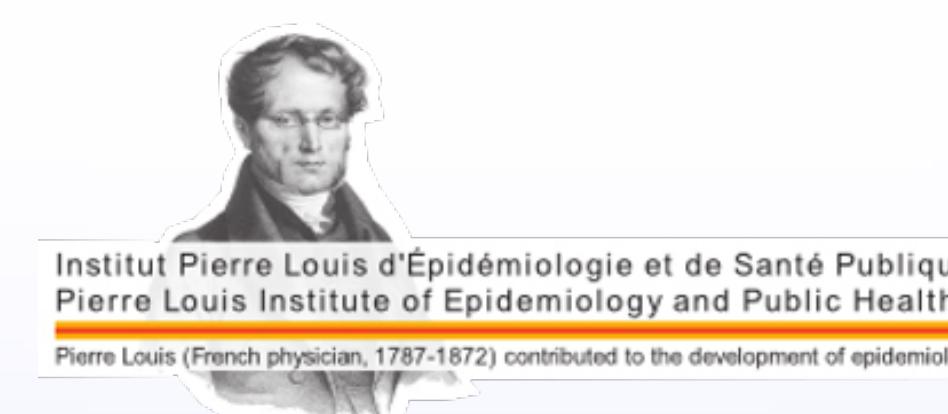


# A comparative analysis of Chikungunya and Zika transmission

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## Introduction

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.

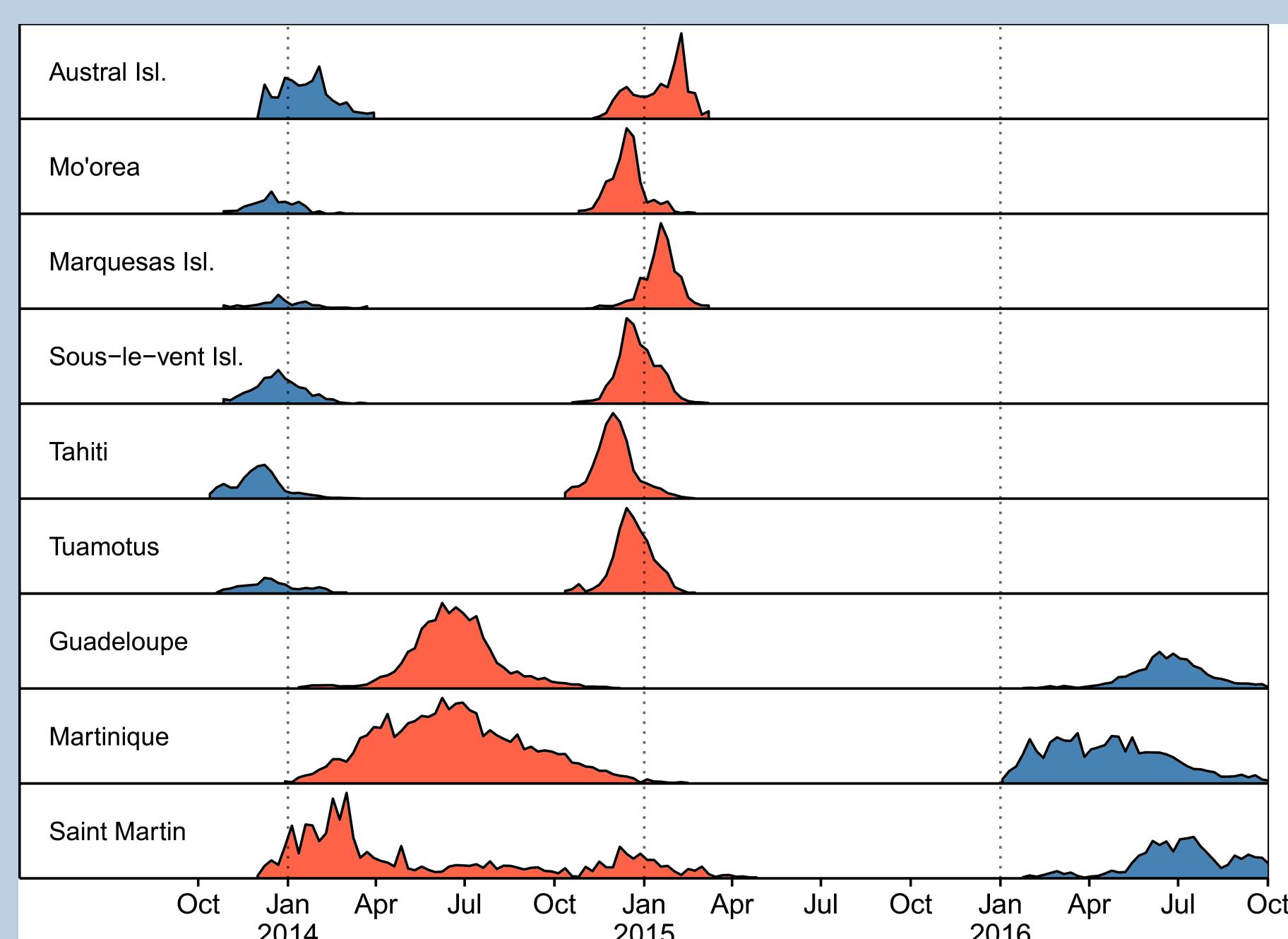


Figure 1: Profiles of CHIKV (red) and ZIKV (blue) outbreaks in the nine territories under study.

## Materials and Methods

We analysed the Zika and Chikungunya epidemics occurring between 2013 and 2016 in 6 islands of French Polynesia and 3 islands of the French West Indies by fitting weekly incidence data with a common hierarchical transmission model. The two main components of this analysis were:

- (1) a mechanistic reconstruction of the distribution of the serial interval of the diseases including the influence of temperature;
- (2) a hierarchical TSIR model<sup>1</sup> for the generation of observed secondary cases  $O_{ijt}$  accounting for the respective effect of virus  $j$ , location  $j$  and weather conditions at time  $t$ :

$$O_{ijt} \sim \text{NegBin} \left( R_{0ijt} \frac{S_{ijt}}{N_j} \sum_{n=1}^5 w_{it,n} O_{ij,t-n}, \phi \right)$$

where: the transmission parameter  $R_{0ijt}$  depends on an island-specific random intercept, on the relative effect of ZIKV on transmission (compared to CHIKV), and possibly on weather conditions;  $S_{ijt}/N_j$  is the proportion of susceptible at time  $t$  (which depends on cumulative incidence until date  $t-1$  and on  $\rho_{ij}$ , the reporting rate parameter, also with an island-specific random component); and  $\sum_{n=1}^5 w_{it,n} O_{ij,t-n}$  summarizes exposure to infectious mosquitoes at time  $t$  (i.e. observed incidence in the last five weeks weighted by the discretized distribution of the serial interval). The model was implemented in Stan<sup>2</sup> using weakly-informative priors.

## References

- <sup>1</sup> A. Perkins et al. Estimating Drivers of Autochthonous Transmission of Chikungunya Virus in its Invasion of the Americas. *PLoS Curr*, 7, February 2015.
- <sup>2</sup> B. Carpenter et al. Stan: a probabilistic programming language. *Journal of Statistical Software*, 2015.

## Results: model fit and parameter estimates

The baseline model (without the influence of weather) captured the essential characteristics of the outbreaks, as shown in Fig. 2.

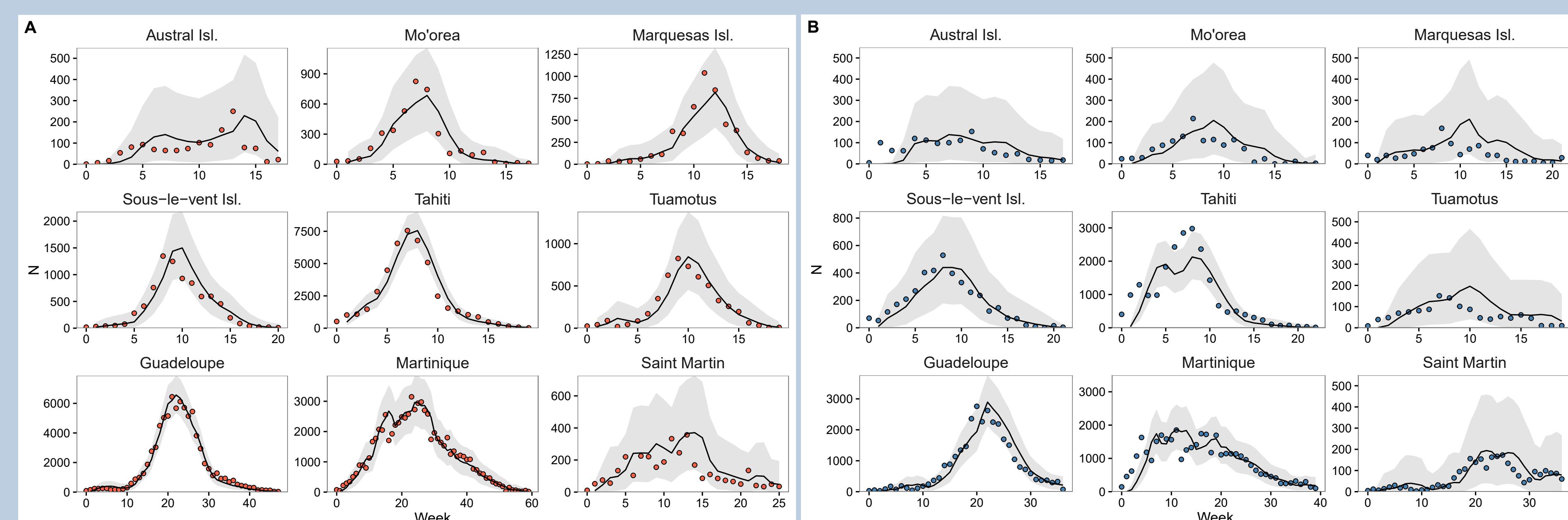


Figure 2: Observed numbers of clinical cases (circles) for CHIKV (panel A) and ZIKV (panel B), and corresponding predicted values from the baseline model.

The island-averaged reporting rate  $\bar{\rho}$  differed according to the disease, estimated at 40% [29%; 54%] for CHIKV and 19% [12%; 28%] for ZIKV. The transmissibility ratio between ZIKV and CHIKV was 1.04 [95%CI: 0.97; 1.13], showing no significant difference in transmissibility between the diseases. Indeed, the island-averaged reproductive ratio was  $\bar{R}_0 = 1.80$  [1.54; 2.12] for CHIKV and 1.88 [1.59; 2.22] for ZIKV. The variance for the random island effects in reporting and in transmission were different from 0, indicating heterogeneity between locations (Fig. 3).

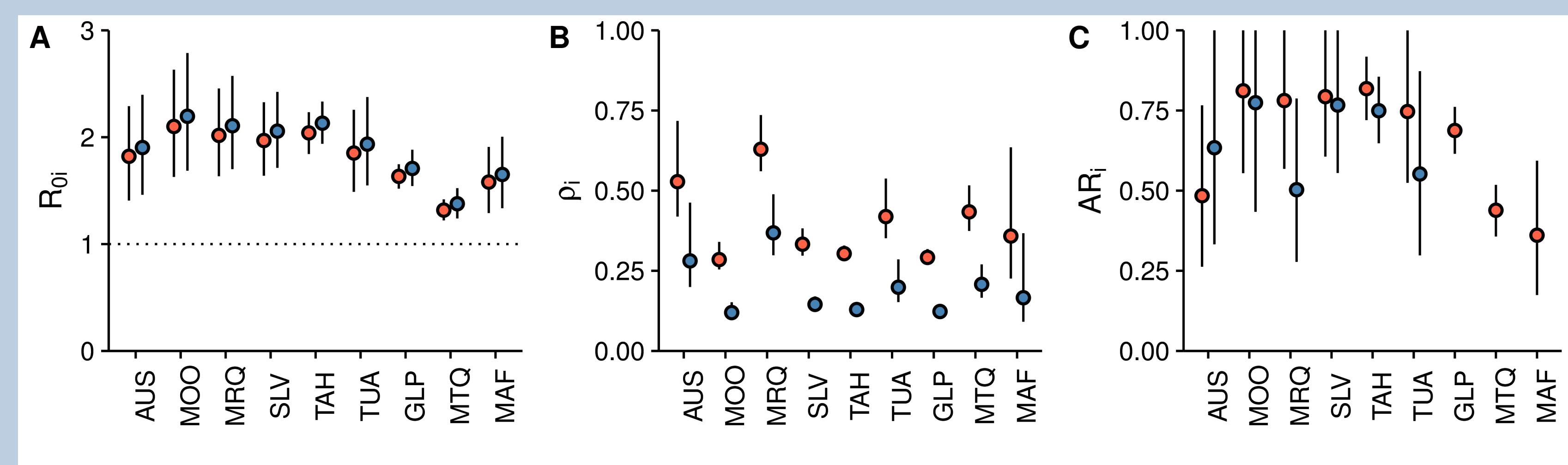


Figure 3: (A) Island-specific basic reproduction ratio  $R_{0i}$ ; (B) reporting rate  $\rho_i$ ; and (C) final attack rate  $AR_i$  for CHIKV (red) and ZIKV (blue).

## Results: weather conditions and disease transmission

We added all combinations of precipitation and temperature on transmission with a lag of up to 8 weeks, and compared models using LOOIC values. Including precipitation in transmission improved the fit (LOOIC difference = -18, standard error = 17), while the effect of temperature was not meaningful (LOOIC difference = +2, se = 13). The effect of local precipitation showed a marked pattern on transmission, with higher rainfall decreasing transmission one to two weeks later and then increasing transmission four to six weeks afterwards (Fig. 4).

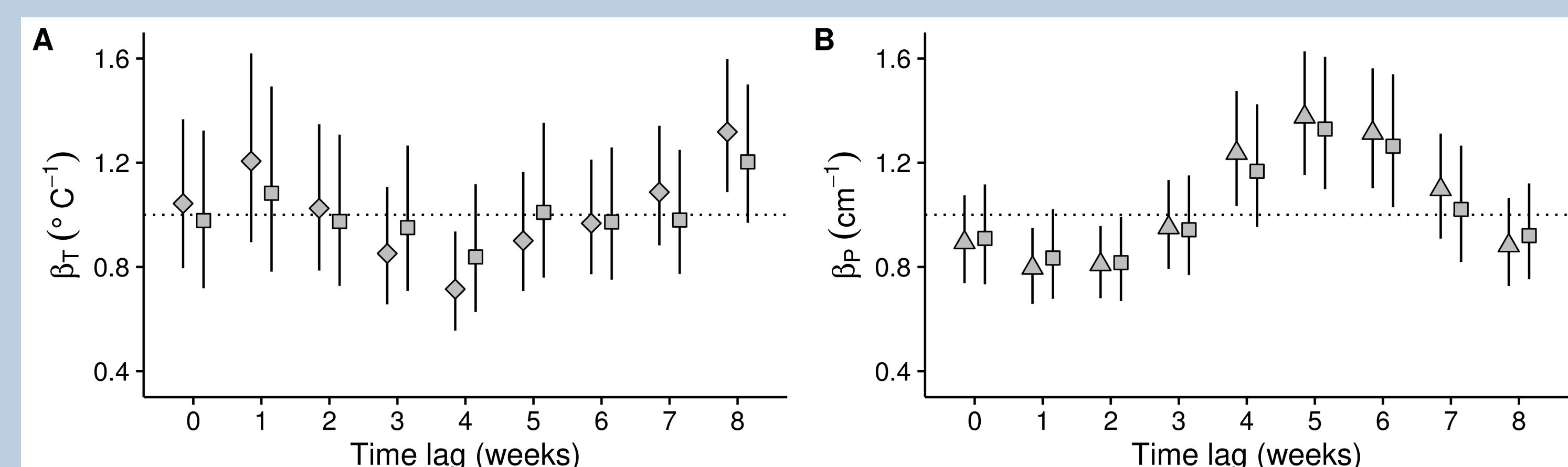


Figure 4: Effect of a variation of 1°C of the weekly-averaged mean temperature (panel A) and of 1 cm of the weekly-averaged precipitation (panel B) on transmissibility according to a given time lag.

## Conclusions

We jointly analysed epidemics of Zika and Chikungunya in nine island territories to quantify the respective roles of the virus, the territory and the weather conditions in the outbreak dynamics. We showed that Chikungunya and Zika have similar transmissibility when spreading in the same location. Accounting for the level of precipitation improved the modelling of the epidemic profiles, notably for the outbreaks of Zika in Tahiti and of Chikungunya in the Sous-le-vent Islands. The absence of effect of temperature can be related to the low variability of temperature in these areas. Eventually, different probabilities of developing symptoms for the two diseases translated in substantial differences in reporting rates. The present study provides valuable information for the assessment and projection of *Aedes*-borne infections spread. In addition, it introduces an approach that can be adopted in other comparative analyses involving multiple arboviruses and locations.