



## HPAI epidemic narrative – Phase 1

A new highly pathogenic avian influenza viral strain was detected on Jolly island about 30 days ago, in a chicken farm producing stage 1 broilers. At this facility, which hosts around 5000 birds, the farmer reported an abnormal increase in mortality combined with neurological and respiratory signs. It is believed that the virus was introduced into this farm via contact with infected wild birds, as the farm is located in the high-risk zone<sup>1</sup> (HRZ), not far from the Southern region where there is a higher poultry farm density. There is very little information available on the viral strain, but preliminary genomic analyses suggest it is likely a new highly pathogenic avian influenza virus, subtype H5N0.

Following detection of the index case, local veterinary authorities immediately implemented our national regulations, which have been largely inspired by those in Europe. In brief, they consist of:

- **National standstill:** upon the detection of the index case, a national standstill of three days was implemented, with all live-poultry movements (between farms and to the slaughterhouses) and imports from the hatchery island strictly forbidden; immediately after the end of the standstill, 2 additional infected farms were detected, one in the southern region and the other in the north, both likely resulting from spillover events from infected wildlife.
- **Suspicion management:** if a poultry flock is suspected because of a sudden increase in mortality, samples are taken on 20 dead or diseased animals, and are immediately sent to the national reference laboratory; results are usually provided in around 2 days.
- **Reactive culling:** if the tests are positive, reactive culling is implemented as early as possible; farms are put under quarantine, culling teams are mobilized, and culling itself generally occurs within the subsequent few days; if the culling capacity of the veterinary services is reached, culling can be delayed to prioritize the culling of infected flocks that have been confirmed earlier; culling of a flock is done in one to three days, depending on the size of the flock; repopulation of depopulated farms is not possible until we have a clearer idea of the epidemiological situation.
- **Contact tracing:** for all stage 2 chicken broiler outbreak farms, a backward tracing of the flock is done to identify the stage 1 broiler farm that sent the batch; subsequent forward tracing is then implemented to identify the other stage 2 broiler farm(s) that received chickens from the same batch as the outbreak farm; these at-risk stage 2 broiler farms are sampled and tested; if they are positive, the flock is culled.

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<sup>1</sup> The high-risk zone (HRZ) corresponds to a composite area where migratory birds stop over during their migration that started a few weeks ago or where high concentrations of *Laridae* (gulls) are found.

- **Zoning:** regulated zones (separate from the high-risk zone associated with HPAI risk from wild birds) are put in place around outbreak farms for 28 days, and consist of both a 3 km protection zone and a 10 km surveillance zone.
  - o **Movement bans in the regulated zones:** three days after the detection of the first outbreak, the nationwide movement ban was lifted for farms outside the regulated zones that are sending a flock to the slaughterhouse and for stage 1 broiler farms that are sending shipments to stage 2 broiler farms; farms located in the regulated zones (irrespective of their farm type) can only move poultry to the slaughterhouse at the end of their production cycle (this also applies to stage 1 broiler farms); note that farms are allowed to restock as long as they have not been culled.
  - o **Enhanced biosecurity and detectability in regulated zones:** all farms located within a regulated zone are visited by their veterinarian at least once, as soon as possible after their inclusion in a zone, to improve farmer awareness of HPAI; the likely consequences of this are that farm workers become a bit more compliant with external biosecurity practices, use additional hygiene precautions to avoid contamination, and suspicions are reported in a timelier fashion than outside these regulated zones.
- **Preventive culling:** from 1 January, given that the virus kept actively circulating, a preventive culling strategy targeting all poultry flocks (irrespective of the species and of the farm type) located within 1 km of infected premises was implemented; RT-PCR tests have been applied to all preventively-culled flocks; in general, reactive culls (depopulation of infected farms) have priority over preventive culls, *i.e.* all infected flocks in the queue for depopulation need to be depopulated before any at-risk flock is preventively culled; the culling capacity of the rendering companies has been reached since 6 January, meaning that we start to see some delays for starting depopulation actions; veterinary services are currently negotiating with the competent authority of the neighbouring island to obtain additional rendering trucks and mobile depopulation sites, with the hope of improving the culling capacities in the coming days.
- **Pre-movement testing in the HRZ:** all stage 1 broiler flocks located in the HRZ and planned to be sent to stage 2 broiler farms require a negative pre-movement RT-PCR test, determined via a single batch test of 20 birds in the three to seven days prior to shipment, in order for the shipment to proceed.
- **Wild bird management:** there is no integrated wild bird surveillance or management, so cases are not reported to Jolly Island veterinary authorities. Any details regarding wild bird cases have been provided only to serve as back story and add to the fun of this experience. However, the effects of infected wild birds are real, and they are known to migrate in early winter with stragglers seen through February.

Despite these measures, we have to say that the situation is NOT under control. As of the morning of 13 January, the virus has been detected in 103 poultry farms, with a majority of them located in the Southern region where the poultry farm density is higher.

The transmission characteristics and host preference of the virus isolated on Jolly Island are still unclear, but early raw epidemic data suggest that galliform (chicken) farms may have been more frequently infected as compared to palmiped (duck) farms, suggesting galliform farms could play a more important role in the spread. Local veterinary authorities managed to obtain daily mortality registers for a few outbreak farms detected by passive surveillance, and have made this data available to you.

Attached to this narrative, you will find a series of files that contain all the phase 1 epidemic data that veterinary services could collate. It is expected that these datasets are accurate. They include:

- **cases**: this spreadsheet provides you with all outbreak information we currently have on these farms, including unique numeric farm ID, date of suspicion, date of laboratory confirmation, method of detection, cull start and end dates (inclusive) and cull status.
- **preventive culls**: this spreadsheet serves as a ledger of all preventive culls that have been planned, completed, or remain in-progress, and contains unique numeric farm ID, cull status, and cull start and end dates (inclusive).
- **movements**: this spreadsheet reports all movements of poultry batches between stage 1 and stage 2 broiler farms. It contains the date of movement, the source farm ID, the destination farm ID, and the movement volume.
- **activity**: this spreadsheet reports, for all registered poultry farms, the dates of farm activity, with the date the batch entered the farm and the date the batch left the farm; the complement of the activity periods correspond to the periods of downtime when the farm is left empty between subsequent poultry batches. If a batch end date is not given, it is because the farm is currently active at the time of data preparation.
- **mortality ledger**: only available as scanned copies, these reports detail the daily mortality incidence as observed in the farm. They are also our only insight into within-farm dynamics. Each ledger must contain the associated farm ID, farm capacity, date of record, and mortality count. These ledgers are not for personal note-taking, and are mandated to be kept in pristine condition.

The file **DataDoc\_Players.pdf** describes these files and the associated variables and modalities.

Your mission is to explore these data to try and address the following items:

1. A general description of the ongoing epidemic, including a table describing the distribution of the outbreaks per species and production types, a timeline of the incidence and a visual representation of the spatial distribution of the outbreaks.
2. A prediction of the likely temporal and spatial evolution of the epidemic over the following four weeks, assuming the management strategy remains as it is today; if you can have it by farm production type, that would be even better.
3. A characterization of the relative contribution of the galliform farms to the virus spread as compared to the palmiped farms;
4. An answer with a justification to the following question: given we have reached the culling capacity and that chicken farms likely are key contributor to the epidemic, how epidemiologically-relevant would it be to focus the preventive culling actions on the chicken farms only?
5. An answer with a justification to the following question: given that outbreak farms are likely more infectious than preventively-culled farms, how epidemiologically-relevant would it be to ignore the preventive culling actions and spend all efforts possible to reduce by 1 day the start of the reactive culling actions in outbreak farms?

Your feedback is due on 28 February 2026.

We acknowledge that we ask a lot, and that not all modelling approaches can address all the questions. Questions 1, 2 and 3 should be addressed in priority. An investigation of questions 4 and 5 would be an immense bonus for us.

### **Reporting outputs**

- First, please fill the **HPAI\_model\_description\_template\_Phase1.docx** file with a description of your model, your feedback on (some of) the requests described above, and your opinion on the modelling approach you developed during this phase 1.
- For any **temporal prediction**, please share raw simulated trajectories as a .csv file with an accompanying description (e.g. README file). If raw trajectories are not

available, please share synthetic metrics of the trajectories at different time points (at least at the end of the four weeks prediction), if possible with distributions (preferably) or at least with confidence/credible intervals, when relevant.

- For **spatial predictions**, please share the spatial risk of the spatial units of interest at specific time points (at least at the end of the four weeks prediction) as a .csv file (preferably) or a .shp file. As for temporal predictions, please provide a description of the file.
- Finally, we would appreciate if you could draft a **one-page (max!) recommendation brief** synthesising your key findings and their implications in terms of epidemic management.

Good luck everyone!