

1106-92-1486

Faina Berezovskaya*, fberezovskaya@howard.edu, and **Georgiy Karev**. *Bifurcation approach to analysis of mathematical model of CRISPR hosts/virus population.*

One of the adaptation mechanisms employed by microbes to curb viruses is the CRISPR-Cas system, a recently discovered adaptive immunity system. Microbes create heritable memory of viruses thus following the Lamarckian modality of evolution that dramatically accelerating adaptation. Population studies and modeling reveal complex behavior of the actual populations. We construct and study a “minimal” 3-dimensional Volterra type analytical model of the CRISPR-Cas system (Berezovskaya et.al., *Biology Direct* 2014, 9:13).

Theorem. Let M be the virus reproduction rate; then for a wide range of other model parameters and any positive initial values the stable mode of the model is the equilibrium for “ $M_j M_{cr}$ ” and stable (pseudo-chaotic) oscillations for “ $M_i M_{cr}$ ”, where “ M_{cr} ” is the parameter value corresponding to supercritical Hopf bifurcation.

Quasi-chaotic regimes of virus-host coevolution are likely to be biologically relevant given the extreme evolutionary instability of the CRISPR-Cas loci revealed by comparative genomics. (Received September 13, 2014)