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Research Paper

Assessing Seasonal Risks for the Introduction and Mosquito-borne Spread of Zika Virus in Europe

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A B S T R A C T

The explosive Zika virus epidemic in the Americas is amplifying spread of this emerging pathogen into previously unaffected regions of the world, including Europe (Gulland, 2016), where local populations are immunologically naïve. As summertime approaches in the northern hemisphere, Aedes mosquitoes in Europe may find suitable climatic conditions to acquire and subsequently transmit Zika virus from viremic travellers to local populations. While Aedes albopictus has proven to be a vector for the transmission of dengue and chikungunya viruses in Europe (Delisle et al., 2015; ECDC, n.d.) there is growing experimental and ecological evidence to suggest that it may also be competent for Zika virus (Chouin-Carneiro et al., 2016; Grard et al., 2014; Li et al., 2012; Wong et al., 2013). Here we analyze and overlay the monthly flows of airline travellers arriving into European cities from Zika affected areas across the Americas, the predicted monthly estimates of the basic reproduction number of Zika virus in areas where Aedes mosquito populations reside in Europe (Aedes aegypti in Madeira, Portugal and Ae. albopictus in continental Europe), and human populations living within areas where mosquito-borne transmission of Zika virus may be possible. We highlight specific geographic areas and timing of risk for Zika virus introduction and possible spread within Europe to inform the efficient use of human disease surveillance, vector surveillance and control, and public education resources.

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1. Introduction

On May 17th, 2015, the Program for Monitoring Emerging Diseases (ProMED-mail) published a report confirming locally acquired cases of Zika virus (ZIKV) in several northeastern Brazilian states, marking the first time this virus is known to have spread within the Americas (Promed, 2015). Eight months later, on February 1st, 2016 the World Health Organization declared the ZIKV epidemic in the Americas a Public Health Emergency of International Concern, in part due to an emerging association with congenital birth anomalies such as microcephaly (Calvet et al., 2016; Mlakar et al., 2016; Rodrigues, 2016) and Guillain-Barré syndrome (Cao-Lormeau et al., 2016). After the virus’ introduction into Brazil, the epidemic has swiftly spread across Latin America and the Caribbean (Faria et al., 2016; Petersen et al., 2016a). Potential reasons for this rapid spread include the presence of immunologically naïve populations and an abundance of Aedes mosquitoes (Kraemer et al., 2015) within a conducive environment.

As the epidemic expands in scale and geographic range, a growing number of travellers are exporting ZIKV to other regions of the world, including Europe, where Aedes vectors are known to be present (Maria et al., 2016; Zammarchi et al., 2015; http://ecdc.europa.eu/en/healthtopics/vectors/vector-maps/Pages/VBORNET_maps.aspx, n.d.). In Europe, Aedes aegypti is known to exist on the island of Madeira, Portugal (http://ecdc.europa.eu/en/healthtopics/vectors/vector-maps/)
and in parts of Georgia and southwestern Russia, whereas *Aedes albopictus* is established along much of the Mediterranean coast (http://ecdc.europa.eu/en/healthtopics/vectors/vector-maps/Pages/VBORNET_maps.aspx, n.d.). While virus importation events could trigger epidemics in distant geographies where competent *Aedes* mosquito vectors exist, this risk has to date, been mitigated by winter temperatures in the northern hemisphere.

Given the growing experimental and ecological evidence to suggest that *Ae. albopictus* may be a competent vector for ZIKV (Chouin-Carneiro et al., 2016; Grard et al., 2014; Li et al., 2012; Wong et al., 2013), health officials must plan for the possibility of locally acquired ZIKV infections in parts of Europe. The imminent arrival of summer in the northern hemisphere, when *Aedes* mosquito populations will peak and viral replication within these vectors will be most efficient, could lead to autochthonous transmission, not unlike the recent localized and transient European epidemics of dengue and chikungunya (Angelini et al., 2007; Wilder-Smith et al., 2014).

To assist public health decision-making, we (i) modeled the risks of ZIKV importation into Europe via airline travellers departing areas in the Americas where ZIKV activity has been confirmed or where suitable conditions exist for its transmission year round (Bogoch et al., 2016), (ii) used a temperature driven vectorial capacity model to quantify the potential for European *Aedes* mosquitoes to support autochthonous transmission of ZIKV, assuming that *Ae. albopictus* is a competent vector, and (iii) quantified the size of populations living in European areas where mosquito-borne transmission of ZIKV may be possible at the height of summer.

### 2. Materials & Methods

#### 2.1. Overview

We developed a mathematical model that outputs basic reproduction numbers (R₀) for ZIKV transmission with biological anchoring in *Aedes* mosquito vectorial capacity and validation against surveillance data from the current ZIKV outbreak in Latin America and the Caribbean. We applied this vectorial capacity model to estimate R₀ potential for ZIKV in Europe this spring to autumn, while superimposing data on airline travellers arriving from areas in the Americas where ZIKV is active, as well as populations living in areas of Europe where mosquito-borne transmission of ZIKV is possible. Finally we discuss model assumptions and limitations in our approach.

#### 2.2. Model Development

R₀ is used to characterize the epidemic potential of a pathogen. It represents the expected number of new infections generated by one infectious individual within a fully susceptible population. In the context of a mosquito-borne illness, R₀ is a function of vectorial capacity (VC), and the period of viremia in humans (Tᵢ) (Anderson and R., 1991), given mathematically by: \( R₀ = VC \times Tᵢ \). Transmission increases when R₀ exceeds 1 (i.e. potential for an epidemic), and diminishes when R₀ is less than 1. VC in turn is a function of vector competence (inherent ability of the vector to transmit a particular pathogen), vector lifespan, and the extrinsic incubation period (Lambrechts et al., 2011). Since *Aedes* mosquitoes are ectotherms, VC is highly dependent upon mean...
temperature and diurnal temperature variation (Lambrechts et al., 2011; Brady et al., 2014; Liu-Helmersson et al., 2014; Liu-Helmersson et al., 2016). It is given mathematically by (Liu-Helmersson et al., 2016):

\[ VC = \frac{ma^2b_dn^2e^{-\mu_in}}{\mu_m} \]

The six vector parameters in the above equation include: 1) the average vector biting rate, 2) the probability of vector-to-human transmission per bite, \( b_n \), 3) the probability of human-to-vector infection per bite, \( b_m \), 4) the duration of the extrinsic incubation period (i.e., this represents the duration between acquisition of a pathogen by a vector and the ability for that vector to transmit the same pathogen to a susceptible host), \( n \), 5) vector mortality rate, \( \mu_m \), and 6) the female vector-to-human population ratio, \( m \).

Dengue virus (DENV), for example, is also transmitted by \( Aedes aegypti \) and \( Aedes albopictus \) mosquitoes, for which the aforementioned parameters and their relationship to temperature has been described (Lambrechts et al., 2011; Brady et al., 2014; Liu-Helmersson et al., 2014; Liu-Helmersson et al., 2016). This has relevance for ZIKV and DENV for both \( Aedes aegypti \) and \( Aedes albopictus \), as the mortality rate, \( \mu_m \), and biting rates, \( a \), for \( Aedes \) mosquitoes are independent of whether they carry ZIKV or DENV. Further, the competence of \( Aedes \) mosquito species to transmit ZIKV, as described by \( n, b_n \), and \( b_m \), is driven by the infection, dissemination, and transmission rates of the virus in an infected vector, measuring the rate of virus presence in the mosquito midgut after a blood meal, and the time and efficiency of its replication to the mosquito’s salivary glands. Recent data suggests that \( Aedes \) mosquitoes may have the same vector competence for ZIKV dissemination and transmission rate as DENV at 29 °C (Chouin-Carneiro et al., 2016; Li et al., 2012; Wong et al., 2013; Lambrechts et al., 2011; Brady et al., 2014; Liu-Helmersson et al., 2014; Liu-Helmersson et al., 2016).

However, geographical differences in vector competence may exist, as \( Aedes \) mosquitoes from Brazil, the U.S. and Martinique have been reported as being less potent in their ability to replicate ZIKV, while \( Aedes \) mosquitoes from French Guiana and Guadeloupe appear competent and efficient (Chouin-Carneiro et al., 2016). The extrinsic incubation period of ZIKV (\( n \)) is not yet determined, but recent studies estimate it to be 7 days (Chouin-Carneiro et al., 2016; Li et al., 2012; Wong et al., 2013), while for DENV is estimated to be 8–9 days at 28–29 °C (Liu-Helmersson et al., 2016).

The duration of viremia for ZIKV (\( T_v \)) is also currently under investigation however recent evidence suggests that the virus may be detectable in blood for 1 to 10 days (Musso et al., 2015a; Lessler et al., 2016). Similarly, DENV is detected in the blood for 3 to 12 days, with most individuals being viremic for about 5 days (Liu-Helmersson et al., 2016). The serial time window between pairs of infected human cases, encapsulating part of the period of viremia and the extrinsic and intrinsic incubation periods, has been estimated to be 15 days for ZIKV and 17 days for DENV (Majumder et al., 2016) indicating similarities between ZIKV and DENV in real-world settings. For both \( Aedes aegypti \) and \( Aedes albopictus \) mosquitoes, the female vector-to-human population ratio (\( m \)), is temperature dependent and presumed to be similar across species. In the absence of valid vector abundance data, as an indicator of vector populations, we used a method described in previous studies relating population density to survival (Lambrechts et al., 2011; Brady et al., 2014; Liu-Helmersson et al., 2014; Liu-Helmersson et al., 2016).

We developed three vectorial capacity models for \( Aedes \) mosquitoes to transmit ZIKV and selected the model that best fit observed transmission dynamics in the Americas. Each model was developed by adapting existing temperature-driven models for DENV transmission via \( Aedes aegypti \) and \( Aedes albopictus \) (Liu-Helmersson et al., 2016) while incorporating current data on ZIKV parameters. Our best fitting model was then adapted to Europe using European climatic data to estimate \( R_0 \).
potential this spring to autumn. Below we synthesize the findings described above into three alternative models describing the vectorial capacity and basic reproduction number of ZIKV:

- **Model 1**: characterized by high vector competence compared with dengue (Liu-Helmersson et al., 2016) in assuming a viremic period of 5 days.
- **Model 2**: similar to model 1 with alternations in \( b_m \) being reduced to 76.7% and \( b_0 \) reduced to 21.4% of the model 1 values for \( A. aegypti \) (Chouin-Carneiro et al., 2016). For \( A. albopictus \), model 2 is similar to model 1 however \( b_m \) are reduced to 50.0% of the model 1 value (Chouin-Carneiro et al., 2016).
- **Model 3**: same configuration as model 2 but with a viremic period of 10 days (Lessler et al., 2016).

The model 1–3 parameters and their relationship to temperature for both vectors are described in the supplementary information, Figs. 7–12.

### 2.3. Model Validation

We collected data on the number, location and time of confirmed and suspected ZIKV infections across Latin America and the Caribbean regions up to the end of March 2016 using data from national surveillance systems (see Table 1). Disease data were reported for individual countries or sub-national administrative regions. We also collected temperature measurements from terrestrial meteorological stations and satellite sensors reading land surface temperatures (see Table 3; extended data).

We estimated \( R_0 \) values for the initial phases of the epidemic in the Americas assuming a Poisson distribution using weekly count data (\textit{R} \textit{package} version 1.2–5, 2014; Wallinga, 2007). The serial time interval range of ZIKV infection was taken to be 10 to 23 days, with a mean of 16 days (Majumder et al., 2016). We then used a lognormal serial time distribution function with a mean of 16 days and standard deviation of 3 days covering the interval. Estimates of observed \( R_0 \) values were made at the sub-national administrative region level and aggregated to national averages as described in Table 1. We selected smaller countries and regions to better fulfill the assumption of homogeneous mixing in the estimation of \( R_0 \).

We tested and validated our three temperature-driven vectorial capacity models by comparing \( R_0 \) values generated for countries in Latin America and the Caribbean to \( R_0 \) estimates derived from the same region using ZIKV surveillance data (Table 1). We used temperature data from one month prior to and two months into the epidemic (Table 3; extended data). \( R_0 \) values were computed assuming that \( A. aegypti \) or \( A. albopictus \) alone were the sole vector for ZIKV transmission.

### 2.4. Estimating \( R_0 \) in Europe

Since Model 1 best fit observed data on ZIKV transmission in the Americas, we used it to estimate potential for mosquito-borne transmission, outputted as \( R_0 \) values, across Europe in 2016. We did this by integrating daily temperature observations (mean, minimum, maximum) from the E-OBS 12.0 dataset at locations gridded at 0.25 × 0.25° (approximately 25 × 25 km at the equator) latitude and longitude (Haylock et al., 2008) for the period between January 1st 2006 to December 31st 2015. Daily \( R_0 \) estimates required interpolating diurnal temperature values from daily temperature observations. We estimated \( R_0 \) values for Europe for geographic areas where \( A. aegypti \) or \( A. albopictus \) mosquito populations have been reported by the European Centre for Disease Prevention and Control in 2016 (http://ecdc.europa.eu/en/healthtopics/vectors/vector-maps/Pages/VBORNET_maps.aspx, n.d.). Maps were presented for each month from May to October after averaging daily \( R_0 \) observations. Model outputs were classified into \( R_0 \) zones for ease of interpretation (<0.5, 0.5–0.99, 1–1.99, 2–2.99, and 3–4).

### 2.5. Airline Travellers into Europe from the Americas

To estimate the potential for travellers infected with ZIKV arriving into European cities from the Americas, we analyzed worldwide airline ticket sales data from the International Air Transport Association (IATA). This dataset includes anonymized, full-route, flight itinerary data on an estimated 90% of all passenger trips on commercial flights worldwide, while the remainder is modeled using airline market intelligence. Each flight itinerary includes information on passengers’ initial point of embarkation, final destination, and where applicable, connecting flights.

To select commercial airports in the Americas where departing travellers might be infected with ZIKV, we assumed that ZIKV would be active in all countries in the Americas except Canada and Chile by the summer of 2016. Subsequently, we narrowed this list of countries to those that have experienced significant transmission of chikungunya virus since the onset of the 2013 outbreak in the Americas (Musso et al., 2015b). In this step, we excluded the United States as it has only experienced limited autochthonous transmission of chikungunya virus in Florida. Conversely, we included Argentina because it is currently experiencing a DENV epidemic (Gil et al., 2016). Within each country in our remaining list, we identified subnational areas with potential for year-round ZIKV transmission by either \( A. aegypti \) or \( A. albopictus \) based upon an ecological suitability analysis (Bogoch et al., 2016). We then created a 50 km buffer zone around these areas to accommodate for the potential movements of individuals travelling by land from areas of ZIKV activity to neighboring commercial airports, where travellers could embark upon international trips. After selecting our final list of commercial airports in the Americas, we quantified and mapped the monthly final European destinations of all travellers departing these airports between May and October 2015.

### 2.6. Populations at Risk for Locally Acquired Infection

To estimate the size of populations living in areas at risk for mosquito-borne ZIKV transmission, we extracted population data from LandScan 2014, a satellite-based dataset of ambient population density worldwide in 1-km² grids (Dobson et al., 2000). To link our vectorial capacity model data with LandScan population density data, our \( R_0 \) map (at 25-km² resolution) was resampled to 1-km² pixels using a nearest-neighbor sampling algorithm. Population estimates were then extracted for each \( R_0 \) zone for each country across Europe in the month of August, when vectorial capacity was at its peak.

### 3. Results

#### 3.1. Travellers Arriving to Europe from the Americas

In continental Europe, the leading final destinations of airline travellers departing areas in the Americas with known ZIKV activity or suitable conditions for year-round autochthonous transmission, from May to October 2015 were i) Paris (~120,000 to 200,000 travellers peaking in July and August), ii) London (~100,000 to 130,000 travellers peaking in August), iii) Madrid (~75,000 to 125,000 travellers peaking in July), iv) Amsterdam (~50,000 to 70,000 travellers peaking in August), v) Frankfurt (~40,000 travellers with no clear peak), vi) Milan (~25,000 to 40,000 travellers peaking in August), vii) Lisbon (~25,000 to 35,000 travellers peaking in September and October), and ix) Rome (~20,000 to 35,000 travellers peaking in August; see Fig. 1). Outside of continental Europe, Madeira, Portugal (where \( A. aegypti \) is established) receives ~500 to 2500 monthly travellers with peak flows in July.
3.2. Basic Reproductive Number for Zika virus in Europe

Based on temperature inputs, our vectorial capacity model predicted a basic reproduction number (R₀) of 3.9 (assuming transmission by Ae. aegypti), and 3.4 (assuming transmission by Ae. albopictus) for the current Zika epidemic in the Americas. We compared these R₀ estimates with those derived using Zika surveillance data in the Americas and found agreement between our predictions and observations as summarized in Table 1. Adapting our vectorial capacity model to Europe using empirical temperature data from 2006–2015, we estimated R₀ values for Ae. albopictus across southern Europe from France and Spain in the west to southwestern Russia in the east (see Fig. 1; higher resolution monthly maps are supplied in the supplementary information, Figs. 1–6). Most of the potential for autochthonous transmission was centered on Italy, southeastern France including the island of Corsica, the southern and eastern coasts of Spain, and western regions of the Balkans from Slovenia and Croatia in the north, to Albania and Greece in the south. While predicted R₀ values begin to exceed 1 (i.e. indicating epidemic potential) across areas of southern Europe in June, they increase in July (R₀ values of 2–3) and peak in August (R₀ values of 3–4) before falling again in September (R₀ values of 1–2) and October (R₀ falls below 1). For the sub-tropical island of Madeira in Portugal, R₀ values for the vector Ae. aegypti, were estimated to exceed 2 from July through October (see Fig. 2).

3.3. Populations at Risk in Europe

Of the total population residing within the geographic range of our analysis (i.e. 779 million people), we find that in the month of August (i.e. when temperatures and vectorial capacity in Europe are peaking), approximately 47% of people (i.e. 366 million) reside in areas with no known occurrences of Ae. albopictus, 35% (i.e. 272 million) in areas where data on Aedes mosquito occurrences are absent, 11% (i.e. 83 million) in areas where R₀ estimates from our model exceed 1, 4% (i.e. 31 million) in areas where R₀ estimates are less than 1 (i.e. low risk for sporadic transmission), and 3% (i.e. 27 million) in areas where our model lacked data to estimate R₀.

Countries with a large proportion of their population residing in areas where our R₀ estimates exceeded 1 in August included: Albania (83%), Croatia (44%), France (20%), Greece (25%), Italy (78%), Montenegro (39%), Slovenia (28%), and Spain (19%). Population sizes in these areas were largest for Italy (45 million people), France (12 million), and Spain (8 million). For Greece and Spain, more than half of their populations resided in areas with either no Aedes mosquito surveillance data or no data outputs from our model. The geographic extents of Ae. albopictus mosquitoes overlaid with our model’s R₀ outputs are shown in Fig. 1, while actual values of populations affected are found in Table 2 (extended data).

4. Discussion

Our analysis indicates that the peak flow of travellers departing areas in the Americas where they might be exposed to Zika (and who have final destinations in Europe) coincides with the peak in vectorial capacity for Zika transmission in Europe (i.e. in July and August). These intersections in risk are most apparent within or adjacent to several major cities such as Barcelona, Milan and Rome.

Since Ae. albopictus mosquitoes might prove to be competent vectors for Zika (Chouin-Carneiro et al., 2016; Grant et al., 2014; Li et al., 2012; Wong et al., 2013), the public, healthcare providers and public health officials across Europe could use these findings to identify regions at greatest risk for the importation of Zika, and its potential transmission within ecologically suitable areas. Although the volume of travellers arriving from the Americas to Madeira, Portugal is substantially lower compared to other major cities in continental Europe, the known occurrence of Ae. aegypti, a longer season with high vectorial capacity, the explosive epidemic of dengue in 2012 (Wilder-Smith et al., 2014), and the recent Zika epidemic in nearby Cape Verde (Attar, 2016), collectively highlight the potential for autochthonous transmission of Zika on this sub-tropical island.

Our analysis highlights necessary, but not always sufficient conditions for autochthonous transmission of Zika. While the introduction of Zika into Europe, the presence of competent mosquito vectors, and suitable climatic conditions are all prerequisites for local mosquito-borne transmission, a multitude of other factors, including but not limited to, population density, housing conditions, and socioeconomic factors, could influence the likelihood of observing Zika epidemics, as seen with other arbovirus infections such as dengue (Clark, 2008; Reiter et al., 2003).

Our model is founded on a number of assumptions, most notably that continental European strains of Ae. albopictus possess competence for the transmission of Zika. While there is growing evidence to suggest that Ae. albopictus can become infected with Zika under experimental conditions (Chouin-Carneiro et al., 2016; Li et al., 2012), empirical data on its role as a vector in nature exist (Grant et al., 2014), but are limited. Recent evidence from the Americas also suggests that Ae. aegypti and Ae. albopictus may be less competent vectors than anticipated (Chouin-Carneiro et al., 2016), and that other factors such as population density, immunologically naive populations, additional modes of transmission (e.g. sexual (Oster et al., 2016; Foy et al., 2011)), and possibly even other mosquito species might play a role in this epidemic (Ayres, 2016). A key strength of our study is that our model’s R₀ outputs were comparable to estimates we derived using Zika surveillance data from the ongoing epidemic in the Americas. However, we assumed that our model, validated against Zika data from the Americas where Ae. aegypti is thought to be the primary driver for transmission, would be transferrable to a European setting where Ae. albopictus is the dominant vector.

Cities across Europe are already experiencing an increase in Zika importations via travellers from the Americas (Maria et al., 2016; Zammarchi et al., 2015). Two recent studies assessed the risk of transmission of Zika in Europe reaching contrasting conclusions (Guzzetta et al., 2016; WHO, 2016). One of the studies finds minimal risk based on an assumed low vectorial capacity of European Ae. albopictus (Guzzetta et al., 2016), while the other study, aligning climatic suitability of vectors and coarse patterns in air traffic, estimate and identify European countries at high risk for Zika transmission (WHO, 2016). Our study increases output resolution through our transmission model and passenger-level air travel data, while drawing from epidemiological data from the current outbreak in the Americas. We conclude, that while there remains uncertainty about the capacity for Ae. albopictus to transmit Zika in nature, European health officials must consider the possibility of mosquito-borne transmission within Europe during warmer periods of the year. With the imminent arrival of summer, our findings could help guide the efficient use of finite resources for human disease surveillance, vector surveillance and control, and public education following guidelines from the European Centre for Disease Prevention and Control (European Centre for Disease Prevention and Control, 2016), for vector and non-vector borne modes of Zika transmission. Furthermore, our travel analysis can help target efforts to educate the public and healthcare providers alike about the potential for Zika virus transmission via travellers returning from Zika affected areas in the Americas to their sexual partners living in Europe (Oster et al., 2016; Petersen et al., 2016b).

4.1. Assumptions and Limitations

The overall range and average values of the basic reproduction number for Zika estimated in our study for Latin America and the Caribbean is supported by several recent studies indicating similarities to dengue (Funk et al., 2016; Kucharski et al., 2016) at least for transmission via Ae. aegypti. Data on the competence of Ae. albopictus as a vector to
transmit ZIKV in natural settings are limited. While recent experimental studies have indicated that North American \textit{Ae. albopictus} strains may not be highly competent (Chouin-Carneiro et al., 2016), others support a higher vector competence (Li et al., 2012; Wong et al., 2013), including one study where \textit{Ae. albopictus} appears to have been the principal vector in an urban ZIKV outbreak in Gabon (Grard et al., 2014). In this analysis, we assumed that \textit{Ae. albopictus} would be capable of transmitting ZIKV in continental Europe. New experimental results indicate European \textit{Ae. albopictus} mosquitoes may exhibit lower competence to transmit ZIKV (Di Luca et al., 2016; Jupille et al., 2016) contrasting to African (Grard et al., 2014) and Asian (Wong et al., 2013) varieties. However, more evidence is needed to fully understand vector competence in Europe.

We also assumed that DENV and ZIKV have similar temperature dependencies in relation to vector competence. While the similarities between our model's \( R_0 \) outputs for ZIKV and \( R_0 \) estimates derived from the current ZIKV epidemic in the Americas supports this assumption, we recognize that other factors, related to human behavior, socioeconomic, and environmental factors may create differential vector-to-human contacts rates between Europe and Latin America. These differences could contribute to different transmission dynamics not accounted for in our predictive models. For example, during a recent DENV outbreak along the Texas-Mexico border, non-climatic factors significantly influenced transmission dynamics (Clark, 2008; Reiter et al., 2003). The observed transmission of chikungunya and dengue in Europe, however, support that European vectors and environment are capable of supporting local transmission (Angelini et al., 2007; Wilder-Smith et al., 2014). We further note that vector populations, as measured by ovitraps, indicate high abundance in Europe (Bellini et al., 2016). We also note that populations of \textit{Aedes} mosquitoes in the Netherlands have not established outside temperate climates. Although DENV and chikungunya viruses may offer certain insights into the unknowns of ZIKV spread and control (Musso et al., 2015b), differences between ZIKV, DENV and chikungunya virus-vector interactions and transmission routes cannot be ignored (Christofferson, 2016). In addition to mosquito-borne transmission, other modes of spread including via sexual contact (Oster et al., 2016) were not accounted for in this analysis. Current data suggest that ZIKV can be found in semen, and hence could potentially be transmitted for months post-infection (Mansuy et al., 2016).

The 2015 IATA data used in this analysis is the most current available to quantify the flow of travellers from the Americas to Europe across this spring to autumn. Although the ZIKV epidemic may decrease traveller flows to and from affected countries, we assumed that the seasonal patterns and proportions of travellers arriving to various European cities would be preserved relative to 2015. Another consideration not accounted for in our analysis is the potential impact of the Summer Olympic Games in Rio in August on travel patterns between Brazil and Europe. However, the local transmission of Zika during the Olympics might decrease due to seasonal transmission changes (Funk et al., 2016; Kucharski et al., 2016).

Our weather-driven models use averaged monthly temperature values over the most recent 10-year period (i.e. 2006–2015). However, 2016 weather patterns may vary under the influence of El Nino this year, which in turn, might increase or decrease vectorial capacity.

Finally, stochasticity plays a key role in the appearance of any epidemic. In this analysis, we present conditions that are necessary, but alone may be insufficient for the emergence of an epidemic. Hence our analysis assesses the potential for ZIKV transmission within Europe, not the probability of ZIKV epidemics. The purpose of this analysis is to highlight geographies and times where epidemic potential is greatest as a way to help guide public health resources to prepare for, and if required, mobilize an appropriate response to mosquito-borne ZIKV transmission in Europe later this year, in accordance with guidelines developed by the European Centre for Disease Prevention and Control (European Centre for Disease Prevention and Control, 2016).

Disclosure Statements

Kamran Khan is the founder of BlueDot, a social benefit corporation that develops public health tools and analytics to help prepare for and respond to global epidemics. Matthew German has been employed by BlueDot and Isaac I. Bogoch has consulted to BlueDot.

Author Contributions

Joacim Rocklöv and Kamran Khan conceived the research idea, made the first analyses and drafted the text. Mikkel Quam helped develop the Zika mathematical models. Bertrand Sudre helped gather the Zika surveillance data and update the manuscript based on literature reviews on Zika epidemiology and entomology. Matthew German conducted the analyses of commercial air travel flows. Moritz Kraemer and Oliver Brady helped to develop the method for the Zika transmission zones in Latin America. Mark Ong produced estimates of populations living in areas at potential risk for autochthonous transmission of Zika virus across Europe. All authors made significant contributions to the editing and critical assessment of the manuscript.

The following are the supplementary data related to this article.

Supplementary data to this article can be found online at http://dx.doi.org/10.1016/j.ebiom.2016.06.009.

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References


Calvet, G., et al., 2016. Detection and sequencing of Zika virus from amniotic fluid of fe-


Delisle, E., et al., 2015. Chikungunya outbreak in Montpellier, France, September to Oc-


Faria, N.R., et al., 2016. Zika virus in the Americas: early epidemiological and genetic find-
ings. Science http://dx.doi.org/10.1126/science.aaf5036.


Tran, A., et al., 2013. A rainfall- and temperature-driven abundance model for Ae-


Majumder, M.S., Cohn, E., Fish, D., Brownstein, J.S., 2016. Estimating a feasible serial inter-
