



IDENTIFICATION OF THE POTENTIAL MOLECULAR TARGETS OF HUMAN HERPESVIRUS 4 USING BIOINFORMATICS TOOLS

Dharmasena W.G.B.P.* and Munasinghe D.H.H.

Department of Botany, University of Sri Jayewardenepura, Sri Lanka

buddhikapolgahawela@gmail.com

Human Herpesvirus 4 (Epstein-Barr virus) is a human pathogenic virus that causes chronic infection leading to severe health problems including cancer. Although, few control strategies are used, a proper medication has not been implemented. The novel gene editing techniques, which are ZFN (Zinc Finger Nuclease), TALEN(Transcription Activator Like Effector Nuclease) and CRISPR/Cas9(Clustered Regularly Interspaced Short Palindromic Repeats/CRISPR associated protein 9) have a potential to be used to control these pathogens and some researches have been carried out to investigate the potential of applying CRISPR/Cas9 on human herpesvirus 4, although the *in vivo* application is controversial. In this study, we carried out a bioinformatic analysis to find the target sites of TALENs. There the viral gene *LMP2A* was selected which shows an important role in the viral persistence inside host cells. If this gene could be altered the viral impact on the host could probably be diminished. We analyzed the *LMP2A* gene for potential TALEN targets with the tool ‘TAL effector nucleotide targeter 2.0’ and the targets with highest possible specificity of binding to the specified TALENs were selected. And we carried out an analysis to find the off-target bindings in human genome and other locations of the viral genome for the selected TALENs. Then among these TALEN sequences, TALENs without off-target bindings were selected. These identified TALEN binding sites would be useful in the medical treatment of the viral infection as an alternative method of treatment.

Keywords: *Human herpesvirus 4, LMP2A, TALEN, Off-targets, Bioinformatics*