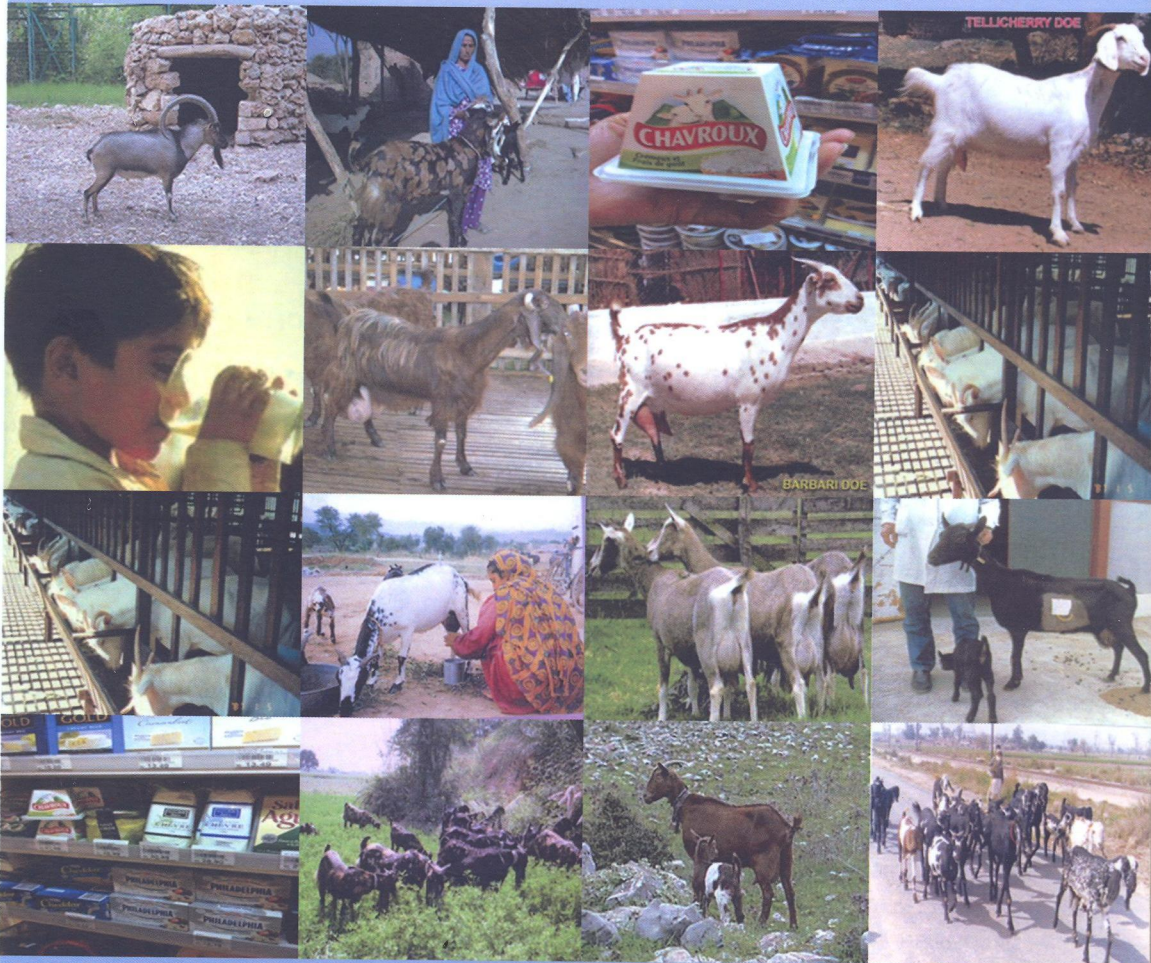


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Paper 37

**Phylogenetic Analysis of Serotype Asia 1 Foot-And-Mouth Disease Virus:
Asia Diversity and the Iran Perspective**

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Introduction

Foot-and-mouth disease (FMD) is an infectious and sometimes fatal viral disease that affects cloven-hoofed animals, including domestic and wild bovids. The virus causes a high fever for two or three days, followed by blisters inside the mouth and on the feet that may rupture and cause lameness. Susceptible animals include cattle, water buffalo, sheep, goats, pigs, antelope, deer, and bison. The disease has had a dramatic impact on the farming industry leading to tremendous economic losses particularly in countries which are naturally FMD-free. Previous studies have shown that Iran has one of the highest reported rates of FMD cases per year. This study was undertaken to compare nucleotide sequences of VP1 gene Asia 1 isolates from Iran with available corresponding sequences from Asian countries deposited in the GenBank database.

Materials and Methods

The published sequences of 60 FMDV type Asia 1 isolates recovered from different parts of the Asia were included in this analysis and compared with the corresponding sequence of Asia 1 isolates from Iran. The phylogenetic tree was constructed using the Neighbour Joining method by using the Alignment and Trees toolbox of the CLC Workbench software (CLC Bio).

Results and Discussion

Nucleotide sequence comparison based upon the alignment of complete nucleotide sequence of the VP1 region indicated that Iran Asia 1 serotypes had the greatest sequence similarity with reported isolates from Afghanistan and Pakistan with a nucleotide identity of approximately 98% (data not shown). Figure 1 shows a phylogenetic tree constructed based on the sequence alignment of 60 genomes, which are distinctly divided into five lineages. The most Iranian reported isolates clustered with Turkish, Afghanistan and Pakistan isolates into a separate branch from other type Asia 1 isolates (lineage D and E). These findings are in accordance with previous study investigated sequence and phylogenetic analysis of Iranian serotype A foot-and-mouth disease (Jelokhani-Niarki et al., 2010). It is thought that FMD virus has a circulation in most areas of Asia. Iran is bordered on the east by Pakistan and Afghanistan and on the west by Turkey. Permeable borders and live animal trade in Asia are likely reasons for virus circulation.



Figure 1. Nucleotide sequence similarity tree based on a comparison of FMDV type Asia 1 isolates, established with VP1 coding sequences (633 bp).

References

Jelokhani-Niaraki, S., M. Esmaelizad, M. Daliri, R. Vaez-Torshizi, M. Kamalzadeh and M. Lotfi, 2010. Sequence and phylogenetic analysis of the non-structural 3A and 3B protein-coding regions of foot-and-mouth disease virus subtype A Iran 05. *J. Vet. Sci.* 11(03):243-247.