Bacterial filamentation accelerates colonization of adhesive spots embedded in biopassive surfaces

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Supplementary information

Computational Model

Geometry and initial conditions. The substrate is described as a 2D lattice, where each lattice site $s_{ij}$ can be either adhesive ($s_{ij}=1$) or nonadhesive ($s_{ij}=0$). The bacterial colony is described as a superimposed lattice of the same size, where each lattice site $c_{ij}$ is either occupied by a single bacterium ($c_{ij}=1$), by a part of a filament ($c_{ij}=2$), or empty ($c_{ij}=0$). For the bridging simulations, the substrate had a size of 50x100 with two round adhesive spots of diameter 10 and edge-to-edge distance of 20. The initial conditions were defined as five isolated bacteria adhering to the lower of the two adhesive spots. For the large area simulations, the surface had a size of 280x390 with a hexagonal array of adhesive spots of diameter 10 and an edge-to-edge distance of 19, to minimize rounding errors on the discrete lattice. Here, the initial conditions were defined such that five adhesive spots in the second row from the bottom were colonized by five isolated bacteria each and separated by one uncolonized spot each.

Growth without filamentation. In each simulation step, one occupied lattice site in the colony is selected and its direction of growth is chosen randomly as one of the four lattice directions (no diagonal growth). The selected cell is duplicated by shifting the part of the colony in the direction of growth by one lattice site, so that as a result the number of occupied lattice sites is increased by one. The duration of the simulation step in units of doubling time is defined as $1/n$, where $n =$ number of occupied sites at the previous time step. This way, the entire colony has doubled its size on average after one doubling period.

The following rules were implemented:

Filamentation. When a single bacterium is selected to divide, it turns into a filament with a probability $P_{\text{filament}}$, implemented by changing the value of the selected lattice site and its neighbor in direction of growth from cell (1) to filament (2). Filaments can only grow along their long axis. When a filament grows, it divides with a probability $P_{\text{divide}}$. Filament division is implemented by changing the value of the
selected lattice site on the filament from 2 (filament) to 1 (single cell), leaving behind two filament fragments.

Surface Detachment. Single bacteria (but not filaments) at the edge of the colony that are not on an adhesive area are washed away by flow with a probability $P_{\text{wash-off}}$. The flow direction is always set from bottom to top in the x-y surface plane. Edge cells at the left and right side of the colony that have no top and bottom neighbours are therefore more likely to detach than edge cells at the sides facing the flow direction which have no left and right neighbours. This asymmetry in the wash-off probability leads to an asymmetric shape of the colony under flow and is implemented in the model by an anisotropy factor $A$, which was set to 1/5 for cells facing the flow and 1 for side-edge cells in order to reproduce the observed colony shapes. Higher flow magnitude leads to higher wash-off probability. Since the relationship between flow rate and detachment probability is not exactly known, we describe the effect of flow magnitude on $P_{\text{wash-off}}$ by introducing a unitless flow factor $F$. In every simulation step, all edge cells are identified and removed with a probability $P_{\text{wash-off}} \leq 1$ that is proportional to $A$ and $F$, multiplied by the duration $\Delta t$ of the current timestep:

$$P_{\text{wash-off}} = \max(A \cdot F \cdot \Delta t, 1)$$

Supplementary Figures

Figure S1. Type 1 fimbriated $E. coli$ adhering to differently patterned RNaseB surfaces after 9 hours of surface colonization under 2.4 ml/min flow. The bacterial surface colonization was strongly dependent on the geometries of the micropatterns, which consisted of 10 µm round adhesive spots with spot-to-spot distances of (a) 5 µm; (b) 10 µm and (c) 20 µm. Even after 9 hours under high flow, no bacteria were observed to adhere to the PLL-g-PEG passivation regions for the patterns with 10 and 20 µm distance indicating that the passivation was stable over time.
Figure S2. Comparison of the length doubling time for non-filamentous and filamentous E. coli as measured from time-lapse movies. For filamentous E. coli, the pole-to-pole length of filaments was measured every 3 minutes over 2 hours. For non-filamentous E. coli the pole-to-pole lengths of all the offspring of an individual bacterium were measured every 3 minutes for 2 hours and summed up. The length doubling time was calculated from an exponential fit of the pole-to-pole lengths. Shown are the mean and standard deviations (n=10). Two-independent sample two-sided t-test was performed (α=0.05) and no significant difference (n.s.) was found between the length doubling times. Population variances were not significantly different as tested by a two-sided F-test (α=0.05).