Appendix A - MCMC Algorithm

A Markov model was developed in which patients were either susceptible (KPC-negative) or colonized (KPC-positive). We looked at floors as separate entities. Patients had a probability f to be colonized on admission. Transmission could occur at rate β, dependent on the number of colonized patients on the floor: $\beta I / N$, with I representing the number of colonized patients on the floor, and N the total number of patients on the floor. Furthermore, transmission of KPC could happen with a constant background rate α, accounting for the endogenous route and transmission from the environment, other wards, visitors, et cetera. Hence, the probability for a susceptible patient to not acquire KPC during a day was $e^{-(\alpha+\beta I / N)}$ and the probability to acquire colonization was then $1-e^{-(\alpha+\beta I / N)}$.

For most patients we had a culture result on the day of admission and a follow-up screening culture. However, since screening cultures are imperfect, we also estimated the sensitivity φ, allowing for false negative results. Specificity was assumed to be 100%. Furthermore, we knew on which floor and in which room patients were during each day of their entire length of stay. For modeling convenience, we assumed that microbiological culture results became available at a fixed time of the day, e.g., at noon, and that admission and discharge occurred at the same fixed time.

The model was developed within a Bayesian framework. We used a data-augmented Markov chain Monte Carlo (MCMC) method with Metropolis-Hastings algorithm to analyze the data and to update α and β. This method allowed for unobserved colonization times. The method was similar to the method described by Worby et al.[29]

First, (uninformative) prior distributions were set for the parameters in the model. For α and β an exponential distribution was chosen, which is an uninformative prior when the parameter of the exponential distribution is chosen to be very small (here, 0.001). In this way, in the most relevant area from 0 to 1 this was almost a constant. For f and φ an uninformative beta distribution was taken as prior distribution with both parameters of the distribution set to 1. f and φ can only adopt values between 0 and 1 and the beta distribution has the same property.

Parameters α and β were updated using a Metropolis-Hastings algorithm. At each iteration, a new value for α was proposed, based on the current sample value plus a value sampled from a normal distribution with mean 0 and standard deviation 0.01. If the change in the posterior likelihood (the likelihood multiplied with the prior distribution) was either in the right direction or the change was smaller than the number sampled from an exponential distribution with parameter 1, the new value for α was accepted and used in the next iteration, otherwise it was rejected and the current value was reused. The same was done for updating β.

The sensitivity φ can be sampled from a from a beta distribution with parameters (a + TP, b + FN) where TP is the number of true positive cases in the augmented data, and FN is the number of false negative cases. Likewise, the admission prevalence f can be sampled from a beta distribution with parameters (a + PA, b + NA). Here, PA is the number of patients who were positive on admission in the augmented data, and NA the number of patients who were negative on admission.

After updating the model parameters, the augmented data were updated. Both the day of colonization and the status on admission (colonized or uncolonized) were updated. Three moves were defined within another Metropolis-Hastings algorithm and these moves could be made with equal probability. See Worby et al.[29] for the exact formulas.

- Move a colonization time: the colonization time is moved to another day, either earlier or later. This could also mean that the patient is now assumed to be colonized on admission or was assumed to be, but not is now assumed to have acquired colonization later. The colonization time of patients with a positive admission screening cannot be moved.

- Add a colonization time: add a colonization time for a patient who was previously assumed to be negative, but now assumed to be either positive on admission or to have acquired colonization.

- Remove a colonization time: remove a colonization time for a patient who was previously assumed to be positive for KPC. Colonization times of patients who have a positive culture result cannot be removed.

When a move was rejected, the augmented dataset was unchanged. In the next step the posterior likelihood was updated. If the change in the posterior likelihood was either in the right direction or the change was smaller than the number sampled from an exponential distribution with parameter 1, then the new colonization times were accepted. Otherwise the current times were used in the next iteration.