

AMD in Action

Innovate • Transform • Protect

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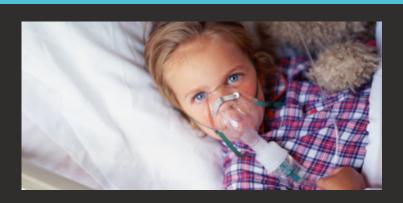
Advanced Molecular Detection and Response to Infectious Disease Outbreaks

In 2014, CDC focused AMD efforts on transforming the response to infectious disease outbreaks by making significant leaps in genomic sequencing and bioinformatics capabilities.



AMD provides quick answers

In early May 2014, AMD methods helped CDC scientists sequence the complete genome of Middle East Respiratory Syndrome Coronavirus, MERS-CoV, in less than 48 hours and provided reassurance that the virus is not rapidly mutating into a more infectious form.



CDC scientists used AMD methods to identify enterovirus D68, EV-D68, as the cause of severe respiratory illness in children. These methods also helped CDC develop a faster diagnostic test and deploy it to states, increasing state laboratories' ability to identify cases. Between August and December 2014, CDC and states confirmed over 1,100 cases of EV-D68 infection, a much greater number than reported in previous years.

A Listeria outbreak affected at least 32 people in 11 states between October and December 2014. Seven of those people died. Using AMD methods, CDC was able to identify the illnesses as a cluster one week faster than would have



occurred with older methods. CDC worked with state and local health departments, the Food and Drug Administration, and industry to identify prepackaged caramel apples as the source of the outbreak. Investigation partners were then able to take action to inform the public and get caramel apples off the shelves to keep more people from becoming ill.

In 2014, AMD methods revealed food sources of **Listeria** that were never suspected before, including lettuce, peaches, and nectarines. Knowing these items can potentially be contaminated will help food safety partners better detect

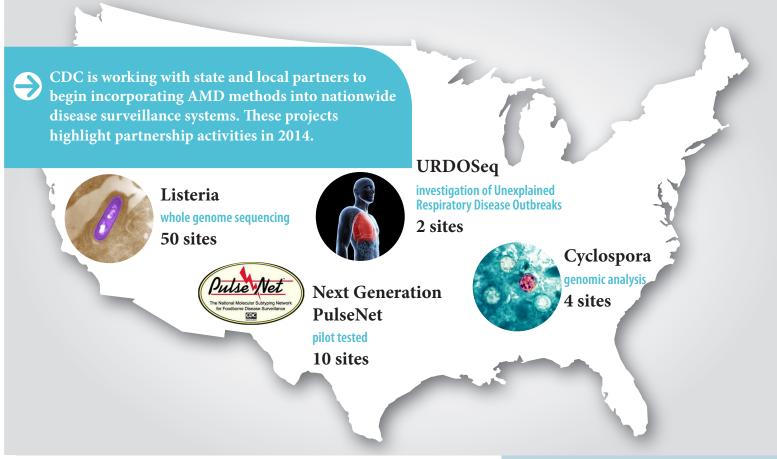


and respond to outbreaks in the future.

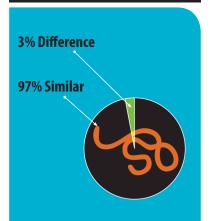


2014 Accomplishments

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Changes in the Ebola Virus From 1976 to 2014



In September 2014, CDC scientists used AMD methods to sequence the complete Ebola virus genome from Liberian isolates within 72 hours of receiving the patient's sample.

This genetic sequence information confirmed the Liberian viral samples were 99% identical to the virus circulating in Guinea and Sierra Leone. Furthermore, CDC could see that the virus in the 2014 outbreak is 97% similar to the virus that was first identified in 1976. Knowing that the virus is not rapidly mutating helps doctors in the field have confidence in the treatments and interventions they are using.

In 2014, CDC used AMD methods to help local and state health departments investigate 20 clusters of tuberculosis. The addition of AMD methods improved the accuracy of outbreak investigations. This partnership gave local and state health departments the information they needed to take action and focus intervention resources.



FY2015 Priorities

- Evaluation
- Partnership engagement
- Innovation
- State and local strategic planning

Increased Server Storage

