Mapping the risk of introduction of highly pathogenic avian influenza to Swedish poultry

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ABSTRACT

Outbreaks of highly pathogenic avian influenza (HPAI) have resulted in severe economic impact for national governments and poultry industries globally and in Sweden in recent years. Veterinary authorities can enforce prevention measures, e.g. mandatory indoor housing of poultry, in HPAI high-risk areas. The aim of this study was to conduct a spatiotemporal mapping of the risk of introduction of highly pathogenic avian influenza virus (HPAIV) to Swedish poultry from wild birds, utilising existing data sources. A raster calculation method was used to assess the spatiotemporal risk of introduction of HPAIV to Swedish poultry. The environmental infectious pressure of HPAIV was first calculated in each 5 km by 5 km cell using four risk factors: density of selected species of wild birds, air temperature, presence of agriculture as land cover and presence of HPAI in wild birds based on data from October 2016-September 2021. The relative importance of each risk factor was weighted based on opinion of experts. The estimated environmental infectious pressure was then multiplied with poultry population density to obtain risk values for risk of introduction of HPAIV to poultry. The results showed a large variation in risk both on national and local level. The counties of Skåne and Östergötland particularly stood out regarding environmental infectious pressure, risk of introduction to poultry and detected outbreaks of HPAI. On the other hand, there were counties, identified as having higher risk of introduction to poultry which never experienced any outbreaks. A possible explanation is the variation in poultry production types present in different areas of Sweden. These results indicate that the national and local variation in risk for HPAIV introduction to poultry in Sweden is high, and this would support more targeted compulsory prevention measures than what has previously been employed in Sweden. With the current and evolving HPAI situation in Europe and on the global level, there is a need for continuous updates to the risk map as the virus evolves and circulates in different wild bird species. The study also identified areas of improvement, in relation to data use and data availability, e.g. improvements to poultry registers, inclusion of citizen reported mortality in wild birds, data from standardised wild bird surveys, wild bird migration data as well as results from ongoing risk-factor studies.

1. Introduction

Outbreaks of highly pathogenic avian influenza (HPAI) in poultry cause substantial economic losses, and have implications for trade, food supply and animal welfare. In Sweden alone, the direct cost for disease control measures and compensation to poultry farmers paid by the state was an estimated 37 million Euro in 2021–2022 (Jordbruksverket, 2022a). In addition, the poultry industry suffered economic losses due to movement restrictions and interrupted trade, and the outbreaks in 2021 led to temporary shortages in table- and hatching eggs.

Since the emergence of the H5 highly pathogenic avian influenza virus (HPAIV) Goose/Guangdong lineage in 1996, there have been several occurrences of global viral spread through migratory waterfowl (Lee et al., 2017; The Global Consortium for H5N8 and Related Influenza Viruses, 2016). Following this, the number of detections of HPAIV in wild and domestic birds have been increasing in Europe during the last

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decade (EFSA et al., 2023a). Since the first detection of HPAIV in Sweden in 2006 (Zohari et al., 2008), the country has experienced several winter seasons with HPAIV presence of varying severity (Jansson et al., 2017), with the worst to date occurring in 2020–2021 (Grant et al., 2022). Outbreaks in poultry were primarily caused by independent viral introductions, most likely through indirect contact with wild birds, notably without confirmed spread between farms.

Viral introduction from wild birds to poultry can occur through direct or indirect contact. Spread via vectors or fomites contaminated with wild bird feces plays a central role in the indirect transmission cycles (Gonzales et al., 2017). The lower temperatures in winter months promote virus survival in the environment (Stallknecht and Brown, 2009), which increases the risk of indirect virus transmission. In recent years, however, HPAIV dynamics have shifted from causing exclusively winter epidemics to now also circulating extensively in wild birds during summer months in European countries (Pohlmann et al., 2022).

A wide range of wild bird species are known to constitute a risk for viral spread to poultry, either as a reservoir (Bodewes and Kuiken, 2018; EFSA et al., 2017; Olsen et al., 2006) or as a bridging species (Shriner and Root, 2020). The presence of wild waterfowl, as the avian influenza virus is well adapted to these species, is known to constitute a particularly high risk (Stallknecht and Shane, 1988). One finding from epidemiological investigations of HPAI outbreaks in Sweden during the 2020–2021 season was that in several cases, large flocks of geese had been noted in close proximity to the farms prior to the outbreaks (Grant et al., 2022). Obtaining reliable wild bird population estimates can be challenging, and different data sources, including standardised surveys and citizen reports, each have specific limitations (Snäll et al., 2011). The number of wintering geese have been increasing in Sweden, with standardised surveys showing an eight-fold increase since the 1980s (Green et al., 2021), pointing to a potential increase in the risk of disease transmission from waterfowl. Indeed, recent studies have identified proxies for the presence of waterfowl, such as bodies of water and agriculture near farms, as risk factors for the occurrence of HPAI in poultry (Gilbert and Pfeiffer, 2012; Schreuder et al., 2022).

Sweden has a low-density poultry population dominated by farms with either broiler chickens or laying hens. Only a very limited number of commercial farms keep ducks or geese. The annual census conducted in June 2022 counted a total of 10.3 million broiler chickens and 7.9 million laying hens (Jordbruksverket, 2022b). The population density per municipality of commercial turkeys, broilers and layers in Sweden is shown in Fig. 1. Approximately 1 % of chicken meat and 13 % of eggs are produced in organic systems (Jordbruksverket, 2023), which require that poultry have outdoor access from early spring to late autumn under normal circumstances. Additionally, 7.4 % of non-organic laying hens normally have outdoor access throughout the year (Jordbruksverket, 2023).

Avian influenza prevention measures are aimed at stopping direct or indirect contact between poultry and wild birds. In order to target such measures, so-called high-risk areas can be identified, as was previously regulated in EU-legislation, but no longer in force (European Commission, 2018). Within a high-risk area, the policy often includes
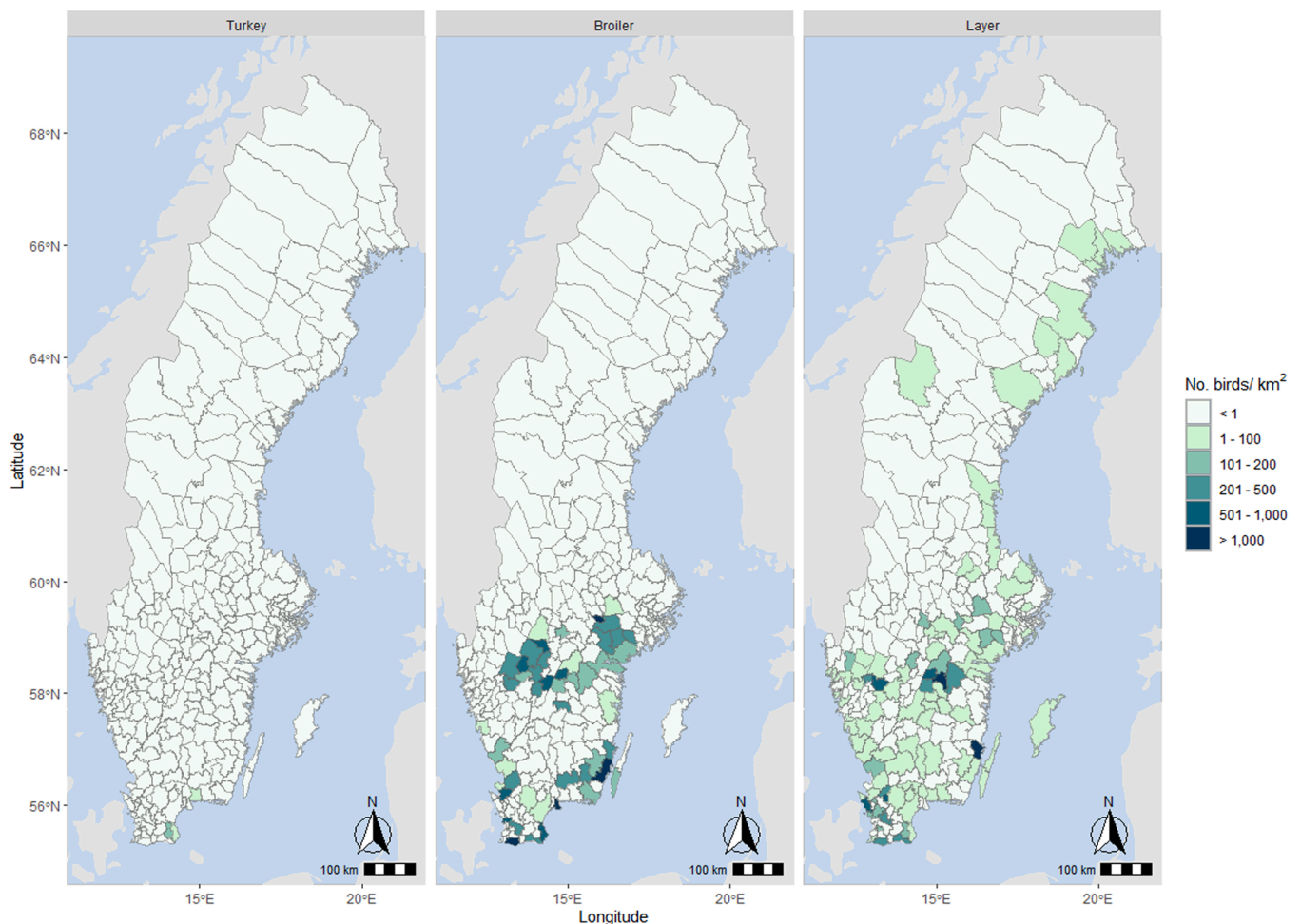

Fig. 1. Poultry population density per municipality in Sweden, expressed as number of birds per km^2, for commercial turkeys, broilers and layers separately. Counts are based on the Swedish poultry register (data accessed in November 2021) and categorisation of species and locations of farms are based on data from the Swedish Egg Association and the Swedish Poultry Meat association (data accessed in June 2022 in both cases).

confinement of poultry indoors, enhancing biosecurity to prevent spread via fomites or mechanical vectors such as rodents or wild birds, and intensifying disease surveillance.

During avian influenza winter seasons prior to 2021, e.g. 2005–2006, 2016–2017 and 2020–2021, the whole of Sweden was considered to be a high-risk area, without any regional differentiation of risk. The reason for not differentiating by region was not due to actual high-risk nationwide, but rather because data and knowledge were lacking at the time. For the 2021–2022 season, high-risk areas were based on a crude risk assessment at county level, only taking into account the geographical location of historical HPAI cases in wild birds and poultry.

As a basis for defining high-risk areas, more detailed mapping which considers data on additional risk factors, such as wild bird abundance and poultry density, can be done. Mapping the risk of HPAIV introduction to poultry has been carried out in several European countries for this purpose (Gierak et al., 2019; Hill et al., 2019; Schreuder et al., 2022). However, results from other settings can only partially be applied to the Swedish context as characteristics of the poultry population, the wild bird populations including migration patterns, land use/cover and climate differ significantly between countries. Furthermore, the risk mapping methodology needs to be adapted to data availability, which is also likely to differ.

The aim of this study was to conduct a spatiotemporal mapping of the risk of introduction of HPAIV to Swedish commercial poultry from wild birds, which ultimately could be used to inform decision makers regarding implementation of targeted preventive measures. The objective was to develop a model for risk mapping, utilising and exploring existing data sources on risk factors.

2. Materials and methods

2.1. Data

Five main risk factors were included in the calculation of risk of introduction to poultry, namely: poultry population, wild bird density, air temperature, land cover and presence of HPAIV in wild birds. These choices were based on literature review, EU guidelines (European Commission, 2018), and data availability. All data were handled and analysed in the statistical program R (R Core Team, 2021) using data. table (Barrett et al., 2024), sf (Pebesma, 2018), raster (Hijmans, 2018), gstat (Pebesma, 2004), unmarked (Kellner et al., 2023) and ggplot2 (Wickham, 2016) packages.

2.2. Data sources and processing

An overview of data sources, inclusion criteria and data processing is provided in Table 1.

Unless otherwise stated, the data were collected for a five-year period spanning from October 2016 to September 2021. Twelve-month periods starting in October were used as offset years based on the European Food Safety Authority (EFSA) definition of an epidemiological year.

2.3. Poultry population data

Data on the geographical location of poultry holdings, species held at the premises, production type and number of birds were retrieved from the Swedish poultry register managed by the Swedish Board of Agriculture. These data were accessed on 3 November 2021 and represented the registered poultry and other captive bird population in Sweden at that time. Because we focused on commercial facilities, we assumed that farm turnover was low enough that this year's data could be used to represent the poultry population in prior years. As the number of birds on a farm can change with the production cycle, we used the registered "maximum capacity", which means the maximum number of birds which at any point of time can be present on the farm (hereafter number

Table 1
Data used in the model, including data sources, inclusion criteria and data processing.

Data	Source	Inclusion criteria	Temporal scale — Original format	Temporal scale — Converted format	Spatial scale — Original format	Spatial scale — Converted format	Weight assigned
Poultry population	Swedish poultry register, Swedish Board of Agriculture	Holdings with production type other than backyard poultry, and registered capacity of at least 50 birds	Active holdings at time of data access on 3 November 2021	-	Point locations of holdings	Sum of the number of birds on holdings within each 5 km cell transformed to natural log scale	-
Wild bird observations	Swedish Species Observation System, SLU Artdatabanken	Observations of ducks, geese, swans, or larids (gulls and terns)	Number of observed birds by species and observation date during October 2016 - September 2021	Monthly raster bands resulting from aggregating observations per month across the five-year period	Point locations of the observations	Counts were fitted with stratified N-mixture models to estimate the population. Observations above the 99th percentile values in each 5 km cell were excluded.	Ducks: 0.19 Geese: 0.17 Swans: 0.10 Larids: 0.07
Air temperature	Swedish Meteorological and Hydrological Institute (SMHI)	-	Monthly average measurements October 2016 - September 2021	Monthly raster bands derived from averaging the rasters per month over the five-year period	Point locations of 350 weather stations across Sweden	Values were predicted based on distance from weather stations and assigned to 5 km cells	0.14
Agriculture	CORINE land cover (CLC)	CLC classes for "arable land", "permanent crops", "pasture", and "heterogenous agricultural area"	2018 data	-	100-meter resolution raster	5 km cells with values equal to the percentage of 100 m cells within the larger cell that were classified as noted in the inclusion criteria.	0.09
Reported cases of HPAI in wild birds	EU's Animal Diseases Information System (ADIS)	All confirmed cases of HPAI in wild birds based on the passive surveillance system in place	Dates of confirmed cases between October 2016 and September 2021	Monthly raster bands resulting from aggregating observations per month during the five-year period	Point locations of cases	Monthly kernel density raster with a 10 km smoothing bandwidth at 5 km resolution	0.24

of birds). We summed the number of birds, of each holding within each 25 km^2 area, excluding holdings classed as keeping backyard poultry and/or had less than 50 registered birds.

2.4. Wild bird observation data

Initially we explored using data from standardised surveys on wild bird presence but as only limited geographical areas and time periods were covered, we opted to use data from citizen-based reports. Data on reports of wild bird distribution, abundance, and occurrence were hence collected from the Swedish Species Observation System, Artportalen (SLU Artdatabanken, 2022). Artportalen is a citizen science-based web reporting system, run by the Swedish Species Information Centre at The Swedish University of Agricultural Sciences (SLU), and to a large extent financed by the Swedish Environmental Protection Agency. Each year several million observations of plant and animal species are added to the database. Data is entered continuously into the national database directly by citizens who make the observations. The minimum requirement for an entry is to report species, date of observation and location (SLU Artdatabanken, 2015). However, most reports also include the number of birds observed and information on activity (e.g. stationary, migrating, foraging).

We focused on four wild bird categories related to live bird observations: ducks, geese, swans, and larids (gulls and terns), based on EU guidelines European Commission (2018), Schreuder et al. (2022) and Green et al. (2023). Point observations were aligned on a 25 km^2 raster surface for each month and wild bird category, and observations above the 99th percentile value within each cell were excluded to reduce the influence of high outlying values. We then fitted stratified negative binomial N-mixture models to estimate population abundance from point observations within each grid cell using the "unmarked" R package (Kellner et al., 2023). Observations were stratified by the species group and the month of observation, derived from the reporting date. A separate model was run for each stratification level for a total of 240 models (60 months in five years and four species groups). The resulting estimates were aggregated monthly by taking the average value within a given cell and wild bird category.

2.5. Air temperature data

Temperature data was included as a risk factor based on Stallknecht and Brown, (2009) and EFSA, (2008). Data on monthly average air temperature were obtained from the Swedish Meteorological and Hydrological Institute (SMHI), collected from approximately 350 weather stations across Sweden (SMHI, 2020). To create a continuous surface from the discrete temperature data, we predicted the intermediate values between the weather stations based on the distance and assigned them to each cell (25 km^2). Monthly rasters for the five-year period were aggregated to produce an overall monthly average raster with 12 bands.

2.6. Land cover data

We initially explored including proximity to water bodies as a risk factor based on Si et al. (2013), and adding data on this land cover variable to the model. In the final model only data on agricultural land cover categories were included based on Gilbert and Pfeiffer (2012) and Schreuder et al. (2022). Data on land cover were obtained from the most recent CORINE land cover (CLC) raster layer, which encompasses a total of 44 land cover and land use classes (Copernicus Land Monitoring Service, 2018). CLC classes for arable land, permanent crops, pasture, and heterogenous agricultural area were reclassified as agricultural area (Kosztra et al., 2017). The raw data with a spatial resolution of 100 m were down sampled to a 5 km resolution. We determined the new value of a 5 km cell based on the proportion of the 25 km^2 area covered by agricultural land cover categories.

2.7. Presence of HPAI in wild birds

For the presence of HPAI in wild birds, we used data reported to EU's Animal Disease Information System (ADIS) (European Commission, 2022) on the locations of wild birds that tested positive for HPAIV in the passive surveillance system (National Veterinary Institute (SVA), 2023; Grant et al., 2022). Species included in the passive surveillance system comprise most wild birds, except small passerines. Birds found dead or sick are reported by members of the public to the National Veterinary Agency and a subset of birds are selected for AIV diagnostics. The selection procedure is risk based, and species not confirmed positive in a given municipality during the preceding 30 days are candidates for sampling and necropsy. We used the point locations of positive wild birds to produce monthly kernel density raster surfaces with a 10 km smoothing bandwidth at 5 km resolution to match the wild bird observation data, using all cases per month in the five-year period. Monthly rasters for the five-year period were aggregated to produce an overall monthly average raster with 12 bands, so reports in March of 2017, 2018, 2019, 2020 and 2021 were all included in the overall kernel density of positive cases for March.

2.8. Data weighting

We calculated weights for the input raster data in the raster calculations based on expert determination of relative risk contributions from the different layers. To do this, we created a custom risk factor matrix similar to Gierak et al. (2019), described in supplementary information. The matrix was sent to eight avian influenza experts, six in Sweden and two in neighboring countries. Answers were received from five experts (four in Sweden and one in a neighboring country). The experts that provided answers were: Two HPAI risk managers at national and regional veterinary authorities respectively, one ornithologist, one poultry veterinary expert and one virologist. The experts represented five different organisations and they were selected based on their experience working with HPAI, either in research or risk management. Monthly average temperature was not included in the matrix as it was deemed to be an overarching variable affecting all other risk factors. Due to its large influence on influenza virus survival in the environment (EFSA, 2008), we assigned a relative risk of 1 between temperature and all other layers, see supplementary information, Table 1. The matrix with the mean values from the experts and the raster layer weights is provided in supplementary information.

2.9. Data analysis

We used a raster calculation method to assess both the environmental infectious pressure of HPAIV, representing HPAIV circulation in wild birds and environmental contamination, and the risk of HPAIV introduction to poultry. The raster layers were combined to a risk raster where a risk value was calculated for each 5 km cell. To put the rasters on the same scale for comparability, the values for all raster layers were normalised to range from 0 to 1 through feature scaling based on the minimum and maximum values of each raster. For multi-banded monthly rasters, this scaling was done using the overall minima and maxima. Additionally, to reduce the effect of outlying high values, we normalised the natural log of values of the wild bird observation and poultry density rasters.

The environmental infectious pressure calculations were performed by summing the weighted, normalised values of the input raster layers with data on: wild bird observations, land cover classed as agriculture, air temperature and cases of HPAI in wild birds (Eq. 1). Multi-banded rasters were summed across matching bands while single-banded rasters were added to all bands. The resulting values were normalised to range from 0 to 1. In this way, environmental infectious pressure was not defined probabilistically, but on a relative scale based on the minimum and maximum values of the input rasters. Then, to examine where

environmental infectious pressure overlapped with poultry density, we multiplied the poultry density raster layer to the environmental infectious pressure raster layer (Eq. 2) to obtain values assessing the risk of HPAIV introduction to poultry. We rescaled the risk values from 0 to 1 and the resulting values were finally summarised within municipalities to aid in communication and outreach.

$$Environmental\ infectious\ pressure = \sum_{i=1}^{n} w_i r_i \qquad (1)$$

where w_i is the weight for each raster layer and r_i is a raster layer.

$$Risk_{introduction} = Environmental\ infectious\ pressure \times PoultryDensity \qquad (2)$$

2.10. Sensitivity analysis

We conducted a sensitivity analysis to assess the impact of each risk factor on the calculated risk to poultry. For each risk factor, we recalculated the weights such that the sum of the weights always equalled 1, ensuring a fair comparison of their effects. Subsequently, we systematically examined the sensitivity of the model by removing one risk factor at a time and proportionally redistributing the weights of the remaining factors to maintain the overall weight constant. This process was repeated for a total of seven sets allowing a comprehensive assessment of potential changes in risk. Each grid cell value of the sensitivity test results was compared with the risk value of HPAIV introduction to poultry. Specifically, we quantified the change in risk value for each cell by

calculating the absolute difference between the value in each sensitivity test set and the corresponding value in the calculated risk. For example, if a grid cell decreased from 0.5 in calculated risk to 0.3 in sensitivity testing, the change in that cell is recorded as 0.2. The effect was assessed by visually comparing the changes to the risk value using box plots. See Figs. 4 and 5 in supplementary information.

2.11. Map validation

To validate the risk map, logistic regression analysis was used to examine the relationship between the maximum risk value in a given municipality and month, as explanatory variable, and HPAI outbreak in poultry as outcome. For this purpose, data on 26 Swedish HPAI outbreaks in poultry reported to ADIS between 2016 and 2024 were used. This data source was also used to visualise outbreak locations on the risk maps in the results. Municipality and month combination with a maximum risk level of zero was excluded from the analysis as these had no or very few registered poultry. The maximum risk level was multiplied with 10 to give an odds per 0.1 (10 %) increase in maximum risk level.

3. Results

Monthly environmental infectious pressure rasters resulting from the expert-weighted environmental infectious pressure calculation at 5 km resolution are shown in Fig. 2. The mean temperature drives the
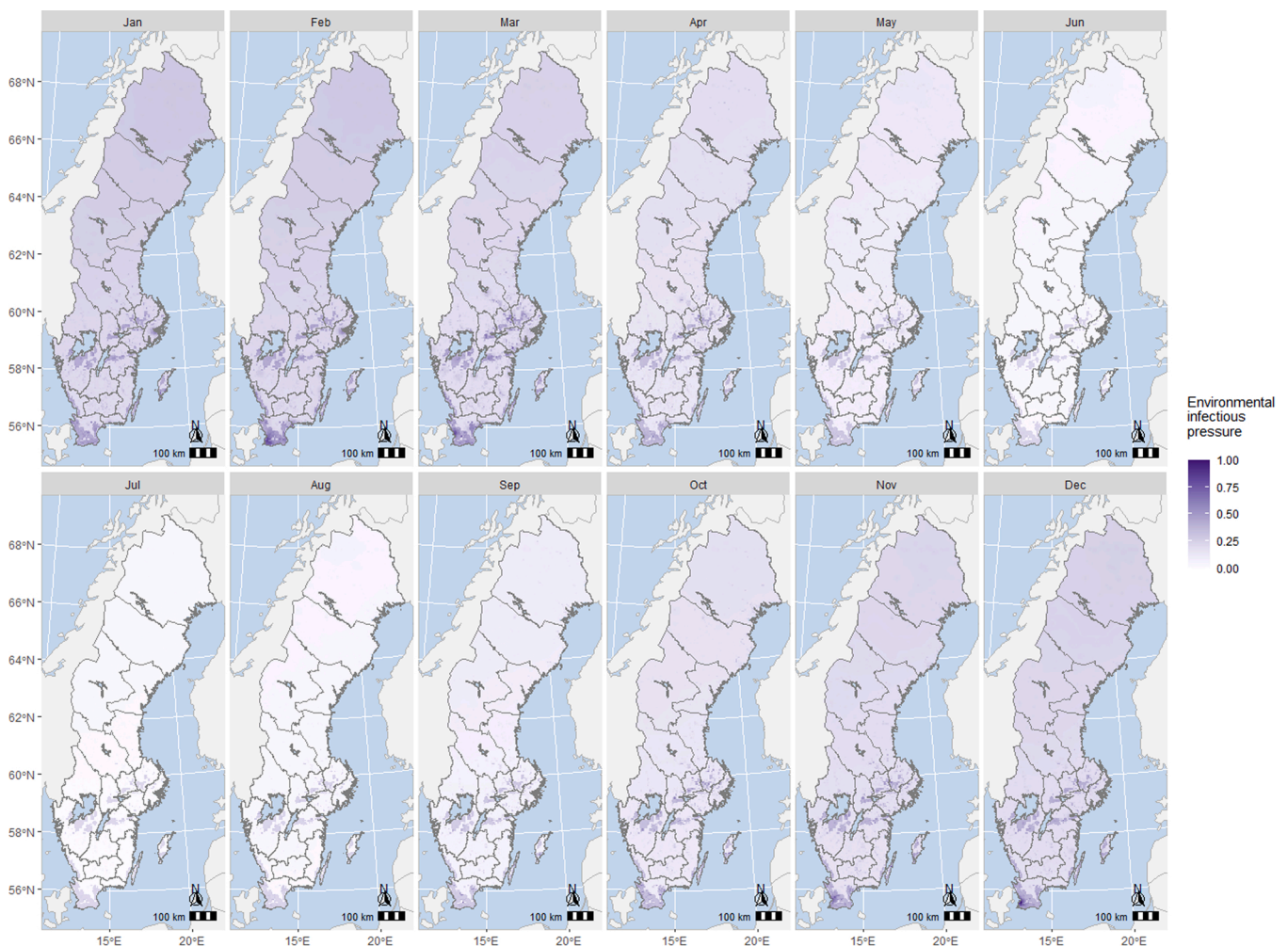

Fig. 2. Monthly environmental infectious pressure rasters resulting from the weighted environmental infectious pressure calculation at 5 km resolution. County boundaries are overlaid on the rasters.

seasonal pattern nationwide, whereas local variation in calculated risk is driven by other environmental risk factors.

The calculated risk is generally higher in the south than in the north of Sweden. The two counties of Östergötland and Skåne are of particular interest as there have been multiple HPAI outbreaks in poultry in these areas and therefore the environmental infectious pressure of the two regions is shown separately in Fig. 3.

The relative risk of introduction of HPAIV to poultry on municipality level by month are shown in the heat map in Fig. 4, and the risk values displayed represents the 99th percentile for cells within each municipality boundary. The municipalities shown are those that had HPAI outbreaks in poultry between October 2016 and January 2024, or where the 99th percentile reached a value of 0.5 or higher for at least one month. Combining the risk value and the information on historical domestic HPAI outbreaks in Fig. 4 reveals that there are municipality-months with relatively high calculated risk values but no outbreaks, and municipality-months with relatively low calculated risk values which have experienced outbreaks since 2016.

The monthly risk of introduction of HPAIV to poultry in Östergötland and Skåne are available in Fig. 5.

The month with the highest average risk for HPAIV introduction to poultry was March, while the month with the lowest average risk was July (Fig. 6). The risk of HPAIV introduction to poultry in other months are available in supplementary information.

Based on the sensitivity analysis, there were no risk factors which had a disproportional impact on the risk level in the model. On a national level, average monthly temperature had a very small contribution to the risk level, whereas the regional effect of temperature was higher in the presence of other risk factors and in poultry dense areas, see supplementary information.

The odds of having an HPAI outbreak in poultry in a given municipality and month increased by 2.2 (95 % CI 1.8–2.6) times for each 10 % increase in maximum risk level ($p < 0.001$).

4. Discussion

The results indicate that the national and local variation in environmental infectious pressure and risk for HPAIV introduction to poultry in Sweden is high and this would support a more detailed risk mapping as a basis for HPAI preventive measures than previously used.

Sweden is characterised by a large variation in land cover, with some areas being highly suitable for agriculture while other areas are unsuitable and forested or rocky and barren. Most poultry farms are located in southern flatlands, which are also attractive wintering and stop-over sites for wild waterfowl along their migratory flyways. These areas were identified as having higher environmental infectious pressure for HPAIV, and these were also the areas where the majority of outbreaks occurred in poultry. The counties of Skåne and Östergötland particularly stood out regarding environmental infectious pressure, risk of introduction to poultry and detected outbreaks of HPAI (Fig. 3 and Fig. 5).

On the other hand, there were also areas, in for example Västra Götaland and Blekinge counties, identified as having higher risk of introduction to poultry which never experienced any outbreaks. The reasons for this are not known, but one possible explanation is the variation in poultry production types present in different areas of Sweden. Some of the higher-risk areas have predominantly broiler farms (see Fig. 1), which have been shown to be at lower risk for HPAI outbreaks (EFSA et al., 2021; Grant et al., 2022; Thomas et al., 2005). There were also outbreaks which occurred in areas with lower risk, which suggests that there may have been risk factors which were not accounted for in the model, including farm-level risk factors. For example, some turkey farms experienced outbreaks during the study period despite not being in areas with highest risk. Production of fattening turkeys tends to be associated with higher risk of HPAI outbreaks (Dargatz et al., 2016; Gierak and Smietanka, 2021). There may be several reasons for turkey farms having higher risk of outbreaks than for example broiler farms. One is that turkeys may require a lower infectious dose (Aldous et al.,
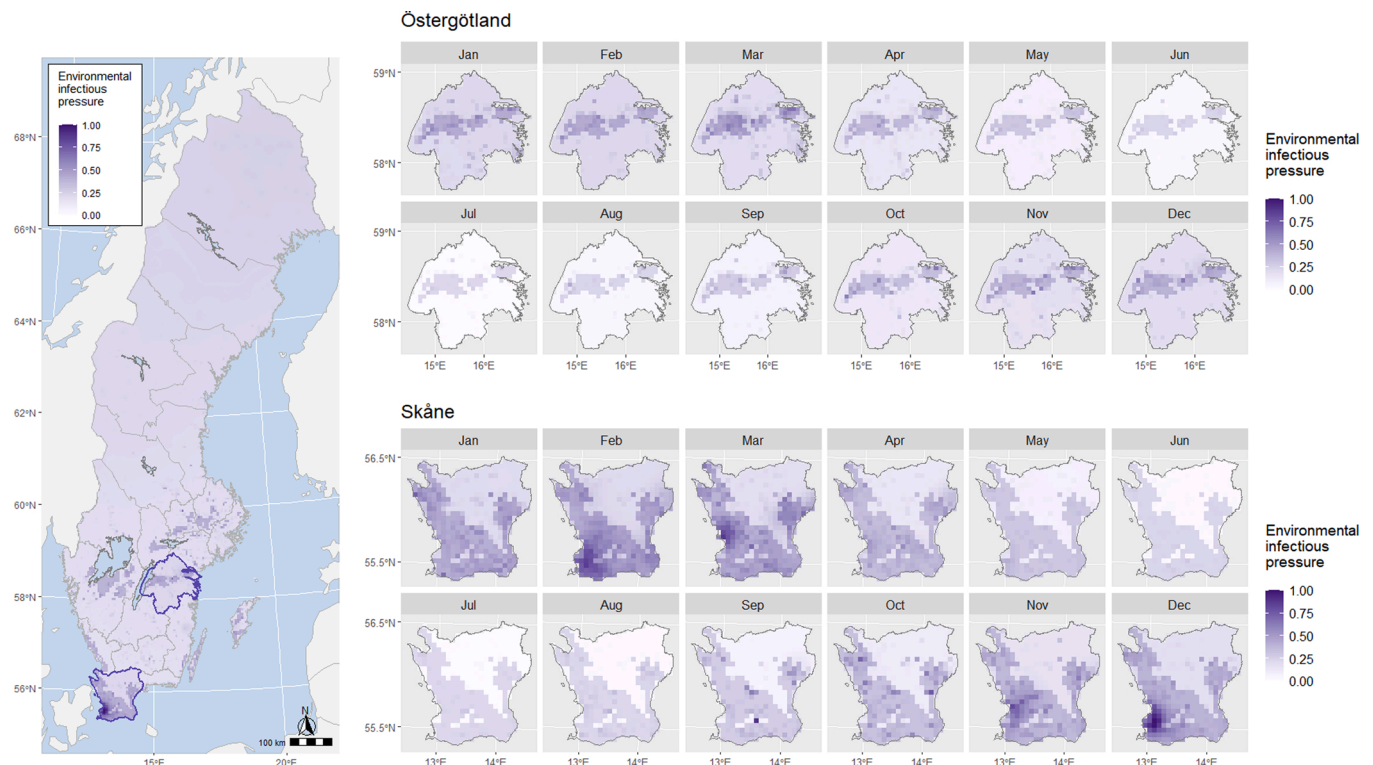

Fig. 3. Monthly environmental infectious pressure rasters resulting from the weighted environmental infectious pressure calculation at 5 km resolution within the counties of Östergötland (top right panel) and Skåne (bottom right panel).
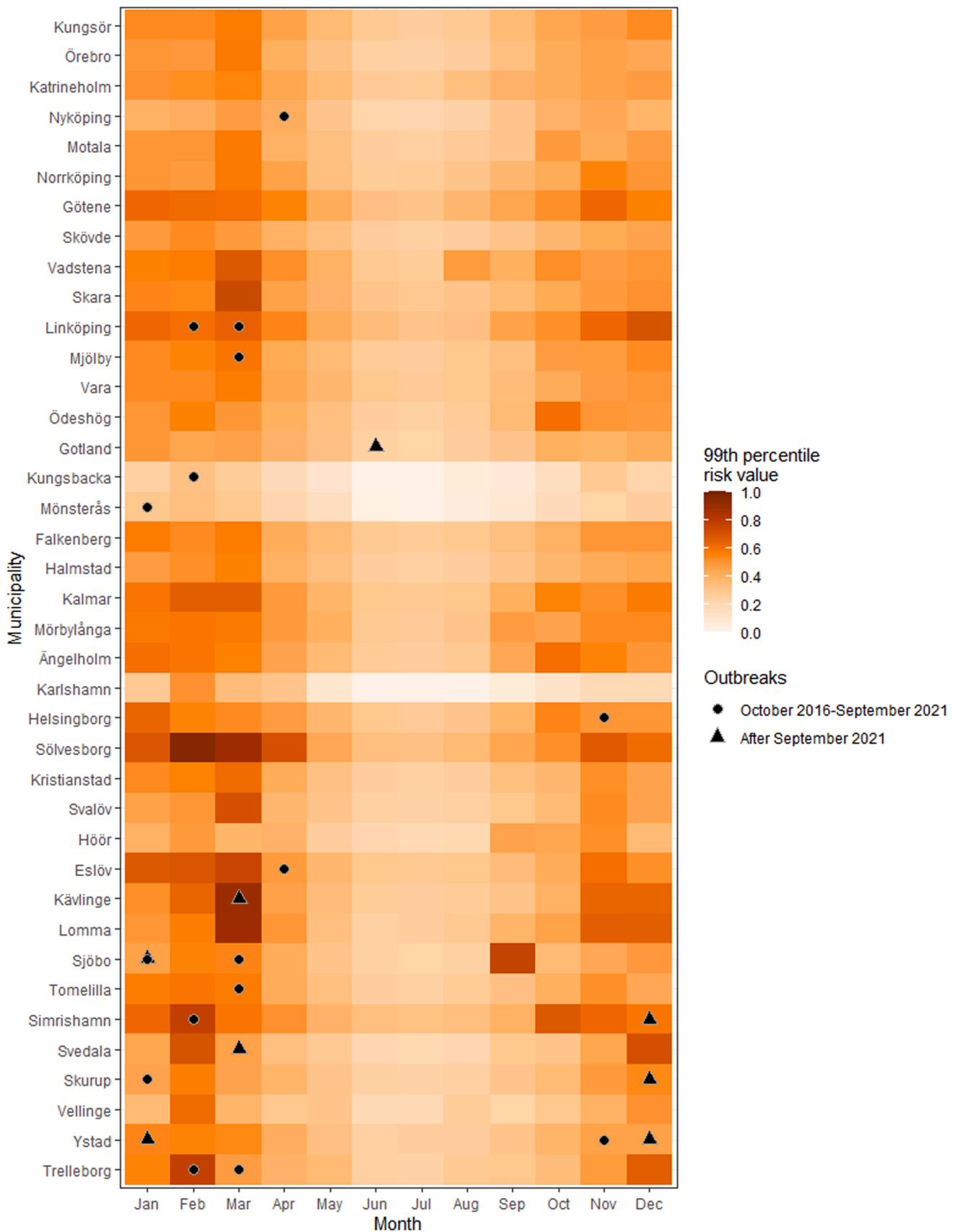
Fig. 4. Heat map of the 99th percentile risk values based on risk of introduction to poultry in municipalities with historical HPAI outbreaks in poultry between October 2016 and January 2024 or where at least one month had a 99th percentile value of 0.5 or higher. Outbreaks between October 2016 and September 2021 are indicated as circles and outbreaks after September 2021 indicated as triangles. Municipalities on the y-axis are ordered from south (bottom) to north (top) by the latitude of the polygon centroids. Monthly calculated 99th percentile risk values for all municipalities in Sweden are available in supplementary information.
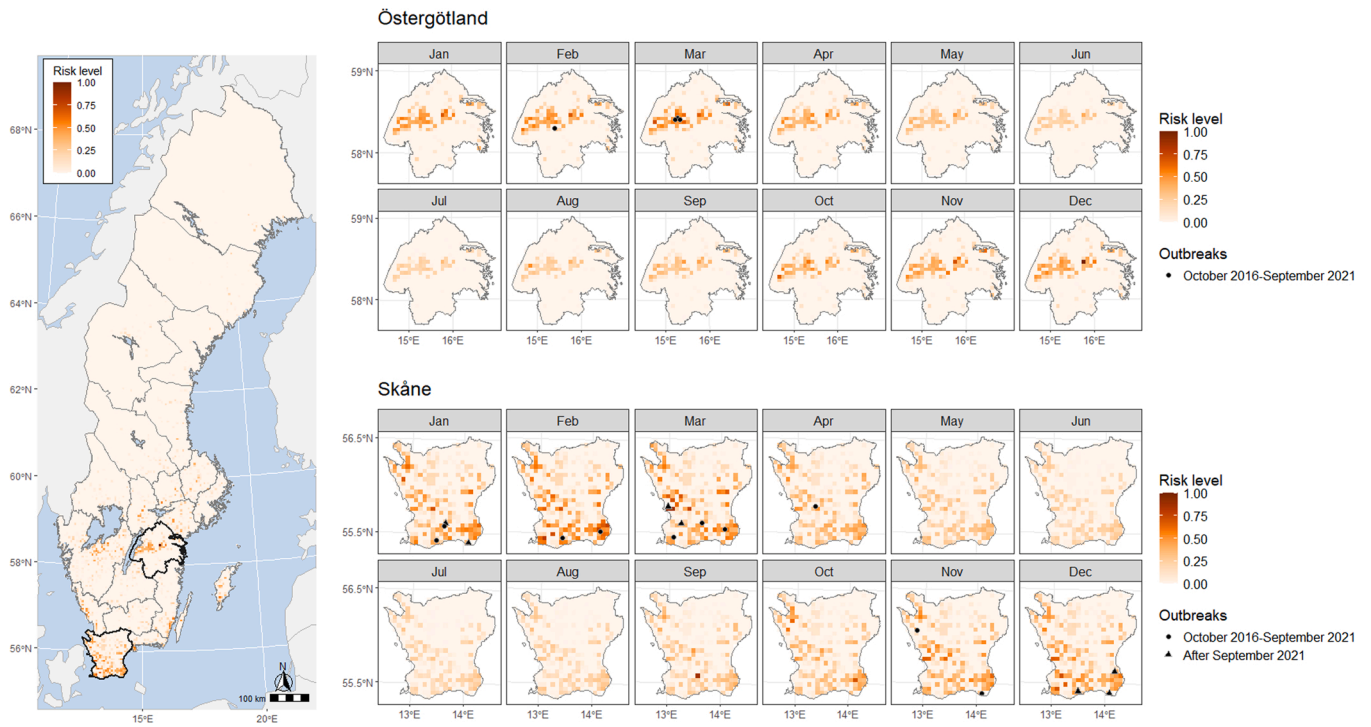
Fig. 5. Monthly risk of introduction of HPAIV to poultry within the counties of Östergötland (top right panel) and Skåne (bottom right panel). The locations and months of HPAI outbreaks in poultry between October 2016 and September 2021 are shown as circles and after September 2021 are shown as triangles.
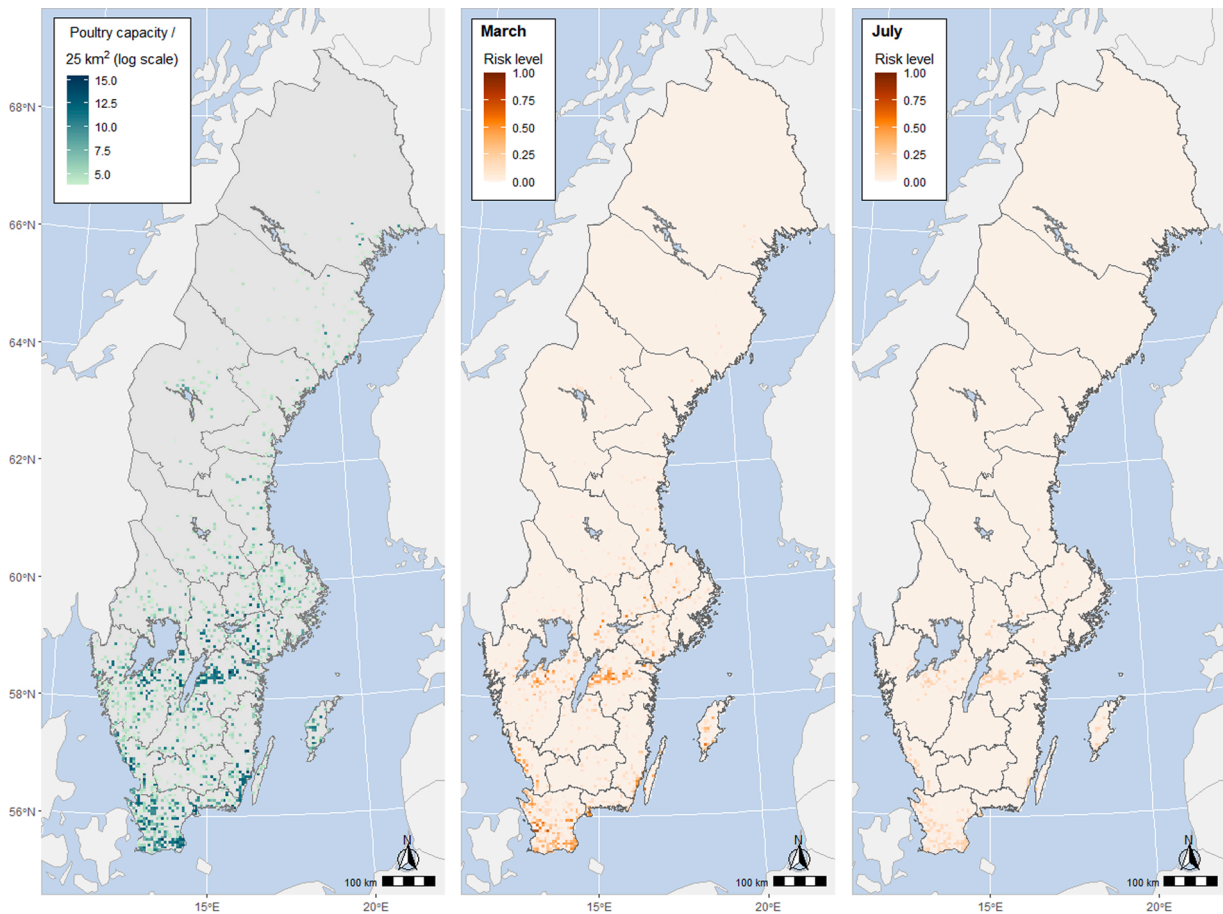

Fig. 6. Risk of HPAIV introduction to poultry per 25 km^2, for March versus July, which were the months with highest and lowest risk, respectively.

2010). Another possible reason is that there are differences in management practices between turkey farms and broiler farms in Sweden. Broiler chickens are often kept in well-sealed, heated buildings, whereas fattening turkeys often have more simple buildings, and are provided with straw several times a week through opening of large doors with increased risk of exposure to pathogens from the outside.

In addition to the variation observed on the national level, large local variation in risk was noted within municipalities. Previously, counties have been used as a basis for preventive risk management decisions, but this finding could support a more targeted approach to reduce unnecessary disruption to normal farm management in free-range or organic production systems.

The seasonal variation of HPAI dynamics is known and this study indicates that March was the month with highest average risk of HPAIV introduction to poultry. March was also the month with the highest number of poultry outbreaks (N=8). Monthly average temperature was included in the model as temperature has been shown to affect HPAIV survival in the environment (Stallknecht and Brown, 2009), and subsequently the risk of indirect spread from wild birds to poultry. Temperature also has an effect on wild bird dynamics, and HPAI cases in wild birds (Reperant et al., 2010), which is already accounted for in the model. These multiple effects of temperature may give an overestimation of risk in the coldest months, but when assessing the model fit against observed HPAI outbreaks in poultry, fit was improved when including monthly average temperature.

The commonly observed seasonal pattern in wild bird occurrence was also noted in our wild bird data. Ducks, geese, and swans (family Anatidae) were more frequently observed, and positive findings of HPAI were more commonly reported, in winter compared to summer months. However, findings from the latest three summers (2021, 2022, and 2023) show a new pattern with viral persistence among wild birds in the summer, but this has so far only resulted in a single outbreak among domestic poultry or captive birds in Sweden. This is likely due to reduced viral survival time in summer months, reducing the risk of indirect viral spread. Furthermore, summer months differ from migratory periods regarding wild bird population dynamics, where birds with different viral and immunological status gather in large groups, thus enhancing viral spread (Lisovski et al., 2018).

To estimate the environmental infectious pressure, we decided to sum the different weighted environmental risk factors (i.e. wild bird observations, agricultural land cover, air temperature, and cases of HPAI in wild birds). Another approach could have been to multiply the risk factors to reduce the risk of overestimating environmental infectious pressure in areas where there are no cases of HPAI in wild birds and the population of waterfowl is very limited. This overestimation would be due to the fact that multiplying near-zero values yields values closer to zero, whereas summing can result in relatively high values even when necessary conditions for active transmission are absent. However, absence of confirmed cases of HPAIV in wild birds and limited population of waterfowl is mainly observed in the north of Sweden, where poultry production is minimal. Therefore, the calculation method used is unlikely to change the relative risk of introduction of HPAIV to poultry in the Swedish setting as we ultimately multiplied the environmental infectious pressure and poultry population layers.

Different wild bird species constitute different risk of HPAIV spread to poultry (Schreuder et al., 2022), but as the virus adapts to new wild bird species this may change over time. We focused on species within the two groups Anatidae (ducks, geese and swans) and Laridae (gulls and terns) in this study, and weights assigned to species category were based on opinion of experts carried out in December 2022. At the time, agreement was high between experts, and most assigned the lowest weight to gulls and terns. Since then, one viral genotype has adapted very well to Larid birds, particularly Black-headed gulls (EFSA et al., 2023b). Such adaptions may change disease dynamics in wild bird populations, which will necessitate regular updates of the risk map.

A limitation to using citizen science-based data on wild bird observations as a basis for wild bird presence is that data collection may be somewhat biased towards more densely populated areas (more observers) and towards areas with known aggregation of birds (observers more prone to visits and report). In addition, the probability of observing and reporting may vary depending on species, time of year, prevailing weather, and ease of access to observation sites, among other factors. Thus, some wild bird flocks may remain unobserved and unreported, and this may result in an underestimation of risk in areas less visited by ornithologists. Here we use a N-mixture model to reduce the effect of these potential biases in the citizen science-based data. Combining citizen-based data with data from standardised surveys could further improve the accuracy of the wild bird population estimates.

As Sweden has a relatively small poultry population with few farms, poultry population density (number of birds per surface area), was chosen as the best way to represent Swedish poultry in the model, rather than number of poultry holdings. However, there is no clear evidence that the risk of HPAI increases with increased number of birds on the farm (Gilbert and Pfeiffer, 2012). This relationship is likely to be much more complex and depends also on which species are kept (Gierak and Smietanka, 2021), contact patterns with other poultry or wild birds, and level of biosecurity (Bavinck et al., 2009). Information about the poultry population was based on data from the Swedish poultry register and the registered number of birds at each holding. Both the number of holdings and number of birds per holding could be an overestimation, as inactive farms may be present in the register and farms may keep fewer poultry than maximum capacity. This may lead to an overestimation in the risk of introduction to poultry in places where inactive farms are located, but we felt that including all potential poultry husbandry in the calculation would result in fewer missed high-risk areas.

Keeping poultry outdoors increases the likelihood of contact with wild birds, and therefore the risk of HPAIV introduction is often higher in outdoor production systems (Bouwstra et al., 2017; Gonzales et al., 2017). In the present study, available data on outdoor access was unreliable, and therefore no additional weight could be assigned to registered free range holdings. This may have contributed to an underestimation of risk in areas with free range holdings. Furthermore, farms with outdoor access often have fewer birds per farm and since we included poultry population density rather than farm density in the model, this may add a further underestimation of risk in these areas.

Holdings with less than 50 birds were excluded from the model, partly because the requirement to register small poultry farms was only introduced in October 2021, one month prior to access of data for this study, and therefore data on this population was incomplete. A reason to set the limit to 50 birds was the EU Animal Health Regulation, where certain derogations may be granted if the HPAI outbreak occurs in an establishment keeping up to 50 birds (European Commission, 2019). Studies have also suggested that contact between backyard flocks and commercial poultry is limited (Van Steenwinkel et al., 2011). Also, backyard flocks have been shown to be less susceptible to HPAIV infection than commercial flocks (Bavinck et al., 2009), so this population may not contribute significantly to the risk of spread to commercial farms, compared to the risk already present from wild birds. The classification of backyard in the poultry register is based on owners own reporting, and there may be some misclassifications, especially as some farms have registered more birds than expected for a non-commercial holding.

As waterbirds are a reservoir for AIV it is fundamental to have this population represented in the model. Previous studies have shown that proximity to water bodies is a risk factor for HPAI outbreaks in poultry, as this is a proxy for presence of waterbirds (Si et al., 2013). Sweden is a country with many water bodies and many poultry farms are located near water in some form (data not shown). However, waterfowl such as ducks, geese and swans prefer certain types of water bodies over others, something which was not possible to incorporate in the model as data on type of waterbody was lacking. Moreover, as reporting of waterfowl is

widely practiced in Sweden, we opted to use this citizen science-based data, and not include water bodies in the final model. Instead, agriculture was the only land cover variable included, based on literature review including results from Schreuder et al. (2022). From interviews with affected poultry farmers as part of epidemiological investigations during HPAI outbreaks (Grant et al., 2022) and in an ongoing study by some of the authors of this paper (data not yet published), several farmers reported observations of geese in close proximity to the farm (agricultural land) prior to the outbreaks. This is consistent with the finding that sightings of wild waterfowl were associated with increased risk of infection with HPAIV in layer farms in the USA in 2022 (Green et al., 2023).

The design of the passive surveillance program for HPAI in wild birds may contribute to an uneven probability of detecting cases of HPAI within municipalities. After one positive HPAI finding in a specific wild bird species, no further birds of the same species are analysed from the same municipality within a 30-day period. Locations that attract birds may be hotspots for HPAIV transmission as well as for ornithologists who report findings of dead birds and submit them for analysis, thus increasing the probability of early detection of HPAI relative to areas less attractive to birds. One further limitation of the current surveillance program is that the magnitude of an HPAI outbreak is not reflected in the number of confirmed HPAI cases. In the model, a single positive wild bird will contribute with as much risk as an area with high wild bird mortality, whereas in reality we would expect the risk to be higher when there is a large number of infected wild birds.

While the focus of this study was to use existing data sources, and to investigate how they could be combined into a risk map to inform about HPAI risk, the next step is to make use of the results. As mentioned, the risk map could be used to target preventive measures on poultry farms, but the map could also be used as a basis for risk-based surveillance or when planning locations of new poultry farms. During the project, preliminary findings were presented to a project reference group with representatives from the risk managing veterinary authority in Sweden and the poultry industry. In discussions with stakeholders, the importance of the communicative step was clear, and choices made to visualise the result may strongly affect interpretation and understanding. In relation to the resolution of the risk map, fear was expressed by some stakeholders that farmers might interpret areas with lower risk as safe and thus may not prioritise implementing biosecurity measures. Regulatory stakeholders emphasised the benefits of risk levels shown following administrative borders to facilitate decision making, but this introduces the need to decide whether to present an average or the maximum observed risk level. Regardless, information on local differences in risk would be lost when summarising values within administrative boundaries, with the consequence of a hotspot raising the risk for a larger area or alternatively risk being diluted and thus missing hotspots in larger areas of lower risk. The conclusion was that one single map will not be sufficient to communicate the results, but several different maps are needed to inform decision making, at the level of the veterinary authority as well as at farm level. Input from the discussion was adopted in relation to colour scheme (monochrome), but as visual communication of risk is a research field of its own, this could be developed even further. It is also important that communication regarding risk should incorporate the uncertainties of the model. A specific cut-off point for high or low risk was deliberately not set in this study, as this is a decision for risk management authorities.

The study has been valuable to explore existing data sources and gain understanding in their potential use and limitations. The collaboration between veterinary epidemiologists and ornithologists was a strength that should be utilised in future work with HPAI risk mapping in Sweden. With the current and evolving HPAI situation in Europe and on the global level, there is a need for continuous updates to the risk map as the virus evolves and circulates in different wild bird species. The study also identified areas of improvement, in relation to data use and data availability, e.g. improvements to poultry registers, inclusion of citizen

reported mortality in wild birds, data from standardised wild bird surveys, wild bird migration data, as well as results from ongoing risk-factor studies.

Author contributions

PS, MG, HK, AC and MN conceived and designed the study. PS and HK performed the data cleaning, data analysis and visualisation. All authors contributed to the analysis and interpretation of the results. PS, MG, HK and MN drafted the first manuscript that all authors reviewed. All authors approved the final version before submission.

CRediT authorship contribution statement

Pascale Stiles: Writing – review & editing, Writing – original draft, Visualization, Validation, Software, Methodology, Formal analysis, Data curation, Conceptualization. **Malin Grant:** Writing – review & editing, Writing – original draft, Validation, Methodology, Formal analysis, Conceptualization. **Hyeyoung Kim:** Writing – review & editing, Writing – original draft, Visualization, Validation, Software, Methodology, Formal analysis, Data curation, Conceptualization. **Arianna Comin:** Writing – review & editing, Validation, Methodology, Conceptualization. **Mikael Svensson:** Writing – review & editing, Methodology, Conceptualization. **Johan Nilsson:** Writing – review & editing, Methodology, Conceptualization. **Maria Nöremark:** Writing – review & editing, Writing – original draft, Visualization, Validation, Supervision, Resources, Project administration, Methodology, Funding acquisition, Formal analysis, Conceptualization.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.prevetmed.2024.106260.

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