

ΔELTA-FLU



DYNAMICS OF AVIAN INFLUENZA IN A CHANGING WORLD

Report on the database of avian influenza outbreaks in EU since 2005 including genetic data of viruses

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SUMMARY

An inventory of potential data sources and available databases on HPAI and LPAI outbreaks in poultry that have occurred since 2005 in Europe has been undertaken and a pilot database established via the WP lead partners P3 Defra-APHA and IZSVe. Poultry outbreak data collected by Defra-APHA in the context of the EFSA grant “Data collection, literature review and spatial models for virus spread in preparation to the mandate on avian influenza” formed the basis of the pilot dataset, which has been populated with outbreaks data up to 31st April 2018 and conveniently amended for Delta-Flu purposes. Included are a data dictionary with the description of each field included in the final record layout and sequence information, when available.

INTRODUCTION

To date no harmonized data collection on Avian Influenza outbreaks in EU exists. Considering the gaps in knowledge, as detailed in the Delta-Flu project, a comprehensive review of the data sources on AI outbreaks in Europe since 2005 was deemed pivotal. Data on avian influenza outbreaks that have occurred since 2005 in Europe have been collated into an initial database that can be updated during the course of the project, all partner countries will contribute. The above data will be also exploited for eco-environmental analyses of avian influenza outbreak occurrence, as described in ‘*Subtask 2.1.1 Determination of environmental factors associated with increased risk of AIV incursion*’, and will form the basis for any other data analysis that will be performed within the Delta-Flu project.

METHODS

An inventory of data sources on AI outbreaks in poultry occurred in EU since 2005 is summarized below:

EUROPEAN COMMISSION: ANIMAL DISEASE NOTIFICATION SYSTEM

The European Commission collects data via the Animal Disease Notification System (ADNS) on a legal basis ([Council Directive 82/894/EEC](#), as last amended by Commission Implementing Decision 2012/737/EU). A disease overview by means of aggregated data is given on the EU website and it is up to date. Raw data can be extracted by the delegate of each member state and include mainly demographical aspects for each primary and secondary cases of HPAI and LPAI in birds. Data can be obtained separately for domestic poultry, wild birds and captive birds. There are potential concerns with extracting this data and making aspects of it publically available. We will discuss this with European Commission officer. Much of the data available though can also be found via EMPRES-i (FAO) and WAHIS (OIE).



FAO: EMPRES-I

The FAO Global Animal Disease Information System is an epidemiologic database that provides information on publicly reported outbreaks of priority animal diseases such as highly pathogenic avian influenza. Data are present since July 2005 onwards for HPAI and LPAI outbreaks in domestic and wild birds and information is up to date. To support epidemiological analysis, disease events can be displayed on geographic maps or described in graphic functions. EMPRES-i also integrates data from other databases, i.e. livestock density or environmental layers from FAO databases (e.g the Global Livestock Production and Health Atlas, GLiPHA) and from other systems. The EMPRES-i influenza includes a genetic module that aims to facilitate the analysis and better understanding of influenza by linking genetic information to detailed epidemiological disease event records. The EMPRES-i genetic module offers combined epidemiological information curated in EMPRES-i (managed by FAO) and genetic information curated in OpenFluDB (managed by the Swiss Institute of Bioinformatics). As a proof of concept, the EMPRES-i genetic module focuses on HPAI H5N1 first and has for the time being a limited number of linkages (30% of the total number of H5N1 disease events).

In addition, a report containing information derived from an epidemiological investigation, as transmitted to the OIE from each country, is given *as PDF file* and contains the following info:

- (i) Location of event with geographical coordinates
- (ii) Status of the event, what disease, serotype and information source
- (iii) Species affected with five categories: at risk, cases, deaths, destroyed, slaughtered
- (iv) Laboratory test, data test, test result

If a genetic link has been found (proposed or validated), the genetic information related will be available for each event

OIE: WAHIS

The WAHIS Interface provides access to all data held within OIE's new World Animal Health Information System (WAHIS), since 2005. It replaces and significantly extends the former web interface named Handistatus II System.

A comprehensive range of information is available from:

- immediate notifications and follow-up reports submitted by Country / Territory Members notifying exceptional epidemiological events occurring in their territory
- six-monthly reports stating the health status of OIE-listed diseases in each Country / Territory
- annual reports providing health information and information on the veterinary staff, laboratories and vaccines, etc.



Information can be derived BY COUNTRY/REGION (in this case the info includes all notifiable diseases in the country/region selected) OR BY DISEASE (in this case the info includes all countries in the world) for a specific year. Information is not always up to date.

EFSA

In the context of a contract between EFSA and a consortium led by Rotterdam University (contract title “Data collection, literature review and spatial models on avian influenza”), data has been collected about HPAI and LPAI outbreaks in domestic poultry and detection of HPAI and LPAI in wild birds in EU from 2005 to 2015, including genetic info.

The record layout for the EU HPAI and LPAI poultry outbreaks consists of 91 and 83 variables, respectively. The following sources of data were used to create a collated dataset: ADNS, consortium partners (from internal epidemiological outbreak investigations), EURL for Avian Influenza (APHA Weybridge), data from presentations made by Member States to the Standing Committee on the Food Chain and Animal Health (SCoFCAH) at the European Commission.

The record layout for the detection of HPAI and LPAI in wild bird in EU consists of 29 variables. The following sources of data were used to create a collated dataset: NewFluBird database (hosted by FLI, Germany), the Influenza Research Database (<http://www.fludb.org/>, this database has ~70,000 samples from wild birds in Europe collected between 2007 and 2013), data from consortium partners.

DELTA-FLU DATABASE

Poultry outbreaks data collected by Defra-APHA in the context of the EFSA grant “Data collection, literature review and spatial models for virus spread in preparation to the mandate on avian influenza” formed the basis of the pilot dataset. Although this work was requested by EFSA, much of the work done and the additional data that was added came from DELTA-FLU collaborating partners.

Data from the sources listed above were combined with the pilot dataset to bring the up to date and fields were added for Delta-Flu purposes. One of the advances of the final dataset will be the additional sequence ID for all those that have been submitted to genetic databases, both full and partial genomes, and those held by consortium partners that are as yet not publically available and/or soon to be submitted. The database is a single flat file with one record per outbreak event. There are currently 83 fields.



KEY FINDINGS FOR EXPERIMENTAL STUDY DELIVERABLES

The dataset includes variables covering the following themes:

- (i) Uploaded data as they appear in the ADNS database
- (ii) managerial and demographical aspects of the farms, as collected by epidemiological investigation
- (iii) laboratory analyses conducted
- (iv) sequence identification and other molecular analyses
- (v) movements of people, poultry, and vehicles

The database concept was discussed and agreed at an interim meeting at the 10th ISAI in Brighton, April 18. Partners agreed with the pilot plan and the initial database was presented and discussed at the first Annual meeting in Rotterdam, 27-28 June 2018.

NUTScode	latitude	longitude	species	reproduction	startY	startM	startD
UKF30	53.429	0.060	TURKEYS	MEAT	2016	12	16
UKL14	51.778	-4.221	BYF		2017	1	3
UKE22	54.047	-2.154	BYF		2017	1	6
UKF30	53.464	0.020	GEESE	MEAT	2017	1	16
UKD43	53.939	-2.942	PHEASANTS	BREED	2017	1	24
UKF30	53.035	-0.017	TURKEYS	BREED	2017	1	26
UKD43	53.925	-2.921	PHEASANTS	BREED	2017	1	27
UKD43	53.933	-2.951	PHEASANTS	BREED	2017	1	30
UKH14	52.367	0.982	CHICKENS	BREED	2017	2	14
UKC21	54.863	-2.507	CHICKENS	EGG	2017	2	24
UKD43	53.868	-2.959	BYF		2017	5	4
UKD43	53.874	-2.958	BYF		2017	5	6
UKH13	52.372	1.164	BYF		2017	6	3
UKM22	56.100	-3.445	CHICKENS	BREED	2016	1	13

Figure 1: Basic Epidemiological fields sample from database

EURLLabTest	EURClade	sequenced	virusName
RRT-PCR, serology, VI, full genome sequencing	2.3.4.4	Y	A/turkey/England/052131/2016 (H5N8) HP
RRT-PCR, serology, VI, full genome sequencing	2.3.4.4	Y	A/chicken/Wales/000023/2016 (H5N8) HP
RRT-PCR, VI, full genome sequencing	2.3.4.4	Y	A/chicken/England/000572/2017 (H5N8) HP
RRT-PCR, serology, VI, full genome sequencing	2.3.4.4	Y	A/turkey/England/003778/2017 (H5N8) HP
RRT-PCR, VI, full genome sequencing	2.3.4.4	Y	A/pheasant/England/8934/2017 (H5N8) HP
RRT-PCR, VI, full genome sequencing	2.3.4.4	Y	A/turkey/England/010538/2017 (H5N8) HP
RRT-PCR, serology, VI, full genome sequencing	2.3.4.4	Y	A/pheasant/England/014146/2017 (H5N8) HP
RRT-PCR, serology, VI, full genome sequencing	2.3.4.4	Y	A/pheasant/England/015238/2017 (H5N8) HP
RRT-PCR, serology, VI, full genome sequencing	2.3.4.4	Y	A/chicken/England/019219/2017 (H5N8) HP
RRT-PCR, VI, full genome sequencing	2.3.4.4	Y	A/chicken/England/026832/2017 (H5N8) HP
RRT-PCR, serology, VI, full genome sequencing	2.3.4.4	Y	A/chicken/England/037977/2017 (H5N8) HP
RRT-PCR, serology, VI, full genome sequencing	2.3.4.4	Y	A/chicken/England/038182/2017 (H5N8) HP
RRT-PCR, serology, VI, full genome sequencing	2.3.4.4	Y	A/chicken/England/042318/2017 (H5N8) HP
RRT-PCR, Serology, VI, HI, NI, IVPI, full genome sequencing		Y	A/chicken/Scotland/532/2016 (H5N1) LP

Figure 2: Laboratory detail fields from database



symptomatic	housing	deconVehicle	deconPeople	protectedFeed	biosecurity	travelAsia
N	free range/outdoor	U	U	U		4 U
U	indoor open to environment	U	U	U		U
N	free range/outdoor	U	U	U		U
U	free range/outdoor	U	U	U		U
Y	indoor open to environment	U	U	U		U
Y	indoor controlled environment	U	U	U		1 U
U	outdoor access	U	U	U		U

Figure 1: Advanced epidemiological detail dields from database

LOCATION OF PRIMARY DATA

It is proposed that the database will be made available initially via Flu-Lab-Net (<https://science.vla.gov.uk/flu-lab-net/>) until the database is completed whereupon it will be hosted permanently in a location agreed upon by consortium partners.

FURTHER DEVELOPMENT OF DELIVERABLE 2.1

Whilst the creation of the database fulfils the deliverable (D2.1 - Report on database of avian influenza outbreaks in EU since 2005, including genetic data of viruses), it is an active deliverable. New data will be added to the database as it is generated through the lifetime of the DELTA-FLU project. Population of the laboratory and virus details alongside advanced epidemiological details is a difficult process and will take time to complete.

