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Introduction

Running from 2010-2013, the "European surveillance network for influenza in pigs (ESNIP) 3" (http://www.esnip3.eu/index.html) represents the only organised surveillance network for influenza in pigs in Europe and seeks to strengthen formal interactions with human and avian surveillance networks.

Materials and Methods

The project consortium comprises 24 participants, contributing a variety of specialities and skills ensuring multi-disciplinary cutting-edge outputs. Among them, 15 partners are actively involved in swine influenza (SI) surveillance. Three work packages aim to increase knowledge of the epidemiology and evolution of SI virus (SIV) in European pigs to inform changes in disease trends and variation in contemporary viruses through organised field surveillance programmes. During the first year of the project, activities focused on the exchange of surveillance systems and standardisation and validation of methods. An inventory of virological and serological surveillance systems has been organised through a questionnaire.

To confirm that all participating laboratories were capable of detecting all relevant SIV subtypes, a PCR ring trial was arranged. The panel consisted of 17 positive samples, 9 negative samples, and 2 'lures' (decoys) – and was sent to 12 participating partners for detection of positive samples.

In order to validate and calibrate the performance of the selected HI protocol to be used for preliminary antigenic subtyping, a standard panel of five sera and antigens was prepared and sent for testing to four laboratories.

Results

An inventory of the surveillance programmes that are currently active in the participating countries , showed that passive surveillance was being (or will be) used in most cases.

Selected virus isolates from the different countries have been collected and curated in a central virus bank at AHVLA, UK. These isolates are presently subjected to detailed antigenic (HI assay characterisation using swine hyperimmune monospecific sera and antigenic cartography) and genomic (full genome sequencing) characterisation. Data derived from surveillance activities have been merged. Briefly, in most countries the European subtypes avian-like (av)H1N1, the 2009 pandemic variant H1N1 (H1N1pdm09), H1N2 and H3N2 constituted the dominating subtypes in 2011. H1N1pdm09 viruses were isolated at an increasing prevalence in some countries, likely indicating that this subtype has become established in the swine population. In contrast, the H3N2 subtype has not been isolated in some geographic areas whereas it was prevalent in other parts of Europe.

Twelve partners participated in the PCR ring trial and the results showed that every laboratory employs diagnostic tests capable of detecting all relevant circulating SIV subtypes, including the H1N1pdm09 virus. Some differences in sensitivity and specificity were seen among the participating labs, depending on the assays used.

Reference panel testing by HI assay in four laboratories revealed small differences in obtained titers, but in general the consistency among the laboratories was good, and the panels were provided to partners.

Conclusions and Discussion

The activities of the ESNIP 3 project will improve SI diagnosis by updating reagents employed in the recommended techniques. These approaches will aid pandemic preparedness and planning for human influenza whilst providing an evidence base for decisions relating to veterinary health. *This work was supported by the ESNIP 3 project (Grant #259949, headed by Prof. IH Brown; AHVLA, UK).*