

Plague proteome reveals proteins linked to infection

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Recreating growth conditions in flea carriers and mammal hosts, Pacific Northwest National Laboratory scientists have uncovered 176 proteins and likely proteins in the plague-bacterium *Yersinia pestis* whose numbers rise and fall according to the disease's virulence.

The team, led by the Department of Energy laboratory staff scientists Mary Lipton and Kim Hixson, identified the proteins as “unique biomarkers related specifically to growth condition,” according to a study in the latest issue of the *Journal of Proteome Research*.

Biomarkers associated with disease progression show promise as detection tools in public health and biodefense and can guide drug and vaccine designers in their quest to disrupt the microbe's ability to infect.

Y. pestis is the bacterium that caused the infamous Black Death plagues. Fleas are vectors for the disease and can spread it to rodent and human hosts. This study mimicked environmental conditions of *Y. pestis* in flea and in mammalian systems.

The proteome is a survey of proteins in a cell. Lipton, Hixson and colleagues at the PNNL-based Environmental Molecular Sciences Laboratory and Lawrence Livermore National Laboratory used proteomic techniques called accurate mass and time tag mass spectrometry and clustering analysis to compare abundance changes in 992 proteins under four different growth conditions, at 26 degrees and 37 degrees Celsius and with and without calcium.

They found 89 candidate proteins with similar abundance changes to 29 known virulence-linked proteins, and an additional 87 disease-condition-associated “hypothetical” proteins. The Institute for Genomic Research defines a hypothetical protein as one identified by a gene-finding algorithm that matches no other known protein sequence or contains no other evidence that it is an actual product of a gene.

The study authors said the same approach is being applied to a search for biomarkers across a wide range of biological systems, from other infectious agents such as Salmonella to soil microbes of interest in cleaning up toxic waste.

Source: DOE/Pacific Northwest National Laboratory

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