

## **Detection and characterization of novel infectious agent**

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The biological threat posed by emerging infectious disease has stimulated the development of technical approaches and bioinformatic methods to detect and assess the risks to military and civilian populations. Many of the challenges and concerns of characterizing such threat agents are shared by those addressing adventitious agents in medical products of biological origin. Increasing emphasis has been placed on next-generation and metagenomic DNA sequencing approaches, as well as computational tools that can distinguish pathogenic and non-pathogenic strains, in order to address issues of sensitivity and determination of likely clinical consequence.

The Defense Threat Reduction Agency has made significant investments in addressing the potential for novel biothreats through its linkage with academic and governmental enterprises. Several such efforts, notably those with the laboratory of Ian Lipkin at Columbia University, have advanced the scope and potential of metagenomic approaches and have supported the discovery of new viral threats. Interagency and private sectors efforts have been established to create pathogen reference datasets that can be shared between the Department of Defense, the Department of Homeland Security and the Centers for Disease Control. This has broadened the base of pathogen information that is available and stimulated creation of response teams for the rapid identification of novel threats. It is anticipated that some of these methods and strategies will be relevant to the area of adventitious agent discovery and validation, particularly in terms of establishing the potential for clinical consequence.