Genome similarities between human-derived and mink-derived SARS-cov-2 make mink a potential reservoir of the virus

Mohammad Khalid

King Khalid University, Saudi Arabia

SARS-CoV-2 has RNA as the genome, which makes the virus more prone to mutations. Occasionally, mutations help a virus to cross the species barrier. The SARS-CoV-2 infection to humans and minks (Neovison vison) are examples of zoonotic spillover. Many studies have been published on the analysis of human-derived SARS-CoV-2, but insight of mutations in mink derived SARS-CoV-2 is still lacking. Here we performed mutation analysis on the mink-derived SARS-CoV-2 genome sequences. We analyzed all available full-length mink derived SARS-CoV-2 genome sequences on GISAID (214 from Netherlands and 133 from Denmark). We found that the mutation pattern in the Netherlands and Denmark derived samples were different. Out of a total of 201 mutations, we found in this study, only 13 mutations were common in the Netherlands and Denmark derived samples. We found 6 mutations prevailed in the Netherlands and Denmark mink derived samples and these 6 mutations are also reported to prevail in human-derived SARS-CoV-2. We found many deletion mutations in the mink derived SARS-CoV-2 genome, man of tehm also reported in human-derived SARS-CoV-2. These resemblances between mink-derived and human-derived SARS-CoV-2 enable the virus to cross the species barrier and suggest mink a potential reservoir for the virus.

Biography

Mohammad Khalid has Completed PhD from Ulm University Medical Centre, Ulm, Germany in 2013 and did posdoctoral fellowship from Linkopink university, Linkopink, Sweden. Published research work in some of prestigious journals in the field of Virology. Presently working as Assistant Professor in the College of Pharamcy, King Khalid University, Abha, Saudi Arabia.