

Scientists make new discoveries in the transmission of viruses between animals and humans

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From left: LLNL scientist Monica Borucki from the Lab's Biosciences and Biotechnology Division looks at cell lines used for viral propagation as members of her multidisciplinary research team, Jonathan Allen and Haiyin Chen look on. Credit: Jamie Douglas/LLNL.

Outbreaks such as the severe acute respiratory syndrome (SARS) Middle East respiratory syndrome coronavirus (MERS) have afflicted people around the world, yet many people think these trends are on the decline.

Quite the opposite is true.

The efforts to combat this epidemic are being spearheaded by a team of Lawrence Livermore National Laboratory (LLNL) scientists. Led by Monica Borucki, a principal investigator (PI) in LLNL's Biosciences and Biotechnology Division in the Physical and Life Sciences Directorate (PLS), the Lab researchers has recently made promising [new discoveries](#) that provide insight into the emergence of inter-species transmittable [viruses](#).

They discovered that the genetic diversity of a viral population within a host animal could allow a virus to adapt to certain conditions which could help it reach a human host. This discovery advances the scientific understanding of how new viruses produced from animal reservoirs can infect people. An animal reservoir is an animal species that harbors an infectious agent, which then goes on to potentially infect humans or other species. Borucki's team is investigating viruses related to SARS and MERS, but not the actual viruses themselves.

"The team's findings are the first steps in developing methods for predicting which viral species are most likely to jump from animals to humans and potentially cause outbreaks of diseases," said Borucki, who is the research project's PI.

Borucki's LLNL multidisciplinary research team includes Jonathan Allen, Tom Slezak, Clinton Torres and Adam Zemla from the Computation Directorate; Haiyin Chen from the Engineering Directorate; and Pam Hullinger, Gilda Vanier and Shalini Mabery from PLS.

Coronaviruses are one of the groups of viruses that most commonly jump to new [host species](#) as evidenced by the SARS and MERS, according to Borucki. These viruses appear to have jumped from

animals to humans and are capable of causing severe diseases in humans.

"Our discoveries indicate that next generation of genetic sequencing technology, combined with advance computational analysis, can be used to characterize the dynamics of certain viral populations," she said.

The team's work on coronaviruses received funding from LLNL's Laboratory Directed Research and Development (LDRD) program and the Defense Threat Reduction Agency (DTRA), an agency of the U.S. Department of Defense.

In June, a research paper published in the *Journal of General Virology* by other scientists cited the Borucki team's findings as pioneering, and it recommended their methodology for studying viral evolution.

Borucki said her team's research findings could eventually be used to influence how vaccines and antivirals are designed and tested.

"Deep Illumina sequencing (a type of genetic sequencing that involves sequencing reads in parallel) is already being used extensively to understand HIV and hepatitis C resistance to antivirals," she said. "We plan to follow up our findings by examining how animal host traits such as nutritional status (being malnourished or obese) influence how viruses evolve."

This latest discovery is part of a string of achievements for Borucki's team.

Provided by Lawrence Livermore National Laboratory

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