

Supporting Information

for

Patterned Biofilm Formation Reveals a Mechanism for Structural Heterogeneity in Bacterial Biofilms

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Table S1. List of *E. coli* strains and plasmids used in this study.

	Genotype	Characteristics	Source/References
<i>E. coli</i> Strains			
RP437	Wild type [<i>thr-1</i> (Am) <i>leuB6</i> <i>his-4</i> <i>metF159</i> (Am) <i>eda-50</i> <i>rpsL1356</i> <i>thi-1</i> <i>ara-14</i> <i>mtl-1</i> <i>xyl-5 tonA31 tsx-78 lacY1 F</i>]	Wild type strain for biofilm study	[1]
RP3087	RP437 (<i>motB</i>) <i>580</i>	Motility mutant (point mutation in <i>motB</i>)	[2]
RP4979	RP437 <i>eda</i> ⁺ Δ <i>m43-10(cheY)</i>	Chemotaxis mutant	[3, 4]
RP3525	RP437 Δ <i>tap-365-4</i> Δ(<i>lac</i>) <i>U169</i> <i>thr</i> ⁺ <i>leu</i> ⁺	Chemotaxis mutant	[5, 6]
KX1485	RP437 <i>luxS</i> ::Cm ^r	Quorum sensing mutant, unable to synthesize AI-2	[7, 8]
BL-19	RP437 Δ <i>motB</i>	Motility mutant (deletion mutation of <i>motB</i>)	[2]
Plasmids			
pRSH109	Amp ^r , <i>gfp</i>	Label cells with constitutive GFP	This study
pDsRed	Amp ^r , <i>rfp</i>	Label cells with constitutive RFP	Life Technologies Inc., Carlsbad, CA, USA
pRHG01	<i>luxS</i> ⁺ , Amp ^r	pCR2.1®-TOPO® with <i>luxS</i> gene controlled by its native promoter	This study

Table S2. Pearson correlation coefficients between Cell Cluster Interaction Index (CII) and pattern size.

Distance (D, μm)	Pattern Size (W, μm)	Correlation Coefficient (r)
10	$\leq 20 \mu\text{m} \times 20 \mu\text{m}$	-0.45 ^{**}
	$>20 \mu\text{m} \times 20 \mu\text{m}$	0.93 ^{**}
15	$\leq 20 \mu\text{m} \times 20 \mu\text{m}$	-0.23 [*]
	$>20 \mu\text{m} \times 20 \mu\text{m}$	0.94 ^{**}
20	$\leq 20 \mu\text{m} \times 20 \mu\text{m}$	-0.20
	$>20 \mu\text{m} \times 20 \mu\text{m}$	0.93 ^{**}
30	$\leq 20 \mu\text{m} \times 20 \mu\text{m}$	-0.20
	$>20 \mu\text{m} \times 20 \mu\text{m}$	0.93 ^{**}
40	$\leq 20 \mu\text{m} \times 20 \mu\text{m}$	-0.25 [*]
	$>20 \mu\text{m} \times 20 \mu\text{m}$	0.92 ^{**}
50	$\leq 20 \mu\text{m} \times 20 \mu\text{m}$	-0.47 ^{**}
	$>20 \mu\text{m} \times 20 \mu\text{m}$	0.95 ^{**}

* P < 0.05.

** P < 0.0001.

Table S3. Biofilm formation of *E. coli* RP437 and its isogenic mutants on patterned surfaces.

Genotype	Attachment on patterns	Interaction among cell clusters
Wild-type	Fully covered patterns	Normal interaction
$\Delta cheY$	Barely covered	No interaction
Δtap	Barely covered	No interaction
<i>motB</i> point mutant	Relatively normal cell clusters (slightly less coverage than the wild type)	Significantly reduced interaction
$\Delta motB$	Barely covered	No interaction
$\Delta luxS$	Relatively normal cell clusters (slightly less coverage than the wild type)	Significantly reduced interaction

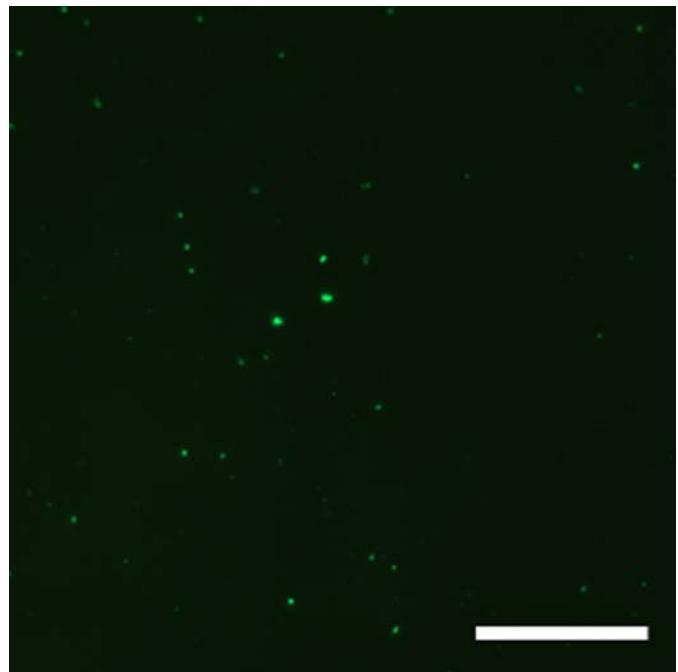


Figure S1. Attachement of *E. coli* BL-19 (RP437 $\Delta motB$) on a surface with 20 $\mu\text{m} \times 20 \mu\text{m}$ SAM patterns after 24 h of incubation. Bar = 50 μm .

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