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Population Balance Modeling in *Enterococcus faecalis*

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ABSTRACT

In the bacteria species *Enterococcus faecalis,* transfer of plasmid pCF10 by conjugation between donor cells that possess sets of genes conferring drug resistance and recipient cells leads to the spread of this resistance in a population. A complex signaling molecule network is responsible for communication between recipient and donor cells. Up to this point, the nature of these signaling molecules has been modeled deterministically from the point of view of an “average” cell. While this view has been cured slightly by stochastic treatments, a model is needed that better accounts for the individual nature of each cell, each cell’s interactions with other cells, and each cell’s distinct effect on the population’s environment. To this end, a population balance model has been formulated that considers these features. Of interest is the distribution of protein PrgB, a membrane-bound protein that indicates the degree to which conjugation has been initiated. As a result of the interactions between cells and the signaling molecules, two steady state levels of protein concentration exist, one for an “off” state of conjugation and one for an “on” state. While the single-cell approach predicts a bimodal distribution of protein resulting from this bistability, the population balance approach demonstrates that a bistable system such as that of plasmid pCF10 can give rise to a unimodal stationary distribution. While there is still much work to be done on understanding conjugation in *Enterococcus faecalis*, this study has delineated two important concepts associated with this complex phenomenon (i.e. bistability versus bimodality).

KEYWORDS

Population balance, stochastic, simulation, gene regulation, convergent transcription, bacteria, signaling molecules, signaling network, plasmid

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