

## In-silico evaluation of Iran NDV fusion protein in order to present effective vaccine candidate

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**Abstract:** Background : Newcastle disease virus (NDV) is one of the major pathogen in poultry (1). Vaccination is intended to control the disease as an effective solution, nevertheless this virus is a growing threat to the poultry industry (2). Fusion protein (F) on surface of NDV has a fundamental role in virus pathogenicity and can induce protective immunity alone (3). The purpose of this study is to find an appropriate vaccine candidate for the Newcastle Virus based on In-Silico study. **Materials and Methods:** In this study, by using bioinformatics software, we compared nucleotide sequence of NDV fusion 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. **Results:** The genomic sequence of Newcastle fusion protein is 1629 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 NDV fusion protein of Iran and NDV fusion protein of Jordan, Ukraine, Adygea and Russia. **Conclusion:** According to predictions, the provision of a protective vaccine against any of the strains mentioned above can also be effective against. By information obtained from this in-silico evaluation, we can develop an effective vaccine against this virus.

**Keywords:** NDV; Fusion protein; in-silico evaluation; vaccine candidate; bioinformatics software

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