Surveillance at the Animal-human Interface and Large-scale Sequencing of Pathogens in Response to Public Health Emergency

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Infectious diseases remain one of the leading causes of death, especially in developing countries. Early identification and classification of the causative agents allow informed interventions for better public health outcomes. Recently emerging zoonotic pathogens, like the H7N9 and highly pathogenic H5Nx avian influenza viruses, the Ebola virus and the Middle East Respiratory Syndrome coronavirus have caused great human suffering and great cost to the community. Sequencing has been one of the main tools that have allowed the identification and classification of these pathogens and the formulation of treatment and vaccine strategies. With next generation sequencing (NGS) viruses, and even viromes, can be identified rapidly from large numbers of patient or animal samples at relatively low cost, whether or not viruses can be isolated. This has changed the effectiveness of zoonotic disease surveillance in the field, and in hospitals as infections can be monitored as they run their course in patients. Large scale surveillance backed by NGS allows a complete picture of the variation of zoonotic agents in the field to be obtained. This can identify changes in threat levels, the emergence of potential new threats and suggest prevention measures. Sequencing of zoonotic agents as a disease progresses allows a better understanding of virus-host interactions and potentially can suggest novel treatment options. I will discuss our use of NGS as part of our surveillance program covering the ongoing H7N9 and H5Nx avian influenza outbreaks and a few other emerging infectious diseases in Asia and show how this gives insights into the emergence and development of these threats.