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Protection and inhibition of antibiotic-resistant mutants in structured bacterial populations NALIN RATNAYEKE, KARISHMA KAUSHIK, PARAG KATIRA, VERNITA GORDON, Center for Nonlinear Dynamics, University of Texas at Austin — Antibiotic resistance is a major issue in public health. Populations of bacteria naturally generate mutants resistant to antibiotics, however the impact of population structure on the subsequent survival of mutants during antibiotic exposure is not well understood. Here we show that resistant mutant survival depends on population structuring such as population density and spatial organization of cells. Mixed populations of *Pseudomonas aeruginosa* susceptible and resistant cells were exposed to antibiotics at various cell densities, and mutant survival was seen to vary non-monotonically with density. We hypothesize that cells in a population during antibiotic exposure are involved in both protection and inhibition of resistant mutants, and that population structure determines which of these processes is dominant. Through performing diffusion assays on agar growth plates, a diffusion constant of $.86 \pm .15$ $\mathrm{mm}^2/\mathrm{hr}$ and molecular weight of 950 ± 500 Da for a putative released inhibitory factor were estimated. Additionally, a model based on antibiotic reaction kinetics was developed in order to describe inhibition in mixed systems. Investigations into these phenomena will lead to an increased understanding of the development and maintenance of antibiotic resistance in nature.

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