Han Xia PhD.

The Ebola outbreak – the arrival of chikungunya in Texas – continued fears about West Nile virus – all hot topics that have placed UTMB’s Galveston National Lab (GNL) in the media spotlight recently. So it’s not surprising to learn GNL researchers are also hard at work on still another emerging infectious disease -- Crimean-Congo hemorrhagic fever (CCHF). One of those researchers is postdoc Han Xia Ph.D. Xia came to UTMB from her home in Wuhan, China a year ago, to work for Dennis A. Bente DVM, Ph.D., who leads the GNL effort on CCHF.

Although the disease appears from Africa to Asia, outbreaks are sporadic in nature and a level 4 biosafety lab (BLS4) is required to study it and the tiny ticks that carry the virus. In the past, these obstacles meant little progress in understanding CCHF, much less how to combat it – a trend Bente and his team determined to reverse.

The work Xia performs each day in the GNL’s BSL4 facility illustrates how far the research has come in recent years. One of her projects involves using next-generation sequencing technology to analyze the CCHF viral genome found in infected cells retrieved from ticks and animal hosts. Xia is also preparing to conduct experiments using a recombinant CCHF virus with a bioluminescence marker. By introducing this marker into the virus, she can follow its path and record the progress of the infection. She explains, “We want to track where the virus goes, its replication rate, which tissues it affects and exactly how it impacts the specimen.” Xia said her overall research goal is to identify useful data about the viral evolution and its diversity at the molecular level. It is hoped this and other GNL research efforts will add important, much-needed information to the limited body of knowledge about the pathology of CCHF.

When asked how she became interested in virology, Xia provides a very telling, one-word answer – SARS. More than 8,000 people were diagnosed with Severe Acute Respiratory Syndrome or SARS during 2002 and 2003, the majority in China and Hong Kong. At that time, Xia was an undergrad studying biology at Wuhan University, about 500 miles north of the outbreak’s epicenter at Guangdong province in China. “The epidemic showed me how a virus can create a very big threat to public health. I think this is part of the reason I chose to study and work in virology,” Xia explained.

Xia expects to continue her research and training at UTMB for one more year and then return to China to work at the Wuhan Institute of Virology, Chinese Academy of Sciences. “I know I am very fortunate
to have the experience working at the GNL,” Xia said with a wide smile. “Very few scientists get a chance to work in a BSL4 environment and I’m really proud to be part of the research work on CCHF.”