

William R. Wiley

# EMSL In Brief

Environmental Molecular Sciences Laboratory

## Fighting Disease One Thousand Proteins at a Time

Using sophisticated bioinformatic methods and a unique suite of proteomic equipment offered at the Environmental Molecular Sciences Laboratory (EMSL), researchers have identified potential biomarkers for virulence in the plague-causing bacterium, *Yersinia pestis*. A biomarker is an indicator of change in a biological system, and biomarkers can yield information about disease state, susceptibility, or exposure.

The team, which includes scientists from EMSL, the Pacific Northwest National Laboratory—on whose campus EMSL resides, and Lawrence Livermore National Laboratory, recreated changes in the environmental conditions that *Y. pestis* experiences in passing from vector (e.g., fleas) to host (e.g., humans), thus inducing the bacteria in culture to express virulence-associated proteins. Applying relatively new bioinformatic and proteomic techniques, some of which were developed by EMSL scientists and users, the team compared the abundance change of nearly 1,000 proteins among control and virulence-mimicking cultures.



EMSL mass spectrometry capabilities were used to identify possible biomarkers for virulence in *Yersinia pestis*, a plaque-causing bacterium.

Of the proteins surveyed, 89 were found to have similar abundance changes to 29 known virulence-associated proteins, indicating they may be biomarkers related to virulence. In addition, 87 so-called hypothetical proteins were determined to be unique biomarkers for the virulence-mimicking conditions under which the bacterial cultures were grown. A hypothetical protein is one identified by a gene-finding algorithm whose sequence matches that of no other known protein and for which there is no other evidence it is an actual gene product. Biomarkers of disease progression show promise as detection tools for public health, medical, and defense applications. For example, drug and vaccine designers may use biomarkers to guide development of an agent that disrupts a biological pathway, resulting in a microbe's inability to infect a host.

The techniques used in this study can be applied across a wide range of biological systems. They are currently being employed to find biomarkers in other infectious agents, including *Salmonella* and soil microbes of interest for bioremediation.

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P.O. Box 999 Richland, WA 99352 • <http://www.emsl.pnl.gov> • 509-376-2553