was reverse transcribed into cDNA and amplified exponentially by PCR. The cDNA was cycle sequenced by termination synthesis and the nucleotide sequences analysed by an automated genetic analyzer. Nucleotide sequence data thus generated was used to detect any differences with reference to the already sequenced S27 African prototype whole genome. The genotypes responsible for the infections were known and their relatedness to each other and to other strains in the world was established by performing phylogenetic analysis. There was over 99% nucleotide sequence homology amongst Comoros 25, KPA 15 and Lamu 33 isolates and they all had about 95% similarity with the S27 African prototype.