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Supporting Material

Cell-Size Homeostasis and the Incremental Rule in a Bacterial Pathogen

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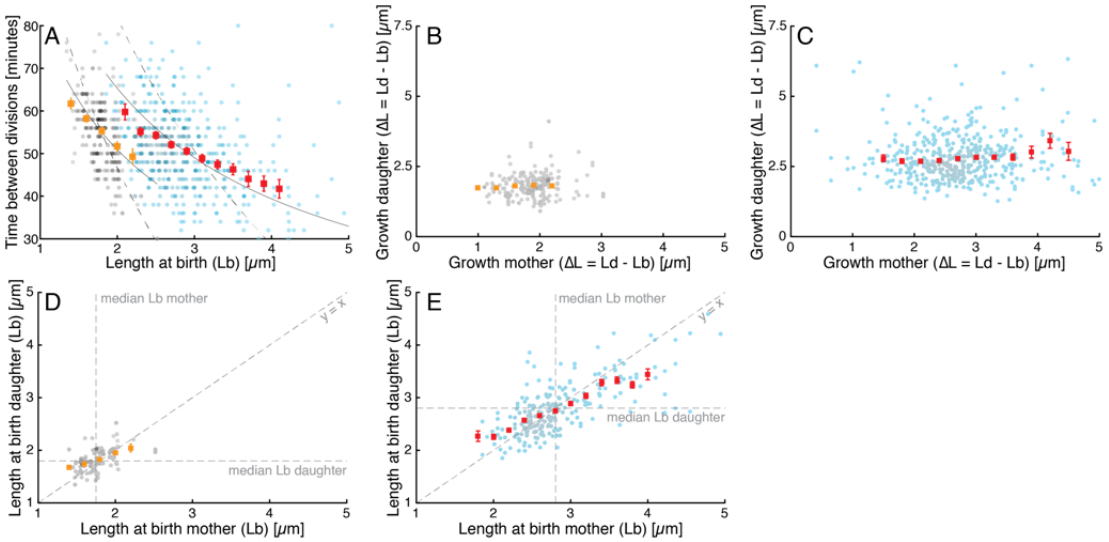

Figure S1: *P. aeruginosa* and the *frik* mutant obey the incremental rule of cell size regulation. For all plots, wt is plotted in black and orange, whereas *frik* is plotted in cyan and red. (A) There is a negative correlation between Lb and ΔT. Solid lines indicate best fits to the incremental model and dash lines indicate best fit to the "sizer" model. (C-D) There is no correlation between Δ^{mother} and $\Delta^{daughter}$. (E-F) $L_b{}^{mother}$ and $L_b{}^{daughter}$ are correlated with a slope of 0.5.

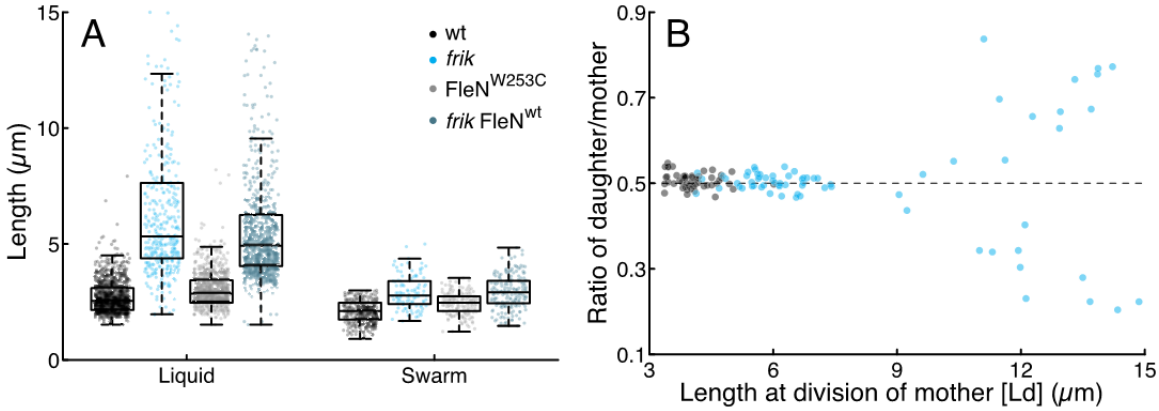

Figure S2: Cell size in *Pseudomonas aeruginosa* and its elongated mutant *frik*. (A) Cell length distributions from exponentially growing liquid cultures and swarms. In liquid culture, *frik* and *frik* $FleN^{wt}$ are longer than wt and $FleN^{W253C}$ (N = 423-897, p <<0.001 by Kruskal-Wallis). *Frik* and *frik* $FleN^{wt}$ are longer than the other two strains when quantifying at swarming edges, as determined by Kruskal-Wallis test (p<<0.001, n = 107-376). (B) Cell division is very symmetric for both wild type (black) and frik cells (cyan), with the exception of the filamentous cell (>10 μm).

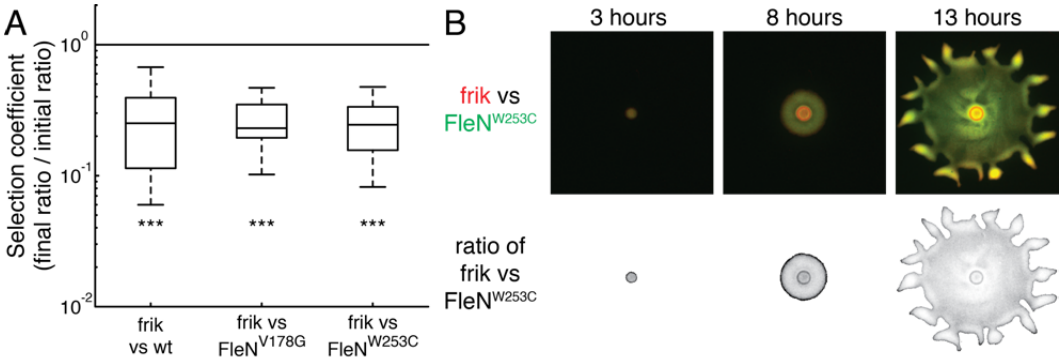

Figure S3: *frik* has a swarming advantage over wild type and other hyperswarmers. (A) Selection coefficients (defined as final ratio over initial ratio) of various clones against *frik*. The horizontal line represents the neutral selection coefficient of 1; anything below that means that the respective clone loses against frik. The (inverse) selection coefficient of *frik* versus wt was previously published [21]. (B) *Frik* segregates at the edge of a swarm from early on. The top row represents fluorescence images and the bottom row is the calculated ratio of *frik* versus FleN^{W253C} based on the fluorescence channels.

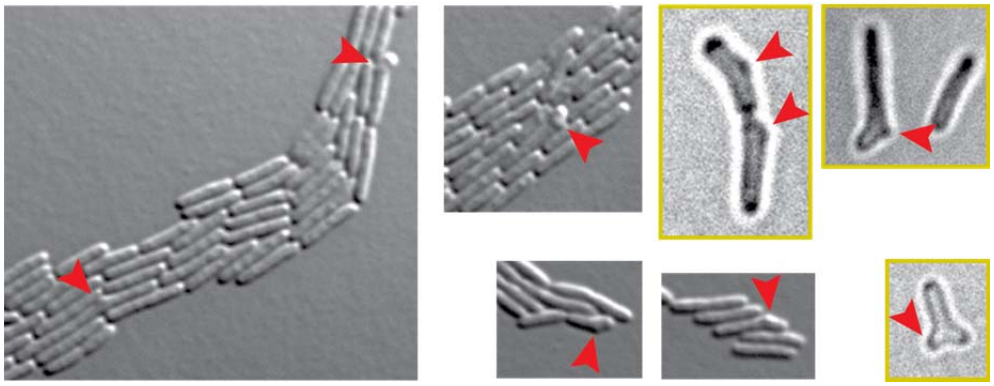

Figure S4: *frik* occasionally shows membrane instabilities. Microscopy pictures taken from either agar pad or liquid culture cells (the latter are outlined in dark yellow) for *frik* shows various cells with membrane instabilities (indicated with red arrowheads).

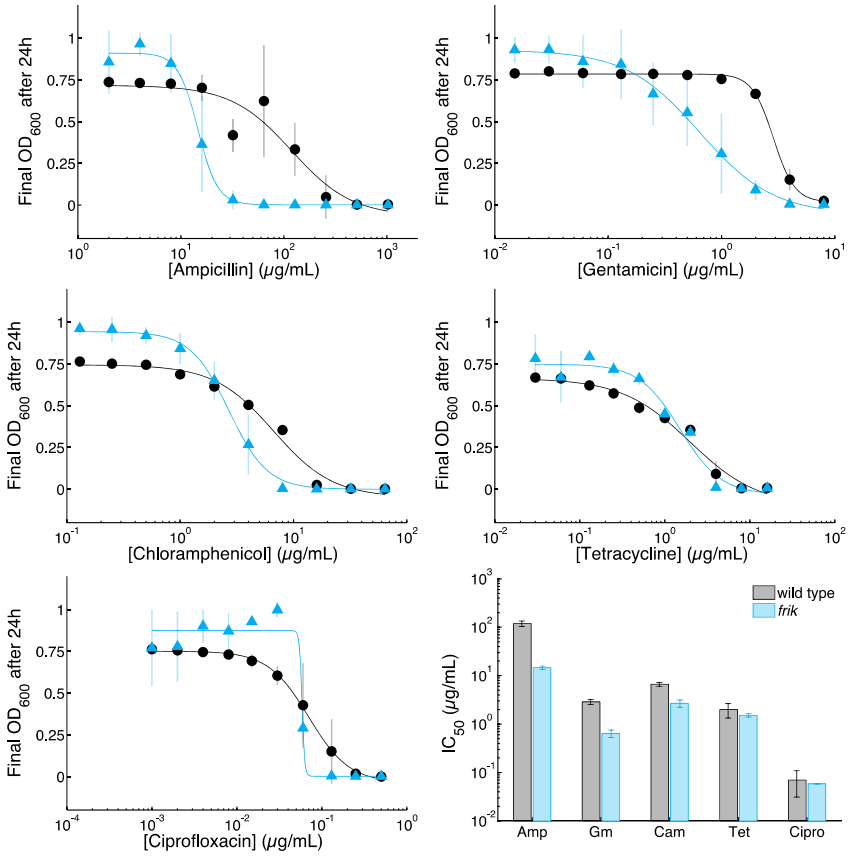

Figure S5: *frik* is sensitive to ampicillin, gentamicin, and chloramphenicol, but not tetracycline, or ciprofloxacin. Minimal inhibitory concentration (MIC) measurements for (A) ampicillin, (B) gentamicin, (C) chloramphenicol, (D) tetracycline, and (E) ciprofloxacin. Black circles represent wild type, cyan triangles represent frik. Mean and standard deviation are plotted. The lines indicate the model fit with which the IC_{50} was determined. (F) The determined IC_{50} values for the various antibiotics with 95%-CI.

wt PA14_65570 amino acid sequence

MTRPTSVKPDNFFLLLFRALRQRRVPIALRLASHSLILVALALLIYAWVMGMQFRQAMQQQADALGQSLITQTAASATELLVSNDILSLNVLLNNLVKNPLVAHAAIYSIDQRILAEAGSRPK(
ATEGLYSTPITFQEVIAGHLRISLDMQQFQQPMMISLQSMGLISLILLILALYFSLRLGRQISTPLLQLRVWLRDPDNPAPGAELQNELGDLARDLEERLVPEKPPAPEPEEAPLPQNFDDILI
ADLRSRKVEASAFEEDDIPLGDALLDETKPVEFTSIDEDPLDQDAFDENGAEAGDQPAAPAAAREPQHSAVLAIQLGAQEQLRRLPRSRLVDLLQRYRDCLEQAARQYKGSLHTLSDGGSLILI
NRADYLTNALCCGELMRALGHALQIEVADSGITLQLQLGLSLGEDLSEQTQADLLLNETVQNALALNQHSRNLLLVERSIADDAVVRERARIRAIASPEGACCVERLLEPYPSMLERQLARMHI

Figure S6: *frik* mutants have a mutation in a putative transmembrane domain in gene PA14_65570. The amino acid sequence encoded by gene PA14_65570 has two predicted transmembrane domains (in red). The 9 base pair deletion found in the *frik* mutant would cause the loss of 3 amino acid residues in one of the transmembrane domains (shown in a rectangle).