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Molecular Characterization and Phylogenetic Analysis of Capripoxviruses from Outbreak in Iran 2021

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Abstract : Sheeppox Virus (SPPV) and goatpox virus (GTPV) are considerable diseases of sheep, and goats, caused by viruses of the Capripoxvirus (CaPV) genus. They are responsible for economic losses. Animal mortality, morbidity, cost of vaccinations, and restrictions in animal products' trade are the reasons of economic losses. Control and eradication of CaPV depend on early detection of outbreaks so that molecular detection and genetic analysis could be effective to this aim. This study was undertaken to molecularly characterize SPPV and GTPV strains that have been circulating in Iran. 120 skin papules and nodule biopsies were collected from different regions of Iran and were examined for SPPV, GTPV viruses using TaqMan Real -Time PCR. Some of these amplified genes were sequenced, and phylogenetic trees were constructed. Out of the 120 samples analysed, 98 were positive for CaPV by Real- Time PCR (81.6%), and most of them wereSPPV. then 10 positive samples were sequenced and characterized by amplifying the ORF 103CaPV gene. sequencing and phylogenetic analysis for these positive samples revealed a high percentage of identity with SPPV isolated from different countries in Middle East. In conclusions, molecular characterization revealed nearly complete identity with all recent SPPVs strains in local countries that requires further studies to monitor the virus evolution and transmission pathways to better understand the virus pathobiology that will help for SPPV control.

Keywords : molecular epidemiology,Real-Time PCR, phylogenetic analysis, capripoxviruses
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