

AMD Projects

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CDC's Advanced Molecular Detection (AMD) initiative fosters scientific innovation to transform public health and protect people from disease threats.

AMD Projects: Better Pneumococcal Disease Vaccines

Harnessing next-generation sequencing to monitor changes in population-based pneumococcal disease

In 2000, children in the United States won the lottery — that is the vaccine lottery — with the introduction of a brand new pneumococcal conjugate vaccine, PCV7, that protects against 7 sets of strains (serotypes) of *Streptococcus pneumoniae* bacteria. Known also as pneumococci, these bacteria can cause life-threatening illnesses such as pneumonia, meningitis, and bloodstream infections.

In the years after PCV7 was introduced, the number of children younger than 5 years old who get invasive pneumococcal disease dropped by 80%. In fact, the vaccine performed so well that even adults benefited because there were no longer so many kids carrying the bacteria in their upper respiratory tracts and passing it to others.

But once the 7 pneumococcal serotypes in the newer conjugate vaccine were nearly eliminated in the United States, other serotypes began taking advantage of the gaps left behind – known as “serotype replacement”. CDC data paved the way for introduction of the next-generation pneumococcal conjugate vaccine that would protect against the most common serotypes of 



Immunization is one of the most important things a parent can do to protect their children's health. Today, we can protect children younger than two years old from 14 serious diseases.



pneumococcal bacteria responsible for severe pneumococcal infections. This vaccine, introduced in 2010, protects against 13 serotypes, including 6 additional serotypes that were not included in the earlier vaccine.

To keep protecting future generations of children from disease, more extensive disease monitoring is critical to answer important questions. Is the new vaccine working as hoped against all 13 serotypes? Is serotype replacement happening again? If so, what are these new serotypes? Will they be resistant to antibiotics?

CDC will use whole genome sequence (WGS) analysis to answer these pressing questions. This faster approach allows for identification of serotypes, predictions of promising vaccine candidate components, and detection of emergence of antibiotic-resistance mechanisms.

For more information on pneumococcal disease and the pneumococcal conjugate vaccine, please visit the CDC websites www.cdc.gov/pneumococcal/about/index.html and www.cdc.gov/pneumococcal/vaccination.html.



2015 Update

In the first year, project investigators used advanced molecular detection (AMD) technologies to develop a new system, called the Automated Bioinformatics Pipeline (ABP), to detect and characterize *S. pneumoniae*. The ABP was created with more than 2,000 samples of pneumococcal bacteria that have caused invasive disease and can quickly determine what serotype a specific sample is and what antibiotics the sample is resistant to. Using the ABP, investigators analyzed over 1,000 samples of pneumococcal bacteria that caused invasive infections in 2015 (as of August 2015). The power of AMD methods was demonstrated in the project's first year when investigators used the ABP to help resolve a multi-state outbreak of pneumococcal disease in 2014.

As this work continues, investigators project that by mid-2016 they will analyze over 3,000 samples of pneumococcal bacteria recovered during 2015. Investigators continue to explore why some serotypes cause certain types of illnesses based on their DNA, ultimately hoping to find better ways to prevent *S. pneumoniae* infections.

Through this work, investigators are currently in the process of performing WGS on samples of invasive groups A and B streptococci collected in 2015 and developing ABPs for these two types of bacteria. They expect to complete WGS analysis of 6,000 samples from 2015 for all three types of bacteria by fall of 2016.