

A discrete dynamical model for natural resistance against HIV

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Human Immunodeficiency Virus (HIV) is a complex and deadly virus that attacks the human immune system. HIV/AIDS remains one of the most pressing global health challenges, affecting millions of individuals and communities worldwide. The CCR5 (Chemokine Receptor type 5) is a crucial key player in HIV infection due to its major involvement in the infection process. Natural resistance, which has come since ancient times, is being built in humankind against some diseases such as Malaria, Galactosemia, etc. This natural resistance is built by changing genetics and it continues to the future generations, providing very suitable examples of Charles Davin's evolution theory. In the recent investigation on HIV, it was found that individuals carrying the CCR5-Δ32 (a-nucleotide deletion in the exon of the CCR5 gene) live a normal life and are warranted a natural barrier to HIV infection. There are many research papers proposing continuous dynamical models for HIV. In this paper, we propose a discrete dynamical model taking into account the evaluation of a gene type, which shows how rapidly the concentration of the CCR5-Δ32 allele converges to its maximum equilibrium level. Graphical methods, including web analysis and analytical methods, were used to find the stable equilibrium value E . $\frac{d(n)-E}{d(n-1)-E}$ were computed for moderately large values of n , where $d(n)$ is the proportion of the CCR5-Δ32 allele in the generation n . We determined the rate at which the frequency of the CCR5-Δ32 approaches its stable equilibrium, and used this rate to estimate what percentage by which the frequency gets closer to equilibrium in one generation compared to the previous generation. There is no surprise that the present and future generations of the human population shall acquire resistance to HIV than in the past.

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