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## Climate Change and the Risk of Highly Pathogenic Avian Influenza Outbreaks in Birds

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### Authors' contributions

*This work was carried out in collaboration between all authors. Author JEM was a postdoc scholar and was involved in the data collection, statistical analyses, results interpretation and manuscript preparation. Author BAM secured funding and was involved in study design, study execution, results interpretation and manuscript preparation. Author XW was involved in statistical analyses and manuscript preparation. Author MPW was involved in results interpretation and manuscript preparation. All authors read and approved the manuscript.*

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### ABSTRACT

In this paper, we examine the association between climate change and outbreak probability of Highly Pathogenic Avian Influenza A virus (HPAI H5N1) in birds. Climate change is a potential factor for the recent spread of H5N1 outbreaks because it can directly alter the conditions involved in persistence of the virus and disease transmission. Also it can contribute indirectly by changing wild bird migration patterns. Econometric analyses using a dynamic Probit model over monthly data from January 2004 to December 2008 found that a 1% rise in winter total precipitation increases the risk of HPAI H5N1 outbreaks by 0.26%. Spring mean temperature was also found to have positive and significant impacts. Our findings are robust across different model specifications and under out-of-sample tests. Using historical data we find the realized climate change of the last 20 years partly explains the recent expansion in outbreaks. Under future climate change projections, we find that countries having higher projected spring temperature or more winter precipitation or both, such as Japan and Romania, will have large increases in outbreak probabilities. This suggests that climate change may play an even greater role in

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the future, although magnitudes will vary across countries and climate projections. From a policy perspective, future climate conditions may give rise to a need for different disease control and prevention strategies.

*Keywords: HPAI H5N1; climate change; general circulation models (GCMs); risk assessment.*

## **1. INTRODUCTION**

Avian Influenza (AI) or "bird flu" is a contagious animal viral disease [1]. Infections can be divided into highly pathogenic avian influenza (HPAI) and low pathogenic avian influenza (LPAI). LPAI is less contagious, and infected species may not display clinical signs. The HPAI A (H5N1) virus spreads rapidly among infected birds with a high mortality rate (up to 90-100% within 48 hours) and may spread to humans [2].

Since 2003, epidemics of HPAI H5N1 have occurred in domestic and wild bird populations with unprecedented frequency across the globe. This strain was first identified in Hong Kong in 1997 and subsequent outbreaks were observed in East and Southeast Asia during 2003 and 2004. In 2005, outbreaks occurred in central Asia, Russia and Europe. Since then, HPAI H5N1 has continued to spread through Europe, the Middle East, and Africa [3]. As of 2007, 60 countries had experienced outbreaks [4,5], and the number of countries with outbreaks is expanding [6]. In addition, as the end of 2013, there have been 648 reported cases of human infection, resulting in 384 deaths [7].

Globally outbreaks of HPAI H5N1 have resulted in the destruction of more than 250 million domestic poultry including chickens, ducks, turkeys, quail and ostriches, causing large socioeconomic and livelihood losses, as well as affecting food and protein supplies, wildlife populations and public health [3,4]. Determining factors causing this HPAI H5N1 spread and estimating risk probabilities of further outbreaks could improve surveillance, control measures, and disease prevention planning to ultimately reduce losses [8].

Climate has been argued to be a driver of disease transmission and persistence plus a driver of wild bird migration patterns [9,10-11]. In particular, experimental evidence shows that cold temperature and low relative humidity are favorable to the spread of influenza virus and suggests that these two environmental factors could contribute to the seasonality of epidemic influenza [12], thus regional weather monitoring may serve as an integral part of a bird flu surveillance system [13]. In empirical studies, Si et al. [9] indicate that lower levels of moisture and humidity affect wild bird food availability and thereby their distribution and migration patterns. Fang et al. [15] find that precipitation is an important risk factor affecting H5N1 virus distribution in China and Si et al. [10] find that HPAI H5N1 occurrences in wild birds in Europe are highly correlated with increased minimum temperatures and reduced precipitation in January. Ottaviani et al. [11] and Kilpatrick et al. [16] conclude that alterations in cold weather trigger winter movements of migratory birds and have contributed to H5N1 spread outside the traditional migration period in Europe. In the future, since climate change alters these environment conditions, it would almost certainly influence virus transmission and survival outside the host [14].

In terms of disease spread vectors, there has been considerable effort investigating how the HPAI H5N1 virus enters previously unaffected countries. The main pathways that have been

identified are wild bird migration, live bird trade and the transport of poultry and poultry products. In terms of migration, studies suggest that wild birds carry HPAI and can introduce it into new areas during migration [9,10,14,16-17]. Wild ducks were found to be able to carry the H5N1 virus asymptotically [18]. Circumstantial evidence from Russia and Mongolia indicates that wild birds play a significant role in disease spread, because they can become infected and travel long distances before dying [9,19,20-21].

Some studies have attributed the increased frequency of outbreaks to the expanding poultry industry as well as greater movements of live poultry and poultry products [22]. Analysis of spring 2006 Romanian H5N1 outbreaks indicates that poultry movement might have facilitated the spread of infection [23]. However, quantification of the contribution is difficult due to the combination of local, unregulated movements of poultry plus illicit bird trade [24,25], particularly in developing countries. Therefore, few studies have examined the influence of poultry movements [16].

Studies in Romania, Thailand, Indonesia and China suggest that human infection and poultry outbreaks can be aggravated by agricultural and socio-demographic factors [26]. These factors include agricultural population density, and poultry density plus incidence of rice paddy fields, water sources and transportation. Ward et al. [23] and Farnsworth and Ward [27] indicate that the environment and landscape factors (specifically the Danube River Delta) played a critical role in the introduction and initial spread of H5N1 in Romania. Fang et al. [15] find that the distance to the nearest main city, distance to the nearest body of water and distance to the nearest highway contributed to disease spread in China. Others find that the risk of outbreaks increases with poultry density (of both chickens and ducks), road density, and is more likely in areas located near major cities and highway junctions [8,23,28].

Despite the importance of predicting the global outbreak spread plus the potentially contributing nature of climate change, little effort has been applied to project HPAI H5N1 risk across regions and countries under climate change scenarios [24,25]. In this study, we examine the extent to which climate is associated with outbreaks of HPAI H5N1 in birds, and then we project future consequences for HPAI H5N1 spread under projected changes in temperature and precipitation.

## 2. MATERIALS AND METHODS

Here we first introduce the conceptual framework of our analyses, the selection of variables, and the data used. Finally we present our econometric model.

### 2.1 Conceptual Framework

Fig. 1 shows a generalized potential relationship between climate change and HPAI H5N1 outbreaks considering direct and indirect influences. Suppose following [18] the probability of HPAI H5N1 outbreaks denoted by  $Y$ , is determined by the virus survival time outside of the host ( $ST$ ), the movement of wild birds ( $MB$ ), and the environmental conditions including temperature ( $T$ ), precipitation ( $P$ ) and extreme weather ( $EX$ ) as given by the equation:

$$Y = f(ST, MB, T, P, EX, X) \quad (1)$$

Where in addition to the factors defined above,  $X$  includes proximity to wild bird migratory flyways, number of live birds traded, per capita gross domestic product (GDP) and population density.

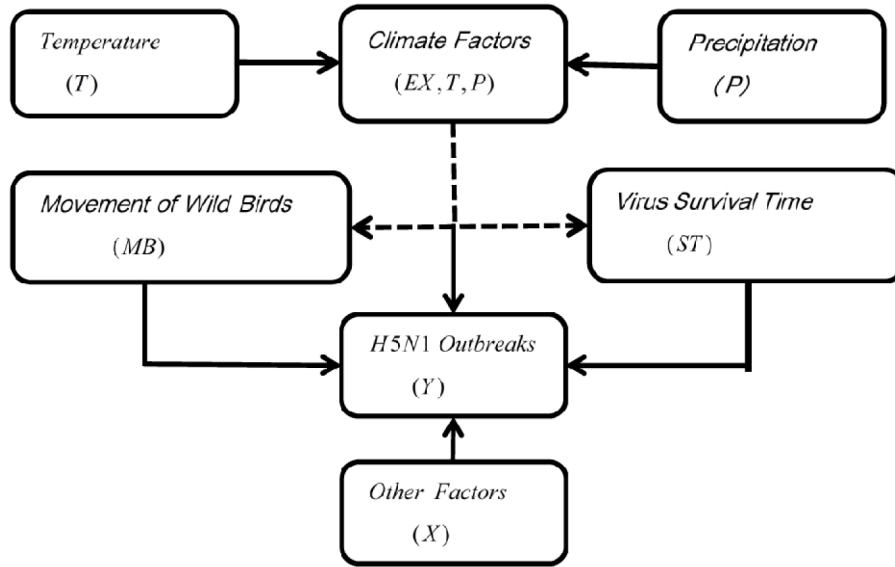
In equation (1),  $ST$  is affected by temperature and humidity of the host environment and  $MB$  forms the distribution of wild birds which is also impacted by temperature and precipitation through the availability of food and water and via their migration patterns [9, 10 and 11]. Consequently, we can rewrite equation (1) as follows:

$$Y = f(ST(T, P, EX), MB(T, P, EX), T, P, EX, X) \tag{2}$$

Therefore, we could develop a statistical model that includes climate variables reflecting both direct and indirect effects and non-climate variables as shown in the equation below:

$$Y = f(T, P, EX, X) \tag{3}$$

Equation (3) is a reduced form model showing the probability of HPAI H5N1 outbreaks as a function of temperature, precipitation, extreme weather and social-economic development.

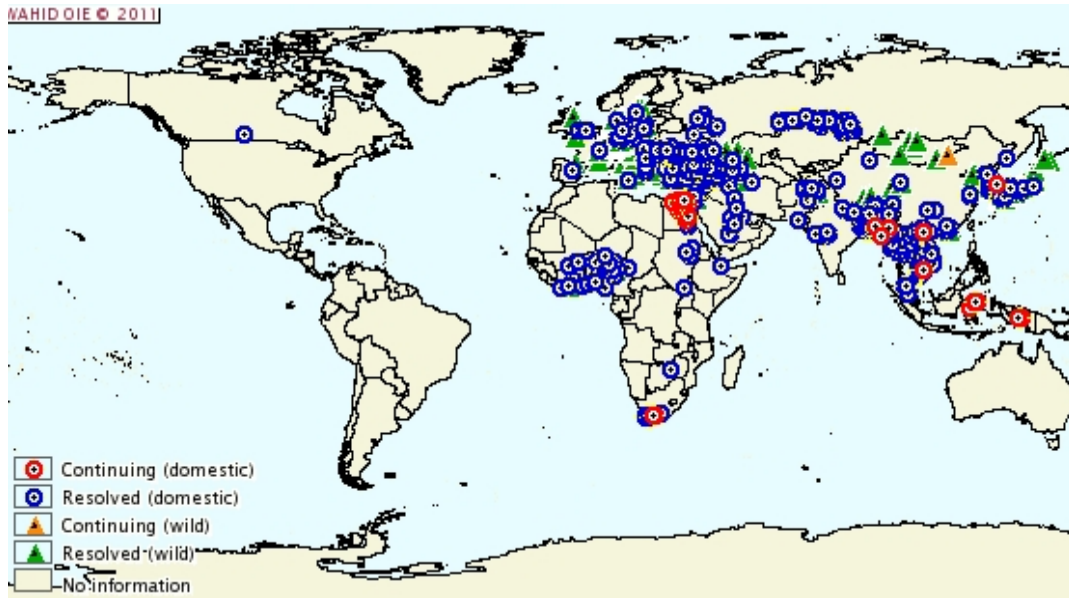


**Fig. 1. A conceptual framework regarding climate effects on HPAI H5N1 outbreaks**  
 (Solid lines indicate direct effects of climate on HPAI H5N1 survival and persistence times. Dashed lines indicate the indirect effects of temperature and precipitation on outbreaks via the distribution of wild birds)

## 2.2 Data and Variables

This study focuses on data regarding HPAI H5N1 outbreaks that occurred between January 2004 and December 2008, the peak period of epidemic activity. The data cover 90 regions in 16 countries in Asia, Africa, Europe and North America. Countries included are Malaysia, South Korea, Cambodia, Indonesia, Thailand, Japan, Vietnam, China, Egypt, Nigeria, Germany, Romania, Turkey, Pakistan, Russia and the United States. Even though there was

no HPAI H5N1 outbreak in the U.S., there was a H5N2 outbreak in February 2004 in Texas. Since the U.S. is on migratory flyways, it is vulnerable to H5N1 introduced via wild bird migration. Fig. 2 shows the distribution of H5N1 outbreaks since 2005 that were reported to the World Organization for Animal Health (OIE), suggesting that there exists heterogeneity across regions with 12% having had at least one HPAI H5N1 outbreak in the past 5 years.



**Fig. 2. Outbreaks of HPAI H5N1 in birds since 2005 as portrayed by OIE (2005)**

The HPAI H5N1 outbreak incidence data were obtained from the World Animal Health Information Database (WAHID) for 2005–2008. The 2004 data were drawn from the Animal Health Database HANDISTATUS II. The HPAI H5N1 outbreak incidence is a binary variable in which a value of one indicates that a region has at least one reported HPAI H5N1 outbreak in domestic poultry or wild birds in a given month while a zero indicates no reported outbreak in that month. We include H5N1 outbreaks in both domestic and wild birds.

Historical monthly climate data were drawn from the National Environmental Satellite Data and Information Service (NESDIS). To construct data on regional climate, we constructed average data across weather stations in each region for temperature and precipitation. Monthly mean temperature was computed in degrees Celsius, and total monthly precipitation including rain and melted snow was computed in millimeters.

Future climate projections were obtained through the Intergovernmental Panel on Climate Change Data Distribution Center (IPCC DDC) for the 2007 IPCC data. Since the projection of future climate change is uncertain, we used multiple General Circulation Models (GCMs) to allow for this uncertainty. Specifically, we choose the following three GCMs:

- The Hadley Center coupled model, version 3 (HAD: CM3), which projects a stable global mean climate [29] and is a mid-sensitivity case [30].
- The Geophysical Fluid Dynamics Laboratory global climate model, version 2.0 (GFDL: CM2.0), which is a model with drastically lower drifts in hydrographic fields

such as temperature and salinity, and display more realistic current climate results that are close to observed values [31,32].

- The Centre National de Recherches Météorologiques coupled atmosphere-ocean climate model, version 3 (CNRM: CM3), which is in close accordance with the present-day climate and predicts a general increase in precipitation throughout the 21<sup>st</sup> century [33].

We assembled projections of monthly changes in temperature and precipitation of these three GCMs under the A1B SRES [34] emissions scenario for 2030 for each country. We obtained the baseline climate data for the period 1961 to 2000 also from the IPCC DDC. We used the historical climate data from 1971-1980 to 1981-1990 and to 1991-2000 to represent the degree of climate change in those two decades.

Per capita GDP and population density were drawn from the U.S. Department of Agriculture Economic Research Service. Data on country-to-country trade in live birds (which excludes illegal movements) were drawn from the United Nations Food and Agricultural Organization and the U.S. Census Bureau, Foreign Trade Division (for the commodity code H1-0105 - live poultry, domestic fowls, ducks, geese, etc.). We also considered trade of live birds by aggregating the totals from three commodity codes: H2-010632 (live birds including parrots, parakeets, macaws and cockatoos), H1-010631 (live birds of prey) and H1-010639 (live birds excluding H1-010632 and H2-010631). However, the data were incomplete and so were not used in the analysis. For each country, trade data were reported either in dollar values or kilograms. Following Kilpatrick et al. [16], we converted the data to numbers of live birds using the median number of birds per kilogram (obtained from trade data) and 10.61 for poultry (most traded poultry are domestic fowl <185g). Table 1 gives definitions and summary statistics of variables used in this study.

**Table 1. Definitions and statistical descriptions of variables**

Variable	Definition	Mean	Std.Dev.	Min	Max
<i>AIotbkProb</i>	Outbreak incidence in a country and month equaling 1 if outbreaks occurred, 0 otherwise	0.12	0.32	0	1
<i>AIotbkProb<sub>t-1</sub></i>	Lagged outbreak incidence	0.12	0.33	0	1
<i>sptemp</i>	Spring mean temperature(°C)	5	9	-7	34
<i>ftemp</i>	Fall mean temperature(°C)	5	9	-8	36
<i>wtemp</i>	Winter mean temperature(°C)	2	7	-21	30
<i>spprecp</i>	Spring total precipitation(mm)	18	59	0	2336
<i>fprecp</i>	Fall total precipitation(mm)	19	62	0	1143
<i>wprecp</i>	Winter total precipitation(mm)	11	48	0	2384
<i>cold_month</i>	Dummy variable for whether the month average temperature is <= 4°C	0.12	0.32	0	1
<i>hot_month</i>	Dummy variable for whether the month average temperature is >= 28°C	0.16	0.36	0	1
<i>lnpimport</i>	Log of imported live birds	8.95	5.06	0	16
<i>lnpexport</i>	Log of exported live birds	6.80	5.98	0	17
<i>popden</i>	Population density (people/ square km)	152	115	8	493
<i>gdpden</i>	Per capita GDP(\$1000)	10	14	0.4	44
<i>EAAFW</i>	East Asia Australian Flyway	0.53	0.50	0	1
<i>CAFW</i>	Central Asian Flyway	0.12	0.33	0	1
<i>BSMFW</i>	Black Sea Mediterranean Flyway	0.30	0.46	0	1
<i>EAFW</i>	East Atlantic Flyway	0.09	0.28	0	1
<i>EFWAFW</i>	East African West Asian Flyway	0.04	0.21	0	1

### 2.3 Econometric Models

We examine the relationship between the probability of HPAI H5N1 outbreaks and climate plus other social-economic and geographic factors using a dynamic Probit model with unobserved individual effects as described in Wooldridge [35-37]. We use this because we are interested in whether there is state dependence after controlling for unobserved heterogeneity. In other words, we estimate how much past HPAI H5N1 outbreaks affect the probability of current outbreaks after controlling unobserved effects. The dynamic Probit model with unobserved individual effects is written as

$$P(y_{it} = 1 | y_{i,t-1}, x_{it}, c_i) = G(\rho y_{i,t-1} + \beta x_{it} + c_i) \quad (4)$$

where  $y_{it}$  is a binary variable, indicating whether an outbreak occurred in region  $i$  at period  $t$ ;  $y_{i,t-1}$  is the lagged dependent variable allowing the current outbreak probability to be altered by whether the region has suffered previous outbreaks;  $x_{it}$  is a  $k \times 1$  vector of explanatory variables;  $c_i$  is an unobserved individual effect in the region that is allowed to be correlated with some elements of  $x_{it}$ ; and  $G$  is a cumulative distribution function that maps the index into the response probability;  $\rho$  and  $\beta$  are parameters to be estimated.

Without loss of generality, we can arrange the observations starting at  $t=0$ , so  $y_{i0}$  is the first observation on  $y$ . For  $t = 1, 2, \dots, T$ , the density function of  $y_{it}$ , under the assumption of normal distribution, can be written as,

$$f(y_{i1}, \dots, y_{iT} | y_{i0}, x_i, c_i, \beta) = \prod_{t=1}^T \Phi(\rho y_{i,t-1} + \beta x_{it} + c_i)^{y_{it}} [1 - \Phi(\rho y_{i,t-1} + \beta x_{it} + c_i)]^{1-y_{it}} \quad (5)$$

Where  $\Phi(\bullet)$  is the standard normal cumulative distribution function.

To estimate  $\beta$  and  $\rho$  consistently, we need to address the existence of outbreaks before the model starts, which is called the initial conditions problem. By making an additional assumption on  $c_i$  as in Wooldridge [35-37], we assume,

$$c_i = \zeta_0 + \zeta_1 y_{i0} + \zeta x_i + a_i \quad (6)$$

Where the conditional distribution of  $a_i | (y_{i0}, x_i) \sim Normal(0, \sigma_a^2)$  and is independent of  $x_i$  and  $y_{i0}$ .

To avoid a large dimensionality problem in estimation<sup>1</sup>, we use the average of  $x_i$  over time

<sup>1</sup> Since we have monthly data from January 2004 to December 2008,  $x_i$  is a  $k \times T$  matrix and  $x_{it}$  is a  $k \times 1$  vector of independent, contemporaneous explanatory variables, which is too large to be estimated based on our sample size.

( $\bar{x}_i$ ) to replace  $x_i$ , as in Chamberlain [38]. Also to identify time indicators, which do not vary across  $i$ , they must be omitted from  $\bar{x}_i$  by setting  $\zeta = 0$ . Therefore the dynamic Probit model with unobserved individual effects becomes

$$f(y_{i1}, \dots, y_{iT} | y_{i0}, x_i) = \prod_{t=1}^T \Phi[(\rho y_{i,t-1} + \beta x_{it} + \zeta_0 + \zeta_1 y_{i0} + \zeta \bar{x}_i) \cdot (1 + \sigma_a^2)^{-1/2}]^{y_{it}} \times \{1 - \Phi[(\rho y_{i,t-1} + \beta x_{it} + \zeta_0 + \zeta_1 y_{i0} + \zeta \bar{x}_i) \cdot (1 + \sigma_a^2)^{-1/2}]\}^{1-y_{it}} \quad (7)$$

Although  $\sigma_a$  cannot be identified in Probit models, we can consistently estimate  $\zeta_{0a}, \rho_a, \zeta_{1a}, \beta_a$  and  $\zeta_a$  applying the conditional Maximum Likelihood Method [37] and estimating a Random-Effects model, which is different from the standard random-effects model since we allow for correlation between the error term and independent variables by specifying the conditional distribution of the unobserved effects.

In the estimation function (7),  $x$  includes,

- Seasonal climate variables (Temperature and precipitation) and their squared terms permit a nonlinear response and allow the model to reflect previous inconsistent results on disease outbreaks as have arose in the literature [10,15,18].
- Dummy variables reflecting temperature extremes as motivated by the fact that AI viruses have been found to survive for long periods in the environment, especially when temperatures are low [15]. Also two studies showed the virus retained its infectivity at 4°C for more than 100 days but lost its infectivity after 24 hours when kept at room temperature (28°C) [39,40]. Therefore, two temperature indices are included: *cold\_month* is 1 when the mean temperature is lower than 4°C, and zero otherwise; *hot\_month* is 1 when the mean temperature is higher than 28°C and zero otherwise.
- A set of migratory bird flyway indicators that identify whether the region is on one of five specific wild bird migratory flyways, or zero otherwise. Disease clusters have occurred throughout the East Asia-Australian flyway since 2003. In the Central Asian flyway, disease clusters started emerging in July 2005 and waned in October 2005. In the Black Sea-Mediterranean flyway, clusters lasted from December 2005 to March 2006. Finally, clusters appeared in the East Atlantic and East Africa-West Asian flyway in March and April 2006, respectively [9].
- Economic variables for country, including per capita GDP, population density, and country-to-country trade in live poultry following Kilpatrick et al. [16].

When applying the econometric model to our data, the empirical model for estimation is,



$$\begin{aligned}
 P(AIOtbkProb_{it} = 1 | x_{it}) = & \Phi(\zeta_{0a} + \rho_a AIOtbkProb_{i,t-1} + \beta_{1a} wtemp_{it} + \beta_{2a} wtemp\_sq_{it} \\
 & + \beta_{3a} sptemp_{it} + \beta_{4a} sptemp\_sq_{it} + \beta_{5a} ftemp_{it} + \beta_{6a} ftemp\_sq_{it} \\
 & + \beta_{7a} wprecip_{it} + \beta_{8a} wprecip\_sq_{it} + \beta_{9a} spprecip_{it} \\
 & + \beta_{10a} spprecip\_sq_{it} + \beta_{11a} fprecip_{it} + \beta_{12a} fprecip\_sq_{it} \\
 & + \beta_{13a} cold\_month_{it} + \beta_{14a} hot\_month_{it} + \beta_{15a} \ln pimport_{it} \\
 & + \beta_{16a} \ln pexport_{it} + \beta_{17a} popden_{it} + \beta_{18a} gdpden_{it} \\
 & + \sum_{k=1}^5 \beta_{19ak} flyway_{it} + \zeta_1 y_{i0} + \zeta \bar{x}_i)
 \end{aligned} \tag{8}$$

We then use estimated coefficients to derive the average partial effects (APE). If  $x_{jt}$  is a continuous variable and  $\phi(\bullet)$  is the standard normal probability density function, the APE can be calculated as,

$$\hat{b}_{aj} f(\hat{z}_{0a} + \hat{r}_a y_{i,t-1} + \hat{z}_{1a} y_{i0} + \hat{b}_a x_{it} + \bar{x}_i \hat{z}_a) \tag{9}$$

If  $x_{jt}$  is a discrete variable, the APE is computed as,

$$\Phi(\bullet) |_{x_{jt}=1} - \Phi(\bullet) |_{x_{jt}=0} \tag{10}$$

### 3. RESULTS AND DISCUSSION

In this section, we present the estimation coefficients, their associated marginal effects and outbreak response elasticities, plus results of the robustness check of using data from 2009 and 2010. We then predict the likelihood of HPAI H5N1 outbreaks under current and future climate scenarios and discuss policy implications.

#### 3.1 Estimation Results

The estimated coefficients from the model are reported in Table 2 as are three model variants included to examine robustness of our results. There the results from the full model given in equation (8) are called model 1, and plus the results from an alternative that excludes the economic variables are labeled model 2 while another variant that excludes the indices of migratory flyways is defined as model 3. The three models give qualitatively similar results for key variables. To save space, we shall focus on model 1, given its greater log-likelihood value and smaller within-sample mean squared error.

Results of Model 1 in Table 2 suggest significant nonlinear effects of climate on HPAI H5N1 outbreaks. For illustration, we plot the marginal effects of spring temperature and winter precipitation in Fig. 3, holding all other variables at their average. Fig. 3 indicates that the probability of disease outbreaks increases as spring temperature increases and then decreases when it reaches a threshold (about 13°C). The pattern is consistent with the cold\_month dummy variable, which is positive and statistically significant (as argued to be the case in Brown et al. [39] and Shahid et al. [40]). Fig. 3 also suggests that higher risks of disease outbreak exist under heavier winter precipitation. It is possible that winter precipitation affects the risk of disease outbreaks through its impacts on water and food

resources and thus affects bird population size and virus survival time [18]. With sufficient precipitation, wild birds might stop for water and food on their migration flyways, which would promote virus transmission among birds [11].

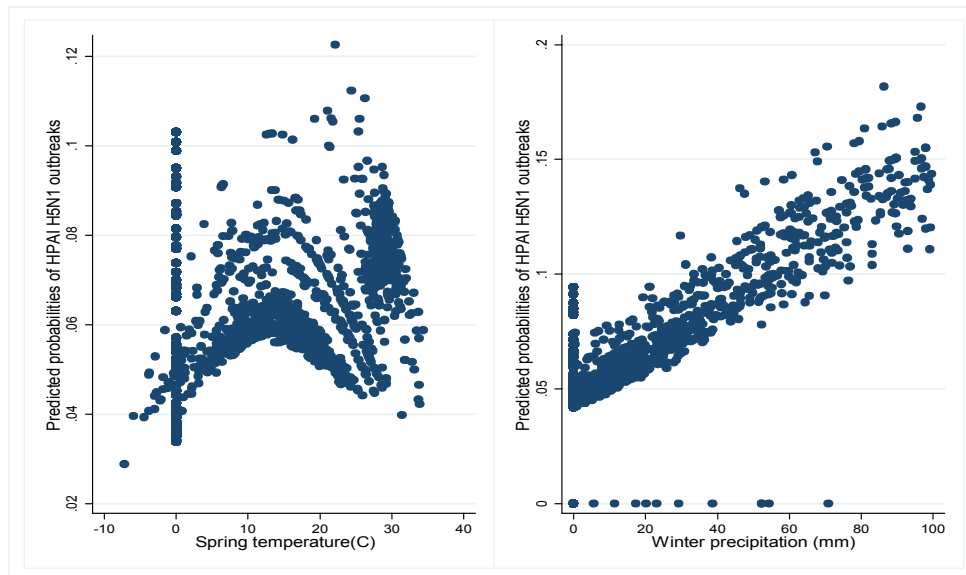
**Table 2. Estimation of the dynamic Probit model with unobserved effects**

Variable	Model1	Model2	Model3
	Coefficients	Coefficients	Coefficients
<i>AIOTbkProb<sub>t-1</sub></i>	1.4382*** (0.0671)	1.4628*** (0.0664)	1.4380*** (0.0671)
<i>Wtemp</i>	0.0108 (0.0124)	0.0100 (0.0124)	0.0099 (0.0124)
<i>wtemp2</i>	-0.0006 (0.0005)	-0.0005 (0.0005)	-0.0005 (0.0005)
<i>Sptemp</i>	0.0350** (0.0174)	0.0339** (0.0172)	0.0355** (0.0174)
<i>sptemp2</i>	-0.0013** (0.0006)	-0.0013** (0.0006)	-0.0013** (0.0006)
<i>Ftemp</i>	0.0299 (0.0207)	0.0281 (0.0204)	0.0298 (0.0205)
<i>ftemp2</i>	-0.0013* (0.0008)	-0.0013* (0.0008)	-0.0013* (0.0008)
<i>wprecip</i>	0.0069*** (0.0021)	0.0063*** (0.0021)	0.0064*** (0.0021)
<i>wprecip2</i>	0.0000*** (0.0000)	0.0000*** (0.0000)	0.0000*** (0.0000)
<i>spprecip</i>	0.0004 (0.0016)	0.0006 (0.0016)	0.0002 (0.0015)
<i>spprecip2</i>	0.0000 (0.0000)	0.0000 (0.0000)	0.0000 (0.0000)
<i>fprecip</i>	0.0008 (0.0012)	0.0008 (0.0011)	0.0007 (0.0012)
<i>fprecip2</i>	0.0000 (0.0000)	0.0000 (0.0000)	0.0000 (0.0000)
<i>cold_month</i>	0.3669** (0.1430)	0.3583** (0.1414)	0.3601** (0.1422)
<i>hot_month</i>	-0.0524 (0.0952)	-0.0614 (0.0944)	-0.0493 (0.0950)
<i>lnpimport</i>	0.0894 (0.0921)		0.0897 (0.0922)
<i>lnpexport</i>	-0.0487** (0.0205)		-0.0476** (0.0203)
<i>popden</i>	0.0411*** (0.0108)		0.0395*** (0.0107)
<i>gdpden</i>	0.1259 (0.0871)		0.1445 (0.0891)
<i>EAAFW</i>	0.1376 (0.3235)	0.7440*** (0.2137)	
<i>CAFW</i>	0.3129** (0.1498)	0.0510 (0.1188)	
<i>BSMFW</i>	0.0224 (0.3640)	0.7805*** (0.2084)	
<i>EAFW</i>	0.9670*** (0.2682)	0.9937*** (0.2618)	
<i>EFWAFW</i>	0.0211 (0.4535)	0.9209*** (0.2861)	

**Table 2 Continued.....**

Intercept	0.0043 (1.2156)	-1.7493* (0.9196)	0.2971 (1.0692)
LR test of rho=0	0.23 (0.3160)	0.99 (0.1600)	3.38** (0.0330)
LR value	-1242.99	-1258.65	-1252.15
MSE	0.0687	0.0690	0.0693
(with-in-sample)	(0.1854)	(0.1874)	(0.1863)
MSE	0.09	0.08	0.09
(out-of-sample)	(0.2187)	(0.2089)	(0.2204)

Note: \*  $p < 0.1$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ ; standard errors are in parenthesis; Model 1 is the full model with all variables; Model 2 is the model without economic variables and Model 3 is the model without indices on wild bird flyways. We omitted estimated results of  $\zeta_1$  and  $\zeta$  because these parameters do not have economic meaning



**Fig. 3. Marginal effects of spring temperature and winter precipitation on HPAI H5N1 outbreak probability**

*(We control all other variables at their sample mean)*

In Table 3, we report the calculated APEs and their associated elasticities. It can be seen that a 1% rise in winter total precipitation increases the risk of HPAI H5N1 outbreaks by 0.26%. Spring mean temperature was also found to have positive and significant impacts. Compared to temperature, precipitation has a larger average partial effect, increasing the risk by 0.12% (model 1).

Previous studies have examined the effect of wild bird movements on HPAI H5N1 spread [9]. Results in both Table 2 and 3 show that countries presence on a migration flyway are statistically significant and positively related to disease outbreaks. The East Atlantic flyway has the largest effects. Previous studies have found that H5N1 outbreaks in some European and African countries were very likely due to earlier seasonal movements of wild birds,

particularly from the East Atlantic flyway [9-11]. Therefore, countries on flyways might need to pay more attention to disease control and prevention plans.

As expected, we find that past outbreaks significantly increase the chance of a current outbreak. A number of Asian countries succeeded in eradicating the disease, notably China, Japan, Malaysia, and South Korea, but then all of these countries experienced re-incursions [41]. These repeated outbreaks indicate virus persistence once introduced into an area [42], suggesting that the dynamics of virus survival are also important to a country's decision making on whether to implement disease prevention and control strategies.

**Table 3. Average partial effects and the elasticity of disease outbreak (change in outbreak probability to change in the independent variable) as derived from regression models**

Variable	Model 1		Model 2		Model 3	
	APE	Elasticity	APE	Elasticity	APE	Elasticity
<i>AIotbkProb<sub>t-1</sub></i>	0.3292*** (0.0251)	0.7318	0.3468*** (0.0253)	0.7197	0.3345*** (0.0253)	0.7135
<i>Wtemp</i>	0.0020 (0.0022)	0.0875	0.0022 (0.0027)	0.0918	0.0012 (0.0014)	0.0497
<i>Sptemp</i>	0.00005** (0.0000)	0.0050	0.0000** (0.0000)	0.0030	0.0001** (0.0000)	0.0060
<i>Ftemp</i>	0.0002 (0.0001)	0.0171	0.0001 (0.0000)	0.0046	0.0000 (0.0000)	0.0000
<i>Wprecip</i>	0.0012*** (0.0004)	0.2627	0.0014*** (0.0005)	0.2714	0.0007*** (0.0002)	0.1446
<i>Spprecip</i>	0.0000 (0.0000)	0.0000	0.0000 (0.0000)	0.0002	0.0000 (0.0000)	0.0001
<i>Fprecip</i>	0.0000 (0.0000)	0.0017	0.0000 (0.0000)	0.0005	0.0000 (0.0000)	0.0000
<i>cold_month</i>	0.0510** (0.0238)	0.1119	0.0520** (0.0244)	0.1065	0.0517** (0.0242)	0.1088
<i>hot_month</i>	-0.0057 (0.0099)	-0.0164	-0.0071 (0.0103)	-0.0192	-0.0056 (0.0102)	-0.0156
<i>Lnimport</i>	0.0103 (0.0102)	1.6981			0.0108 (0.0105)	1.7059
<i>Lnexport</i>	-0.0055** (0.0023)	-0.6954			-0.0056** (0.0023)	-0.6750
<i>Popden</i>	0.0045*** (0.0012)	12.6509			0.0045*** (0.0013)	12.2528
<i>Gdpden</i>	0.0144 (0.0096)	2.5948			0.0164 (0.0101)	2.8406
<i>EAAFW</i>	-0.0124 (0.0364)	-0.1221	0.0871*** (0.0254)	0.8001		
<i>CAFW</i>	0.0306 (0.0223)	0.0689	-0.0085 (0.0137)	-0.0178		
<i>BSMFW</i>	-0.0269 (0.0341)	-0.1491	0.1301*** (0.0421)	0.6722		
<i>EAFW</i>	0.2023** (0.0822)	0.3317	0.2207** (0.0880)	0.3378		
<i>EFWAFW</i>	-0.0268 (0.0314)	-0.0220	0.2180** (0.0981)	0.1668		

Note: \*  $p < 0.1$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ ; standard errors are in parentheses; Model 1 is the full model with all variables; Model 2 is the reduced model without economic variables and Model 3 is the reduced model without indices of wild bird flyways. Please see equation (9) and (10) for the calculation of APE; the elasticities show the effects of a 1% change in the independent variable on the outbreak probability

We also find the probability of disease outbreaks is positively related to human population density. Apparently a country with a denser population is more likely to spread the disease through contact or trade as found in [14,16]. In addition, we find a statistically significant, negative effect of exporting live birds, showing that trade is another important factor as argued in [16]. Countries with more exports of live birds have less disease outbreaks perhaps because of a combination of a need for more careful management to meet international standards and possible underreporting.

Under alternative model specifications (i.e., model 2 and model 3), we find qualitatively similar results, suggesting that our model exhibits substantial robustness. To further test the model robustness, we use an out of sample evaluation using data from 2009 to 2010. In that case, we predict the probability of disease outbreaks and then calculate the out-of-sample mean squared errors (MSEs). We find that the MSEs across models are very close (see the bottom of Table 2), indicating that our models are stable in both specifications and predictions. Therefore, we continue our analyses to predict the disease outbreak risk using climate data from existing and future climate projections.

### **3.2 Outbreak Probability under Effects of Climate Change**

Using estimated parameters from model 1, we first examine the shift in outbreak probability if we had or did not have the climate change of the last 20 years. Additionally, we examine the effects of projected climate change until 2030.

#### **3.2.1 Outbreaks under past climate change**

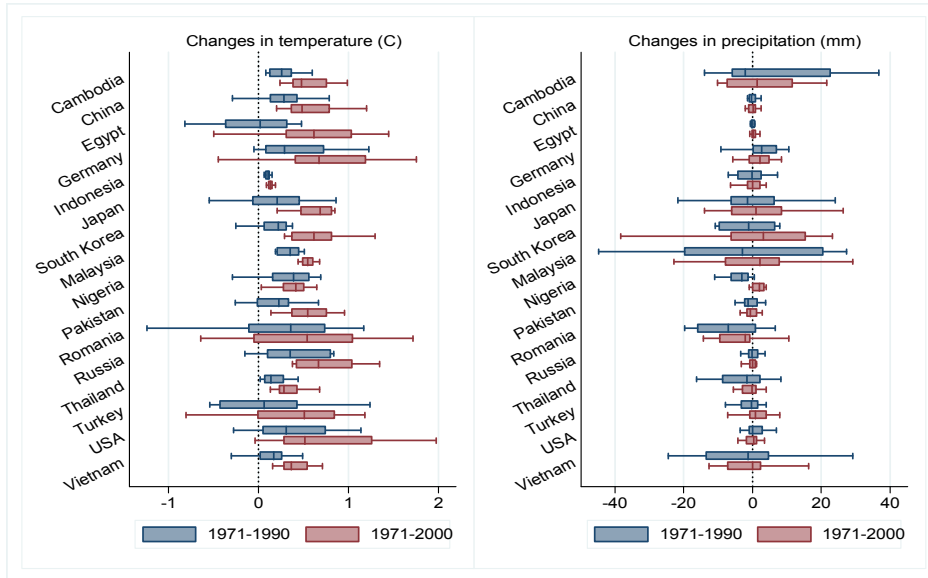
IPCC (2007) reports that the global average temperature has increased by 0.55°C per decade from 1970-2006 [43]. Changes in overall precipitation vary by regions and seasons, but globally there has been a statistically significant 2 to 4% increase in the frequency of heavy and extreme precipitation events [44,45].

For countries in this study, Fig. 4 shows the changes in mean temperature (°C) and total precipitation (mm) for recent periods. We use the climate in 1971-1980 as the baseline, and calculate the average difference in temperature and precipitation between 1971-1980 and 1981-1990 for a 10-year comparison and the difference between 1971-1980 and 1991-2000 for a 20-year comparison. These data show temperature has increased in all northern hemisphere countries relative to 1971-1980, while changes in precipitation vary across countries and time periods. In most countries, changes in precipitation are close to zero, while in others, for example, Cambodia, Japan, South Korea, Malaysia and Viet Nam, there are large variations of precipitation changes.

To predict the effect of climate change of the last few decades on outbreak probability, we use the changes between decadal average climate data for 1971-1980, 1981-1990 and 1991-2000. We evaluate this using the model 1 parameters, holding all but the climatic variables constant. We compute probability under the climate of 1971-1980, and then compute the change under 1981-1990 and 1991-2000 conditions.

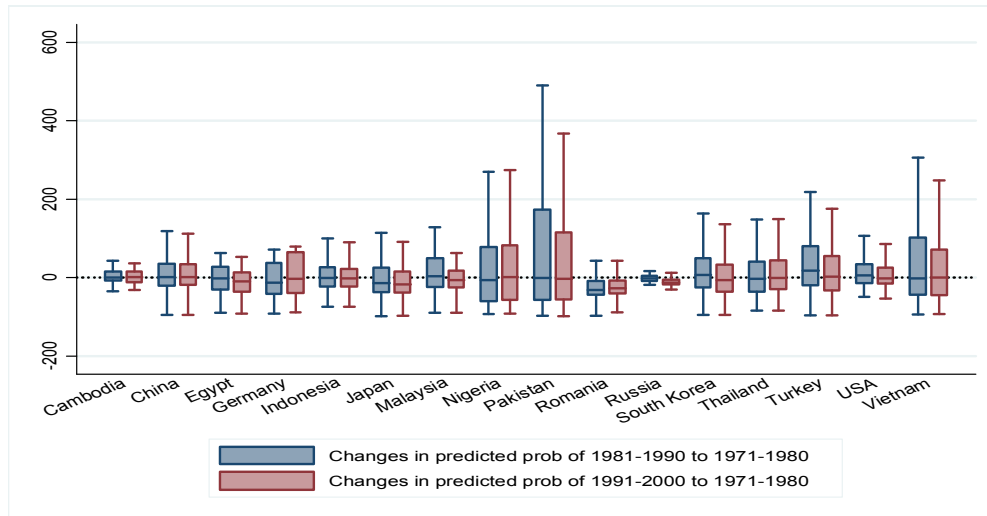
Fig. 5 presents these predicted probabilities for each country and shows little change in disease outbreak probability during the 1980s and 1990s. This is because with mixed changes in temperature and precipitation, effects on disease outbreak may trade-off. For example, Romania has a large increase in temperature and a modest decrease in precipitation, but since our statistical results suggest that precipitation plays a more important role in disease outbreaks, the predicted risk decreases. On the other hand, Turkey

has increased risk of disease outbreaks because it has increased temperature as well as slightly increased precipitation. Although impacts from past climate change on the risk of disease outbreaks are insignificant for some countries, overall results suggest that temperature and precipitation plays a significant role in outbreaks of HPAI H5N1.



**Fig. 4. Changes in winter precipitation and spring temperature between 1971-1980 and recent periods**

(we use the climate in 1971-1980 as the baseline to calculate the difference of temperature (left) and precipitation (right) from 1971-1990 and 1971-2000)



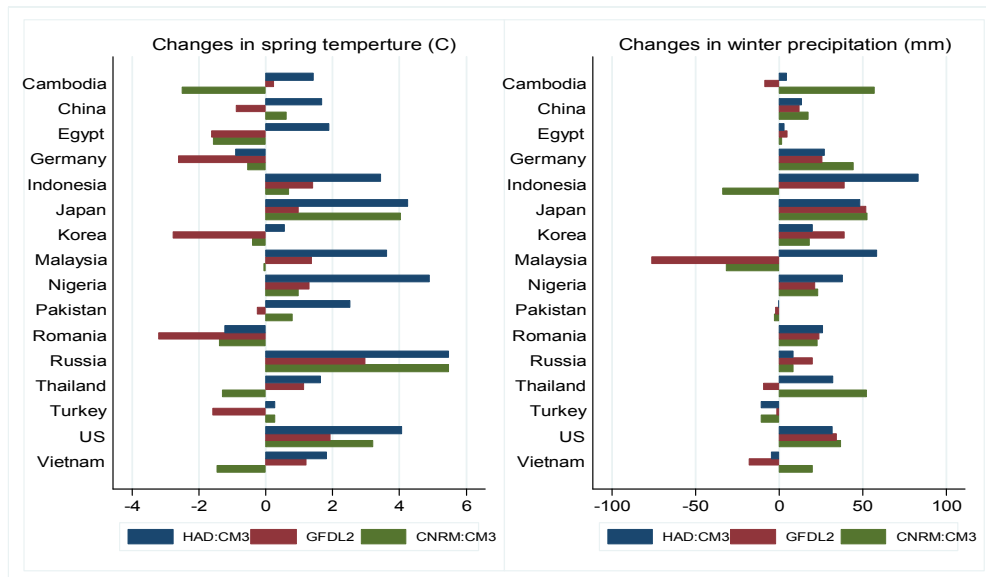
**Fig. 5. Percent changes in predicted probabilities of HPAI H5N1 outbreaks under past climate change**

(We use the predicted probabilities from 1971-1980 as the baseline and calculate the percent change in predicted probabilities under 1981-1990 and 1991-2000 climate conditions from the baseline, respectively)

### 3.2.2 Outbreak probability shifts under future climate change

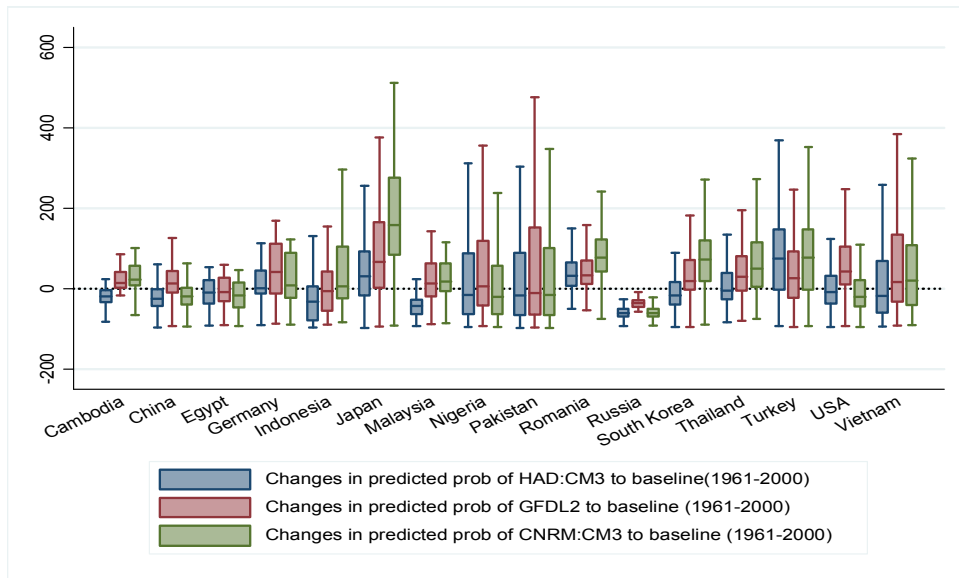
For the effects of future climate change on outbreak risks, we use projected climate data from three GCMs used in IPCC AR4 (2007) under the A1B emission scenario [34] because we note that by 2030, the degree of climate change is not very sensitive to the choice of scenarios across the SRES alternatives [43].

In the climate projections (Fig. 6) all three GCMs project an increase in spring temperature in Indonesia, Japan, Nigeria, Russia, and the US, and an increase in winter precipitation in China, Germany, Japan, Korea, Nigeria, Romania, Russia and the US. There are large variations of changes in temperature and precipitation across countries and GCMs.



**Fig. 6. Changes in spring temperature and winter precipitation under three GCMs**  
 (we use the climate in 1961-2000 as the baseline to calculate the difference of temperature (left) and precipitation (right) from climate models by 2011-2030)

Fig. 7 shows the predicted probabilities of HPAI H5N1 outbreaks across climate scenarios. We find that projected climate change increases the risk of HPAI H5N1 outbreaks in certain countries, mainly depending on the changes in temperature and precipitation or both. In particular, we find increases in disease outbreak probabilities in Japan and Romania, because Japan is projected to have increased temperature and precipitation, and Romania will have increased precipitation and decreased temperature. Additionally, Russia has decreased risk of HPAI H5N1 outbreaks although it has increased temperature and precipitation, but with increased temperature projected in the future, there are fewer cold months with temperature below 4°C. We caution that results in Fig. 7 are not necessarily in accordance with those in Fig. 6 because results in Fig. 7 are generated by changing all climate variables in the model – not only spring temperature and winter precipitation. Note we also include the effects of climate variables that are insignificant in Table 2.



**Fig. 7. Percent changes in predicted probabilities of HPAI H5N1 outbreaks under projected climate change**

*(We set the predicted probabilities from 1961-2000 as the base and compute the percent changes in predicted probabilities under three GCMs climate conditions from the base, respectively)*

### 3.3 Discussion

Results in Fig. 7 suggest that climate change is likely to increase the risk of HPAI H5N1 outbreak in a number of countries although different GCMs provide different ranges of increase or decrease. Given this information, those countries with shifts in outbreak levels could use this information to design more aggressive disease prevention, surveillance, and control plans.

From a methodology development perspective, by including more climate models it would be possible to better capture uncertainties associated with climate projections, which has been an important topic for climate modelers and agronomic researchers [46]. This approach is applicable to risk assessment of epidemic diseases, which could provide useful insight into underlying uncertainties.

### 4. CONCLUSION

We examined the relationship between HPAI H5N1 outbreaks and climate change. We used an econometric model to estimate the effects of climate on the probability of disease outbreaks. The results suggest that the risk of HPAI H5N1 outbreaks is positively related to spring temperature and winter precipitation. Using projected climate data from three GCMs, we find that countries with higher spring temperature and more winter rainfall, or both, are likely to have more disease outbreaks during the future 20 years.



Our results indicate that climate change is a likely factor affecting HPAI H5N1 outbreaks in the past and the future. Two policy implications flow from our statistical and predicted results,

- Countries which are projected to have higherspring temperatures or more winterprecipitation might enhance their planning regarding disease prevention and surveillance so as to reduce the likelihood of future disease outbreaks.
- Climate change mitigation strategies would also have co-benefits in reducing the risks of HPAI H5N1 outbreaks in the future.

Our results also show there are other important factors that influence the risk, including history of past outbreaks, human population density and amount of international trade in live birds. These factors are related to the technology and social-economic development in a country, and are difficult to project in the future. Nonetheless, further research could examine what would happen if social-economic scenarios change together with climate change.

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## **COMPETING INTERESTS**

Authors have declared that no competing interests exist.

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