Abstract

Infections caused by antibiotic–resistant bacteria are posed to be one of the most pressing health concerns of the twenty–first century. A common mechanism of resistance involves production of an antibiotic–degrading enzyme. In this case, neighboring, nonproducer bacteria can "cheat" by sharing the benefits of resistance while the metabolic cost of enzyme production falls solely on producer cells. The objective of this work is to explore how the spatial population dynamics of producers and nonproducers maintain the resistance found in biofilms. A three–dimensional spatial model was used to simulate growth of both producers and nonproducers under antibiotics with different characteristics. Standard antibiotics resulted in a heterogeneous populations with stable, homogeneous community structure. The population of resistant bacteria was most sensitive to altering the fitness cost of enzyme production. These results could suggest novel antibacterial treatments in order to create therapies less likely to favor the evolution of resistance.

Keywords: antibiotic resistance, spatial simulation, clustering analysis, biofilm, public good