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Molecular cloning and characterization of the pseudorabies virus *US1* gene

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ABSTRACT. Using polymerase chain reaction, a 1050-bp sequence of the *US1* gene was amplified from the pseudorabies virus (PRV) Becker strain genome; identification of the *US1* gene was confirmed by further cloning and sequencing. Bioinformatics analysis indicated that the PRV *US1* gene encodes a putative polypeptide with 349 amino acids. The encoded protein, designated PICP22, had a conserved Herpes_IE68 domain, which was found to be closely related with the herpes virus immediate early regulatory protein family and is highly conserved among the counterparts encoded by Herpes_IE68 genes. Multiple nucleic acid sequence and amino acid sequence alignments suggested that the product of PRV *US1* has a relatively higher homology with ICP22-like proteins of genus Varicellovirus than with those of other genera of Alphaherpesvirinae. In addition, phylogenetic analysis showed that PRV *US1* has a close evolutionary relationship with members of the genus Varicellovirus, especially Equid herpes virus 1 (EHV-1), EHV-4 and EHV-9. Antigen prediction indicated that several potential B-cell epitopes are located in PICP22. Also, subcellular localization analysis demonstrated that PICP22 is predominantly located in the cytoplasm,

suggesting that it might function as a cytoplasmic-targeted protein.

Key words: Pseudorabies virus; *US1*; ICP22; Cloning; Bioinformatics; Molecular characterization

