

In-silico evaluation of Human papilloma virus L1 protein in order to present effective vaccine candidate

Dehghan SH¹, Haji beigy N¹, Ebadi M², Shafaati MR^{1,3*}

1- Department of Biology, Faculty of Sciences, Islamic Azad University Central Branch, Tehran, 14676-86831, Iran

2-Department of Biology, Faculty of Sciences, Damaghan Branch, Islamic Azad University, Damghan, Semnan, Iran

3-Department of cellular & molecular biology, Faculty of Basic Sciences, Hamadan Branch, Islamic Azad University, Hamadan, Iran

* Shafaati@iauh.ac.ir

Abstract: The human papilloma virus (HPV) was introduced as the major etiological agent in outbreak of cervical cancer in 1970 (1). HPV vaccines available in the market are not effective against different strains of papillomavirus, therefore there is a need to develop a new prophylactic epitopic vaccine, which can work against different strains of HPVs and may lead to protection of cervical cancer against new pandemic viruses (2). The purpose of this study is to find an appropriate vaccine candidate for the HPV based on In-Silico study. In this study, by using bioinformatics software, we compared nucleotide sequence of HPV L1 protein of Iran strain with other countries. Also, by using the online software of the **IEDB** website, the hydrophobic, hydrophilic and antigenic regions of the Iran strain were predicted and evaluated. The genomic sequence of HPV L1 protein is 1518 bp. The similarity of this sequence with 25 other sequences was evaluated by using the Bio-Edit software. The information obtained from these bioinformatics studies and the evaluation of the phylogeny tree showed that there is a large similarity between HPV L1 protein of Iran and HPV L1 protein of Thailand, China, and Turkey.

Conclusion: Our results propose, the provision of a protective vaccine against any of the strains mentioned above can also be effective against another. therefor similarly to the information obtained from this in-silico evaluation, we can develop an effective vaccine against this virus.

Keywords: HPV; in-silico evaluation; vaccine candidate; bioinformatics software

References:

1. Romero-Pastrana F. Detection and Typing of Human Papilloma Virus by Multiplex PCR with Type-Specific Primers. International Scholarly Research Notices. 2012;2012.
2. Eslami G, Golshani M, Rakhshon M, Fallah F, Goudarzi H. The study on relation of Human Papillomavirus with bladder transitional cell carcinoma. Cancer Therapy. 2008;6:355-60.