

AMD Accomplishments 2015

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Innovate • Transform • Protect

Advanced Molecular Detection and Response to Infectious Disease Outbreaks In 2015, CDC's AMD initiative continued to revolutionize the response to disease outbreaks by implementing high-priority programs that improve detection and tracking of infectious pathogens.

AMD Speeds Development of Diagnostic Methods for Zika Virus



When mosquito-borne **Zika virus** spread to the Western Hemisphere in 2015, doctors in Brazil saw increased numbers of babies born with microcephaly and suspected these were linked to the virus. Brazilian health officials sent samples of several Zika virus strains to CDC.

Using AMD methods, CDC scientists were able to sequence genomes of the viral strains and develop, validate, and distribute a molecular diagnostic assay protocol to detect emerging strains of the virus within approximately 3 weeks of receiving Zika-positive samples; a process that would have required 3–4 months with older methods.



In collaboration, CDC and USDA used AMD to examine gene sequence data of **two avian influenza H5 viruses** — H5N8 and H5N2. Hundreds of virus samples were taken from domestic poultry populations across the U.S. Results showed that the emerging H5 viruses in poultry were **genetically different from the H5N8 candidate vaccine virus (CVV)** developed during 2014–15. CDC used this genetic data to **rapidly create new panel of H5 CVVs** for use by vaccine manufacturers, in case human vaccine against these emerging H5 viruses becomes necessary.



CDC scientists used AMD to **link a case of Valley fever** from a person in south-central Washington State to *Coccidioides* fungus in soil samples taken in the state, far from its endemic range in the Southwestern United States. Investigators later found additional human and animal cases in the region. AMD revealed the Washington strain of this fungus is genetically different from the strain found in the Southwestern United States. CDC is using AMD to better understand the range of *Coccidioides* fungus in soil.



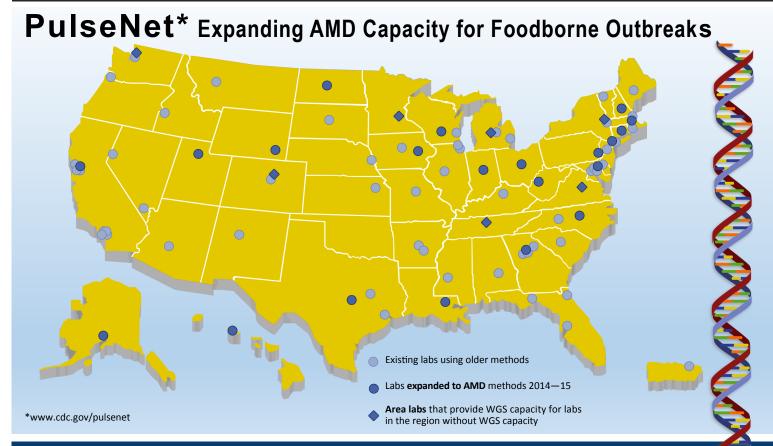
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U.S. Department of Health and Human Services Centers for Disease Control and Prevention

Updated: March 2016

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CDC completed the first step in developing methods for sequencing DNA of *Mycobacterium tuberculosis* directly from sputum. These methods have the potential to determine the antimicrobial susceptibility of TB bacterium within days rather than the weeks currently required, leading to earlier initiation of treatment and decreased spread of antimicrobial-resistant TB.

AMD methods helped trace links between HIV infections associated with injection drug use in a rural Indiana outbreak. The outbreak affected 190 people, 90% of whom were co-infected with hepatitis C virus (HCV). CDC also used **AMD to**

identify the overlap of HCV and HIV transmission

clusters. By combining HIV laboratory data, case demographic data, and viral genetic sequences for each infected person's HIV strain, researchers could monitor for spread of the outbreak in **near real-time**, allowing public health officials to **focus prevention efforts**, including outreach for HIV testing and pre-exposure prophylaxis, where they will be most effective.

FY 2016 Priority Areas

- Innovation
- Data integration
- Expansion of AMD capacity
- State and local workforce development

CDC Sequence Data Submitted to Public Gene Repositories



BEFORE AMD 7,749 Up until 2012

AFTER AMD 155,797 (2013 – 2015)

20X More