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Contents lists available at ScienceDirect

Environmental Research

journal homepage: www.elsevier.com/locate/envres



A time-trend ecological study for identifying flood-sensitive infectious diseases in Guangxi, China from 2005 to 2012



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ARTICLE INFO

Keywords: Floods Infectious diseases Spectrum of sensitive infectious diseases Time-trend ecological study

ABSTRACT

Background: Flood-related damage can be very severe and include health effects. Among those health impacts, infectious diseases still represent a significant public health problem in China. However, there have been few studies on the identification of the spectrum of infectious diseases associated with floods in one area. This study aimed to quantitatively identify sensitive infectious diseases associated with floods in Guangxi, China.

Methods: A time-trend ecological design was conducted. A descriptive analysis was first performed to exclude infectious diseases with low incidence from 2005 to 2012 in ten study sites of Guangxi. The Wilcoxon rank-sum test was applied to examine the difference in the ten-day attack rate of infectious diseases between the exposure and control periods with different lagged effects. Negative binomial, zero-inflated Poisson and zero-inflated negative binomial models were used to examine the relationship and odd ratios (ORs) of the risk of floods on infectious diseases of preliminary screening.

Results: A total of 417,271 infectious diseases were notified. There were 11 infectious diseases associated with floods in the preliminary screening process for flood-sensitive infectious diseases. The strongest effect was shown with a 0–9 ten-day lag in different infectious diseases. Multivariate analysis showed that floods were significantly associated with an increased the risk of bacillary dysentery (odds ratio (OR) = 1.268, 95% confidence interval (CI): 1.072–1.500), acute haemorrhagic conjunctivitis (AHC, OR = 3.230, 95% CI: 1.976–5.280), influenza A (H_1N_1) (OR = 1.808, 95% CI: 1.721–1.901), tuberculosis (OR = 1.200, 95% CI: 1.036–1.391), influenza (OR = 2.614, 95% CI: 1.476–4.629), Japanese encephalitis (OR = 2.334, 95% CI: 1.119–4.865), and leptospirosis (OR = 1.138, 95% CI: 1.075–1.205), respectively.

Conclusion: The spectrum of infectious diseases which are associated with floods are bacillary dysentery, AHC, influenza A (H_1N_1) , tuberculosis, influenza, Japanese encephalitis and leptospirosis in Guangxi. Floods can result in differently increased risk of these diseases, and public health action should be taken to control a potential risk of these diseases after floods.

1. Introduction

Many extreme weather events, such as heavy rains, heat waves and droughts, have increased in frequency or magnitude due to global warming (Rahmstorf and Coumou, 2011). Floods are the most frequent natural disaster and have been more widely documented than any other

natural disaster. Their frequency has tended to intensify in recent decades as well as in China, and this trend is projected to increase with climate change (Cao et al., 2013; Milly et al., 2002). Floods are widespread in China, and particularly noteworthy in coastal areas, such as Guangxi, where most of the precipitation is concentrated in rainy seasons. A study suggested that a significantly increasing trend has been

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observed in the population's vulnerability to floods, and the areas include the southwestern provinces, such as Chongqing, Sichuan, Guizhou, Yunnan and Guangxi and the central provinces, such as Hubei and Jiangxi (Wang et al., 2014). In Guangxi, the floods between 2005 and 2012 forced an evacuation of thousands of people from homelands, with over 89.65 million people affected (The Office of State Flood Control and Drought Relief Headquarters, 2013). The floods hit 5.10 million hectares of crops, of which 2.40 million hectares were demolished (The Office of State Flood Control and Drought Relief Headquarters, 2013). The economic damage was estimated at approximately 55.11 billion Yuan (US\$ 8.24 billion) (The Office of State Flood Control and Drought Relief Headquarters, 2013), Floods not only cause enormous losses of people's lives and property, but also pose a major public health threat. It is important to study the impact of floods on human health for forecasting and informing the population, in order to help minimise negative consequences.

At the global level, infectious diseases amounted to an estimated 18% of the total disability adjusted life years (DALYs) of the Global Burden of Disease (GBD) in 2016 (GBD 2016 DALYs and HALE Collaborators, 2017). At present, infectious diseases still represent a significant public health problem in China, with over 7 million cases (incidence rate was 509.54 per 100,000) reported in 2017(Bureau of Disease Control and Prevention, 2018). The health effects of floods are complex and far-reaching, which may include increased mortality and morbidity from some infectious diseases. Flood disasters may lead to infectious disease outbreaks when they result in substantial population displacement, microbes, vectors and reservoir animal hosts exploit the disrupted social and environmental conditions for disease transmission (Kouadio et al., 2012; McMichael, 2015). Studies at home and abroad show that floods can increase the risk of infectious diseases, e.g., cholera (Rieckmann et al., 2018; Sidley, 2008), bacillary dysentery (Liu et al., 2015, 2017), leptospirosis (Mohd Radi et al., 2018), malaria (Ding et al., 2014) and dengue fever (Davrit et al., 2018). However, evidence on the association between floods and infectious diseases is far from clear. Few studies have been conducted about the identification of flood-sensitive infectious diseases. To our knowledge, although previous studies have confirmed an increased risk of individual infectious diseases during a flooding, there are few relevant studies on the identification of the spectrum of infectious diseases associated with floods in one area. Flood-sensitive infectious diseases remain unclear in China. At present, further strong epidemiological evidence is still needed to study the impact of floods on infectious diseases.

In view of the background summarised above, this study aimed to identify sensitive infectious diseases associated with floods in Guangxi, China from the quantised perspective. Results will contribute to provide reliable epidemiological information for the control programmes in Guangxi and lead to a better understanding of the public health consequences of floods.

2. Material and methods

2.1. Study sites

Fig. 1 hows the geographic position of the study areas in Guangxi, China, which are located in the middle reaches of the Pearl River. It has a longitude of 104°26′E and 112°04′E, and latitude of 20°54′N and 26°24′N, covering an area of 236,700 km² and hosting a population of 56 million in 2017. Most of local residents are ethnic Han or Zhuang. Guangxi is divided into Eastern Guangxi, Southern Guangxi, Western Guangxi, Northern Guangxi, and Central Guangxi according to geographical location. There are 111 administrative regions at the county level in Guangxi, including 39 municipal districts, 8 county-level cities, 52 counties and 12 autonomous counties. Two county-level administrative districts were selected for each region as the study sties, and our study areas covered ten county-level administrative districts (i.e., Guiping, Mengshan, municipal district of Nanning, municipal district of

Qinzhou, municipal district of Baise, municipal district of Hechi, municipal district of Guilin, Xing'an, municipal district of Liuzhou and Rong'an). The similar geographic locations determine the characteristics of the subtropical monsoon climate in the study sites. The annual average temperature in these study sites is 16.5–23.1 °C, and the annual average rainfall is above 1070 mm. The study sites have clear dry and rainy seasons, with the rainy season from April to September and dry season from October to March. Precipitation in the rainy season accounts for 70–85% of the annual precipitation, making them prone to floods.

2.2. Data collection

2.2.1. Disease surveillance data

In China, each month is divided into 3 ten-day, i.e., the first, middle and last ten-day periods of a month. The ten-day number of 39 notifiable infectious disease cases were collected for the period of 2005–2012 from the China Information System for Disease Control and Prevention (CISDCP). All cases were defined based on the diagnostic criteria and principles of management for notifiable infectious diseases issued by the Ministry of Health of the People's Republic of China. Only the cases confirmed both clinically and by laboratory tests, including microscopic examination and biochemical identification, were included in our study. In China, The Direct Network Report system for infectious diseases has been applied since Jan 1, 2004, and the surveillance system for notifiable infectious diseases is mainly hospital-based. According to the law of the People's Republic of China on the Prevention and Treatment of Infectious Diseases, all hospitals and clinics are obliged to report every case of notifiable infectious diseases to their nominated CDC within 24 h through the Direct Network Report system. Hence, it is assumed that the disease notification of the research duration is consistent and trustworthy.

2.2.2. Floods and meteorological data

Data on floods from 2005 to 2012 were collected from the Yearbooks of Meteorological Disasters in China and Chinese Agri-meteorological Disasters Information Dataset (http://data.cma.cn/data/ cdcdetail/dataCode/AGME_AB3_CHN_TEN.html). The extent and intensity of floods, as well as the damage to the population, crops and economy ascribed to one specific event, are approximately described in the yearbooks and dataset. During the study period, floods killed 498 and collapsed 0.56 million buildings in Guangxi. The number of floods in each district was as follows: Baise municipal district (26), Guilin municipal district (11), Guiping (34), Hechi municipal district (30), Liuzhou municipal district (3), Mengshan (33), Nanning municipal district (20), Qinzhou municipal district (39), Rong'an (3) and Xing'an (29) between 2005 and 2012, respectively. After receiving permission from the National Meteorological Information Centre of China, meteorological data were obtained from China Meteorological Data Service Centre (http://data.cma.cn/). Ten meteorological stations, including Guiping (23°24'N, 110°05'E), Mengshan (24°12'N, 110°31'E), Nanning (22°38'N, 108°13'E), Qinzhou (21°57'N, 108°37'E), Baise (23°54′N, 106°36′E), Hechi (24°42′N, 108°02′E), Guilin (25°19′N, 110°18′E), Xing'an (25°61′N, 110°66′E), Liuzhou (24°21′N, 109°24′E), and Rong'an (25°13'N, 109°24'E) were used for our study. The meteorological variables included ten-day mean temperature (MT), tenday mean minimum temperature (MinT), ten-day mean maximum temperature (MaxT), ten-day accumulative rainfall (AR), heavy rain (25-49.9 mm per day) days (HRD), rainstorm (> 50 mm per day) days (RD), ten-day mean relative humidity (MRH), ten-day mean air pressure (MAP), ten-day mean wind velocity (MWV) and ten-day accumulative sunshine duration (ASD).

2.3. Study design and statistical analysis

A time-trend ecological study was performed to identify flood-

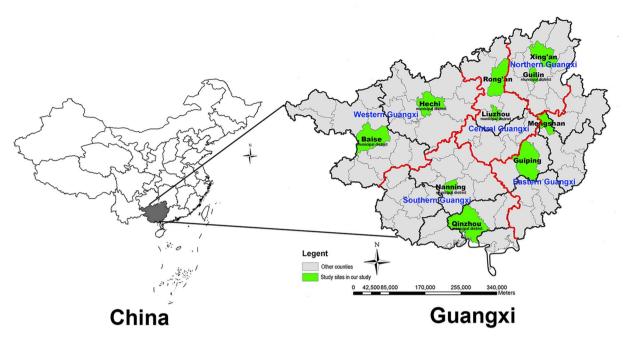


Fig. 1. Location of study sites in Guangxi, China.

sensitive infectious diseases in the study sites. Time-trend ecologic studies can compare variations in aggregate exposures and outcomes over time within the same study site (Morgenstern, 1995). In the following three stages we examined the association of floods and infectious diseases.

Firstly, we performed a descriptive analysis to illustrate the distribution of infectious diseases from 2005 to 2012. There are currently 39 notifiable infectious diseases in China. Epidemiological reviews have suggested that floods may be contributing to the spread of the most notifiable infectious diseases, in addition to blood and sexually transmitted diseases (hepatitis B, hepatitis C, syphilis, gonorrhoea and acquired immunodeficiency syndrome) and neonatal tetanus (Ahern et al., 2005; Alderman et al., 2012; Du et al., 2010; Hajat et al., 2005; Ivers and Ryan, 2006; Llewellyn, 2006). Therefore, the blood and sexually transmitted diseases and neonatal tetanus were no longer identified in this study according to the mechanism of disease transmission and biological plausibility of these diseases during floods. Then, the descriptive analysis was conducted to describe the incidence and temporal distribution of infectious diseases. Based on the interquartile range, diseases with annual average incidence rates less than the lower quartile were defined as low-incidence infectious diseases. The diseases with low incidence during the study period were not incorporated in the next analysis because a small number of cases of these diseases may result in uncertainty and instability of the study results when assessing the effect of floods.

Secondly, the exposure periods and control (or "reference") periods were selected according to floods in the study sites. Guangxi is located at low latitude with a subtropical monsoon climate. Seasonal variation in Guangxi is not obvious, but dry and rainy seasons are distinct. Hence, the period of April–September between 2005 and 2012 was selected as our study period in order to control for seasonality. The exposure periods were the ten-day period with flooding in the study sites and the ten-day period without flooding or other meteorological disasters (e.g., heat wave) was a candidate for control periods during the rainy season. In this study, the control periods were selected according to the time-stratified approach of a time-stratified case-crossover design (Levy et al., 2001; Lumley and Levy, 2000). Thus, every ten-day period within the same rainy season and year of the exposure period was considered a control period. If more than one flood occurred in the same rainy season, other ten-day periods with flooding were excluded as control

periods. Because floods may occur any time during the same rainy season, all control periods may be distributed before one exposure period, or after one exposure period, or before and after the exposure period (i.e., several control periods were randomly distributed, and the exposure period was not fixed at a certain location). A study indicates that this referent selection is not subject to bias resulting from time trend and can be used as a control for seasonality (Janes et al., 2005a). In addition, this referent selection avoids overlap bias associated with a multifactor model (Janes et al., 2005b). The Wilcoxon rank-sum test was applied to examine the difference in the ten-day attack rate of infectious diseases between the exposure and control periods with different lagged effects. Relative risks (RRs) were derived by comparing the attack rate of infectious diseases between exposure and reference periods. The optimal lag time was selected based on the maximum RRs because the best estimate of duration had minimal non-differential misclassification at this point (Maclure, 1991).

Thirdly, because there was a strong linear correlation between meteorological factors (Fig. S1), a principal component analysis (PCA) was constructed using meteorological data from 2005 to 2012 to extract principal components. After fitting the lags, multivariate count outcome models were performed to evaluate the relationship between each infectious disease and floods with adjustment for potential confounding factors. The selection procedures of multivariate count outcome models are shown in Fig. S2.

A Poisson distribution is not an appropriate model for infectious diseases because of infectivity and clustering of infectious diseases. A negative binomial (NB) distribution is usually used to describe the distribution of infectious diseases (Cameron and Trivedi, 2013). So, in the final models, the NB regression models were selected to evaluate the relationship between bacillary dysentery, other infectious diarrhoea and tuberculosis and floods due to a large number of cases of these infectious diseases.

However, data of some infectious diseases, such as the counts of amoebic dysentery, measles, leptospirosis, etc. examined in the present study, were often characterised by overdispersion and excess zeros in a given ten-day period, which was beyond the predictive ability of the NB regression (Greene, 1994). Zero-inflated regression is a practical way to model count data with both excess zeros and positive counts, as such models, incorporating covariates, can be estimated simultaneously in the extra zeros and the count distributional components of the model

(Carrel et al., 2010; Cheung, 2002). Zero-inflated Poisson (ZIP) and zero-inflated negative binomial (ZINB) are the two most popular models (Zuur et al., 2009). In our study, we first determined whether zero-inflation existed in the count data of infectious diseases. Then, a likelihood ratio test that alpha = 0 was performed for overdispersion, which compares the sample mean with the sample variance (Böhning et al., 1997; Xu et al., 2017). If the likelihood ratio test of alpha was not significant, the ZIP was adopted to explore the relationship between floods and infectious diseases; otherwise, the ZINB was adopted. The Vuong test was also performed to determine whether the apparent overdispersion was induced by the extra number of zeros and which regression model was more suitable for this study (Vuong, 1989). In the final models, the ZINB models were selected to examine the relationship between amoebic dysentery, acute haemorrhagic conjunctivitis (AHC), influenza, measles, rabies, Japanese encephalitis and floods; the ZIP models were selected to explore the influence of floods on influenza A (H_1N_1) and leptospirosis.

Lastly, the goodness of fit of regression models were determined by the likelihood ratio test statistics: log-likelihood. Odds ratios (ORs) and 95% confidence intervals (CI) of the floods on the above-mentioned infectious diseases were calculated in each model. The diseases with statistical significance in the models identified our flood-sensitive

Table 1The incidence of each kind of infectious diseases in study sites during the study period.

Disease	Time-period	Number of cases	Av. incidence rate $(/10^5)$
Cholera ^a	2005.01-2012.12	0	0
Hepatitis A	2005.01-2012.12	1618	2.296
Hepatitis E	2005.01-2012.12	1606	2.218
Poliomyelitis ^a	2005.01-2012.12	0	0
Bacillary dysentery	2005.01-2012.12	17302	25.044
Amebic dysentery	2005.01-2012.12	331	0.481
Typhoid fever	2005.01-2012.12	2591	3.668
Paratyphoid fever	2005.01-2012.12	698	1.007
Other infectious diarrhoea	2005.01-2012.12	46625	65.506
AHC	2005.01-2012.12	32218	44.312
HFMD	2008.06-2012.12	166937	350.996
SARS ^a	2005.01-2012.12	0	0
Influenza A (H ₁ N ₁)	2009.05-2012.12	3648	9.998
Measles	2005.01-2012.12	2082	3.118
Tuberculosis	2005.01-2012.12	87266	123.830
Meningococcal meningitis ^a	2005.01-2012.12	6	0.009
Pertussis ^a	2005.01-2012.12	15	0.023
Scarlet fever	2005.01-2012.12	1466	2.063
Diphtheria ^a	2005.01-2012.12	0	0
Influenza	2005.01-2012.12	6074	8.429
Mumps	2005.01-2012.12	42652	59.125
Rubella	2005.01-2012.12	2902	3.927
Plague ^a	2005.01-2012.12	0	0
HFRS ^a	2005.01-2012.12	26	0.038
Rabies	2005.01-2012.12	424	0.607
Dengue fever ^a	2005.01-2012.12	24	0.033
Japanese encephalitis	2005.01-2012.12	170	0.247
Anthrax ^a	2005.01-2012.12	4	0.006
Brucellosis ^a	2005.01-2012.12	6	0.009
Schistosomiasis japonica ^a	2005.01-2012.12	2	0.003
Leptospirosis	2005.01-2012.12	267	0.377
Malaria	2005.01-2012.12	157	0.219
Kala-azar ^a	2005.01-2012.12	0	0
Typhus fever	2005.01-2012.12	154	0.201
Hydatidosis ^a	2005.01-2012.12	0	0
Filariasis ^a	2005.01-2012.12	0	0

AHC, acute haemorrhagic conjunctivitis; HFMD, hand-foot-and-mouth disease; SARS, severe acute respiratory syndrome; HFRS, hemorrhagic fever with renal syndrome; Av., average.

Table 2 Distribution of ten-day attack rate ($/10^5$) of each kind of diseases which were significantly in the strongest lagged time between exposure and control periods.

Disease	Exposure period	Control period	Lag (ten- day)	RRs	Z	p
Bacillary dysentery	0.773	0.707	1	1.093	2.226	0.026
Amebic dysentery	0.046	0.023	2	1.986	2.828	0.005
Other infectious	1.942	1.910	6	1.017	2.148	0.032
diarrhoea						
AHC	2.834	2.762	0	1.026	2.470	0.014
Influenza A (H ₁ N ₁)	0.108	0.039	7	2.767	2.048	0.041
Tuberculosis	4.011	3.476	9	1.154	2.546	0.011
Influenza	0.606	0.250	0	2.425	2.086	0.037
Measles	0.104	0.076	0	1.368	2.520	0.012
Rabies	0.030	0.016	9	1.881	3.072	0.002
Japanese encephalitis	0.032	0.008	0	3.971	3.853	0.000
Leptospirosis	0.013	0.005	5	2.593	2.877	0.004

RRs, relative risks; AHC, acute haemorrhagic conjunctivitis.

infectious diseases. All statistical analyses were performed using Stata 12 (StataCorp., USA).

3. Results

3.1. Descriptive analysis for the infectious diseases

There were 417,271 cases of infectious diseases in total in the study sites over the study period. Table 1 shows the incidence of each kind of infectious disease in study sites during the study period. No cases had been notified in cholera, poliomyelitis, severe acute respiratory syndrome, diphtheria, plague, kala-azar, hydatidosis and filariasis in the study sites. Twenty-eight other infectious disease cases were reported during this period, with annual average incidences ranging from 0.003 to 350.996 per 100,000. It was difficult to assess the effect of floods on meningococcal meningitis, pertussis, haemorrhagic fever with renal syndrome (HFRS), dengue fever, anthrax, brucellosis and schistosomiasis japonica because of the small number of cases in these diseases. Therefore, these diseases were not incorporated in the next analysis.

3.2. Preliminary screening for flood-sensitive infectious diseases

The primary sensitive diseases were screened through comparing the morbidity of infectious diseases between exposure and reference periods by the Wilcoxon rank-sum test. Table 2 demonstrates the results of distribution of ten-day attack rate of infectious diseases, which were significant in the strongest lagged time between exposure and control periods. The results suggested that floods were not associated with the attack rate of hepatitis A, hepatitis E, typhoid fever, paratyphoid fever, HFMD, scarlet fever, mumps, rubella, malaria and typhus fever. Wilcoxon rank-sum test results showed that bacillary dysentery, amoebic dysentery, other infectious diarrhoea, AHC, influenza A (H₁N₁), tuberculosis, influenza, measles, rabies, Japanese encephalitis and leptospirosis were significantly associated with floods (p < 0.05). The strongest lagged effects were observed at 1 ten-day for bacillary dysentery, 2 ten-day for amoebic dysentery, 6 ten-day for other infectious diarrhoea, 0 ten-day for AHC, 7 ten-day for influenza A (H1N1), 9 tenday for tuberculosis, 0 ten-day for influenza, 0 ten-day for measles, 9 ten-day for rabies, 0 ten-day for Japanese encephalitis, and 5 ten-day for leptospirosis; and the RRs between exposure and reference periods were 1.093, 1.986, 1.017, 1.026, 2.767, 1.154, 2.425, 1.368, 1.881, 3.971 and 2.593, respectively.

a These diseases were not incorporated in the next analysis.

Table 3Parameters of the floods on the risk of infectious diseases in the multivariate models.

Diseases	β	SE	Z	p	OR (95% CI)
Bacillary dysentery	0.237	0.086	2.77	0.006	1.268 (1.072–1.500)
Amebic dysentery	0.511	0.322	1.59	0.112	1.667 (0.887-3.133)
Other infectious diarrhoea	0.017	0.112	0.15	0.880	1.017 (0.816-1.267)
AHC	1.172	0.251	4.68	0.000	3.230 (1.976-5.280)
Influenza A (H ₁ N ₁)	0.592	0.025	23.31	0.000	1.808 (1.721-1.901)
Tuberculosis	0.182	0.075	2.43	0.015	1.200 (1.036-1.391)
Influenza	0.961	0.292	3.30	0.001	2.614 (1.476-4.629)
Measles	0.009	0.180	0.05	0.959	1.009 (0.709-1.436)
Rabies	0.358	0.198	1.81	0.070	1.431 (0.971-2.109)
Japanese encephalitis	0.847	0.375	2.26	0.024	2.334 (1.119-4.865)
Leptospirosis	0.129	0.029	4.47	0.000	1.138 (1.075–1.204)

SE, standard error; OR, odds ratio; CI, confidence intervals. AHC, acute haemorrhagic conjunctivitis.

3.3. Multivariate regression analysis

After fitting the lags, flood variable, the four principal components and the ten-day cases of infectious diseases were added into the multiple regression models with adjustment for the influence of the population base in the study sites. The parameters of the multivariate regression models and ORs of floods on the risk of infectious diseases are presented in Table 3 and Fig. 2. Results showed that floods were significantly associated with an increased risk of bacillary dysentery, AHC, influenza A ($\rm H_1N_1$), tuberculosis, influenza, Japanese encephalitis and leptospirosis. After adjustment for potential confounding factors, the ORs of the above-mentioned diseases for floods were 1.268 (95% CI: 1.072–1.500), 3.230 (95% CI: 1.976–5.280), 1.808 (95% CI: 1.721–1.901), 1.200 (95% CI: 1.036–1.391), 2.614 (95% CI: 1.476–4.629), 2.334 (95% CI: 1.119–4.865) and 1.138 (95% CI: 1.075–1.205), respectively.

4. Discussion

During heavy rains and floods, due to the widespread existence of infectious sources, it is easy to produce various hidden dangers and conditions conducive to the spread of infectious diseases. This study helps determine the spectrum of sensitive infectious diseases, which are associated with floods in Guangxi, China. Although increased risk of some infectious diseases has been noted after floods in some studies, this was first time that the study quantitatively screened flood-sensitive

infectious diseases extensively and systematically using monitoring data. The results confirm that exposure to floods will affect the risk of transmission of some communicable diseases. Identification of floodsensitive infectious diseases would be beneficial for providing a basis for the policy making for control technologies of these infectious diseases during floods.

This study has indicated that floods are positively associated with the morbidity of bacillary dysentery, amoebic dysentery, other infectious diarrhoea, AHC, influenza A (H₁N₁), tuberculosis, influenza, measles, rabies, Japanese encephalitis and leptospirosis. An increased risk of enteric infectious diseases following floods has been reported in some developing countries. For example, a cholera outbreak hit Mozambique after severe flooding in 2008, with many people dying from the disease (Sidley, 2008). During flood-associated epidemics, Vibrio cholerae is the most commonly identified cause of diarrhoea, and rotavirus is the second most frequently identified flood-associated pathogen in Dhaka, Bangladesh (Schwartz et al., 2006). In Bangladesh, approximately two-thirds of the tube-wells and all toilets became unusable during the floods of 1998 and 2004 and approximately half of the affected population suffered from diarrhoeal diseases (Shimi et al., 2010). Even in high-income countries, although the risk of outbreaks of gastrointestinal illness during floods is low, the risk of gastrointestinal illness increases with the severity of the disaster (Reacher et al., 2004; Wade et al., 2004). After floods, there is great concern for respiratory infection from exposures to these extraordinary conditions, especially among those at higher risk of developing illnesses from exposure to respiratory pathogens. Approximately 30% of displaced individuals seeking medical care in Sri Lanka after the 2004 tsunami disaster complained of respiratory problems (Lim et al., 2005). After the 2005 floods in England, many of the respondents had suffered a number of minor ailments, which included recurring flu-like symptoms, such as coughs, sore throats, etc. (Carroll et al., 2010). One study from rural Bangladesh shows evidence of a moderate elevation in risk of acute respiratory infection during the 2 years after flooding (Milojevic et al., 2012). Floods can potentially increase the spread of vector-borne diseases, such as leptospirosis, Japanese encephalitis, malaria, dengue, rabies, etc. (Afzal and Sultan, 2013; Ding et al., 2014; Matsushita et al., 2018; Mohd Radi et al., 2018; Saeed and Piracha, 2016; Smith et al., 2013; Zhang et al., 2016). Similar findings have been reported in our study. Our study shows that the attack rates of bacillary dysentery, amoebic dysentery, other infectious diarrhoea, AHC, influenza A (H₁N₁), tuberculosis, influenza, measles, rabies, Japanese encephalitis and leptospirosis in the exposure periods were significantly higher than those in the control periods. The results indicate that floods may play an

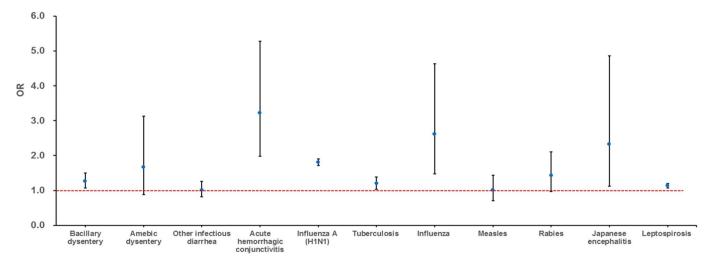


Fig. 2. OR estimates of the risk of infectious disease due to floods.

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important role in the risk of those diseases in the study sites. Due to the delayed environmental transport of pathogens and delayed onset of clinical symptoms, this study has identified a lagged effect of floods on bacillary dysentery, amoebic dysentery, other infectious diarrhoea, influenza A (H_1N_1), tuberculosis, rabies and leptospirosis. The factors that may affect the lagged effect include the growth of pathogens under suitable environmental conditions, spread through contaminated food or water and other health infrastructures, spread through the expansion in the number and range of vector habitats and the incubation period of those diseases. However, this study showed no association between floods and some infectious diseases (e.g., cholera, malaria, dengue fever, etc.), which were linked to floods in the literature review. This may be because the prevention and control of these infectious diseases has high priority in this region.

In our study, results of the NB and ZINB models have identified that bacillary dysentery and AHC are associated with floods after controlling potential confounding factors. In flood conditions, there is potential for increased transmission of enteric infectious diseases, especially in areas where the population does not have access to clean water and sanitation. The underlying mechanisms by which floods influence bacillary dysentery and AHC are not yet clear. We propose that the disruption of sewage systems and contamination of drinking water during floods may contribute to bacillary dysentery and AHC epidemics (Kunii et al., 2002). Heavy rainfalls have also been associated with increases in measurable Shigella and pathogenic viruses (such as Enterovirus 70) in water. One study from Pakistan indicated that twenty percent of the drinking water samples collected during the flood period were contaminated with Shigella and other enter pathogens, including Vibrio cholerae, Salmonella, Staphylococcus aureus and Enterovirus (Khan et al., 2013). In addition, lack of clean water, overcrowding, insufficient understanding of personal and domestic hygiene, nutritional deficiency, and overall poor sanitation are the major contributing factors for the spread of diarrhoeal diseases. A study showed that post-flood resettlement, overcrowding and compromised quality of water and hygiene in Ethiopia contributed to a high incidence of diarrhoeal disease (Wakuma Abaya et al., 2009). A German study also showed that the major risk factor for enteric infectious diseases was contact with floodwater (OR = 5.8, 95% CI: 1.3-25.1) (Schnitzler et al., 2007).

Results from the NB, ZINB and ZIP models show that floods were associated with an increased risk of influenza A (H1N1), tuberculosis and influenza after adjustment for lagged effect, meteorological factors, seasonality and long-term trend. Overcrowding and an interruption in public health campaigns after natural disasters (e.g., earthquakes, floods, Tsunami, etc.) can impact the incidence of a number of vaccinepreventable illnesses, including measles, meningitis and influenza (Ivers and Ryan, 2006). According to a systematic review, measles case fatality rates in complex emergencies may be as high as 33%, compared with a mortality rate in stable populations of approximately 1% (Wilder-Smith, 2005). Therefore, we speculate that the possible reasons for the increase in influenza A (H₁N₁), tuberculosis and influenza caused by floods were: the cold chain work was interrupted by flood disasters, and many vaccination stations stopped their public health services; floods caused a large number of displaced people and resulted in the accumulation of susceptible populations; poor health resources, poor nutrition and irregular life during the floods were also a possible factor to increase the risk of respiratory infectious diseases (Ivers and Ryan, 2006). In addition, the temporary shelters and the humid and crowded living environment where the victims live provide more opportunities for respiratory infections. For example, it was reported in some studies that the humid and crowded living environment were risk factors for tuberculosis (Dheda et al., 2016; Luo et al., 2014).

Our results indicate that an increased risk of Japanese encephalitis and leptospirosis was significantly associated with floods in the multivariate analysis models. One Chinese study has confirmed that exposure to floods can increase the incidence of Japanese encephalitis (Zhang et al., 2016). As we know, stagnant water provides a breeding ground

for many vectors, such as mosquitoes. This situation can result in an increase of the vector population and potential for disease transmission (Watson et al., 2007). A certain amount of precipitation during the floods not only provides the medium for breeding but also increases the relative humidity that enhances the longevity of adult mosquitoes, which in turn facilitates the transmission of Japanese encephalitis virus to humans (Bi et al., 2003; Zhang et al., 2016). Considering the incubation periods of the virus in the mosquito and the human, the lagged time of 0 ten-day periods between floods and increased Japanese encephalitis transmission is not biologically feasible. Therefore, we also assume that the floods could indirectly affect the intermediate stage of Japanese encephalitis virus infection through providing proper environmental conditions (i.e., rainfall, humidity and temperature) for activity of adult mosquitoes, rather from the beginning of the infection process (Zhang et al., 2016). There have been reports of flood-associated outbreaks of leptospirosis from a wide range of countries (Ahern et al., 2005). Leptospirosis is caused by pathogenic spirochaetes of the genus Leptospira. Humans usually become infected through contact with water or soil contaminated by the urine of infected animals, such as rodents, dogs, cattle, pigs and wild animals (Karande et al., 2003). Leptospirosis has the potential to cause widespread epidemics when large numbers of the population are exposed to wet conditions for prolonged periods (Sehgal et al., 2002). Floods may result in the scattering of garbage, debris and food that may contribute to the amplification of rodent populations. Animal displacement commonly occurs during periods of floods. Displaced domesticated animals, rats, pigs, cattle and reptiles often result in contaminating floodwaters. Therefore, when flood victims were in anti-flood rescue, they directly or indirectly come into contact with contaminated water and then be infected by spirochaetes.

A key advantage of our study is that we applied the time-trend ecological design to screen the impact of floods on three categories of infectious diseases in Guangxi, China, allowing us to flexibly examine the possible relationships between extreme weather events and disease. We have adopted the time-stratified approach to select the control periods, which allows unbiased multivariate regression estimates and avoids bias resulting from time trend in the exposure series (Janes et al., 2005a). In addition, we have controlled other meteorological factors in the multivariate models with consideration of lagged effects of the floods. Therefore, the longitudinal data in our study sites are beneficial to identify more reliable flood-sensitive diseases.

Several limitations of this study must also be acknowledged. The first limitation is that the relationship between floods and infectious diseases was analysed from group level, which may result in a certain ecological fallacy. The ecology of infectious diseases is very complicated. Some infectious diseases may have been missed in flood-sensitive infectious diseases that we screened. Secondly, not all environmental factors were considered for analysing the risk of infectious diseases caused by floods. For example, the information about human activities, socioeconomic status, availability of health services, environmental hygiene and the activity and numbers of vector habitats was not available from our data sources and thus could not be included in this analysis. In addition, we chose only ten study sites in southern China to identify flood-sensitive infectious diseases. Moreover, the transmission of infectious diseases is very complicated, and more studies in other flood-affected regions in China with different climatic, ecological and human conditions are still needed to assess the risk of floods from ecology.

To control the epidemic and outbreak of flood-sensitive infectious diseases effectively during floods, the timeliness and accuracy of the disease surveillance should be strengthened. Secondly, hygienic supervision on environmental hygiene, drinking water quality and food safety should be conducted by the institution of disease prevention and control. We should carry out timely environmental cleaning, disinfection and vector control. Thirdly, routine immunisation should be provided for vulnerable populations during floods. Health education and

health promotion should be undertaken to improve disaster victims' awareness and capacity of disease prevention for flood-sensitive infectious diseases.

5. Conclusion

A key conclusion of this study is that the spectrum of sensitive infectious diseases associated with floods has been identified for the first time in the study region. Floods have significantly increased the different risk of bacillary dysentery, AHC, influenza A (H_1N_1) , tuberculosis, influenza, Japanese encephalitis and leptospirosis in the study areas, and floods may bring more risk of AHC and influenza. Therefore, effective preventive and treatment interventions should be developed to avoid and control a potential risk of flood-sensitive infectious disease epidemics after floods.

Conflicts of interest

The authors have declared that no competing interests exist.

Source of support

This study was supported by Medicine and Health Science Technology Development Program of Shandong Province (Grant NO.2016WS0605 and 2016WS0602), Science and Technology Development Plan of Taian City (Grant NO.2016NS1206), High-level Research Topic of Shandong First Medical University for the Cultivated Program (Grant No.2015GCC16 and 2016GCC05), and Doctoral Scientific Research Foundation of Shandong First Medical University (Xuena Liu). We thank Chinese Center for Disease Control and Prevention, National Meteorological Information Center of China, and Data center for Institute of Geographic Sciences and Natural Resources Research of China sharing with us the data needed for this study.

Ethical statement

Disease surveillance data used in this study were permitted by Chinese Center for Disease Control and Prevention. All data are unidentified. The study was approved by the research institutional review board of Shandong First Medical University.

Author contributions

Conceived and designed the experiments: GD HH XL. Performed the experiments: XL BZ. Analyzed the data: BJ DL WX. Contributed reagents/materials/analysis tools: QL BJ. Wrote the paper: GD XL.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.envres.2019.108577.

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