

**THÈSE DE DOCTORAT DE
L'UNIVERSITÉ PIERRE ET MARIE CURIE**

Spécialité

Épidémiologie

Ecole doctorale n°393

Épidémiologie et Sciences de l'Information Biomédicale

Présentée par

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Pour obtenir le grade de

**DOCTEUR de l'UNIVERSITÉ PIERRE ET MARIE
CURIE**

Sujet de la thèse :

**Analyse comparative et prédictabilité des épidémies
transmises par les moustiques du genre *Aedes***

soutenue le

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Remerciements

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Résumé de la thèse

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Thesis summary

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Productions scientifiques

Publications

Posters

Table des matières

1	L'invasion mondiale des moustiques du genre <i>Aedes</i> et leur conséquences	3
1.1	Origines, adaptations et invasions d' <i>Aedes aegypti</i> et d' <i>Aedes albopictus</i>	3
1.1.1	Les moustiques du genre <i>Aedes</i> : éléments entomologiques	3
1.1.2	La domestication d' <i>Aedes aegypti</i>	3
1.1.3	L'invasion d' <i>Aedes albopictus</i>	3
1.2	Émergences et réémergences	3
1.2.1	Dengue	3
1.2.2	Fièvre jaune	3
1.2.3	Fièvre West Nile	3
1.2.4	Encéphalite équine de l'Est	3
1.2.5	Chikungunya	3
1.2.6	Zika	3
1.2.7	Le futur : Mayaro, Usutu, Ross River	3
2	Techniques et concepts en modélisation des épidémies vectorielles émergentes	5
2.1	Les modèles de maladies vectorielles	5
2.1.1	SIR	5
2.1.2	Ronald Ross et le paludisme	5
2.1.3	Extensions : immunité, saisonnalité, écologie, spatialisation	5
2.2	Contourner le vecteur : discretisation et temps de génération	5
2.2.1	Discretisation du modèle SIR	5
2.2.2	Reconstruire le temps de génération	5
2.2.3	Différences avec les approches classiques	5
2.3	Apports de l'inférence Bayésienne	5

2.3.1	Mieux prendre en compte les incertitudes . .	5
2.3.2	Intégrer l'information <i>a priori</i>	5
2.3.3	Mise en commun de plusieurs sources d'infor- mation	5
2.3.4	Efficacité computationnelle : la méthode HMC	5
3	Analyse comparative des épidémies transmises par les moustiques du genre <i>Aedes</i>	7
3.1	Distinguer les facteurs influençant la transmissibilité	7
3.1.1	Vecteurs	7
3.1.2	Hôtes	7
3.1.3	Virus	7
3.2	Analyse comparative de la transmission du Chikun- gunya et du Zika aux Antilles et en Polynésie fran- çaise entre 2013 et 2017	7
3.2.1	Résumé de l'article en français	7
3.2.2	Article : Riou, Poletto, Boëlle, A comparative analysis of Chikungunya and Zika transmis- sion, <i>Epidemics</i> , 19 :43–52, 2017	7
3.3	Commentaires et perspectives	9
4	Utiliser les ressemblances entre les maladies trans- mises par <i>Aedes</i> pour améliorer les outils de prédic- tion épidémique	11
4.1	Guider les interventions de prévention et de contrôle en situation d'épidémie émergente	11
4.1.1	Approches classiques en prédiction	11
4.1.2	Récents développements : les challenges . . .	11
4.2	Améliorer les prédictions à la phase précoce d'une épidémie de Zika grâce aux données historiques sur la transmission du Chikungunya	11
4.2.1	Résumé de l'article en français	11
4.2.2	Article : Riou, Poletto, Boëlle, Improving early epidemiological assessment of emerging <i>Aedes</i> - transmitted epidemics using historical data .	11
4.3	Commentaires et perspectives	13
5	Conclusions	15

Introduction

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Chapitre 1

L'invasion mondiale des moustiques du genre *Aedes* et leur conséquences

1.1 Origines, adaptations et invasions d'*Aedes aegypti* et d'*Aedes albopictus*

1.1.1 Les moustiques du genre *Aedes* : éléments entomologiques

1.1.2 La domestication d'*Aedes aegypti*

1.1.3 L'invasion d'*Aedes albopictus*

1.2 Émergences et réémergences

1.2.1 Dengue

1.2.2 Fièvre jaune

1.2.3 Fièvre West Nile

1.2.4 Encéphalite équine de l'Est

1.2.5 Chikungunya

1.2.6 Zika

1.2.7 Le futur : Mayaro, Usutu, Ross River

Chapitre 2

Techniques et concepts en modélisation des épidémies vectorielles émergentes

2.1 Les modèles de maladies vectorielles

2.1.1 SIR

2.1.2 Ronald Ross et le paludisme

2.1.3 Extensions : immunité, saisonnalité, écologie, spatialisation

2.2 Contourner le vecteur : discretisation et temps de génération

2.2.1 Discrétisation du modèle SIR

2.2.2 Reconstruire le temps de génération

2.2.3 Différences avec les approches classiques

2.3 Apports de l'inférence Bayésienne

2.3.1 Mieux prendre en compte les incertitudes

2.3.2 Intégrer l'information *a priori*

2.3.3 Mise en commun de plusieurs sources d'information

2.3.4 Efficacité computationnelle : la méthode HMC

Chapitre 3

Analyse comparative des épidémies transmises par les moustiques du genre *Aedes*

3.1 Distinguer les facteurs influençant la transmissibilité

3.1.1 Vecteurs

3.1.2 Hôtes

3.1.3 Virus

3.2 Analyse comparative de la transmission du Chikungunya et du Zika aux Antilles et en Polynésie française entre 2013 et 2017

3.2.1 Résumé de l'article en français

3.2.2 Article : Riou, Poletto, Boëlle, A comparative analysis of Chikungunya and Zika transmission, *Epidemics*, 19 :43–52, 2017



A comparative analysis of Chikungunya and Zika transmission



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ARTICLE INFO

Article history:

Received 30 September 2016

Received in revised form

23 December 2016

Accepted 3 January 2017

Available online 18 January 2017

Keywords:

Zika virus

Chikungunya virus

Outbreak analysis

Multilevel analysis

Weather

ABSTRACT

The recent global dissemination of Chikungunya and Zika has fostered public health concern worldwide. To better understand the drivers of transmission of these two arboviral diseases, we propose a joint analysis of Chikungunya and Zika epidemics in the same territories, taking into account the common epidemiological features of the epidemics: transmitted by the same vector, in the same environments, and observed by the same surveillance systems. We analyse eighteen outbreaks in French Polynesia and the French West Indies using a hierarchical time-dependent SIR model accounting for the effect of virus, location and weather on transmission, and based on a disease specific serial interval. We show that Chikungunya and Zika have similar transmission potential in the same territories (transmissibility ratio between Zika and Chikungunya of 1.04 [95% credible interval: 0.97; 1.13]), but that detection and reporting rates were different (around 19% for Zika and 40% for Chikungunya). Temperature variations between 22 °C and 29 °C did not alter transmission, but increased precipitation showed a dual effect, first reducing transmission after a two-week delay, then increasing it around five weeks later. The present study provides valuable information for risk assessment and introduces a modelling framework for the comparative analysis of arboviral infections that can be extended to other viruses and territories.

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1. Introduction

Arboviral infections are increasingly becoming a global health problem (WHO, 2016). Dengue fever and yellow fever viruses have been re-emerging in many tropical areas since the 1980s (Gubler, 2004), but new epidemic waves have recently been caused by lesser known arboviruses: the Chikungunya virus (CHIKV) since 2005 (Renault et al., 2007), and the Zika virus (ZIKV) since 2007 (Duffy et al., 2009). Interestingly, the spread of ZIKV and CHIKV have shared many epidemiological characteristics. While discovered in the 1940–50s, the global spread of these viruses to previously unaffected areas has only begun in recent years, and large outbreaks have affected the immunologically naive populations of the Indian and Pacific oceans and of the Americas (Weaver and Lecuit, 2015; Musso et al., 2015; Zhang et al., 2016). Case identification and counting has been an issue for epidemiological surveillance since symptoms caused by ZIKV and CHIKV infection are most of the times mild and not specific. Finally, both diseases can be transmitted by the same mosquitoes of the *Aedes* genus (Richard et al., 2016; Li et al., 2012). The most common vector, *Ae. aegypti*, is well adapted to the human habitat (Brown et al., 2011), is resistant to many insecticides (Lima et al., 2011), and bites during the day so that

prevention by bed nets, for example, is ineffective (Christophers et al., 1960).

Obviously, transmission of the disease has been facilitated due to the joint occurrence of large susceptible human populations and competent vectors. However, other aspects are involved in the transmission of arboviruses, since vector abundance and behavior change with the environment. A joint analysis of CHIKV and ZIKV epidemics may provide a better understanding of the commonalities and differences among these two *Aedes*-transmitted diseases. Up to now, these diseases have been studied separately, with a special focus on the reproduction ratio of CHIKV (Boëlle et al., 2008; Poletti et al., 2011; Yakob and Clements, 2013; Robinson et al., 2014) or ZIKV (Kucharski et al., 2016; Champagne et al., 2016; Nishiura et al., 2010; Chowell et al., 2016). The uncertainty regarding several parameters, such as the under-reporting ratio and the rate of asymptomatic individuals, have made it difficult to assess the attack rates in naive populations, the relative transmissibility of the viruses, and whether meteorological conditions may alter these parameters.

Here, building on common aspects in location and vectorial transmission, we study in detail the main factors that impacted disease spread. With this objective, we propose a joint model of Chikungunya and Zika transmission based on the time-dependent susceptible-infectious-recovered (TSIR) framework (Perkins et al., 2015), using data from nine distinct territories in French Polynesia and the French West Indies, where both diseases circulated

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3.3 Commentaires et perspectives

Chapitre 4

Utiliser les ressemblances entre les maladies transmises par *Aedes* pour améliorer les outils de prédiction épidémique

4.1 Guider les interventions de prévention et de contrôle en situation d'épidémie émergente

4.1.1 Approches classiques en prédiction

4.1.2 Récents développements : les challenges

4.2 Améliorer les prédictions à la phase précoce d'une épidémie de Zika grâce aux données historiques sur la transmission du Chikungunya

4.2.1 Résumé de l'article en français

4.2.2 Article : Riou, Poletto, Boëlle, Improving early epidemiological assessment of emerging *Aedes*-transmitted epidemics using historical data

Improving early epidemiological assessment of emerging *Aedes*-transmitted epidemics using historical data

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Abstract

Model-based epidemiological assessment is useful to support decision-making at the beginning of an emerging *Aedes*-transmitted outbreak. However, early forecasts are generally unreliable as little information is available in the first few incidence data points. Here, we show how past *Aedes*-transmitted epidemics help improve these predictions. The approach was applied to the 2015-2017 Zika virus epidemics in three islands of the French West Indies, with historical data including other *Aedes*-transmitted diseases (Chikungunya and Zika) in the same and other locations. Hierarchical models were used to build informative *a priori* distributions on the reproduction ratio and the reporting rates. The accuracy and sharpness of forecasts improved substantially when these *a priori* distributions were used in models for prediction. For example, early forecasts of final epidemic size obtained without historical information were 3.3 times too high on average (range: 0.2 to 5.8) with respect to the eventual size, but were far closer (1.1 times the real value on average, range: 0.4 to 1.5) using information on past CHIKV epidemics in the same places. Likewise, the 97.5% upper bound for maximal incidence was 15.3 times (range: 2.0 to 63.1) the actual peak incidence, and became much sharper at 2.4 times (range: 1.3 to 3.9) the actual peak incidence with informative *a priori* distributions. Improvements were more limited for the date of peak incidence and the total duration of the epidemic. The framework can adapt to all forecasting models at the early stages of emerging *Aedes*-transmitted outbreaks.

Author summary

In December, 2015, *Aedes* mosquito-transmitted Zika outbreaks started in the French West Indies, about two years after Chikungunya epidemics, spread by the same mosquito, hit the same region. Building on the similarities between these epidemics – regarding the route of transmission, the surveillance system, the population and the location – we show that prior information available at the time could have improved the forecasting of relevant public health indicators (i.e. epidemic size, maximal incidence, peak date and epidemic duration) from a very early point. The method we describe, together with the compilation of past epidemics, improves epidemic forecasting.

Introduction

Model-based assessments must be done in real time for emerging outbreaks: this was the case in recent years for MERS-CoV in the Middle East [1–3], Ebola virus in West

4.3 Commentaires et perspectives

Chapitre 5

Conclusions

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