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Molecular characterization of the pseudorabies virus *UL2* gene

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ABSTRACT. A 948-bp sequence of the *UL2* gene was amplified from the pseudorabies virus (PRV) Becker strain genome using polymerase chain reaction, and the gene identity was confirmed through further cloning and sequencing. Bioinformatic analysis indicated that the PRV *UL2* gene encodes a putative polypeptide with 315-amino acid residues. Its encoding protein, designated UL2, has a conserved uracil-DNA glycosylase (UDG)_F1 domain, which is closely related to the herpesvirus UDG family and is highly conserved among its counterparts encoded by UDG genes. Multiple nucleic acid and amino acid sequence alignments suggested that the product of PRV *UL2* has a relatively higher homology with UL2-like proteins of Alphaherpesvirinae than that of other subfamilies of Herpesviridae. In addition, phylogenetic analysis showed that PRV UL2 had a close evolutionary relationship with members of Alphaherpesvirinae, especially members of the genus *Varicellovirus* of bovine herpesvirus 1 and bovine herpesvirus 5. Antigen prediction indicated the presence of several potential B-cell epitopes in PRV UL2. In addition, secondary structure and 3-dimensional structure prediction revealed that PRV UL2 consisted predominantly of

an α-helix. Taken together, these results provide molecular biological insight for the further study of the function and mechanism of *UL2* during PRV infection.

Key words: Pseudorabies virus; Cloning; Bioinformatic analysis; *UL2*; UDG; Molecular characterization

