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VIROLOGICAL SURVEY OF MORBILLIVIRUS INFECTION IN CASPIAN SEALS

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Morbillivirus infections in Caspian seals (*Phoca caspica*) have been reported since 1997 and implicated in mass mortality of this species in 2000. In this study, we conducted virological survey on circulation of morbilliviruses in Caspian seals in interepizootic period. Seals were live sampled during tagging with satellite transmitters in late fall of 2007-2009, on their hauling out sites in Northern Caspian. Totally 149 specimens as nasal, tonsil, uro-genital, rectal swabs and blood were collected from 31 animals. The samples were screened for morbillivirus nucleic acid by reverse-transcriptase polymerase chain reaction (RT-PCR), with a set of universal morbillivirus primers targeted on conserved sequences in the phosphoprotein (P) gene. All swab samples of six individuals (one adult, five juveniles) out of 13 animals sampled in 2008 were positive, giving products of expected size 429 base pairs. The samples of adult seals tagged in 2009 were negative for morbillivirus presence. For phylogenetic analysis the nucleotide sequences of selected fragment were defined by sequencing of P gene of PCR-positive materials. Thirteen partial sequences of canine distemper virus sequences from public databases were used for analysis. On the base of P gene phylogenetically seal morbillivirus interepizootic variant of 2008 was close to epizootic strain CDV/Caspian seal/Baku/1997 and clustered together with viruses isolated from Caspian seals died during CDV infection outbreak among them in 2000. These data demonstrate that the CDV viruses similar to epizootic strains still circulating in Caspian seal population without clinical manifestation of morbillivirus infection and their re-emerging in certain circumstances will be a threat to those endangered species.