AMD Projects

Innovate • Transform • Protect

CDC's Advanced Molecular Detection (AMD) program fosters scientific innovation in genomic sequencing, epidemiology, and bioinformatics to transform public health and protect people from disease threats.

AMD Projects: Attacking Legionnaires' Disease

Rapid molecular detection of *Legionella* for outbreak response

First discovered in 1976 at an American Legion convention in Philadelphia, Pennsylvania, Legionnaires' disease continues to cause outbreaks in the United States. Even though it is a leading cause of potable waterborne outbreaks in the United States, reliable, rapid, and consistent analysis techniques have not been developed.

Available genetic techniques to determine the most likely source of transmission require matching clinical and environmental samples and can be used for only 1 of the more than 60 species of *Legionella*. Right now, it can take more than 3 weeks to completely identify the bacterium, if a specimen is even collected from a patient. These hurdles leave many cases and outbreaks uncharacterized. State and local health departments often rely on CDC laboratories because they do not have the specialized skills and extensive

People with Legionnaires' disease have pneumonia (lung infection) since the Legionella *bacteria grow and thrive in the lungs. Pneumonia is confirmed either by chest x-ray or on physical exam.*

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resources required to analyze *Legionella* specimens.

CDC is creating a database of *Legionella* genomes that will improve capacity for identifying and comparing outbreak-causing strains.

Advance molecular detection (AMD) techniques are revolutionizing how assessments are made about the source of disease transmission, which is the cornerstone of controlling *Legionella* outbreaks. Rapid identification of a source will allow faster implementation of prevention efforts. This project will help streamline methods for state and local public health laboratories investigating their own outbreaks, leading to quicker public health response. Ultimately, the methods developed through this project are the first critical steps in being able to detect *Legionella* directly from environmental or clinical samples,

For more information on Legionnaires' disease, please visit the CDC website, www.cdc.gov/legionella/index.html.

→ 2017 Update

Since the project began, investigators used AMD to develop and implement a new method called whole genome Multilocus Sequence Typing (wgMLST) to quickly compare *Legionella pneumophila* strains. Previously researchers could only characterize small areas of DNA at once. Using wgMLST, researchers are currently able to look at several thousand specific sections (alleles) of DNA. The data from wgMLST can be shared easily between public health laboratories investigating an outbreak allowing for reliable, rapid, and consistent analysis. This new testing method, along with another type of test—single nucleotide polymorphism (SNP)—that looks at variations in shared DNA regions, were evaluated through a joint project with the New York State Department of Health. Both wgMLST and SNP analysis allow for a better view of DNA than traditional methods helping researchers identify new differences between strains. Additional laboratories will test these new methods in the upcoming year. Researchers will also continue to expand the wgMLST database by adding hundreds of new informative alleles as more highly diverse strains of *Legionella* are sequenced. With these improved and standardized methods of analyzing isolates, laboratories will be able to match environmental samples and clinical specimens quickly and accurately. This will allow state and local public health laboratories to share results faster and help prevent additional cases of Legionnaires' disease.

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