

5th International Congress on

INFECTIOUS DISEASES

March 01-02, 2018 Berlin, Germany

Genetic and evolutionary characterization of a novel picornavirus in Algerian *Miniopterus schreibersii* bats

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Despite the fact that bats are reservoir hosts of numerous viruses with zoonotic potential, the presence of the Picornaviridae family members in these flying mammals remains little known, however they may have the potential to cross species barriers. Picornaviruses are non-enveloped small positive sense-single stranded-RNA viruses, which evolve very fast: 80 species are counted to date. In order to be prepared to face newly emerging viral diseases our knowledge about the viruses circulating in animals of high zoonotic potential, is highly important in order to rapidly detect zoonotic spillovers. For this purpose, we accomplished co-phylogenetic analyses of host-virus relationship on *Miniopterus schreibersii* bat guano samples collected in Algeria in 2017, through both metagenomic and phylogenetic analyses. In this study, we report the first molecular data and genomic characterization of a novel picornavirus from the bat species *M. schreibersii* in Algeria. Phylogenetic analyses showed that this novel picornavirus belongs to Mischivirus genus and is closely related to *Mischivirus B*, also within the Mischivirus group there is no host jumping phenomenon observed comparing to other members of Picornaviruses.

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Biography

Zeghib Safia is a PhD student at University of Pécs in the virological research group. She completed her MSc in Genetics from U.S.T.H.B University in Algeria. She worked as a medical representative for three years, then joined Pasteur institute in Tunisia for six months where she worked on congenital deafness, after that she had been awarded a Stipendium Hungaricum scholarship and started her work on zoonosis in Algeria.

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