

MODERNIZING INFLUENZA SURVEILLANCE



Influenza is a serious and persistent public health threat with as much as 20% of the population contracting the flu each year. Flu leads to hospitalizations, lost wages, and as many as 49,000 deaths annually.

Flu vaccines are one of the most effective prevention measures, but flu viruses are constantly changing which requires close public health monitoring of the viruses and frequent, sometimes annual, vaccine updates. Public health laboratories provide critical influenza surveillance data which inform how flu viruses change over time. Understanding these virologic changes provide public health officials with vital information about severity of the flu, who may be the most susceptible, and pertinent changes needed for next season's flu vaccines.

With the advent of next generation sequencing (NGS) capabilities, a form of advanced molecular detection (AMD), laboratories can now sequence the genome of the flu virus very quickly. Prior to the availability of this technology, vaccine surveillance solely relied on traditional methods that were laborious and not always effective for characterizing some virus strains. NGS allows CDC to get a better sense of how genetic alterations can lead to changes in the flu viruses that will impact vaccine and therapeutic effectiveness. Until this year, the final step in the testing algorithm for national surveillance was NGS, which was only being performed at CDC. This led to an additional one to two months for the generation of sequence data. Since flu viruses are

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constantly changing, it is important to have timely data to inform vaccine compositions each year. Any efficiencies that can be gained allowing for faster generation of surveillance data can have huge impacts on vaccine composition decisions, which must be made each spring to allow time for vaccine development in time for the next flu season.

In 2015, CDC and APHL conducted a pilot study with the Wisconsin State Laboratory of Hygiene, which serves as a National Influenza Surveillance Reference Center. As a national reference center, Wisconsin receives influenza specimens from other public health laboratories to perform surveillance testing on behalf of CDC. Wisconsin became the first state to be trained by CDC to use NGS for national influenza surveillance purposes. Within three months, Wisconsin had established the necessary equipment and technology infrastructure, trained laboratory staff and was successfully performing sequencing and sharing data with CDC. Having public health laboratories, such as Wisconsin, with sequencing capacity allows for a faster turnaround time and more real-time view of how flu viruses are evolving.

The pilot project allowed Wisconsin to begin the 2015-2016 influenza season performing NGS on all specimens submitted for surveillance testing. This has reduced the burden on CDC for sequencing testing and has provided this data for analysis faster than ever before. The experiences and expertise Wisconsin has gained through this project will pave the way for implementing sequencing at the remaining two National Influenza Surveillance Reference Centers and potentially other public health laboratories. The use of AMD technologies to enhance our existing national influenza surveillance system will result in a more complete picture of how flu viruses change overtime and the impact of those changes on important policy and public health decisions such as seasonal influenza vaccine composition.