



A spatially distributed model for the future evolution of the current Haiti cholera outbreak

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As a major cholera epidemic spreads through Haiti, and the figures of the infection, up to the end of 2010, climb to 146,000 cases and 3,300 deaths, the development of models to track and predict the evolution of the outbreak in order to guide the allocation of medical supplies and staff is gaining notable urgency. However, early data exhibit a clear signature of the spatial spreading of the disease, which started from the Artibonite river and has progressively involved all the surrounding departments, that is not completely integrated into baseline cholera models. We propose here an epidemic model that accounts for the dynamics of susceptible and infected individuals as well as the redistribution of *Vibrio cholerae*, the causative agent of the disease, among different human communities in a spatially explicit framework. Spreading mechanisms include the diffusion of pathogens in the aquatic environment and the dissemination due to the movement of asymptomatic hosts. The model capability to reproduce the spatial-temporal features of the epidemic up to date grants robustness to the foreseen future development. We estimate that the aggregated number of cases for the whole country should peak around mid January. During this month the epidemic should mainly involve the "Ouest" (Port-au-Prince) department while it should be fading out in the northern regions. The development of these models might also help to evaluate the effectiveness of alternative intervention strategies. Our results show that vaccination strategies (using an estimate of 300,000 doses currently available) at this stage of the epidemic would have negligible impact. We also evaluate the effect of sanitation strategies like clean water supply and educational campaigns which prove still able, however feasible, to significantly weaken the force of the infection.