

It is estimated that each year, seasonal flu epidemics cause from 2 to 5 million cases and 250 000 to 500 000 deaths worldwide. The emergence of a new strain of influenza A virus in 2009 resulted in pandemic that lasted over two years and was responsible for more than 60 million cases in the United States of America alone. These figures show that the newly emerging strains of influenza A virus pose a serious threat to public health.

Reassortment of genetic segments during coinfection of one organism with strains from different hosts could serve as a potential source of new, dangerous strains of influenza A virus, and may lead to overcoming species barriers and adaptation of the virus to new host. The World Health Organization (WHO), the Food and Agriculture Organization of United Nations (FAO), and the World Organization for Animal Health (OIE) issued many reports about mixed infections between humans and animals, describing the gravity of the problem. All the organizations recommended specific procedures to limit the mixing of different strains of the virus. They also clearly stated that the adaptation of human viruses among farm animals would create a potential for reassortment with other viruses of swine or avian origin and emergence of a novel, more virulent strain. According to the concept of "One Health", which is now the basis for cooperation between the CDC, WHO, FAO and OIE, human health is related to the animal health and the environment, so we should put great emphasis on monitoring, diagnostics and control of influenza virus infections not only in humans but also in animals remaining in our immediate vicinity in order to collect data and evaluate potential hazard which may result in emergence of dangerous human and/or animal strain of the virus.

The aim of this project is to assess the genetic variability of influenza A virus strains prevalent among the swine herds and bird flocks in Poland. This will allow to gain knowledge about epidemiological situation we are in, being a part of a common ecosystem in which individual species, susceptible to infection with the same type of virus remain in close contact.

With the assist of Polish Veterinary Institute, we will collect the samples both from sick animals and animals without influenza symptoms, from farms across the country. The presence of influenza A virus in collected isolates will be confirmed by standard diagnostic methods. Subsequently, we will gather information about the whole genome sequence of confirmed influenza A strains found in isolates using Next Generation Sequencing methods. This will allow to characterize the genetic variability of the virus. Collected data will be used to assess the risk for public health associated with influenza A virus strains circulating among the livestock in Poland. This will enable the preparation and timely introduction of appropriate directives and procedures regarding contact with breed animals, of course if a high risk of reassortment and the emergence of new strains is confirmed. If, however, the study does not demonstrate such a risk, we will be aware of the epidemiological situation prevailing in the country and equipped with the procedures and tools needed to maintain that state of knowledge.