GMR Genetics and Molecular Research
Online Journal
ISSN:1676-5680

# Molecular cloning and characterization of the pseudorabies virus *UL31* gene

**M.L. Li[1,2], Z.Y. Zhao[1], W. Cui[1], C.C. Mo[1], J.L. Wang[1] and M.S. Cai[1,2]**

[1]Department of Pathogenic Biology and Immunology,
School of Basic Science, Guangzhou Medical University, Guangzhou, China
[2]Institute of Immunology, Sino-French Hoffmann Institute,
School of Basic Science, Guangzhou Medical University, Guangzhou, China

Corresponding author: M.S. Cai
E-mail: mingshengcai@hotmail.com

Genet. Mol. Res. 13 (1): 1832-1847 (2014)
Received January 2, 2013
Accepted August 13, 2013
Published March 17, 2014
DOI http://dx.doi.org/10.4238/2014.March.17.11

**ABSTRACT.** We amplified a 816-bp sequence of the *UL31* gene from the pseudorabies virus (PRV) Becker strain genome. Evidence that this was the *UL31* gene was confirmed by cloning and sequencing. The PRV *UL31* gene encodes a putative protein of 271-amino acid residues, which was designated the UL31 protein. Bioinformatic analysis indicated that PRV UL31 contains a conserved PHA03328 domain, closely related with the herpes virus nuclear egress lamina protein *UL31* family and highly conserved among counterparts encoded by herpes UL31 genes. Nucleic acid sequence and amino acid sequence alignments demonstrated that PRV *UL31* has a relatively higher homology with UL31 homologous proteins of subfamily Alphaherpesvirinae than other subfamilies. In addition, phylogenetic analysis showed that PRV *UL31* has a close evolutionary relationship with members of the subfamily Alphaherpesvirinae, especially bovine herpesvirus 1 (BoHV-1), BoHV-5, equine herpesvirus 4 (EHV-4), EHV-9 and EHV-1. Antigen prediction demonstrated that several

 

potential B-cell epitopes are located in PRV UL31. Additionally, secondary structure and three-dimension structure prediction revealed that PRV UL31 predominantly consists of α-helix. Taken together, these results provide insight on the function and mechanism of UL31 during PRV infection.

**Key words:** Pseudorabies virus; *UL31*; Cloning; Bioinformatic analysis; Molecular characterization

 