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**Genetic and antigenic characterization of Foot and mouth disease virus in cattle and buffalo**

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	<p><b>English Abstract</b></p> <p>A total of 209 vesicular fluid and tongue epithelium samples were collected from cattle and buffaloes in Sharkia (131), Ismailia (49) and Dakahlia (29) Governorates during 2018. Collected samples were screened for detection of FMD virus using antigen ELISA and serotyping. Thirty three samples were positive (15.7%) for SAT2 using antigen ELISA. Pan serotyping primers were used in a real time PCR assay for detection of FMDV SAT2 virus RNA in 45 samples with positive percentages of 21.7% and no serotype A or O were detected. Real time PCR proved to be more sensitive than antigen ELISA. FMDV is more prevalent in cattle than buffaloes with percentages of 31.5 % and 13.6 % respectively. The highest prevalence was recorded in Belbes, sharkia Governorate, while the lowest rate was recorded in El-Tal Al keeper, Ismailia Governorate with percentages of 100 and 14.2% respectively. Three FMDV SAT2 positive samples represented as Sharkia 2018 and Sharkia 2019 and Ismailia 2020 were selected for sequencing and phylogenetic analysis of VP1. Sequencing and phylogenetic analysis of VP1 of the three Egyptian strains demonstrated that these strains are closely related to other Egyptian strains in gene bank as Alex 2018 (MK4933346), Ismailia 2018 (MK4933341) and Menofia 2018 (MT199283) with homology ranged from 95.8% to 98.2%. Phylogenetic tree of FMDV SAT2 showed clustering of Sharkia 2018, Sharkia 2019 and Ismailia 2020 with Libya 2012 topotype VII with three amino acid substitutions at the site 24, 28 and 52. Keywords: CPE, BHK21, qRT-PCR,</p> <p>UTR, FMD, WRLFMD</p>

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