Epidemics 5 (2013) 146–156

Contents lists available at ScienceDirect

Epidemics

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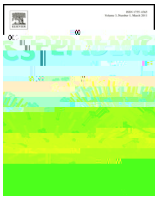

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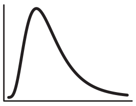
**Table 1**
List of epidemics used in the smallpox outbreak models.

| Epidemic | Date(s) | Population size |
|---|---|---|



affected transmission dynamics, like that seen in measle epidemics (Finkenstädt and Grenfell, 2000; Rohani et al., 2002).

The data consist of 13 monthly time series, with total number of individuals who died during each month of an outbreak in each community. The data for the populations of European/African descent are counts of smallpox deaths only (Creighton, 1891; Anderson, 1918), while the Native-American population data include all deaths during the outbreak (Fenn, 1999). Given the low background mortality rates, and the fact that not all smallpox deaths were recorded in the registries (Fenn, 1999), in addition to the relatively short duration of each outbreak, the assumption that deaths in the Native-American populations were entirely due to smallpox

**Table 2**

Comparison of the fit of nine candidate models for estimating $R_0$ from the smallpox epidemics using BIC scores, ΔBIC, and BIC weights.

| Model (summary) | *K* | BIC | ΔBIC | BIC weights |
|---|---|---|---|---|
| 1. Native-American and European/African | | | | |

**Table 3**
Prior and posterior parameter estimates with 95% posterior credible intervals (CI) for three of the candidate models.

| Parameter | Models | | | |
|---|---|---|---|---|
| | Prior | Model 1 – $R_{\mathbf{0},EA/NA}$ | Model 3 – $R_{i,EA/NA}$ | Model 5 – $R_{i,EA/NA}$ spatial autocorrelation |
| $R_{0,EA}$ | 4 (0.7, 23.7) | 6.2 (5.18, 7.68) | 6.7 (3.17, 14.43) | 6.8 (2.96, 15.21) |
| $R_{0,NA}$ | 4 (0.7, 23.7) | 8.0 | | |

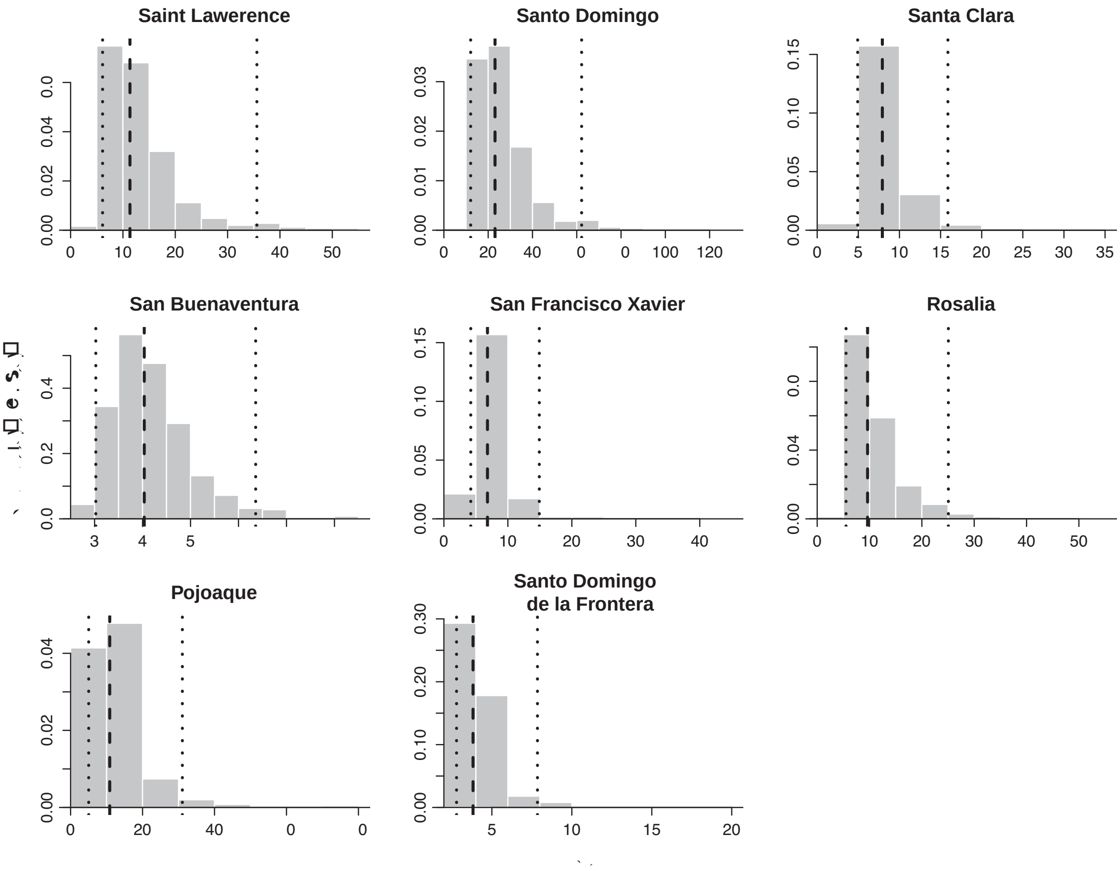


**Fig. 5.** Posterior distribution of the basic reproductive rates $R_i$ for Native-American populations. The dashed line represents the posterior median and the dotted lines include the 95% posterior credible intervals. Note the

(0.38, [−0.296, 0.785]). Whether this pattern arose from differences between the population types or due to overall population size remains to be seen. However, it does suggest a population size relationship may exist for smallpox. For other diseases, such as measles, there may be no such relationship (Bjørnstad et al., 2002).

In the best-fit model, each population has an $R_i$ value that is drawn from a global $R_0$ distribution. Allowing for this hierarchical structure slightly increases the overall uncertainty in global $R_0$ for populations of European/African descent, but it results in a better fit of the model to the data. In particular, the improved likelihood under the $R_i$ model (Model 3) is at least partly due to the improved fit of the European/African population data sets. By contrast, allowing for spatial correlation in $R_i$ values for the Native-American populations did not improve model fit and the corresponding models had little relative support (Table 2). This was also true for any of the models in which we assumed that there was heterogeneity between individuals in the risk of contracting smallpox. Given

Dushoff, J., 1999. Host heterogeneity and disease endemicity: a moment-based approach. Theoretical Population Biology 56, 325–335.

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