

GENETIC DIVERSITY AMONG FOOT AND MOUTH DISEASE VIRUS ISOLATES OF SRI LANKA THROUGH MOLECULAR CHARACTERIZATION

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Foot and mouth disease (FMD) is caused by single stranded positive sense RNA virus. Although there are seven viral serotypes namely A, O, C Asia-1, SAT-1, SAT-2 and SAT-3, the serotype O is only present in Sri Lanka. Foot and mouth disease virus (FMDV) can infect cloven-hoofed domestic animals such as cattle, pig, sheep, goat and buffalo. Out of these hosts, infection of cattle by FMDV is economically very important. In Sri Lanka, FMD outbreaks can be seen with significant peaks in every five to six years. The DNA sequence analyses of *VPI* region of the FMDV genome is the general practice to identify new topotypes which is crucial in developing new vaccines or selecting appropriate vaccines from the international FMDV vaccine pool. In Sri Lanka limited studies have been conducted in this manner to determine the genetic relationship of field isolates of FMDV. Therefore, the objective of the current study was to genetically characterize FMDV isolates in recent outbreaks by DNA sequencing of the *VPI* genomic region.

FMDV isolates were collected as epithelial samples from the infected cattle populations in *Kundasale* (2010), *Polonnaruwa, Waharei, Oddusudan*, (2011), *Siyambalanduwa* and *Samanthurai* (2012). Viral particles were purified and inoculated in to *BHK21C13* cell line for multiplication. RNA was extracted from multiplied viral particles. RT-PCR was conducted using the primers *IC-ROD1, NK 61, NK 72* to amplify *VPI* genomic region of the FMDV serotypes. PCR products were purified and sequenced. The DNA sequences were aligned and examined for genomic dissimilarity using Clustal Omega package.

There is a strong possibility that in comparison to the *VPI* reference sequence of FMDV genome two possible topotypes at 83.3% of genetic similarity were prevalent in studied isolates. All the other strains except *Siyambalanduwa* (2012) represented one topotype and viral isolates from *Siyambalanduwa* (2012) represented the other topotype. These two topotype variants strongly suggest the requirement of at least two vaccines to control the outbreaks at *Siyambalanduwa* and at other studied areas separately. It seems very probable that FMDV was spreading from North to South in Sri Lanka supporting the general hypothesis that new variants are coming to Sri Lanka from South India.

