

Chemists weigh intact virus mixture with mass spectrometer

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Carnegie Mellon University chemists, led by Mark Bier, have separated and weighed virus particles using mass spectrometry (MS). This is the first time that researchers successfully used matrix-assisted laser desorption ionization MS to analyze a mixture of intact virus particles.

Bier, research professor of chemistry and director of Carnegie Mellon's Center for Molecular Analysis, and graduate student Logan Plath will present their findings in a poster session at the American Society for Mass Spectrometry Conference on Mass Spectrometry and Allied Topics today, June 2, in St Louis.

"It is important to study virus particles because they are everywhere on our Earth and in enormous numbers. They are not all bad for humans and, in fact, it could be said that bacteriophages are essential for life as we know it," Bier said. "We need to understand the good from the bad to better understand nature and how we can best take advantage of these molecular forms."

Mass spectrometers separate ionized molecules based on their mass-to-charge ratio. One limitation of [mass spectrometry](#) is in the analysis of macromolecules. Most instruments are unable to efficiently detect such large molecules at low charge states or must resort to creating high charge states that require high-resolution mass analysis. As a result, most researchers don't analyze whole macromolecules. Instead, they break down macromolecules into smaller parts in wet chemistry laboratories and analyze the subunits. While effective, this wet lab process can be

time consuming and doesn't allow researchers to study intact macromolecules directly in the gas phase.

Because of their size, which can be more than a million times larger than a water molecule, viruses are one type of molecular complex that has seen only limited study by scientists using mass spectrometry. To overcome the high mass limitations, Bier's group uses a cryodetector-based matrix-assisted laser desorption/ionization time of flight mass spectrometer, called a Macromizer, that has 16 superconducting tunnel junction detectors. The 3.75 meter-long apparatus can analyze low charge heavy ions with a significantly higher signal than mass spectrometers with standard ionizing detectors. Carnegie Mellon is home to the only known active cryodetector mass spectrometer research lab in the U.S. and Bier's group also is developing the next generation cryodetector [mass spectrometer](#).

Using samples of cowpea mosaic virus gathered and purified by the lab of Case Western Reserve University's Nicole Steinmetz, Bier's team used mass spectrometry to weigh and separate a mixture of two variants of the virus. One contained RNA1 and weighed 5.65 megadaltons; the second contained RNA2 and weighed 4.84 megadaltons. These weights were close to the theoretical weights that had been proposed for the [virus particles](#).

Bier hopes that the technique, which he calls a form of "heavy [ion mass spectrometry](#)," can be used to analyze and study other viruses, and will be helpful in understanding the robustness of viral structure, the mechanics behind viral infection and provide new ways of virus detection and treatment. He also plans to continue to use the technique to study other types of heavy ions.

Provided by Carnegie Mellon University

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