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MATHEMATICAL MODELING OF LUNG INFECTION  
AND ANTIBIOTIC RESISTANCE

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**Motivation and Aim:** At various times it was shown that restricting the use of antibiotics in clinical practice resulting in successful decrease in antibiotic resistance (Barbosa T.M. & Levy S.B. 2000). Some authors have attributed this phenomenon to the fitness cost (Andersson D.J. & Hughes D. 2010). However, most researchers pay attention to the development of resistance and transmission. Various models considered these processes in order to develop new treatment strategies (D'Agata E.M.C. et al. 2007). The aim of this work was to develop a model of the observed reversal of antibiotic resistance in therapy of pulmonary infections.

**Methods and Algorithms:** The process considered of treatment of the infected organism. At its initial stage, the bacteria infected of organism. Further starting treatment organism of some antibiotic. Consequently, the number of bacteria is reduced, and a complete recovery may occur. However, due to mutations appear bacteria resistant to the action of this antibiotic. Over time the effectiveness of the antibiotic is substantially reduced. Treatment continued for a new drug. After some time, the sensitivity of bacteria to the initial antibiotic is gradually recovering. The mathematical model of the observable process is proposed. This is a system of nonlinear differential equations. The model characterizes the variation of the general bacterial population, and as well as mutants resistant to antibiotics. The differential equations theory is applied for the qualitative analysis of this model. The numerical solution of the system is found for the large enough scope of process parameters. The experimental data is used for the assessment of the model efficiency.

**Results:** The general stages of the observable process are determined by means of the approximate qualitative analysis of the suggested mathematical model. These results are corroborated by computer analysis. The clinical material prepared for validation of the developed model.

**Conclusion:** By dint of the proposed model is used to simulate the reversal of antibiotic resistance in pulmonary infectious diseases. This will not only describe the process of reversion of antibiotic resistance, but also to develop a new treatment strategy.

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