

# Enhanced Molecular Attribution through Proteomic Signatures (EMAPS) for Biothreat Agent Forensics

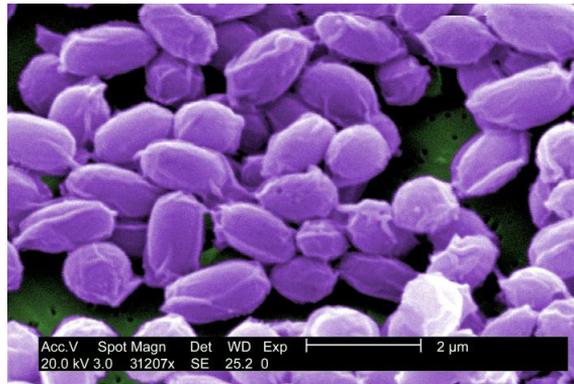
*There is a critical need for methodologies that generate a detailed signature of a biothreat agent (BTA). Genetic analysis alone cannot provide a full description of a BTA; information on how the material was prepared, by whom and the resources available to the operator cannot be obtained by genetic means.*

## The Challenge

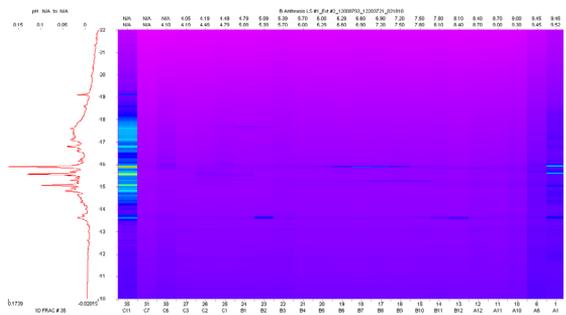
Obtaining useful information will require novel methods that provide a signature of the BTA that is highly sensitive and detailed enough for attribution. In some scenarios, the signature must be sufficiently reliable to withstand legal challenges in court. The proteome, which is the set of expressed proteins in a given type of cells or an organism, is the most appropriate source of molecular signatures.

## The Solution

Argonne researchers have developed a novel forensic methodology specific to BTA attribution called Enhanced Molecular Attribution through Proteomic Signatures (EMAPS). *Bacillus anthracis* spores, which cause anthrax, are the model organism for validation of the methodology. EMAPS technology can provide detailed information regarding the methods used to culture, purify and store the spores. This can help identify not only the specific organism used, but also the facilities used in its preparation and the technical sophistication of the operator.



*This scanning electron micrograph depicts spores from the Sterne strain of *Bacillus anthracis* bacteria. A key characteristic of the Sterne strain is the wrinkled surface of the protein coat of these bacterial spores.*



*A fingerprint of anthrax using Argonne's EMAPS technology.*

## The Results

This approach is an innovative improvement on previous spore analytic methods because of its molecular separation and protein chip fabrication technologies and the manner in which they are integrated into a single system. The methodology is particularly well suited for security missions because it combines sensitivity with a highly robust, semi-automated platform that does not require a specialized laboratory or expensive mass spectral analysis.

*“The EMAPS technology provides the most informationally rich molecular signature of any proteomic technology and does so at a fraction of the cost,”* said Dan Schabacker, biochemist, Argonne National Laboratory.