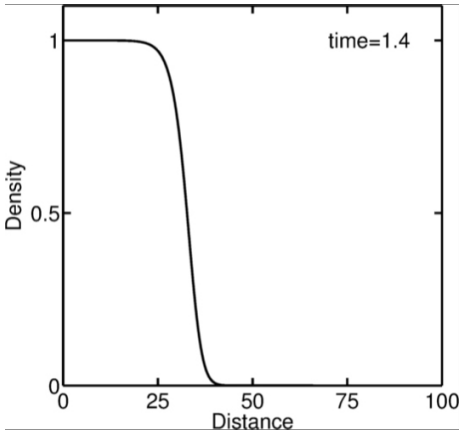
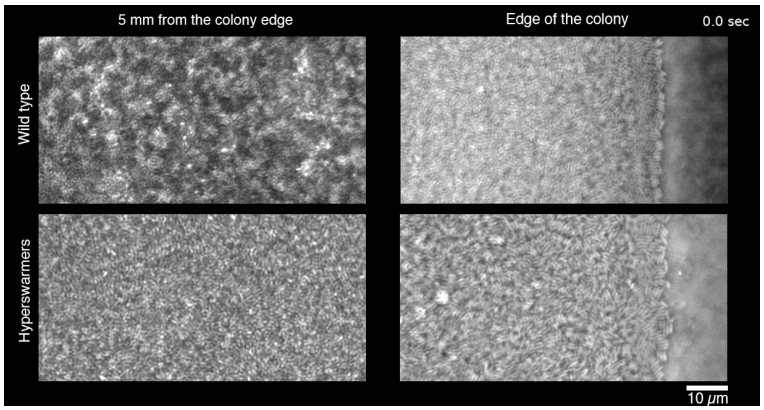
Figure legends

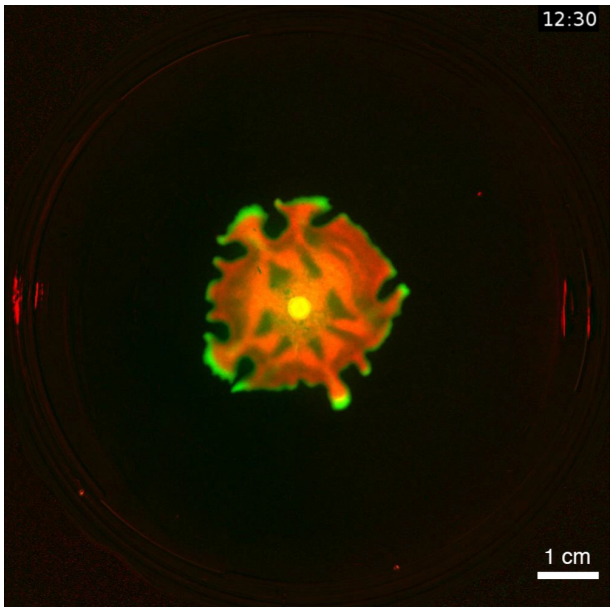


Video 1: Traveling wave solution of the F-KPP equation, advancing at the speed $v = 2\sqrt{(rD)}$.

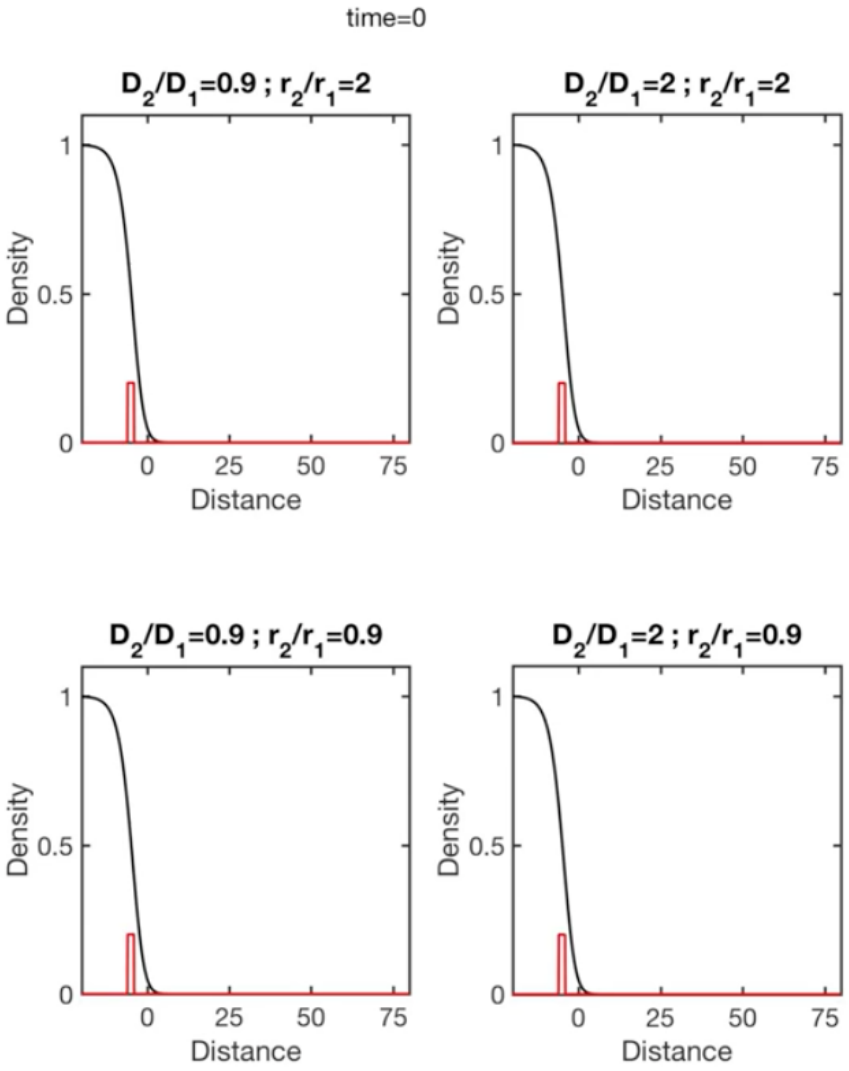
Online figure legends



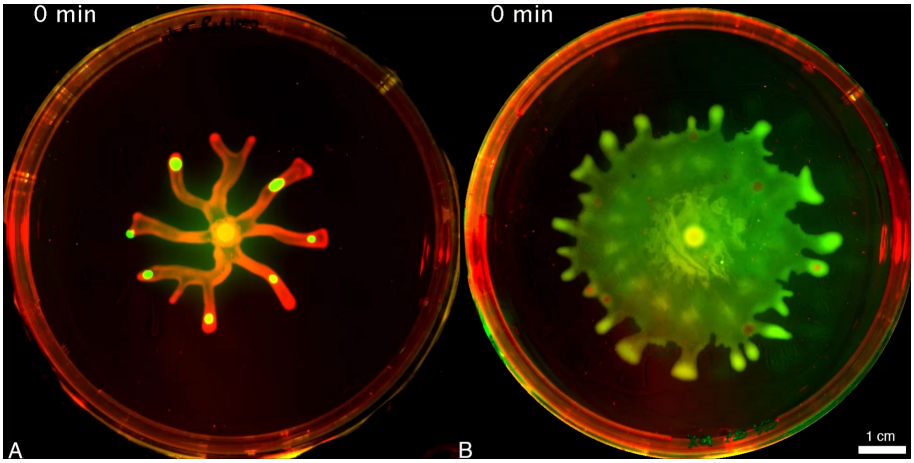
Video 2: Phase-contrast video-microscopy images of *P. aeruginosa* swarming colonies. Top row: *P. aeruginosa* wild-type colony. Bottom row: Hyperswarmer mutant colony. Left side: 5 mm from the edge. Right side: edge of the swarming colony. Note the active turbulence patterns displayed by the hyperswarmer colony, whereas wild-type cells seem more static.



Video 3: Fluorescence video of a swarming colony formed by a mixed population *P. aeruginosa* wild type / Hyperswarmers (initial ratio 10:1). *P. aeruginosa* wild-type constitutively expresses DsRed (red). Hyperswarmer mutant constitutively expresses GFP (green).



Video 4: Introduction experiments performed in numerical simulations. The black line represents the density of species 1. The red line represents species 2, implanted at t=0 at the distance L=5 from the edge.



Video 5: Implantation experiments. A: Hyperswarmers (green) are implanted into wild type (red) swarming branches. B: Wild type (red) are implanted into a hyperswarmer colony.

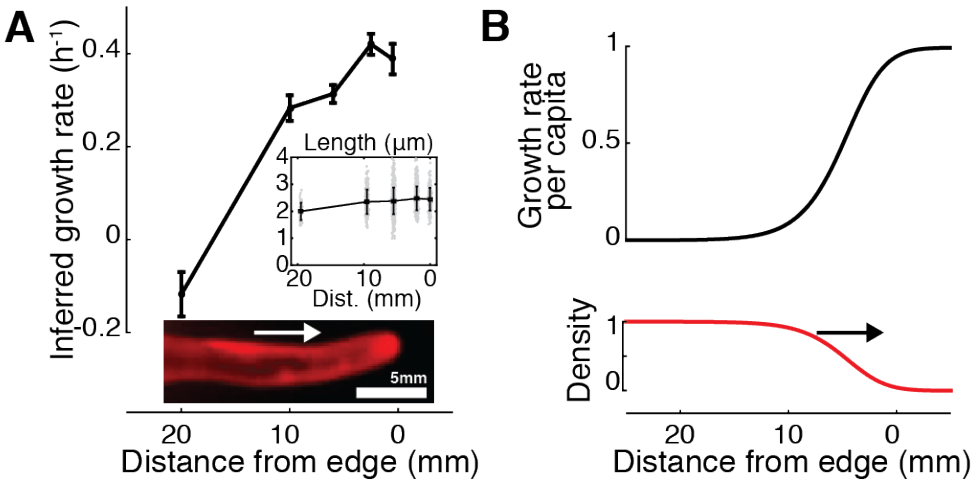


Figure S1: Bacterial swarming can be modeled by FKPP equation where growth is greatest at the edge. A: The length of each bacterium is converted into a growth rate, using the results a previous study (Deforet et al. 2015) linking cell length to growth rate, where this fit is obtained: $L = 2.18 + 0.89\mu$ (L is the length of a bacterium and μ is its growth rate in casa-aminoacids). Errors bars are standard error of the mean ($N \simeq 100$). Inset: Cells length measured by fluorescence microscopy and automated image analysis. Error bars are standard deviations. Data points are randomly distributed around each value of distance for better visualization. The picture represents a wildtype branch growing on agar gel. The white arrow depicts the direction of expansion. B: The growth rate per capita ($r(1-u)$, with $r = 1$, black line), and the density (u) of the population simulated by the FKPP equation (black line). The black arrow depicts the direction of expansion.

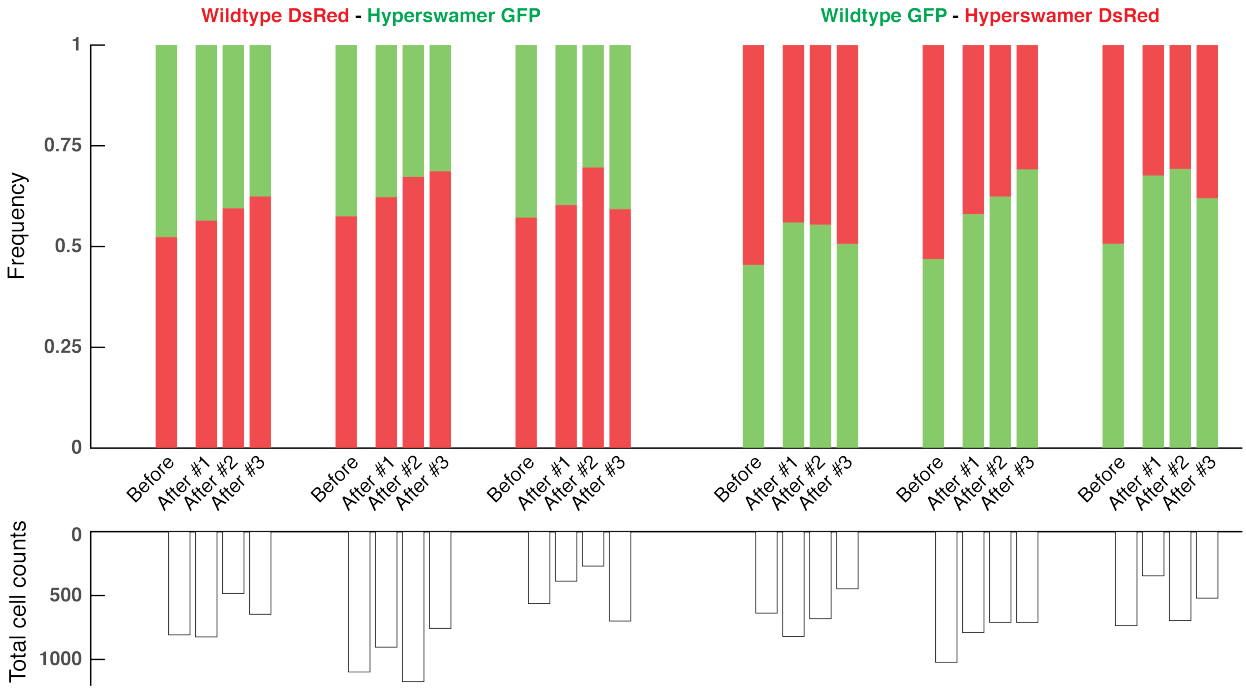


Figure S2: Wild type *P. aeruginosa* outcompetes its hyperswarmer mutant on a plate when the spatial structure is suppressed. Swarming plates (0.5% agar) are inoculated with a loan of a mixed population of wildtype and hyperswarmers (approximate initial ratio 1:1) and incubated for 4 hours of incubation at 37°C. The ratios of wild type before and after the competition are estimated using CFUs counting. GFP and DsRed fluorescent proteins (constitutively expressed) are used to take apart the two bacterial strains. Swapped experiments confirm that despite toxicity of DsRed proteins, wild type cells outcompete hyperswarmers ($p = 5.8 \times 10^{-5}$, generalized linear model for binomial data). N=3 biological replicates x 3 technical replicates per color combination.

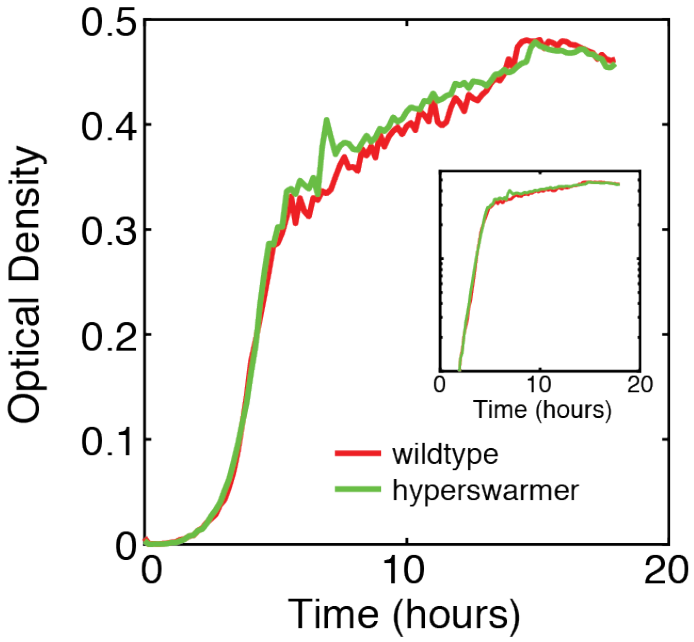


Figure S3: Wild type *P. aeruginosa* and its hyperswarmer mutant have comparable carrying capacities. The bacterial density is measured in a plate scanner as optical density. Inset: Growth curves in logarithmic scale.

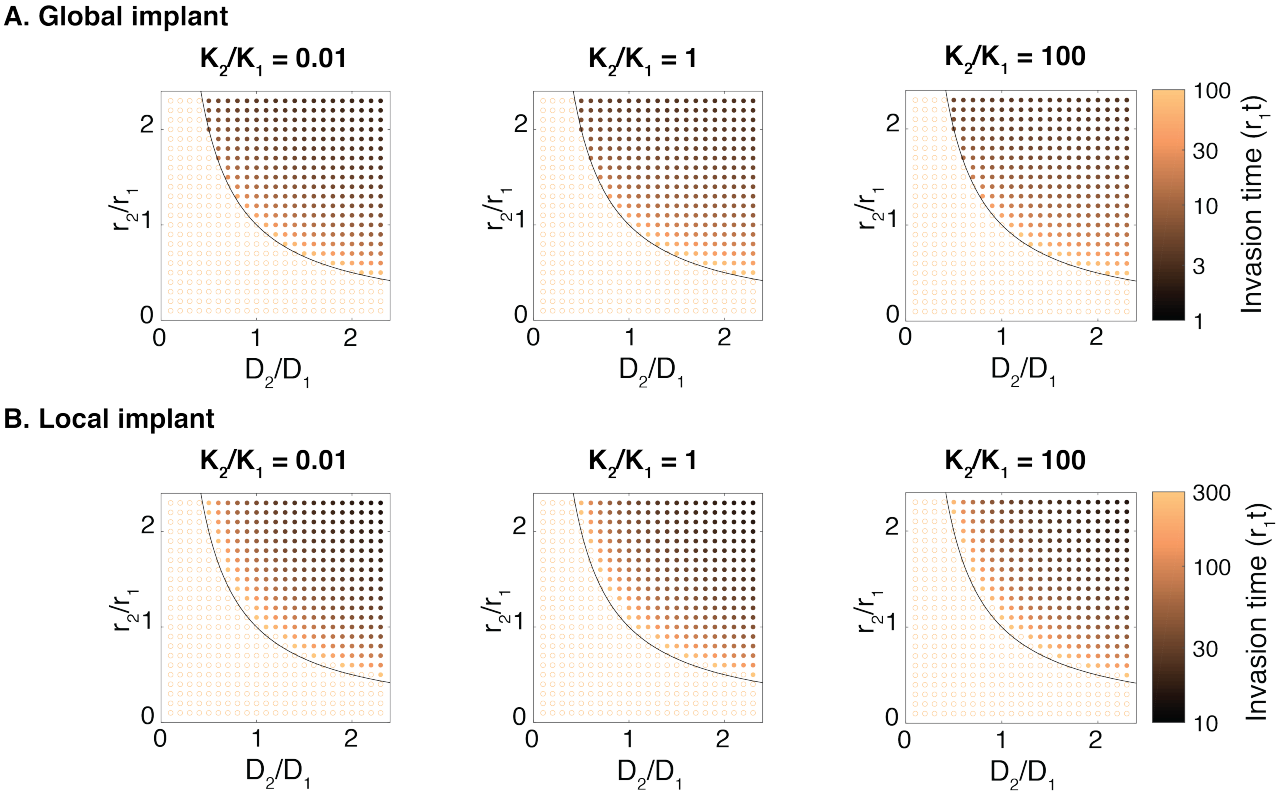


Figure S4: Different carrying capacities do not affect the evolutionary processes. A: Species 2 is introduced globally with $u_2 = u_1/100$. B: Species 2 is introduced locally with $u_2(x) = 0.2$ where $-16 < x < -14$ (with the edge of the population being at $x = 0$).

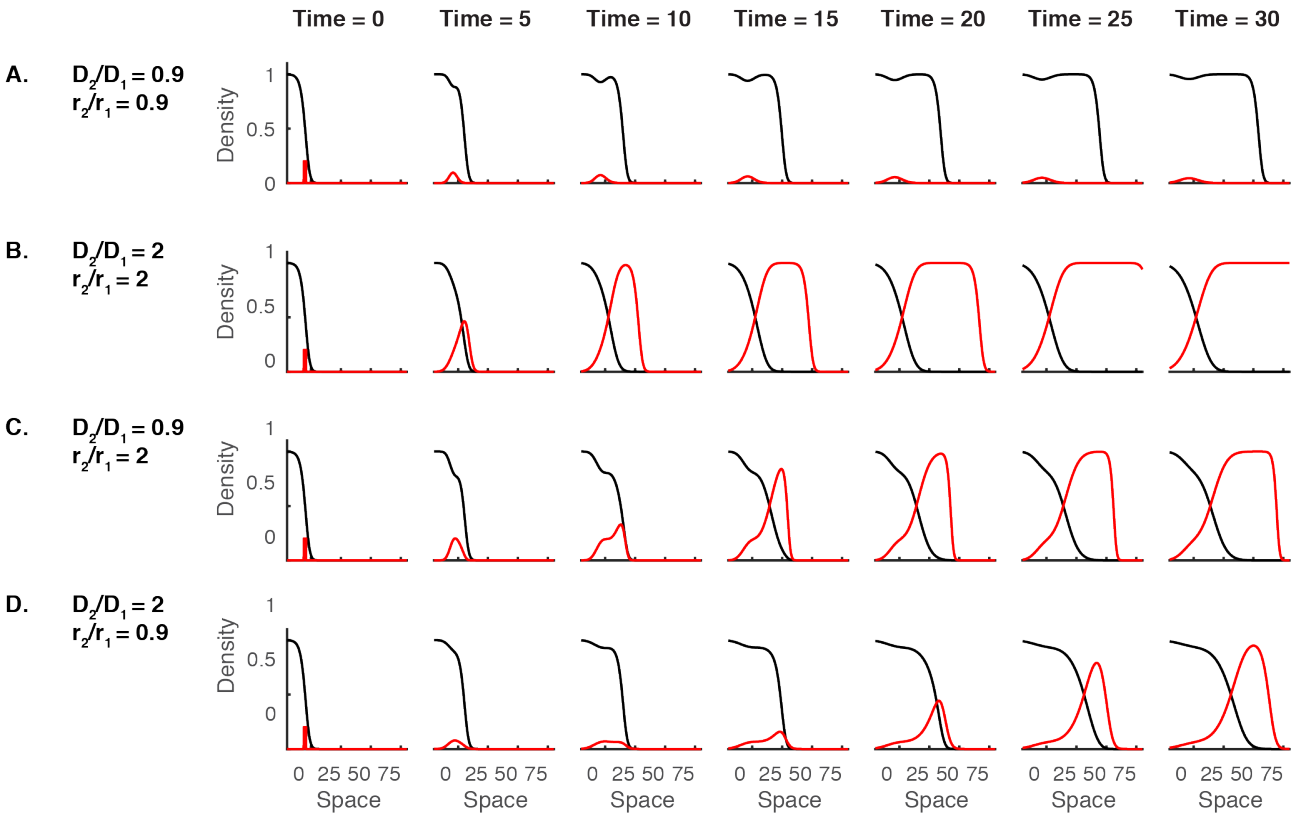


Figure S5: Snapshots of takeover (or no takeover) after introduction of species 2. A: No takeover case with lower growth and lower dispersal. B: Takeover case with greater growth and greater dispersal. C: Takeover case with greater growth but lower dispersal. D: Takeover case with lower growth but greater dispersal. See also Video 4.

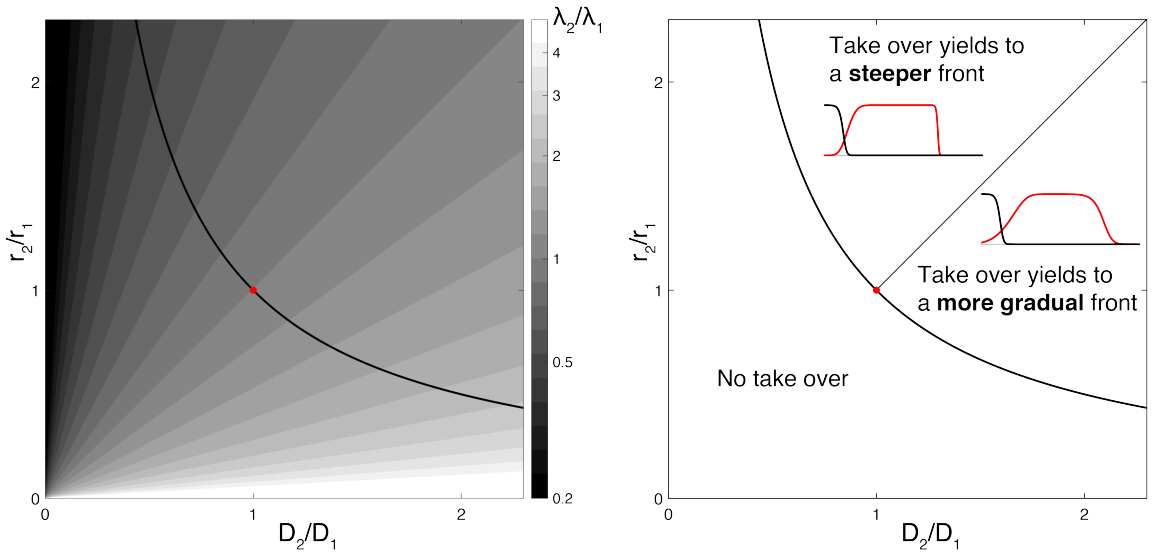


Figure S6: The lengthscale of the front is modified when another phenotype takes over. The lengthscale of the front ($\lambda = \sqrt{D/r}$) depends on the phenotype of the population sitting at the front. Here is a map of the change of lengthscale (λ_2/λ_1) in the space (r,D). The red dot depicts the phenotype of the ancestral (reference) species. The black line represents the success rule. Note the chosen colormap is not smooth to highlight the shape of the map. Right panel: a chart representing domains of takeover with a steeper front and with a more gradual front.

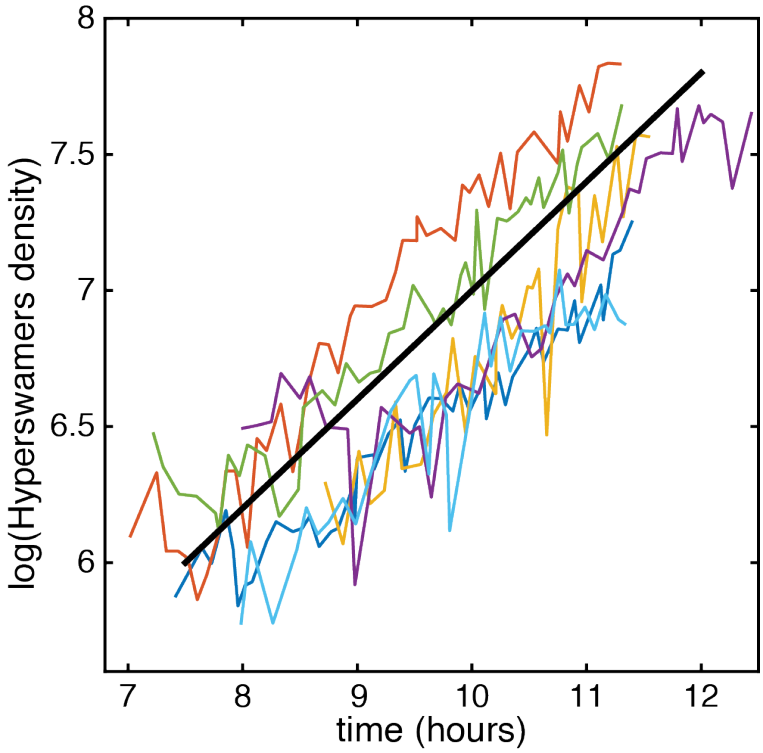


Figure S7: Hyperswarmers density dynamics at the edge of the colony, from Video 1. The dynamics of the density of hyperswarmers is governed by the eigenvalue $\tilde{r}_{\max} = r_2 - \frac{v_1^2}{4D_2}$, in the limit of low density. Experimental parameters (Table 1) yields to $\tilde{r}_{\max} = 0.4\ \mathrm{h}^{-1}$. The black line is a visual guide with a rate of $0.4\ \mathrm{h}^{-1}$. The average slope of the six curves is $0.39\ \pm 0.08 \mathrm{h}^{-1}$ (Standard deviation).

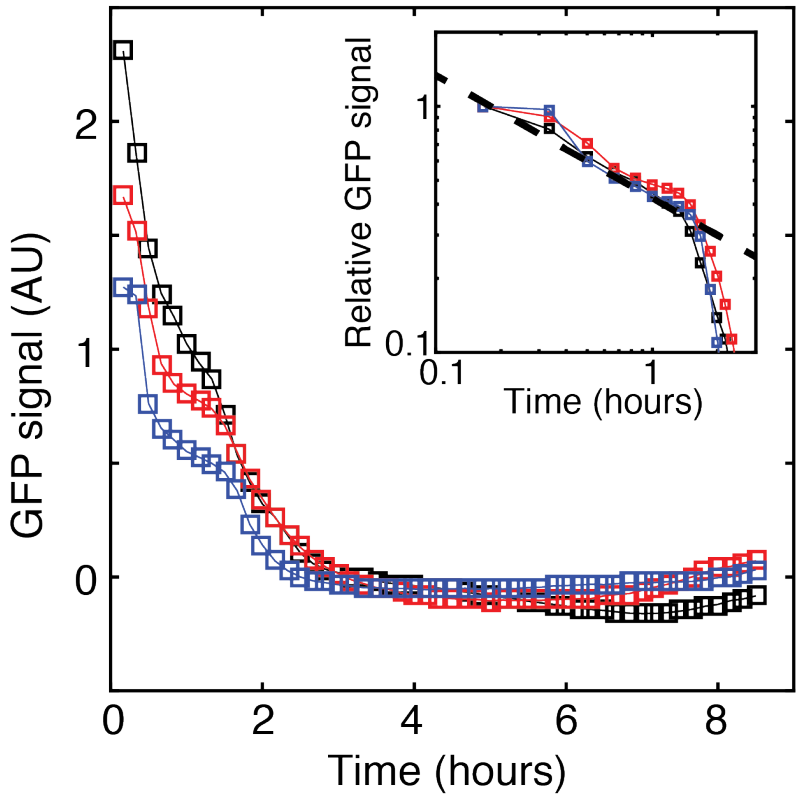


Figure S8: Hyperswarmers introduced into a wildtype swarming colony spread by diffusion. Three representative implant sites are analyzed. The data represents the average GFP signal at the site of introduction. GFP signal 1 cm closer to the center of the colony is used for background correction. Data extracted from video 5A. Inset: the first 1.5 hours can be modeled by a diffusive decay. The dashed line is the prediction from 1D diffusion decay, using $D = 4\,\mathrm{mm}^2/\mathrm{h}$ and a inoculum size of 3 mm ($C \sim \frac{C_{\max} L}{\sqrt{4\pi D t}}$).

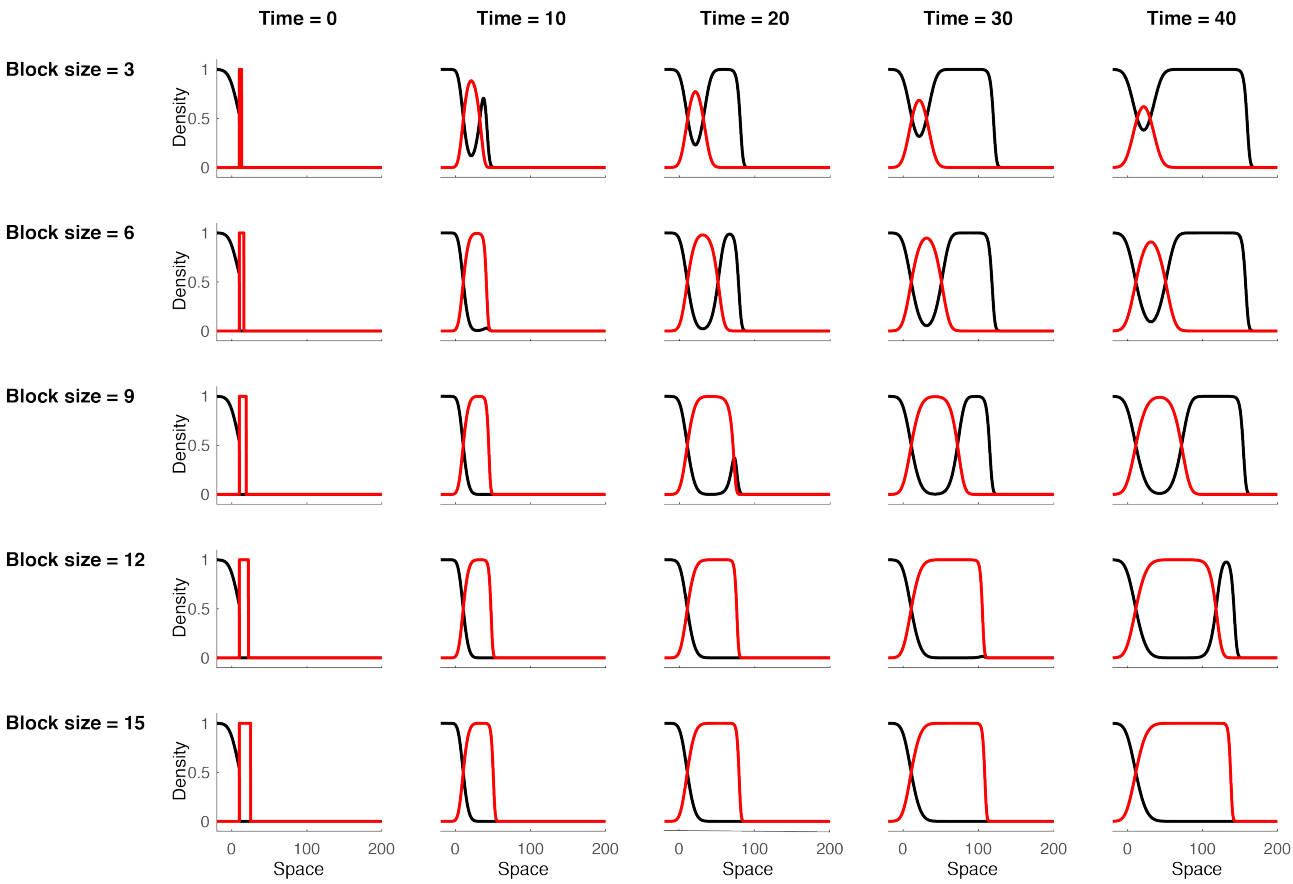


Figure S9: Wild-type cannot prevent hyperswarmers from taking over. A $t = 0$, a block of species 2 (red curve, $r_2 = 1.1$ and $D_2 = 0.5$) is implanted at the edge of the population of species 1 (black curve, $r_1 = 1$ and $D_1 = 1$). Formally, the simulation starts with the steady-state profile of species 1, where individuals are entirely removed at the edge (u_1 is unchanged for $x < 10$, $u_1 = 0$ for $x > 10$). For species 2, $u_2 = 1$ for $10 < x < 10 + \textit{Block size}$ (with *Block size* from 3 to 15), and $u_2 = 0$ everywhere else. A larger block size delays the takeover, but does not prevent it. Take over is nearly immediate for block size lower than 3. For larger blocks, species 2 forms a traveling wave for a short time before being taken over. For block size greater that 15, take over is not observed, even at longer simulation time, possibly because of numerical precision issues at very low population densities. Similar behavior is observed for all values of r_2 and D_2, as long as $v_2 < v_1$.

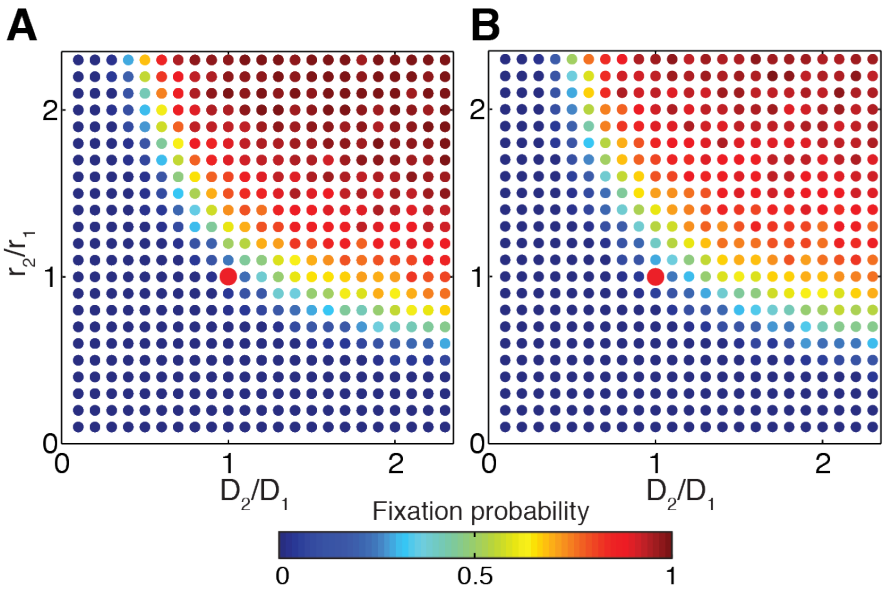


Figure S10: Evolutionary diagram in stochastic models. Fixation probability obtained from the stochastic model without death rate (A), and with death rate (B). For the stochastic simulations, $S = 1$, $K = 100$, $L = 2\lambda_1$. The red dot depicts the reference point ($D_2 = D_1$ and $r_2 = r_1$).

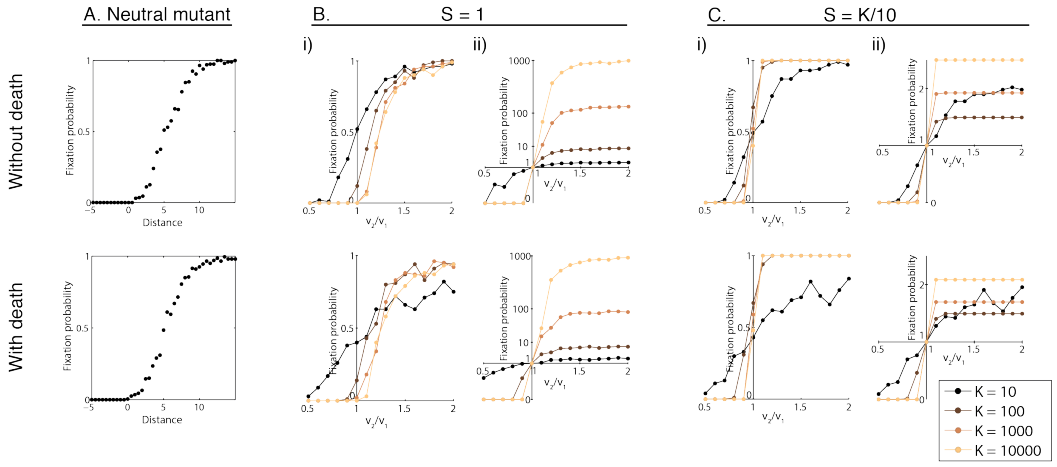


Figure S11: Fixations probability in stochastic models. The first row shows results of the stochastic model without death. The second row shows results of the stochastic model with death. A. Fixation probability of a neutral mutant with respect to the distance to the front ($S = 1$). B. Fixation probability of a mutant with respect to v_2/v_1 (with $r_2/r_1 = D_2/D_1$), for various carrying capacities. The introduction occurs in fixed size implant ($S = 1$ individual) at $L = 3$. i) represents the raw data in linear scale. ii) represents the data normalized by the fixation probability of a neutral mutant (note power-law scale on the y-axis, exponent=0.2). C. Fixation probability of a mutant with respect to v_2/v_1 (with $r_2/r_1 = D_2/D_1$), for various carrying capacities. Unlike in B, the number of introduced individuals scales with carrying capacity ($S = K/10$). i) represents the raw data in linear scale. ii) represents the data normalized by the fixation probability of a neutral mutant, in linear scale. Note that in B and C, for the model with and without death, the fixation probability curves get steeper as the carrying capacity gets larger.

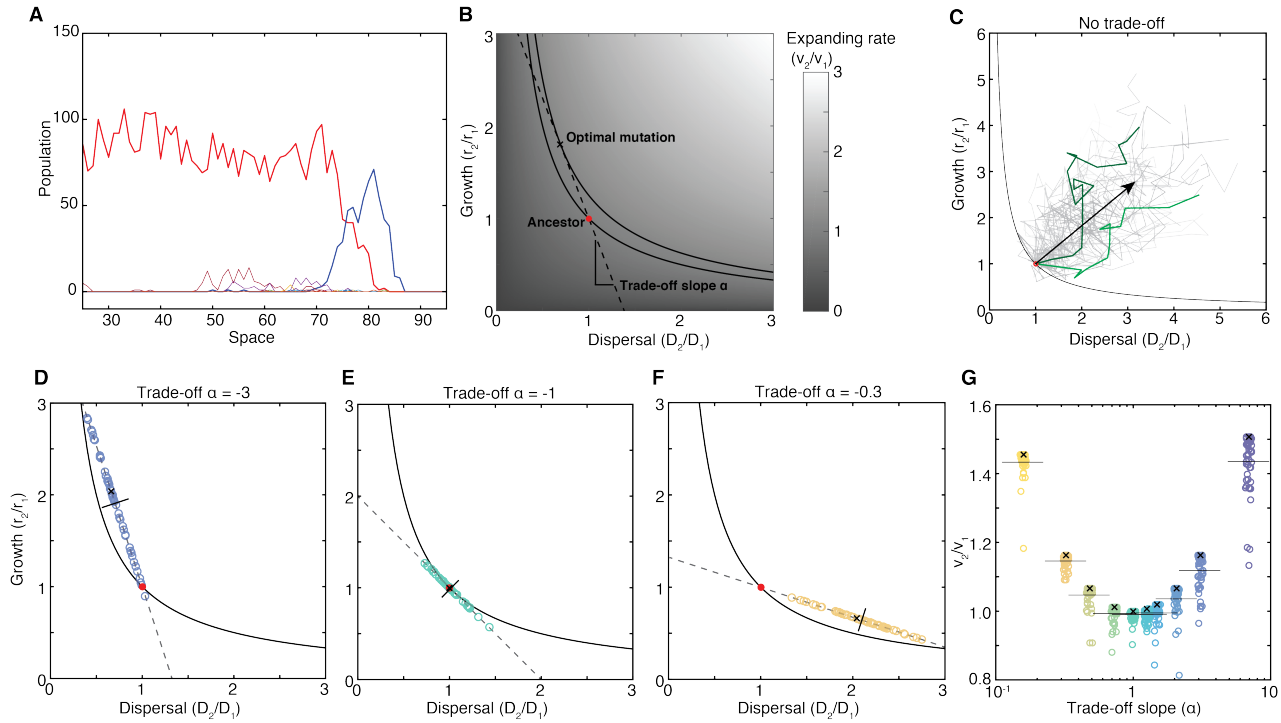


Figure S12: Stochastic simulations of population expansion with mutations reveal that evolution tends to maximize the expansion rate $v = 2\sqrt{rD}$. A: Representative snapshot of the spatial distributions of a population (red) and mutant populations it has generated. B: Diagram representing the success rule (black line), the ancestral phenotype (red dot), a trade-off line (dashed line), the expansion rate (grey levels), and the phenotype that maximizes the expansion rate along the trade-off line (cross symbol). C: Without trade-off between growth and dispersal, evolution tends to improve both traits simultaneously. 50 evolutionary trajectories of the majority phenotype sitting at the edge are represented. Two trajectories are highlighted in green. The black arrow depicts the average trajectory (average from 50 simulations). D-E-F: Phenotypes obtained after $r_1 t = 1000$ with 3 trade-off slopes: -0.5, -1, -2. The black line is the average phenotype from 50 simulations, the cross is the theoretical optimal phenotype. G: Summary of the results for 10 trade-off slopes.

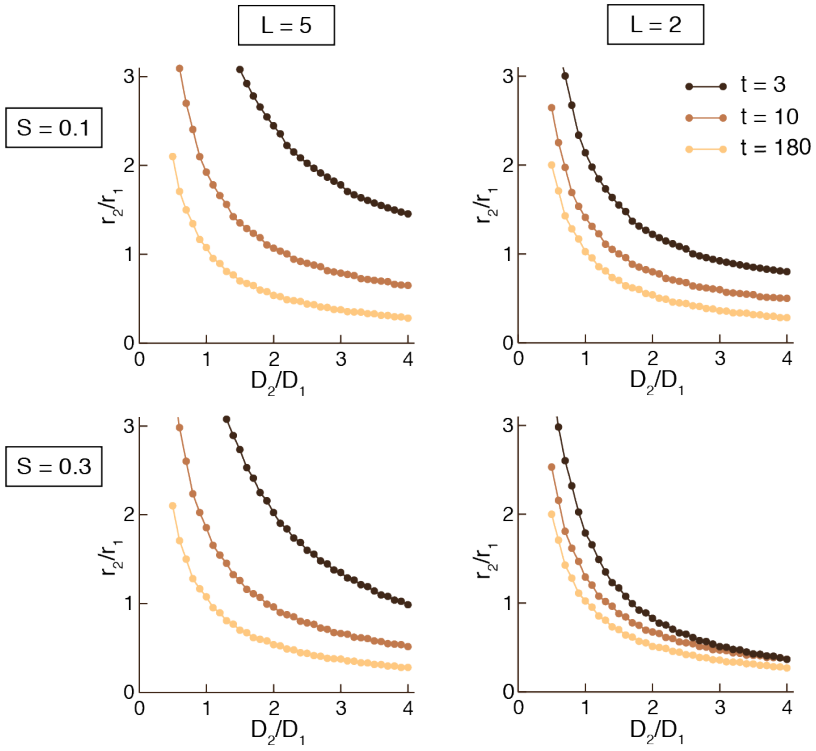


Figure S13: Evolutionary domain boundaries for various simulation times, sizes of introduction S, and distances of introduction L.

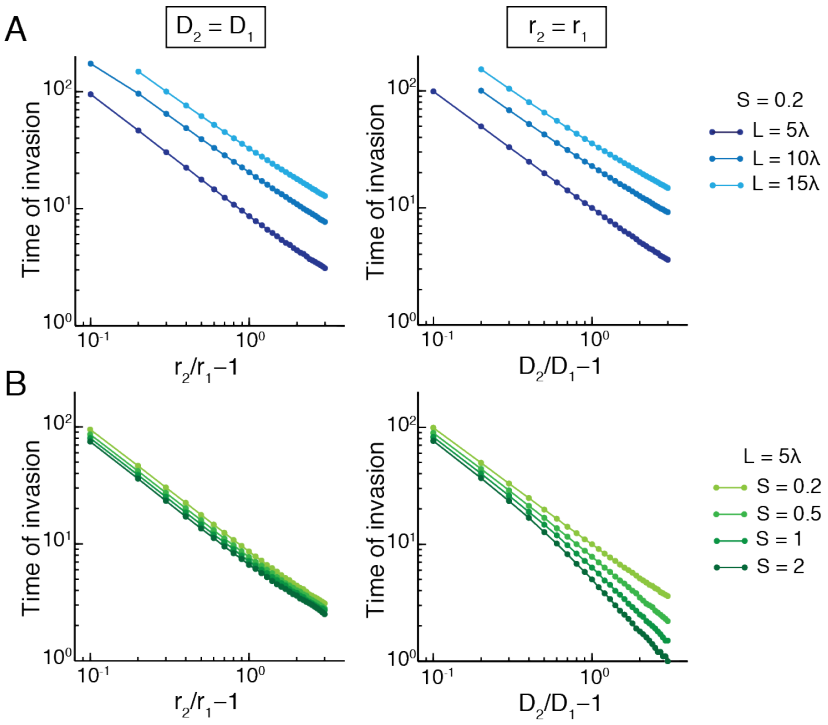


Figure S14: Implanting further away or lower amounts delays takeover. A: Time of takeover for different implantation sites. B: Time of takeover for different implant sizes.