Universität Basel

Publication

A virtual look at Epstein-Barr virus infection: biological interpretations

JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)

The possibility of using computer simulation and mathematical modeling to gain insight into biological and other complex systems is receiving increased attention. However, it is as yet unclear to what extent these techniques will provide useful biological insights or even what the best approach is. Epstein-Barr virus (EBV) provides a good candidate to address these issues. It persistently infects most humans and is associated with several important diseases. In addition, a detailed biological model has been developed that provides an intricate understanding of EBV infection in the naturally infected human host and accounts for most of the virus' diverse and peculiar properties. We have developed an agent-based computer model/simulation (PathSim, Pathogen Simulation) of this biological model. The simulation is performed on a virtual grid that represents the anatomy of the tonsils of the nasopharyngeal cavity (Waldeyer ring) and the peripheral circulation–the sites of EBV infection and persistence. The simulation is presented via a user friendly visual interface and reproduces quantitative and qualitative aspects of acute and persistent EBV infection. The simulation also had predictive power in validation experiments involving certain aspects of viral infection dynamics. Moreover, it allows us to identify switch points in the infection process that direct the disease course towards the end points of persistence, clearance, or death. Lastly, we were able to identify parameter sets that reproduced aspects of EBV-associated diseases. These investigations indicate that such simulations, combined with laboratory and clinical studies and animal models, will provide a powerful approach to investigating and controlling EBV infection, including the design of targeted anti-viral therapies.