Impact factor 5.49

Eurosurveillance

Europe's journal on infectious disease epidemiology, prevention and control

Vol. 19 | Weekly issue 28 | 17 July 2014

Editorials

Rapid communications

Research articles

ecdc EUROPEAN CENTRE FOR DISEASE PREVENTION AND CONTROL

www.eurosurveillance.org

Spread of chikungunya from the Caribbean to mainland Central and South America: a greater risk of spillover in Europe?

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Citation style for this article:
Noël H, Rizzo C. Spread of chikungunya from the Caribbean to mainland Central and South America: a greater risk of spillover in Europe? . Euro Surveill. 2014;19(28):pii=20855. Available online: http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=20855

Article submitted on 15 July 2014 / published on 17 July 2014

After a decade of outbreaks in Africa, the Indian Ocean and Asia, chikungunya virus (CHIKV) is stepping out of the shadow of dengue virus [1]. Although these two mosquito-borne viruses share clinical characteristics and their main vectors, *Aedes albopictus* (the tiger mosquito) and *Ae. aegypti*, CHIKV has long remained exotic to the western hemisphere [2]. The emergence of the Indian Ocean lineage changed the views on CHIKV when it caused an unprecedented disease burden in India and the islands of the Indian Ocean between 2005 and 2008 [3,4].

More than the reports of single events of locally-acquired cases of chikungunya fever in Italy and France [5,6], the recent occurrence of autochthonous transmission of CHIKV in the Americas has redesigned the geographic distribution of the virus. An outbreak in the Caribbean caused by an Asian strain of the virus started in Saint Martin in October 2013 with *Ae. aegypti* as the primary vector. The dynamics of the spread of CHIKV was in line with that in outbreaks that occurred in the Indian Ocean [2].

In this issue of *Eurosurveillance*, Cauchemez et al. estimate the basic reproductive number (the mean number of new host cases generated by one infectious host in a completely susceptible human population) at between 2 and 4 in the initial phase of the outbreak in the French Caribbean [7]. This is close to estimates from the outbreaks in Italy in 2007 and on Réunion Island in 2006 (3.5 and 3.7, respectively) [8,9].

Data from epidemiological surveillance suggest that so far, six months after its introduction to the Caribbean, CHIKV has been responsible for over 350,000 suspected cases of chikungunya fever that have occurred throughout the region [10].

The consequences of the outbreaks in the Caribbean have ripples in Europe, as Paty et al. and Requena-Méndez et al. document in this issue [11,12]. Paty et al. report the increased detection through surveillance of infected travellers arriving in mainland France from the French West Indies [11]. Likewise, the importation of chikungunya cases presented by Requena-Méndez et al. in this issue are likely to continue for months in Spain and other countries with intense exchanges with South America [12]. Cauchemez et al. stress that if circulation of CHIKV settles in mainland South and Central America, the international spillover of cases could escalate [7]. At this moment, public health surveillance has already detected local transmission of CHIKV on the continent, in Costa Rica, Guyana, El Salvador, Suriname and French Guiana [10].

Based on the recent rapid risk assessment from the European Centre for Disease Prevention and Control (ECDC), the chikungunya epidemic in the Americas represents a tangible threat to public health in Europe that goes beyond the scope of travellers' health [13]. In this globalised world, it could ignite local diffusion of CHIKV in Madeira that is colonised by *Ae. aegypti* and in the constantly expanding areas in Europe where *Ae. albopictus* is established. Vector competence studies are ongoing, but it is highly likely that *Ae. albopictus* will be found competent for transmission of the CHIKV strain circulating in the Caribbean. Local tiger mosquitoes were able to transmit CHIKV strains of the Indian Ocean lineage to more than 250 cases in Italy in 2007 and to two cases in France in 2010 [5,6].

Local foci or even large outbreaks are more likely to occur in Europe now because of the synchronicity between CHIKV transmission on the other side of the Atlantic and the season of vector activity in Europe. Preventing the spillover of the chikungunya outbreak to Europe in this challenging context requires the mobilisation of the population and cross-sector collaboration between clinicians, medical biologists, entomologists

and public health professionals at local, national and European level in as part of the One Health concept.

The odds of controlling CHIKV dissemination to Europe will become lower if, as expected, CHIKV spreads during the summer to continental South America. Indeed, it is plausible that the long feared epidemic in South America will be ongoing for months and maybe years, continuously fuelling the flow of imported cases.

There are no prospects of a human vaccine or curative antiviral treatment available in a near future. Therefore, the only opportunity of preventing dissemination to Europe consists in reducing the vector density and its contacts with humans. People living in an area colonised by *Aedes* vector mosquitoes should be taught how to prevent and eliminate man-made breeding sites to reduce the overall vector density around their homes and workplaces. They should be informed about personal protective measures to avoid mosquito bites such as wearing long-sleeve shirts and long trousers and using repellent on exposed skin. Travellers should strictly observe the recommendations for personal protection against mosquito bites while visiting areas where CHIKV transmission is active. In case of fever upon return to an area where the vector is established, travellers should seek medical attention and prevent mosquito bites while symptomatic. Because both vector mosquitoes are day biters, nets are of limited use. But they can be useful to protect in particular young children and infected patients that are resting. Healthcare professionals should become increasingly aware of the clinical presentation and diagnostics of chikungunya, as well as treatment relieving symptoms. They should advise travellers and cases about protective measures against mosquitoes.

Vector control measures should target both adult mosquitoes and larvae and rely on a limited set of insecticides that are active against *Aedes* spp. These insecticides should be used sparingly and only for targeted responses so as to avoid toxic effects on humans and the surrounding fauna as well as the emergence of resistant insects. For this reason, implementing surveillance systems for local entomological indicators in Europe is crucial in order to estimate the risk of local transmission associated with imported cases and to guide vector control measures in time and space.

Thus, it is crucial to be prepared. European Union (EU) Member States are advised to develop preparedness planning for identifying new health threats at national level according to the recent *Decision 1082/2013/EU* on serious cross-border threats to health [14]. The CHIKV control measures at EU level require: entomological surveillance, surveillance of imported and autochthonous cases and rapid diagnosis to detect local outbreaks. Moreover, vector control measures should be included in the planning around cases, either after rapid diagnosis or, in patients returning from epidemic areas, without waiting for laboratory confirmation results.

However, underreporting of cases can be substantial. Published reports suggest that the estimated number of imported cases generally exceeds the number of notified cases by a factor 10 and over [15,16]. Active mobilisation of clinicians and medical biologists in targeted geographical areas has proven efficient to improve completeness of the surveillance of dengue virus and captured up to 69% of cases [16].

At this stage, surveillance should be based primarily on laboratory confirmation. At EU level, new case definitions for dengue and chikungunya fever are being developed, based on the group discussion that took place during the meeting of ECDC Emerging and Vector-borne Diseases (EVD) network in December 2013 [17]. A case definition including only epidemiological and clinical criteria should be considered to monitor large outbreaks when systematic laboratory confirmation is not feasible any more.

The threat that the chikungunya outbreak in the western hemisphere represents for public health in Europe, should not overshadow the risk posed by other arboviruses such as dengue virus. Globalisation and environmental changes affect the dynamics of both viruses in Europe in the same way. Recent reports of limited autochthonous transmission of dengue virus and large-scale outbreaks in Europe call for continued vigilance and involvement [18-20]. When confronted with a febrile patient returning from tropical and subtropical areas, practitioners should now consider both diagnoses. Both mosquito-borne viral diseases can be tackled by the same surveillance and response efforts.

Laboratory capacity for CHIKV infections in the EU is limited and should be increased for early detection of cases. In 2007, the European Network for Diagnostics of 'Imported' Viral Diseases (ENIVD) conducted an external quality assurance survey of serological and molecular methods used for CHIKV detection [21]. That study unveiled great differences in the availability and performance of CHIKV diagnostics among the 24 participating laboratories from 15 countries across Europe. There is little available information to make us believe that the situation since has notably improved. Most of these laboratories are still using in-house techniques and may not be able to cope with a considerable increase in activity. New and reliable commercial serological and molecular tests are needed to improve access to CHIKV diagnostics in Europe.

CHIKV also represents a threat for blood safety in Europe. The recent detection of CHIKV among blood donors from Guadeloupe and Martinique in early 2014 alerts us to the risk of transfusion-transmitted infections [22]. Temporary deferral of donors returning from areas of active transmission of CHIKV is an effective way of preventing transfusion-transmitted infections.

In case of local transmission of CHIKV in the EU, different measures should be considered according to the intensity of vector-borne transmission in the community. These measures include discontinuing blood collection in affected areas, screening donors for symptoms, post-donation quarantine and CHIKV RNA detection in donations.

In summary, the introduction of chikungunya in the Caribbean and the Americas illustrates how quickly diseases can spread with international travel. In the coming months, chikungunya cases among travellers visiting or returning to Europe are likely to increase. European public health authorities should therefore not underestimate the transmission potential of CHIKV and should remain vigilant. These imported cases could trigger local outbreaks in Europe where the competent vector is established. Levels of risk and preparedness appear very heterogeneous between and within countries. We believe that ECDC can lend support to EU Member States in preparing for potential local chikungunya outbreaks by building capacity and strengthening networks in collaboration with internationals stakeholders in this global event.

Conflict of interest

None declared.

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Cases of chikungunya virus infection in travellers returning to Spain from Haiti or Dominican Republic, April-June 2014

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Citation style for this article:
Requena-Méndez A, García C, Aldasoro E, Vicente JA, Martínez MJ, Pérez-Molina JA, Calvo-Cano A, Franco L, Parrón I, Molina A, Ruiz M, Álvarez J, Sánchez-Seco MP, Gascón J. Cases of chikungunya virus infection in travellers returning to Spain from Haiti or Dominican Republic, April-June 2014 . Euro Surveill. 2014;19(28):pii=20853. Available online: http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=20853

Article submitted on 08 July 2014 / published on 17 July 2014

Ten cases of chikungunya were diagnosed in Spanish travellers returning from Haiti (n=2), the Dominican Republic (n=7) or from both countries (n=1) between April and June 2014. These cases remind clinicians to consider chikungunya in European travellers presenting with febrile illness and arthralgia, who are returning from the Caribbean region and Central America, particularly from Haiti and the Dominican Republic. The presence of *Aedes albopictus* together with viraemic patients could potentially lead to autochthonous transmission of chikungunya virus in southern Europe.

We report 10 cases diagnosed with chikungunya virus (CHIKV) infection in Spain after returning from Haiti or the Dominican Republic. These are the first cases reported in Spain from travellers returning from Latin America and this should alert clinicians to consider CHIKV infection in any traveller with febrile illness or arthralgia returning from Central America and/or the Caribbean, particularly from Haiti and the Dominican Republic.

Case reports

Case definition

In this report, a probable case was defined as a person who was residing in or visited epidemic area within 15 days before onset of symptoms, was presenting with fever and arthralgia or arthritis, and had a positive IgM CHIKV antibody test result; a confirmed case was defined as a positive tests for one of the laboratory criteria, irrespective of clinical manifestations: (i) presence of viral RNA, (ii) specific IgM antibodies or (iii) four-fold increase in IgG titres in paired samples.

Clinical and epidemiological data

Between April and June 2014, 10 patients were diagnosed with chikungunya in Spain. Their age ranged from 21 to 57 years (mean age: 45.7) and six were male. All patients presented with fever (>37.7°C) and arthralgia. Four patients also had an itchy rash. Clinical and epidemiological features of the cases of chikungunya are presented in the Table.

Travel history

Nine cases resided in Catalonia and one in Cuenca, Spain. However, all 10 had a history of recent travel to Haiti and/or the Dominican Republic and for all symptoms had started either when abroad or within five days of their return to Spain.

Seven of the 10 cases had travelled to the Dominican Republic, while two had been to Haiti. One case had visited both of these countries. The seven cases whose travel was limited to the Dominican Republic had done short trips there, which lasted less than a month. These cases included two persons who were visiting friends and relatives (VFR) in very small village near Santo Domingo and another person VFR who stayed in San Cristobal (south of the Dominican Republic). The remaining four of the seven cases had travelled separately all over the Dominican Republic, one during a short period for work and three as tourists. The two cases who had only visited Haiti had been there as part of their job, as they worked for the same company. During their stay, they lived together in the town of Jacmel for eight months before returning to Spain. The case who had been both to Haiti and the Dominican Republic was a tourist who had travelled there for a total period of four months.

Table

Clinical and epidemiological characteristics of cases of chikungunya in travellers returning from Haiti and/or the Dominican Republic, Spain, April–June 2014

Cases	Sex	Approximate age in years	Country visited	Duration of stay (days)	Clinical symptoms[a]	Diagnosis[b,c]	Treatment required
1	M	In the 40s	Haiti	240	Fever, rash, arthralgia	PCR	NSAID
2	M	In the 50s	Haiti	240	Fever, rash , arthralgia	Serology	NSAID
3	F	In the 30s	Dominican Rep.	15	Fever, rash, arthralgia	PCR	Nothing
4	F	In the 50s	Dominican Rep.	15	Fever, arthralgia	PCR	NSAID
5	M	In the 50s	Dominican Rep.	15	Fever, headache, arthralgia	Serology	Nothing
6	M	In the 40s	Dominican Rep./Haiti	120	Fever, rash, arthralgia	Serology	NSAID
7	M	In the 40s	Dominican Rep.	5	Fever, weakness, polyarthralgia	Serology	Steroids
8	F	In the 50s	Dominican Rep.	7	Fever, arthralgia	PCR	NSAID
9	M	In the 40s	Dominican Rep.	24	Fever, headache, polyarthralgia	PCR	NSAID
10	F	In the 20s	Dominican Rep.	30	Fever, arthralgias	Serology	Nothing

Dominican Rep.: Dominican Republic; F: female; M: male; NSAID: Non-steroidal antinflammatory drug; PCR: polymerase chain reaction.
For all 10 cases, symptoms started either when abroad or within five days of their return to Spain.

[a] Fever was defined as a temperature >37.7°C.

[b] Diagnosis by PCR was done by a real-time reverse transcription-PCR (RT-PCR) (Realstar CHIKV kit, Altona diagnostics).

[c] Diagnosis by serology included detection of both IgM and IgG against CHIKV in the first sample obtained, using a commercial immunofluorescence assay (Euroimmun). These cases were classified as probable cases.

Laboratory confirmation

For all cases, dengue virus infection was excluded through either polymerase chain reaction (PCR) or serological tests. In five of the 10 cases, chikungunya diagnosis was confirmed by real-time reverse transcription-PCR (RT-PCR) (Realstar CHIKV kit, Altona diagnostics). In the five remaining patients, chikungunya diagnosis was based both on IgM and IgG antibodies against CHIKV, which were detected by immunofluorescence (Euroimmun). PCR was not performed for such patients because the first diagnostic samples were obtained between 10 and 21 days after the onset of symptoms and the probability of viraemia was very low.

Treatment

Although their condition significantly improved one or two weeks after symptom onset, the majority of cases required anti-inflammatory therapy. Three weeks after the onset of symptoms, only three patients were still taking anti-inflammatory drugs and one of them required steroids therapy during 15 days due to the persistence of polyarthralgia.

Background

CHIKV is an arbovirus of the genus Alphavirus transmitted by *Aedes* mosquitoes (mainly *Ae. aegypti* and *Ae. albopictus*) [1].

Clinical manifestations of chikungunya

The disease caused by CHIKV has an incubation time that ranges from one to 12 days, with an average of two to four days [2] and clinical presentation has similarities with dengue fever. Chikungunya is characterised by fever, headache, rash and both acute and persistent arthralgia. Polyarthralgia is common in cases CHIKV infection and is the most disabling symptom [2]. Around 75% of infections are symptomatic [3] and general complications are rare but include myocarditis, hepatitis, ocular disorders, central nervous system involvement (encephalitis), and haemorrhagic fever [4]. Although the mortality rate associated with CHIKV is low, the arthralgia can persist or can recur for weeks or months [5] and the likelihood of developing persistent arthralgia is highly dependent on age, being more prevalent in those older than 45 years-old [2].

Diagnosis

The diagnosis should be based on clinical, epidemiological and laboratory criteria [2]. The laboratory confirmation is crucial to distinguish from other disorders with similar clinical manifestations, such as dengue fever, other diseases caused by alphaviruses, or malaria. In the acute phase of illness, detection of viral nucleic acid in serum by RT-PCR is possible [6]. After this period, diagnosis relies on detection of specific antibodies against CHIKV [7-8]. Laboratory confirmation of CHIKV infection is usually achieved by detection of viral genome or demonstration of seroconversion in paired serum samples [9].

Geographical distribution of chikungunya virus

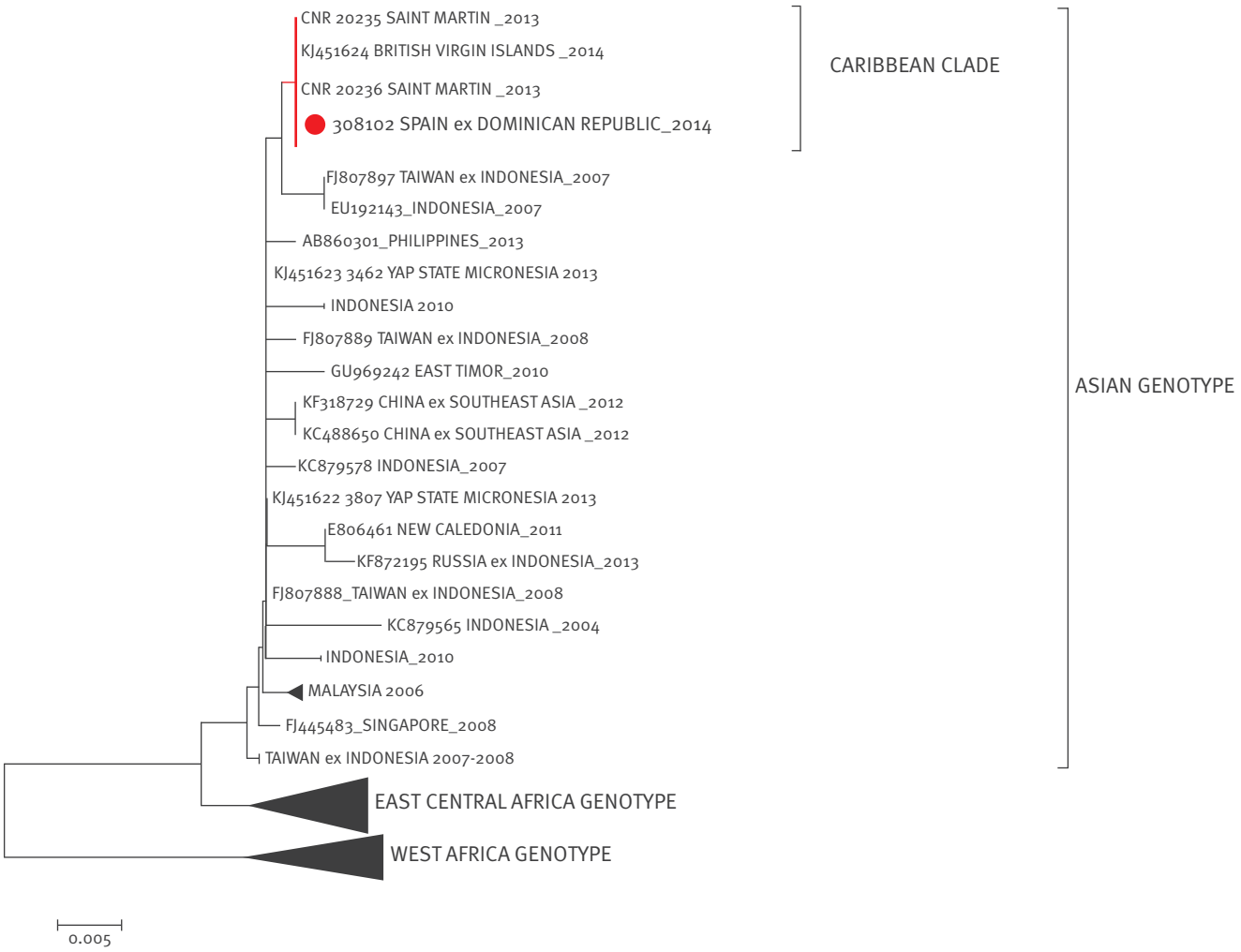
Until 2005, CHIKV infection was endemic in some parts of east Africa and southeast Asia and cases were also reported from the Indian subcontinent [2,10]. Following outbreaks of chikungunya in islands of the Indian Ocean and in peninsular India in 2005 [11], the virus also caused localised outbreaks in some countries in Europe, such as Italy (2007) and France (2010) [12-13]. Before 2013, CHIKV infections had not been detected in the Americas but in December of that year, the first confirmed autochthonous case of CHIKV was reported in the Caribbean, in Saint Martin [14]. Since then, almost 800 confirmed cases of CHIKV infection have been reported from Saint Martin [15] and the virus has spread to the whole Caribbean. As of the end of June 2014, almost 255,000 suspected cases have been reported from the Latin Caribbean and there are almost 180,000 suspected cases in the Dominican Republic and Haiti, with 18 confirmed cases in the Dominican Republic and 14 in Haiti [15-16].

Investigation of the chikungunya virus sequence derived from a case

A PCR targeting the partial envelope protein (E) 1 gene was done in addition to the real-time RT-PCR for one case (case 9), who had travelled to the Dominican Republic [17]. Following amplification and sequencing of the gene, basic local alignment search tool (BLAST) analysis revealed a 100% similarity index of the case's sequence with sequences from strains recently identified in the British Virgin Islands (strain 99659; GenBank accession number: KJ451624) and Saint Martin (strain CNR-20235/STMARTIN/2013, retrieved from the European virus archive (http://www.european-virus-archive.com)) [18]. Phylogenetic analysis, using MEGA5 software showed the strain affecting the patient to be of the Asian genotype, and in the

Figure

Phylogenetic analysis of a sequence derived from a case of chikungunya virus infection in a traveller returning from the Dominican Republic to Spain, April 2014



The phylogenetic tree was constructed by neighbour-joining method and based on partial (450 nt) sequences of the chikungunya virus Envelope protein 1 gene. The sequences analysed included one derived from the case reported here, which is highlighted (sequence 308102/2014), and 90 sequences retrieved from Genbank. Sequences from East and Central and West Africa were collapsed.

phylogenetic tree, the sequence derived from the case clustered together with other CHIKV sequences from the Caribbean (Figure). The sequence was deposited in GenBank under accession number KM192348.

Discussion

We report 10 cases of chikungunya in Spain between April and June 2014. Five of these can be considered as laboratory confirmed based on a positive specific real-time RT-PCR. The other five that tested positive for both IgM and IgG CHIKV antibodies can be classified as probable cases.

All cases had a clear epidemiological link to the Dominican Republic and/or Haiti, two countries where they had recently travelled and which were concurrently affected by chikungunya. Symptom onset for all cases occurred either before returning to Spain or within a period compatible with infection abroad, based on the incubation time. Phylogenetic analysis of a viral sequence derived from one of the cases moreover showed 100% similarity with sequences from strains recently identified in the Caribbean.

After December 2013, when autochthonous transmission of CHIKV was first reported in Saint Martin, the virus spread within a few weeks to most countries of the Caribbean, where an outbreak is currently taking place [18]. A concomitant dengue outbreak in the region complicates differential diagnosis. Chikungunya presents a good example of the interaction between globalisation and emerging infections. During the last 10 years, the virus has spread throughout the Indian Ocean, Asia, and localised outbreaks have also been reported in Europe [2]. Local transmission has been detected in the Americas in recent months. It is predicted that CHIKV will spread in most American areas where *Aedes* mosquitoes are endemic [14].

Cases of autochthonous transmission have not been reported in Spain but imported cases from countries affected by CHIKV have been documented in the past years [19,20] and a retrospective study reported 14 to 15 cases per year in the period between 2006 and 2007 [21]. Since April 2014 however, due to the situation in the Caribbean region, the numbers of cases have increased and in addition to the cases presented here further more recent cases have occurred (data not shown). According to last data from the World Tourism Organization (data from 2008–2012), Spain is one of the European countries with a largest number of travellers to Haiti and the Dominican Republic [22]. Moreover, the presence of immigrants in Europe from the Caribbean [23, 24] may also account for trips to these countries. The number of imported cases of CHIKV into Europe is likely to increase in the following weeks.

Aedes aegypti, one of the main vectors of CHIKV, is present in some areas of Europe, such as Madeira [25]. *Ae. albopictus*, the other vector, is already established in various countries in Europe, such as Italy, the south of France and some regions in Spain [26, 27-29]. In Spain, the mosquito is found in most parts of Catalonia, the region where most of our cases (9/10) were residing, and in the Baleares islands as well as some territories of Murcia and Valencia [26]. Although *Ae. Albopictus* is currently not established in Cuenca, where one of the cases lived, this town is approximately 200 km away from Valencia.

The presence of a chikungunya vector together with travellers, who are still in the period of viraemia, as for five of our cases, could be a source of local transmission of CHIKV infection. In fact, an outbreak of autochthonous CHIKV infection already occurred in north-eastern Italy in 2007 after an index case arrived from India [30]. This led to an estimate of 254 locally-acquired infections [30]. With vectors established in parts of Europe and the intense circulation of people between this continent and America, there is a threat for new localised outbreaks of CHIKV infection in Europe [18].

At this time, surveillance in the Catalonian region [31] where the vector is established is based on active-case finding. The surveillance is activated when either a confirmed case is detected or when a probable case in Catalonia could be viraemic. Moreover, primary healthcare centres belonging to the local area where the probable or confirmed case is detected are warned and, in parallel, the regional government in Catalonia is trying to activate measures to control the vector in the affected areas.

The set up of a surveillance system that can accurately identify chikungunya cases presents difficulties since the symptoms of the infection are not very specific. However, although confusion between dengue and chikungunya is possible, in most cases the symptoms of chikungunya are specific enough to be recognisable in travellers by clinicians who are aware of the disease.

Conclusions

CHIKV infection might be suspected in any people returning from the Caribbean with fever, particularly if disabling arthralgias are present. In regions infested with *Ae. albopictus* or *Ae. aegypti*, health authorities should be aware of the risk of local outbreaks and the need to implement control measures for both vectors.

Acknowledgements

The CRESIB Research group receives funds from AGAUR, (project 2009SGR385) and also from the project RICET (RD12/0018/0010) within the Spanish National plan of R+D+I and co-funded by ISCIII-Subdireccion General de Evaluacion and the Fondo Europeo de Desarrollo Regional (FEDER). CRESIB institution belongs to the TROPNET network. This work has been partially funded by the project PI10/00069FIS (Fondo de Investigaciones Sanitarias)

Conflict of interest

None declared.

Authors' contributions

AR, CG, EA, AC, JAV, AM, MR, IP and JA took clinical care of the patients, since admission to hospital and at outpatient clinic once discharged. MJM, LF and MPSS, performed the laboratory investigations and phylogenetic analysis of the virus, JG and JAPM were the senior supervisor of the article. All authors participated in writing the manuscript.

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Large number of imported chikungunya cases in mainland France, 2014: a challenge for surveillance and response

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Citation style for this article:
Paty MC, Six C, Charlet F, Heuzé G, Cochet A, Wiegandt A, Chappert JL, Dejour-Salamanca D, Guinard A, Soler P, Servas V, Vivier-Darrigol M, Ledrans M, Debruyne M, Schaal O, Jeannin C, Helynck B, Leparc-Goffart I, Coignard B. Large number of imported chikungunya cases in mainland France, 2014: a challenge for surveillance and response. Euro Surveill. 2014;19(28):pii=20856. Available online: http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=20856

Article submitted on 08 July 2014 / published on 17 July 2014

During the summer of 2014, all the pre-requisites for autochthonous transmission of chikungunya virus are present in southern France: a competent vector, *Aedes albopictus*, and a large number of travellers returning from the French Caribbean islands where an outbreak is occurring. We describe the system implemented for the surveillance of chikungunya and dengue in mainland France. From 2 May to 4 July 2014, there were 126 laboratory-confirmed imported chikungunya cases in mainland France.

In November 2013, locally acquired cases of chikungunya were laboratory-confirmed in the French Caribbean island of Saint Martin [1]. The chikungunya virus rapidly spread in the surrounding French territories (Martinique, Guadeloupe, Saint Barthélemy and French Guiana) in December 2013 and then in most of the islands of the Caribbean [2,3]. By 15 June 2014, there were more than 80,000 clinically compatible cases in the French Caribbean Islands, based on the estimation of the sentinel surveillance [4]. Given the epidemic situation in the French Caribbean, and due to the large amount of travel between mainland France and the Caribbean, it is expected that a large number of chikungunya cases will be imported to mainland France in 2014.

During the summer of 2014, all the pre-requisites for autochthonous transmission of chikungunya virus, and to a lesser extent, dengue virus, will then be present in southern France: a competent vector [5], a large number of viraemic travellers, and favourable climatic conditions for mosquito reproduction and viral replication in the mosquitoes. The likelihood of chikungunya transmission in mainland France is therefore particularly high.

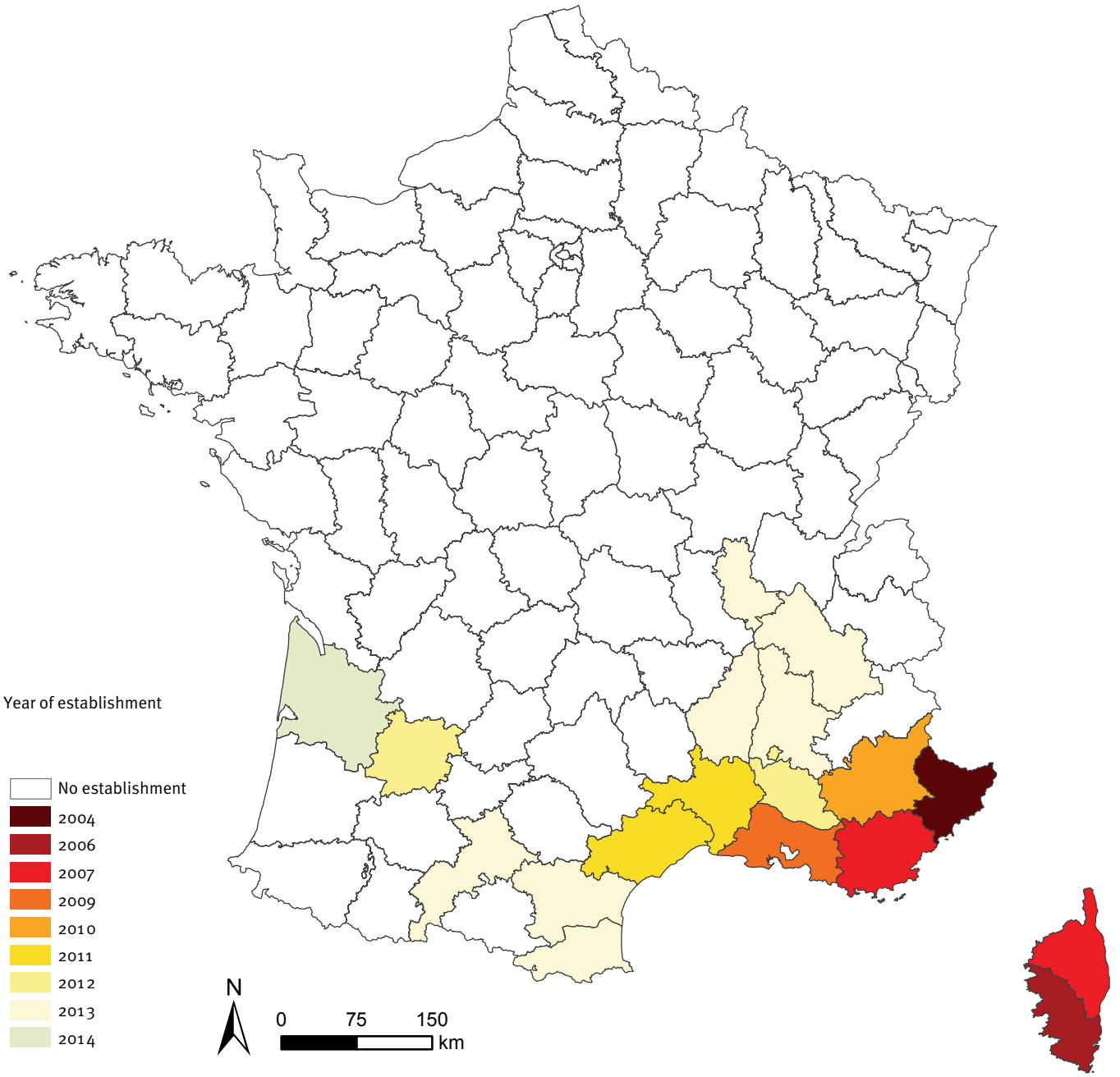
Surveillance of chikungunya and dengue in mainland France

Chikungunya and dengue are mosquito-borne viral diseases, transmitted by *Aedes* mosquitoes, in particular *Aedes aegypti* and *Aedes albopictus*, the latter being present in Europe [6,7]. Since it was identified in 2004 in the French administrative district of Alpes-Maritimes, *Ae. albopictus* has continued to spread in southern France [8,9].

Since 2006, in response to *Ae. albopictus* establishment in southern France, the French Ministry of Health has implemented a dengue and chikungunya preparedness and response plan to monitor and prevent the risk of dissemination of the two viruses in mainland France [10]. Because the two diseases present a number of similarities regarding the clinical and entomological

Figure 1

Establishment of *Aedes albopictus*, by administrative district and year, mainland France, 2004–2014



Source: IGN-GéoFLA, 1999: French Institute for Public Health Surveillance (Institut de Veille Sanitaire, InVS), 2014.

features, a common system has been set up comprising entomological and epidemiological surveillance.

Entomological surveillance for chikungunya and dengue

The entomological surveillance is operated by public local structures of mosquito control, under the coordination and responsibility of the Ministry of Health.

The presence and the spread of *Ae. albopictus* is monitored using ovitraps placed along the French Mediterranean coastline and land inwards along motorways. Traps are checked at least monthly for presence of *Ae. albopictus* eggs. Mosquitoes and eggs are not tested routinely for the presence of dengue and chikungunya viruses.

The administrative districts, according to the year of establishment of *Ae. albopictus*, are shown in Figure 1: from one district in 2004, *Ae. albopictus* has become established in 18 administrative districts in six regions (Provence-Alpes-Côte d'Azur, Corsica, Languedoc-Roussillon, Rhône-Alpes, Aquitaine, Midi-Pyrénées) in 2014.

Epidemiological surveillance for chikungunya and dengue

A suspected case is defined as a person with acute fever (>38.5 °C) and joint pains (chikungunya) or at least one of the following symptoms: headache, retro-orbital pain, joint pains, myalgia or lower back-pain (dengue), not explained by another medical condition. For both diseases, cases are confirmed by serology (IgM positive or a fourfold increase in IgG titre) or detection of viral nucleic acids in plasma by real-time reverse transcription polymerase chain reaction (RT-PCR), or for dengue, a positive dengue nonstructural protein 1 (NS1) antigenic test.

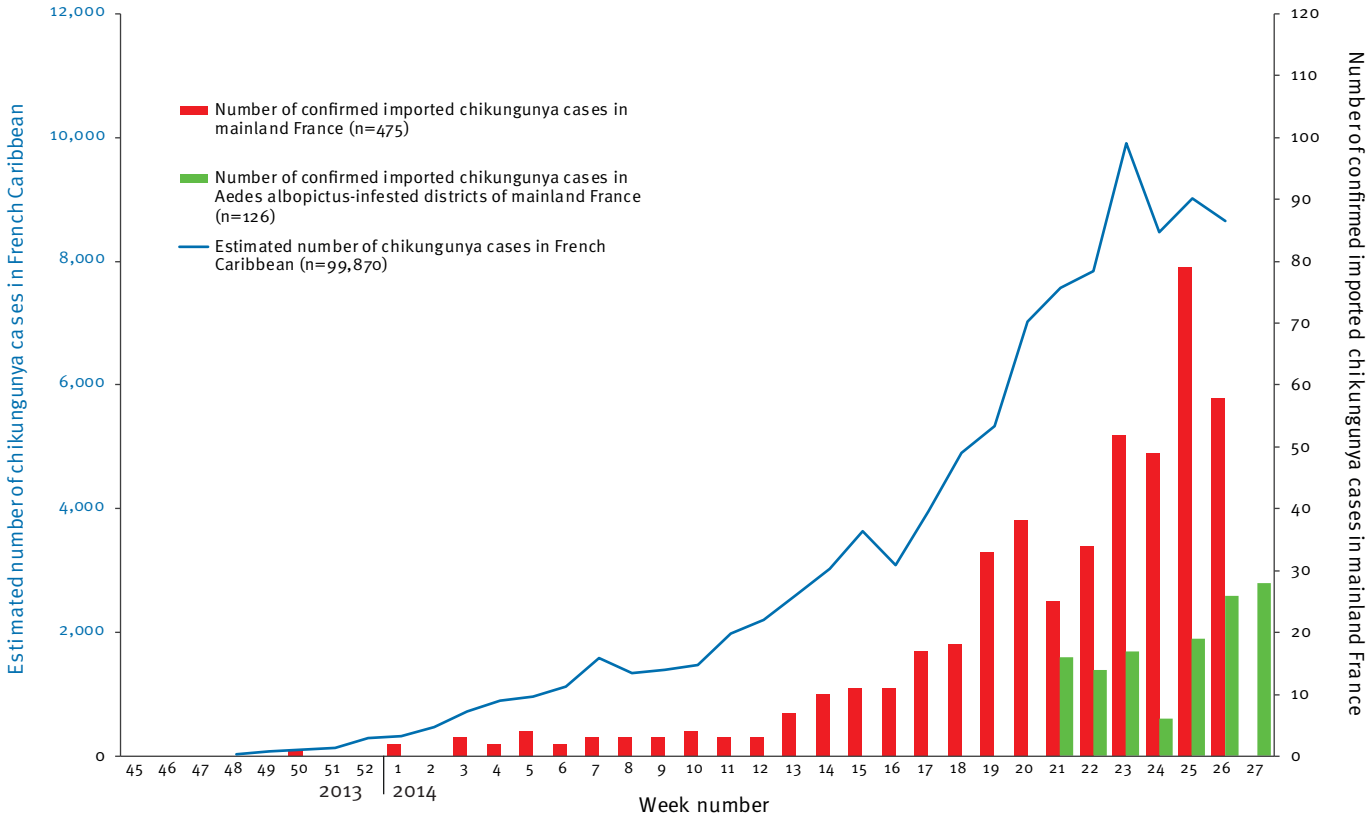
The surveillance system aims to prevent or to contain autochthonous transmission of dengue and chikungunya, and comprises three components:

- nationwide year-long mandatory notification of laboratory-confirmed cases of chikungunya and dengue;
- seasonal enhanced surveillance in the administrative districts where the vector is established. From May to November, when the vector is active, all suspected imported cases must be immediately reported to the regional health authorities (Agences Régionales de Santé, ARS). Appropriate vector control measures are then implemented within 200 metres of the places visited by the patients during the likely viraemic period (from the day before until seven days after the onset of symptoms [11]), without waiting for laboratory confirmation of the infection;
- daily reporting from a network of laboratories of the results of chikungunya and dengue serological or RT-PCR tests to the French Institute of Public Health Surveillance (Institut de veille sanitaire, InVS). This catches cases who have not been reported through the notification system and the seasonal enhanced surveillance, and thus serves to improve the completeness of reporting of the surveillance system.

The notification of a laboratory-confirmed locally acquired case triggers immediate epidemiological and entomological investigations, in order to assess the

Figure 2

Laboratory-confirmed imported chikungunya cases in mainland France[a], laboratory-confirmed imported chikungunya cases in *Aedes albopictus*-established districts in mainland France during the period of vector activity[b] and estimated number of clinically compatible chikungunya cases in the French Caribbean[c]



[a] Per week, week 45 2013 to week 26 2014 (1 November 2013 to 27 June 2014), source: laboratory network. Data for week 26 2014 are not yet consolidated and are not available for week 27 2014.

[b] Per week, weeks 18 to 27 2014 (2 May to 4 July 4 2014), source: enhanced surveillance.

[c] Per week, week 48 2013 to week 26 2014 (25 November 2013 to 29 June 2014). Data are not available for week 27 2014, source: French Caribbean sentinel surveillance.

Table 1

Suspected and laboratory-confirmed cases of chikungunya and dengue, by region involved in seasonal enhanced surveillance, mainland France, 2 May–4 July (weeks 18 to 27) 2014

Regions	Number of administrative districts where Aedes albopictus is established	Resident population in administrative districts where the vector is established[a]	Number of suspected cases	Number of laboratory-confirmed imported cases		Number of laboratory-confirmed autochthonous cases	
				Chikungunya	Dengue	Chikungunya	Dengue
Provence-Alpes-Côte d'Azur	5	4,777,464	121	43	17	0	0
Corsica	2	314,486	4	0	0	0	0
Languedoc-Roussillon	4	2,592,890	55	28	6	0	0
Rhône-Alpes	4	3,764,718	76	27	12	0	0
Aquitaine	2	1,794,528	31	14	5	0	0
Midi-Pyrénées	1	1,260,226	63	14	7	0	0
Total	**18**	**14,504,312**	**350**	**126**	**47**	**0**	**0**

[a] Source: French national institute of economic and statistical information (Institut national de la statistique et des études économiques, INSEE

autochthonous transmission and to guide vector control measures. The investigation and control measures include: (i) active case finding in the neighbourhood of the case's residence and in other areas visited by the case; (ii) recommending personal protection measures for the viraemic patient; (iii) encouraging health professionals to screen suspected cases; (iv) carrying out perifocal vector control activities, within 200 metres of the case's residence, including destruction of mosquito breeding sites and spraying targeted at adult mosquitoes; (v) giving information to the public about personal protection and reduction of mosquito breeding sites.

Chikungunya cases in mainland France

Throughout mainland France, 475 laboratory-confirmed imported cases of chikungunya were notified through the laboratory network from 1 November 2013 (the month of confirmation of the first cases in Saint Martin) to 27 June 2014 (Figure 2), whereas during the whole of 2011 and 2012, there were 33 and 17 cases, respectively.

From 2 May to 4 July 2014, of 350 suspected cases who were notified to the regional health authorities, 126 were laboratory-confirmed imported cases of chikungunya and 47 laboratory-confirmed imported cases of dengue were detected in the *Ae. albopictus*-established districts (Table 1 and Figure 2). A large majority of the laboratory-confirmed imported cases of chikungunya arrived from the French Caribbean (85% (107/126), as shown in Table 2). More than 80% of cases (n=103) were in an *Ae. albopictus*-established district while potentially viraemic (the remaining 20% were diagnosed retrospectively). No autochthonous case has been confirmed to date. More information and updated surveillance results are provided on the InVS website [4].

Discussion

From 2006 to 2013, the number of laboratory-confirmed imported cases of chikungunya reported in *Ae. albopictus*-established districts from May to November ranged from 2 to 6 [4]. From 2 May to 4 July 2014, the number of laboratory-confirmed imported cases of chikungunya was much higher (126) than in previous years, as a consequence of the chikungunya outbreak in the Caribbean region.

Although no autochthonous case has been confirmed to date in 2014, the conditions required for autochthonous transmission of the chikungunya virus are met: the population in mainland France is immunologically naive to the virus; a competent vector exists, *Ae. albopictus* [5] and its distribution has been constantly and rapidly spreading for the past 10 years [10]; and the probability of introduction of the virus by travellers coming from affected areas is high. The possibility of occurrence of autochthonous transmission of arboviruses has been demonstrated in the recent past in southern France, with the identification of two autochthonous dengue cases in 2010 and one in 2013, as well as two autochthonous chikungunya cases in 2010 [12-14].

Passenger traffic between mainland France and Martinique and Guadeloupe is high, with more than 2.5 million plane passengers in 2013 [15]. During this summer of 2014 – when the mosquito is active – large numbers of travellers will return from the French Caribbean islands where an outbreak is currently occurring. Among them, a high proportion will possibly be viraemic upon their arrival, increasing the probability of the occurrence of autochthonous cases of chikungunya in the administrative districts where *Ae. albopictus* is established, and increasing the risk of a chikungunya outbreak in mainland France.

Table 2

Laboratory-confirmed chikungunya cases imported to mainland France, by place of origin, as of 4 July (week 27) 2014

Place of origin	Number of cases imported to mainland France
Guadeloupe	70
Martinique	36
Haiti	10
Dominican Republic	3
Tonga	1
Sierra Leone	1
Saint Martin	1
Indonesia	1
Côte d'Ivoire	1
Costa Rica	1
Cambodia	1
Total	**126**

Source: seasonal enhanced surveillance system, mainland France.

The preparedness and response plan developed in mainland France since 2006 has proved to be effective for the early detection of cases and implementation of vector control measures to prevent or contain autochthonous transmission of dengue and chikungunya viruses. However, it is currently challenged by the increased number of imported chikungunya cases. It is thus crucial to maintain a high level of mobilisation of all actors within the surveillance system. They are also an important source of information for the general population, to encourage the use of personal protection against mosquito bites and control of mosquito breeding sites.

The challenge that we face is to avoid the establishment of a local cycle of transmission in mainland France and, beyond, in other European areas where competent vectors are also present.

Acknowledgements

We would like to thank the personnel of diagnostic laboratories and the clinicians involved in the surveillance system.

Conflict of interest

None declared.

Authors' contributions

Marie-Claire Paty coordinates the chikungunya and dengue surveillance system at the national level. Brigitte Helynck and Marie-Claire Paty co-drafted the manuscript. Caroline Six, Francis Charlet, Guillaume Heuzé, Amandine Cochet, Axel Wiegandt, Jean Loup Chappert, Dominique Dejour-Salamanca, Anne Guinard, Pauline Soler, Véronique Servas, Martine Vivier-Darrigol, Martine Ledrans are responsible at regional level for the surveillance and epidemiological investigations. Monique Debruyne, Oriane Schaal and Isabelle Leparc-Goffart are in charge of virological analysis and transmit the results on a daily basis to the surveillance teams. Charles Jeannin is an entomologist in charge of entomological investigations and mosquito control activities. Bruno Coignard reviewed the final document for accuracy. All authors contributed to the review of the manuscript and approved the final version.

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Local and regional spread of chikungunya fever in the Americas

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Citation style for this article:
Cauchemez S, Ledrans M, Poletto C, Quenel P, de Valk H, Colizza V, Boëlle PY. Local and regional spread of chikungunya fever in the Americas. Euro Surveill. 2014;19(28):pii=20854. Available online: http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=20854

Article submitted on 01 July 2014/ published on 17 July 2014

Chikungunya fever (CHIKV), a viral disease transmitted by mosquitoes, is currently affecting several areas in the Caribbean. The vector is found in the Americas from southern Florida to Brazil, and the Caribbean is a highly connected region in terms of population movements. There is therefore a significant risk for the epidemic to quickly expand to a wide area in the Americas. Here, we describe the spread of CHIKV in the first three areas to report cases and between areas in the region. Local transmission of CHIKV in the Caribbean is very effective, the mean number of cases generated by a human case ranging from two to four. There is a strong spatial signature in the regional epidemic, with the risk of transmission between areas estimated to be inversely proportional to the distance rather than driven by air transportation. So far, this simple distance-based model has successfully predicted observed patterns of spread. The spatial structure allows ranking areas according to their risk of invasion. This characterisation may help national and international agencies to optimise resource allocation for monitoring and control and encourage areas with elevated risks to act.

Introduction

Chikungunya fever is caused by the chikungunya virus, an alphavirus that is transmitted by several species of mosquitoes, including *Aedes albopictus* and *Ae. aegypti* [1]. In the last decade, large outbreaks of chikungunya fever have been reported in the Indian Ocean region [2], with millions of people experiencing incapacitating arthralgia, fever and rashes [3,4]. Transmission was sustained even in places with high standards of sanitary organisation [5].

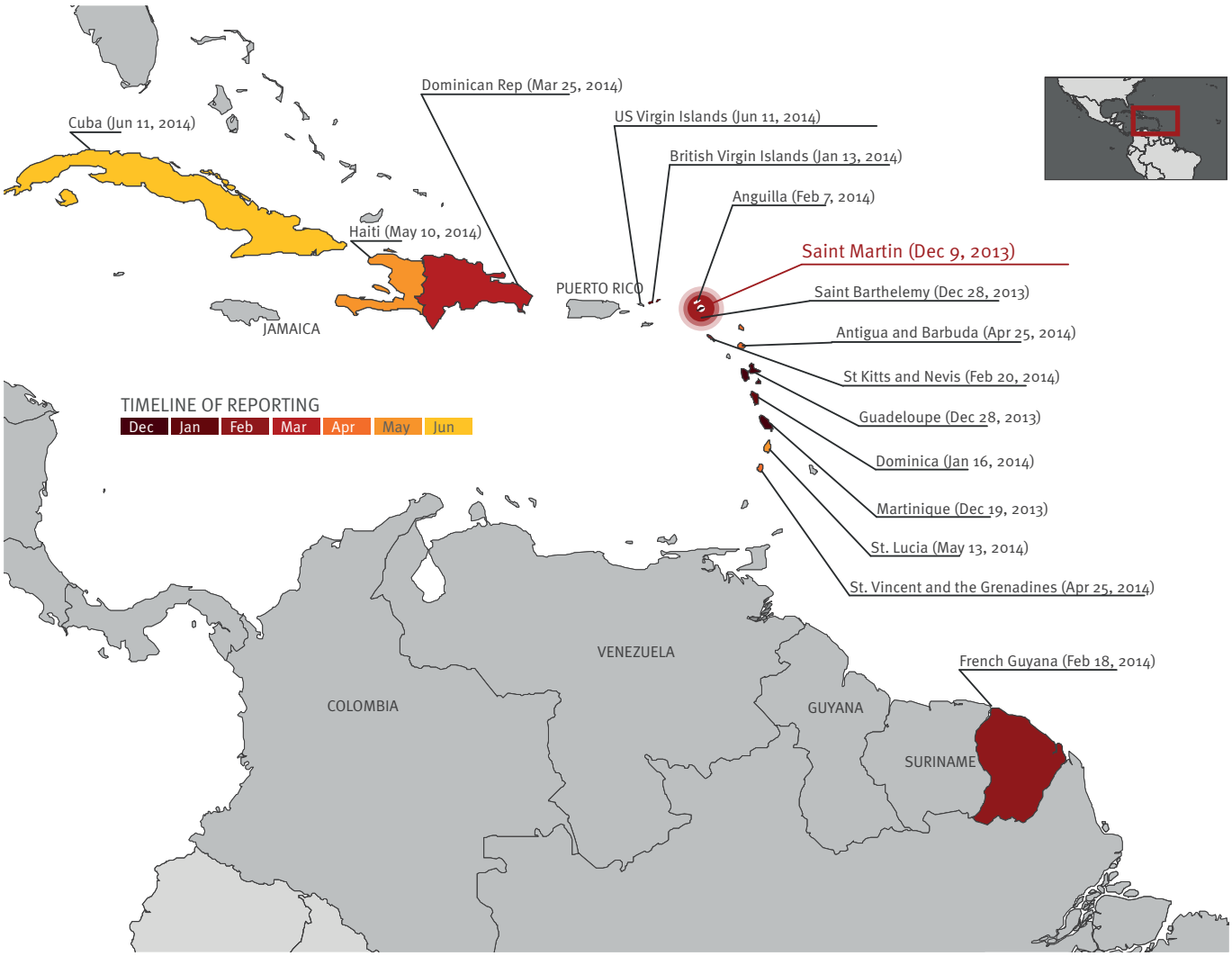
An outbreak of chikungunya fever is currently affecting an increasing number of areas in the Caribbean [6-8]. Figure 1 shows areas that reported at least one autochthonous case by 15 June 2014. The figure also shows the timeline of reporting. The first area reporting cases was Saint Martin (9 December 2013) with symptom onset of the first documented case on 5 October 2013. Further reports quickly followed from two other French territories, Martinique on 19 December 2013 and Guadeloupe on 28 December 2013. By 15 June 2014, 16 areas had reported at least one autochthonous case.

This rapid expansion constitutes a source of concern for public health in the Americas [8]. The mosquito vector is found in a wide geographical zone that goes from South Florida to Brazil [10]. The potential for geographical expansion is therefore considerable and extends far beyond the areas currently affected. Moreover, the Caribbean is a highly connected area with frequent exchanges among the islands in the region, with mainland America and with Europe: more than 10 million international visits are reported each year by the World Tourism Organization, including 25% from Europe [11]. These important connections increase the risk of the current epidemic expanding quickly to a wider area in the Americas. Furthermore, the epidemic generates importations of cases into Europe, where the mosquito species *Ae. albopictus* is well established in many countries, primarily around the Mediterranean [9,12]. As of 1 July 2014, 98 imported laboratory-confirmed cases have been reported for metropolitan France alone [13].

In order to support preparedness and response planning in affected areas and those at risk of invasion (i.e. arrival of the disease in the area), it is important that we understand better the local and regional

Figure 1

Chikungunya fever in the Caribbean, as of 15 June 20141



Areas that reported at least one laboratory-confirmed autochthonous case of chikungunya fever are coloured according to the timeline of reporting [6]. The first date of symptom onset was 5 October 2013, on Saint Martin.

Box

List of areas included in the assessment of chikungunya virus transmission (n=40)

Anguilla, Antigua and Barbuda, Aruba, Bahamas, Barbados, Belize, British Virgin Islands, Cayman Islands, Colombia, Costa Rica, Cuba, Curacao, Dominica, Dominican Republic, El Salvador, Florida, French Guiana, Grenada, Guadeloupe, Guatemala, Guyana, Haiti, Honduras, Jamaica, Martinique, Mexico, Netherlands Antilles, Nicaragua, Panama, Puerto Rico, Saint Barthelemy, Saint Kitts and Nevis, Saint Lucia, Saint Martin, Saint Vincent and the Grenadines, Suriname, Trinidad and Tobago, Turks and Caicos Islands, United States Virgin Islands, Venezuela.

dynamics of spread of chikungunya fever in the Caribbean. Firstly, how effective is transmission of the disease in the Caribbean? Answering this question is important to assess the potential for large and explosive outbreaks as seen previously in the Indian Ocean region. Secondly, we need to understand the regional dynamics of spread and their determinants to assess which areas currently are at risk of invasion, to help national and international agencies with resource allocation, technical support and planning, and to encourage areas with elevated risks to act. This is essential in order to reduce disease burden in the Americas, but also to reduce the number of imported cases in Europe.

Here, we provide the first assessment of the effectiveness of transmission of the virus in the Caribbean and of the factors explaining the spread at the regional level.

Methods

Data collection

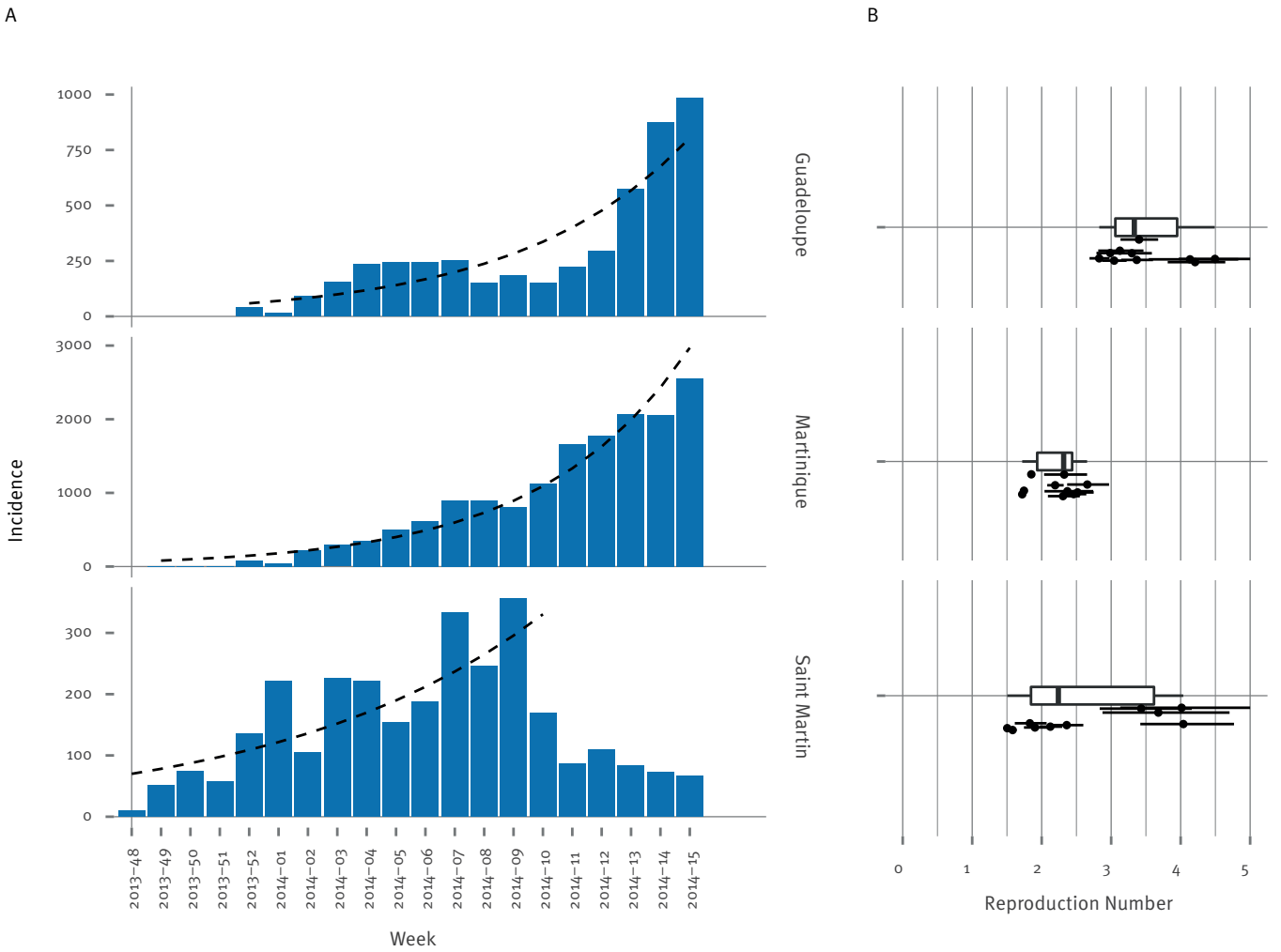
We selected 40 areas (countries or territories) around the Caribbean which overlap with areas infested by *Ae. aegypti* mosquito [10] and where dengue is present [14,15] in central America (Box).

We defined areas officially affected by chikungunya fever as those reported to have had at least one laboratory-confirmed autochthonous case of chikungunya fever in the ProMED-mail alerts [6], the Pan American Health Organization [16] or the Caribbean Public Health Agency [17]. The date of the first report was also recorded.

In the French overseas territories (Saint Martin, Martinique and Guadeloupe), detailed data were collected by Cire Antilles-Guyane, using different approaches as the health authorities adapted to the situation. At first, an investigation was started around suspected or clinical cases with retrospective identification of other suspected cases in the neighbourhood. Virological confirmation was undertaken for most of the clinically suspected cases by the two laboratories of the national reference centre (Marseille and Cayenne). As the number of cases increased, existing surveillance networks based on general practitioners (GP) were asked to monitor clinical cases according to the case definition (patient with onset of acute fever >38.5 °C and severe arthralgia of hands or feet not explained by another medical condition). The surveillance network comprised 100% of the GPs on Saint Martin (15

Figure 2

Reproduction number of chikungunya fever in the Caribbean, 2014

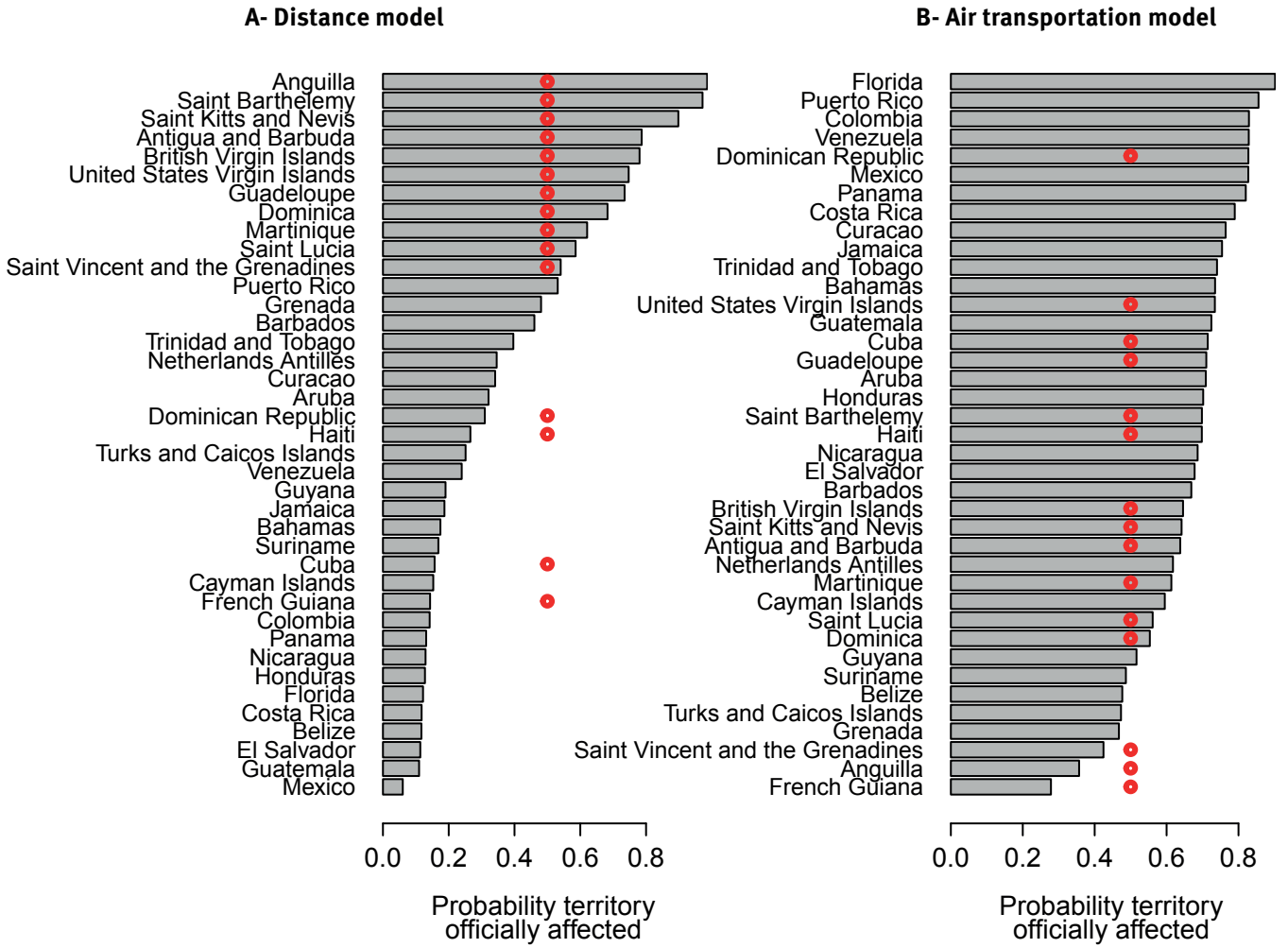


A Epidemic curves based on clinical surveillance systems in general practice on three French islands (bars). An exponential fit to the whole epidemic is shown as a dashed line.

B. Estimates of the reproduction number based on the exponential growth for the 10 time periods of four weeks or more with the best fits. The boxplots show the median, interquartile interval and range of the 10 point estimates.

Figure 3

Areas in the Caribbean officially affected by chikungunya fever on 15 June 2014 and prediction in the distance model (A) and the air transportation model (B)



The grey bars give the probability predicted by the model that the area should be officially affected by 15 June 2014, sorted in decreasing order. The red dots indicate areas that were officially affected by 15 June 2014 according to the (data). The red dots indicate areas that actually were officially affected by 15 June 2014 according to the data. A good fit is suggested when most of the red dots appear at the top of the pyramid.

of 15) and around 20% on Martinique and Guadeloupe. Virological confirmation was no longer systematically undertaken as the number of cases increased.

Commercial air connections and 2013 data for volume of passengers between airports of the region were obtained from the International Air Transport Association [18,19]. These data correctly captured multi-leg flight trajectories, i.e. if a person flew from Florida to Jamaica via Puerto Rico, the recorded itinerary would be the Florida to Jamaica journey. Distances between the centroids of the areas were computed.

Characterising local transmission on Saint Martin, Martinique and Guadeloupe

The human-to-human initial reproduction number *R* (mean number of secondary cases generated by a human case) was computed using the exponential growth method [20]. We explored the variability of these estimates by analysing all time periods of four weeks or more in the epidemic curves and reporting the 10 periods for which our exponential growth model had the best fit to the data (as measured by the deviance *R*-squared statistic [21]). Additional details can be found in the supplementary material* that can be accessed at https://docs.google.com/file/d/0BopDXBmlKKGMRW9ucWRpaVV5bDQ/edit?pli=1.

Characterising regional spread

The transmission paths between areas were analysed under the hypotheses that the risk of invasion arose from previously invaded areas with data available as of 15 June 2014 [22]. We considered that Saint-Martin was the first invaded territory, with a first case on 5 October 2013. For other areas, a delay of on average 30 days

was allowed between invasion and reporting. Different mathematical models were developed in which the instantaneous risk of transmission between areas depended on population size, distance, air traffic volume or a combination thereof. The models were fitted by Markov chain Monte Carlo sampling [23]. Goodness of fit was assessed by determining how well the models agreed with the set of areas officially affected by the time the analysis was performed. Finally, we used the best model to predict areas with the highest risk of invasion. As we have been using this model since early 2014, we also evaluated retrospectively short-term predictions that were made with data available on 15 January 2014 and on 30 March 2014. Technical details are available in the supplementary material*.

Results

Local transmission on Saint Martin, Martinique and Guadeloupe

Surveillance of clinically suspected cases started in weeks 48, 49 and 52 of 2013 on Saint Martin, Martinique and Guadeloupe, respectively. The fit of an exponential increase to the first weeks of each outbreak was reasonable, leading to estimates of the reproduction number in the range 2 to 4 (Figure 2). The reproduction number was estimated to be slightly higher on Guadeloupe than on Martinique, due to a renewed outbreak starting in week 10 of 2014 on Guadeloupe.

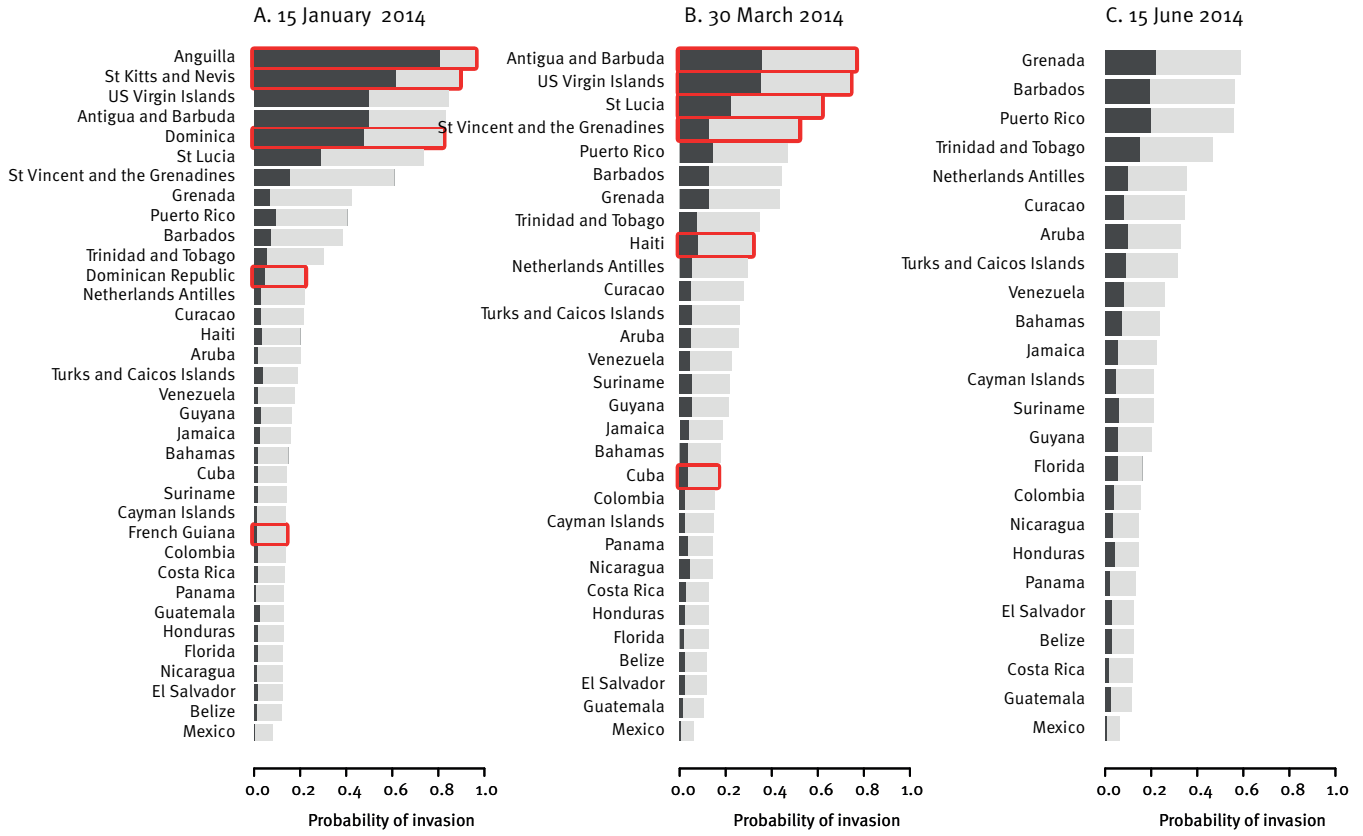
Regional spread

A marked geographical pattern of the spread was apparent (Figure 1), as 12 of 16 officially affected areas were situated in a relatively small geographical zone between the British Virgin Islands in the north-west and Saint Vincent and the Grenadines in the south-east.

We found that this pattern was best explained by making the risk of transmission between areas inversely proportional to distance. If we exclude the seed location Saint Martin, 15 areas were officially affected. Of these 15, 11 were at the top of the list of areas predicted to be at highest risk of invasion by this simple model based on distance (Figure 3A). In contrast, only one of 15 officially affected areas was at the top of the list if the risk of transmission was instead assumed to depend on air passenger flows, indicating that air passenger flow was a poor predictor of transmission

Figure 4

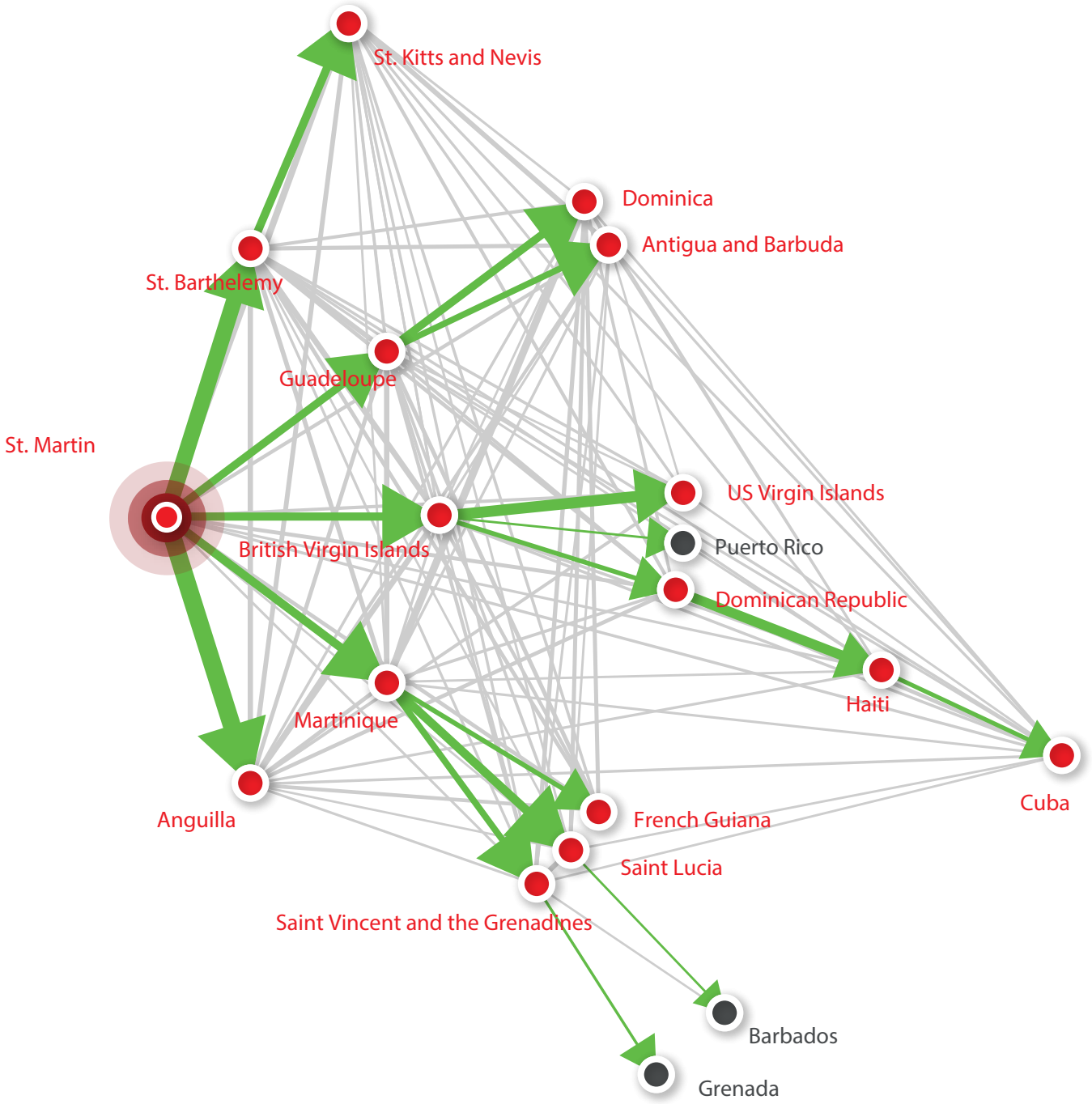
Short-term predictions of the distance model performed on different dates in the chikungunya fever epidemic in the Caribbean with data as available on these dates



Dark bars indicate the probability of areas already invaded at the time the analysis was performed. Light bars give the probability that the area would be invaded in the 75 days following the time of the analysis. For analyses performed on 15 January and 15 June 2014, we highlight in red the areas that became officially affected in the 75 days following the date of analysis.

Figure 5

Most probable source of transmission for areas that are officially affected by chikungunya fever and for those that may already be invaded but have not yet reported cases



Transmission tree for areas officially affected (in red) and for those that have at least 20% probability of already being invaded (in grey). The transmission tree is visualised in a topological space where areas are organised in successive layers starting from Saint Martin according to their most probable source of transmission. Most probable transmission links are plotted in green; other links with probability larger than 3% are plotted in grey. The thicker the arrow, the higher the probability of transmission.

(Figure 3B). Population sizes of areas were not found to significantly affect transmission (see supplementary material*).

Figure 4 presents predictions made with this model on 15 January 2014 (Figure 4A) and on 30 March 2014 (Figure 4B). It shows the risk of being already invaded at the time of the analysis or of being invaded in the following 75 days, based on data available at the time. Overall, performance of the model has been good, as most areas officially affected in the following 75 days were among those that had the highest predicted risk of invasion. Of 11 areas officially affected during this period, French Guiana and Cuba were the only two with low predicted risks.

Figure 4C shows predictions of the model with data available on 15 June 2014. Grenada, Barbados and Puerto Rico currently have the largest predicted probability of being invaded in the 75 days following the analysis (36%). We note that heterogeneity in the predicted risk of invasion has decreased as Chikungunya has expanded in the region, with the standard deviation in the predicted risk declining from 27% on 15 January 2014 to 15% on 15 June 2014.

Assuming that Saint Martin was the seed of infection in the region, Figure 5 shows the most likely path of transmission for areas that were either officially affected or likely to be already invaded although autochtonous cases had not been reported. The first round of invasion included Martinique, Guadeloupe, Saint Barthélemy, British Virgin Islands and Anguilla. The second round of invasion eventually led to eight new invaded areas, including Dominica and French Guiana. Four rounds were necessary for the disease to reach Cuba. Looking at the reconstructed transmission tree and restricting the analysis to areas that were officially affected, we found that the median distance between two areas predicted to have transmitted chikungunya to each other was 476 km (95% CI: 16–2,040). It was 173 km (95% CI: 16–451) and 626 km (95% CI: 54–2,043), respectively, for areas in the first and in subsequent rounds of the regional epidemic.

Discussion

The chikungunya virus has found a propitious environment for transmission in the Caribbean. All areas of the Caribbean and Central America are at risk of invasion, although with important heterogeneities in their predicted risks. Our analysis provides a quantitative basis for informed policy making and planning.

Transmission of chikungunya fever was consistently estimated to be effective in the three French territories that first reported cases (Saint Martin, Martinique and Guadeloupe). Estimates of the reproduction number R ranged from 2 to 4, similar to what was reported in the Indian Ocean region [5,24], making large and fast-growing outbreaks possible. With the largest estimate, Guadeloupe may end up with the largest attack rate if transmission goes on unchanged. Interestingly, incidence there showed sustained increase only after the epidemic entered the largest city (Pointe à Pitre), suggesting heterogeneity in transmission. In Saint Martin, incidence has notably slowed down in the last weeks, despite large growth at first. Further investigation is required to find out how vector abundance, heterogeneity in population mixing and exposure explain these outcomes. These estimates of R were obtained under the assumption that the serial interval was 23 days (see supplementary material*). Using a shorter duration for the gonotrophic cycle (three days vs four days) led to little change in the serial interval distribution (two days) and less than 5% variation on the estimates of R. With higher daily mortality in mosquitoes (15% instead of 10%), the serial interval was shorter, and the estimates of R were reduced by ca 20%.

Sustained transmission in the French islands has been in contrast with the limited number or absence of cases reported in some nearby areas. This could partly be explained if French territories were invaded first so that they had more time to build up large numbers of cases. However, heterogeneity in reporting is also likely to be involved, as some areas only reported the disease when it had already been responsible for hundreds of cases.

Indeed, a difficulty in the analysis of the regional diffusion of chikungunya fever has been the imperfect documentation of areas that were affected and of the dates when they were invaded. This is due to variable delays between (unobserved) dates of invasion and reporting of the first autochthonous cases. We did not model heterogeneities in the capabilities of the different areas to identify cases, as supporting data are lacking and this would therefore have been mostly subjective and added uncertainty to the analysis. But we used state-of-the-art data augmentation techniques [25-27] to overcome uncertainty about timing. In our baseline scenario, we assumed an average 30-day reporting delay but analysed alternative scenarios with shorter and longer delays in the supplementary material*. Reducing the reporting delay did not change the relative order of areas by risk of invasion but led to reduced probabilities of invasion in the near future. Unfortunately, we did not have independent data to back up the baseline assumption of an average 30-day delay in reporting.

To understand and predict regional spread, we postulated that importation of infected humans or mosquitoes by usual transportation routes was likely to be responsible for invasion of new areas. Most islands are served by air carriers, but travelling by boat, ferries and cruisers is also very common. Up to now, areas officially affected by chikungunya fever have presented smaller air passenger flows than those not yet affected (daily average: 797 as opposed to 2,476). It is therefore not surprising that air transportation data could not reproduce the patterns of spread seen so far

(Figure 3B). A direct assessment of alternative modes of transportation, including boats and cruises, was not possible due to a lack of detailed data on these routes. To overcome this limitation, we used standard geographical models where connections between areas depend on distance and population sizes [28-30]. We found that the spatial structure of the epidemic was most consistent with a model in which the strength of a connection was inversely proportional to the distance. Overall, our results suggest that short-range transportation such as boats and cruises hopping between islands are likely to have played a substantial role in the spread observed in the early phase of the chikungunya outbreak in the Carribean.

The good fit of this distance model to current data (Figure 3A) and its successful predictions so far (Figure 4, panels A and B) give us some confidence in the short-term predictions of this model (Figure 4C). However, the relative importance of the transmission routes may change as the epidemic spreads, which could increase the risk to more distant areas in the longer term. In that respect, we note an apparent increase in the median distance of transmission between the first and subsequent waves in the regional epidemic. Given the current absence of correlation between available long-range air transportation data and disease spread, long-term predictions for international spread are harder to make.

The propensity of an area to get invaded and to transmit is expected to depend on vector activity and case numbers, respectively. Here, we used qualitative data on the presence of the *Ae. aegypti* mosquito [10], which are supported by recent reports on dengue virus circulation [14,15], to characterise vector activity. The vector was present in all areas included in our analysis [10,14,15]. Due to the lack of adequate data, we were unable to modulate the risk of invasion with more quantitative indicators of vector activity. Efforts to construct quantitative maps of vector activity should be a priority to improve model predictions. If they become available, data on incidence of cases in the invaded areas may improve the fit further, although this was not shown to be the case in the spatial analysis of other outbreaks [22]. Despite these limitations, short-term predictions of the model have been good (Figure 4, panels A and B). Improved predictions may require taking seasonality into account, as vector abundance may change with the seasons. The range of temperature is limited in the Caribbean islands (between 26 °C and 29 °C in Saint Martin), but larger changes are expected as we move away from the equator. Seasonal changes in the number of passengers to and from the Caribbean must also be considered when studying the risk of importation to Europe.

In conclusion, we have shown that chikungunya fever is an important threat in the Americas. The high transmissibility may lead to fast-growing and large outbreaks. Regional dissemination is under way, so far with a simple geographical pattern, which is relevant for optimising the monitoring of areas.

*Note:

Supplementary information made available by the authors on an independent website is not edited by Eurosurveillance, and Eurosurveillance is not responsible for the content. The material can be accessed at: https://docs.google.com/file/d/0BopDXBmlKKGMRW9ucWRpaVV5bDQ/edit?pli=1.

Acknowledgements

We thank IMMI, EU FP7 PREDEMICS, Labex IBEID, NIH MIDAS and HARMSflu for research funding.

Conflict of interest

None declared.

Authors' contributions

ML, PQ, HDV provided the data. SC, CP, VC, PYB analysed the data. SC and PYB designed the analysis and wrote the first draft. All authors edited and commented the paper.

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