

Lab researchers hunt for clues in transmission of deadly Middle Eastern respiratory virus

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Monica Borucki, a scientist from Lawrence Livermore Lab's Biosciences and Biotechnology Division, looks at cell lines used for viral propagation.

Lawrence Livermore Lab researchers have used new genetic sequencing technology and bioinformatics analysis to define how a novel and deadly respiratory virus changes when it passes from one host to another.

The Middle East Respiratory Syndrome Coronavirus (MERS-CoV), an RNA [virus](#) related to Severe Acute Respiratory Syndrome (SARS), can cause serious respiratory illness, fever, cough and shortness of breath in carriers and has killed roughly 40 percent of diagnosed patients. Since first being reported in Saudi Arabia in 2012, scientists have determined MERS likely originated in camels, but not much is known about how it is transmitted to humans or other animals.

As described in a paper published by *PLOS ONE* on Jan. 20, using ultra-deep sequencing and [polymerase chain reaction](#) tests, LLNL researchers obtained data from nasal samples of three camels infected with the human MERS virus. While only five mutations were detected in the virus' genome sequence, nearly 500 genetic variants were identified within the samples.

The findings, according to LLNL virologist and lead author Monica Borucki, suggest a high number of genetic mutations occur throughout the [viral genome](#), previously undetected by consensus sequencing, making MERS readily transmittable from camels to humans, and potentially allowing it to survive in new environments.

Borucki said the findings are an early step in determining the regions in the viral genome that mutate easily, and this information could prove important to designing detection assays for MERS.

Since its discovery, more than 20 countries have reported cases of MERS, including South Korea, which experienced an outbreak last summer that resulted in 36 deaths, closed schools and required thousands to be quarantined. So far, just two cases have been reported in the United States. Both patients, who likely contracted the disease while visiting Saudi Arabia, fully recovered.

"There's still an incredible amount of work to be done," Borucki said.

"MERS is something that needs to be monitored carefully. It should not be ignored."

More information: Monica K. Borucki et al. Middle East Respiratory Syndrome Coronavirus Intra-Host Populations Are Characterized by Numerous High Frequency Variants, *PLOS ONE* (2016). [DOI: 10.1371/journal.pone.0146251](https://doi.org/10.1371/journal.pone.0146251)

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