Supporting Information 1. Calculations.

Differential equations

The model used (Figure S1) can be described by the differential equations below. In the equations, \( W \) represents the number of uncolonized hospitalized patients (K- C-), \( X \) the number of hospitalized patients colonized with \( E.\ coli_{OXA-48} (K- C+) \), \( Y \) the number of hospitalized patients colonized with \( K.\ pneumoniae_{OXA-48} (K+ C-) \), and \( Z \) the number of hospitalized patients colonized with both (K+ C+). Since the hospital population size is constant, \( Z = N - (W + X + Y) \).

\( Ah \) to \( Dh \) represent the same types of individuals in the community with a high risk of readmission: \( Ah \) represents the number of uncolonized individuals (K- C-), \( Bh \) the number of individuals colonized with \( E.\ coli_{OXA-48} (K- C+) \), \( Ch \) the number of individuals colonized with \( K.\ pneumoniae_{OXA-48} (K+ C-) \), and \( Dh \) the number of individuals colonized with both (K+ C+). \( Al \) to \( Dl \) represent the same types of individuals in the community with a low risk of readmission.

\[
\frac{dW}{dt} = -\alpha W + \phi_1 Ah + \phi_2 Al - \beta_K \frac{Y + Z}{N} W - \beta_C \frac{X + Z}{N} W \\
\frac{dX}{dt} = -\alpha X + \phi_1 Bh + \phi_2 Bl + \beta_C \frac{X + Z}{N} W - \beta_K \frac{Y + Z}{N} X - \lambda_{CK} X \\
\frac{dY}{dt} = -\alpha Y + \phi_1 Ch + \phi_2 Cl + \beta_K \frac{Y + Z}{N} W - \beta_C \frac{X + Z}{N} Y - \lambda_{KC} Y \\
\frac{dAh}{dt} = \alpha W - \phi_1 Ah - \chi Ah + \gamma_C Bh + \gamma_K Ch \\
\frac{dBh}{dt} = \alpha X - \phi_1 Bh - \chi Bh + \gamma_K Dh - \gamma_C Bh - \lambda_{CK} Bh \\
\frac{dCh}{dt} = \alpha Y - \phi_1 Ch - \chi Ch + \gamma_K Dh - \gamma_C Ch - \lambda_{KC} Ch \\
\frac{dDh}{dt} = \alpha Z - \phi_1 Dh - \chi Dh - \gamma_K Dh - \gamma_C Dh + \lambda_{CK} Bh + \lambda_{KC} Ch \\
\frac{dAl}{dt} = \chi Ah - \phi_2 Al + \gamma_C Bl + \gamma_K Cl \\
\frac{dBl}{dt} = \chi Bh - \phi_2 Bl + \gamma_K Dl - \gamma_C Bl - \lambda_{CK} Bl \\
\frac{dCl}{dt} = \chi Ch - \phi_2 Cl + \gamma_K Dl - \gamma_C Cl - \lambda_{KC} Cl \\
\frac{dDl}{dt} = \chi Dh - \phi_2 Dl - \gamma_K Dl - \gamma_C Dl + \lambda_{CK} Bl + \lambda_{KC} Cl 
\]
Figure S1. OXA-48 model.
(a) Model of population flow
(b) Within-host model in the hospital
(c) Within-host model in the community with a high risk of readmission
(d) Within-host model in the community with a low risk of readmission

K- C-: bla_{OXA-48} negative (both *K. pneumoniae* and *E. coli* are susceptible)
K- C+: *E. coli*_{OXA-48} (K. pneumoniae is susceptible)
K+ C-: *K. pneumoniae*_{OXA-48} (E. coli is susceptible)
K+ C+: *K. pneumoniae*_{OXA-48} and *E. coli*_{OXA-48}
Calculation of $R_0$ and $R_A$

$R_0$ was calculated using the methodology described in the book of Diekmann et al. [18] First, the transition matrix $\Sigma$ was determined. In $\Sigma$, all changes of states except for cross-transmissions are incorporated:

$$
\begin{pmatrix}
-a - \lambda_{CK} & 0 & 0 & \phi_1 & 0 & 0 & \phi_2 & 0 & 0 \\
0 & -a - \lambda_{KC} & 0 & 0 & \phi_1 & 0 & \phi_2 & 0 & 0 \\
\lambda_{CK} & \lambda_{KC} & -a & 0 & 0 & \phi_1 & 0 & 0 & 0 \\
\alpha & 0 & 0 & -\gamma_{KC} - \lambda_{CK} - \phi_1 - \chi & 0 & \gamma_K & 0 & 0 & 0 \\
0 & \alpha & 0 & 0 & -\gamma_K - \lambda_{KC} - \phi_1 - \chi & \gamma_K & 0 & 0 & 0 \\
0 & 0 & \lambda_{CK} & \lambda_{KC} & -\gamma_{KC} - \phi_1 - \chi & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & \chi & 0 & -\gamma_{KC} - \lambda_{CK} - \phi_2 & 0 & \gamma_K & 0 \\
0 & 0 & 0 & 0 & \chi & 0 & 0 & -\gamma_K - \lambda_{KC} - \phi_2 & \gamma_K \\
0 & 0 & 0 & 0 & 0 & \chi & \lambda_{CK} & \lambda_{KC} & -\gamma_{KC} - \phi_2 & \gamma_K
\end{pmatrix}
$$

Next, minus the inverse of $\Sigma (-\Sigma^{-1})$ is calculated. The elements of $-\Sigma^{-1}$ have a clear interpretation: the element $-(\Sigma^{-1})_{ij}$ is the expected time that an individual will spend in state $i$, given that it is currently in state $j$.

Thereafter, the next-generation matrix (NGM) can be calculated, using the cross-transmission parameters ($\beta_K$ and $\beta_C$). Element $ij$ of the NGM can be interpreted as the expected number of new colonizations starting in state $i$, caused by an infected individual in state $j$. Since a newly colonized person always starts his ‘colonized life’ in state $X$ or $Y$, the NGM can be reduced to:

$$
\begin{pmatrix}
\beta_C \ast (-\Sigma^{-1})_{11} + (-\Sigma^{-1})_{31} & \beta_C \ast (-\Sigma^{-1})_{12} + (-\Sigma^{-1})_{32} \\
\beta_K \ast (-\Sigma^{-1})_{21} + (-\Sigma^{-1})_{31} & \beta_K \ast (-\Sigma^{-1})_{22} + (-\Sigma^{-1})_{32}
\end{pmatrix}
$$

$R_0$ is then the dominant eigenvalue of the NGM. An explicit expression for $R_0$ in terms of the model parameters does exist, but is too large to write down here.
For the calculation of $R_A$ we only focused on the hospital dynamics (Figure S1B), ignoring readmissions. The transition matrix $\Sigma$ is then:

$$
\begin{pmatrix}
-a - \lambda_{CK} & 0 & 0 \\
0 & -a - \lambda_{KC} & 0 \\
\lambda_{CK} & \lambda_{KC} & -a
\end{pmatrix}
$$

Using the same methodology as described above, the following NGM is obtained:

$$
\begin{pmatrix}
\beta_C & \beta_{C\lambda_{KC}} \\
\frac{\beta_C}{a} & \frac{\beta_{C\lambda_{KC}}}{a^2 + a\lambda_{KC}} \\
\frac{\beta_K}{a^2 + a\lambda_{CK}} & \frac{\beta_K}{a}
\end{pmatrix}
$$

Again, $R_A$ is the dominant eigenvalue of this NGM.
Calculation colonization duration with HGT

In order to determine the influence of HGT on the duration of colonization with \(K.\ pneumoniae_{OXA-48}\) or \(E.\ coli_{OXA-48}\), we focused on the situation outside the hospital, where loss of colonization is possible (Figure S2). We will elaborate on the calculation of \(K.\ pneumoniae\); the calculation for \(E.\ coli\) is analogous.

The mean duration of colonization with \(K.\ pneumoniae_{OXA-48}\), as calculated from the data, is \(1/\gamma_k\). If HGT is included, then an individual can ‘start’ being colonized in state \(K+C^-\), or in state \(K+C^+\). \(T\) is defined as the mean duration of colonization with \(K.\ pneumoniae_{OXA-48}\) given a start in \(K+C^-\) and \(U\) is defined as the mean duration of colonization with \(K.\ pneumoniae_{OXA-48}\) given a start in \(K+C^+\). The following expressions can then be derived for \(T\) and \(U\):

\[
T = \frac{1}{\gamma_k + \lambda_{KC}} + \frac{\lambda_{KC}}{\gamma_k + \lambda_{KC}} U
\]

\[
U = \frac{1}{\gamma_k + \gamma_c} + \frac{\gamma_c}{\gamma_k + \gamma_c} T + \frac{\gamma_k}{\gamma_k + \gamma_c} \frac{\lambda_{CK}}{\gamma_c + \lambda_{CK}} U
\]

Solving these equations for \(T\) and \(U\) gives the following expression for \(T\):

\[
T = \frac{\gamma_c^2 + \lambda_{CK} \lambda_{KC} + \gamma_c \left( \gamma_k + \lambda_{CK} + \lambda_{KC} \right)}{\gamma_c \gamma_k \left( \gamma_c + \gamma_k + \lambda_{CK} + \lambda_{KC} \right)}
\]

The ratio of the duration of colonization with \(K.\ pneumoniae_{OXA-48}\) with and without HGT can then be calculated as:

\[
\frac{T}{\gamma_k T} = \gamma_k T
\]

**Figure S2. OXA-48 model (community).**

Representation of the model used to calculate the influence of HGT on the duration of colonization.