Optimal viral immune surveillance evasion strategies

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Abstract

Following cell entry, viruses can be detected by the cellular immune system. The detecting CD8 T cells can lead to the host cell apoptosis and following it to the destruction of the infecting virus. This detection is mediated by viral protein epitopes. Thus, viruses with fewer epitopes have a higher survival probability and are selected through evolution. Given the high viral mutation rate, one could assume that strains with mutations erasing all epitopes should rise. However, mutations have a fitness cost and on the evolutionary long term, viruses maintain some epitopes. The number of such epitopes in each viral protein is a balance between the selective advantage of having less epitopes and the costs of the mutations. Here we present a bioinformatic analysis of the number of epitopes in various viral proteins and an optimization framework to explain these numbers. We show, using the genomic analysis and the theoretical optimization framework, that the most critical factor affecting the number of presented epitopes is the expression stage in the viral life cycle of the gene coding for the protein. The early expression of epitopes can lead to the destruction of the host cell, before budding can take place, and thus to the destruction of the virus. A lower number of epitopes is expected in early proteins even if the late proteins have a much higher copy number.