chickens. Some isolates possessed the F protein of a virulent type, which contained a pair of dibasic amino acids at the cleavage site. The present results suggest that potentially virulent strains, which showed avirulent character, of NDV are maintained in migratory waerfowl populations. Some of those may transmit to domestic poultry and acquire pathogenicity during passages in chicken population.

These results indicate that pathogenicity of NDV strains was not necessarily correlated to the amino acid sequence at the cleavage site of the F protein. Pathogenicity, i.e. the ability of a virus to induce disease in the infected organism, is the results of a complex interplay of a multitude of factors that are determined by the biological, biochemical, and genetic characteristics. Thus, a molecular basis for viral pathogenicity is not easy to define. It is reasonable, however, to assume that disease becomes manifest, if the infecting virus has the ability to multiply to high amounts and to spread in the organism, and if cells containing vital functions are altered or killed by the virus. Since cell tropism represents primarily an interaction between the surface components of the virus and receptors of the host cell, it is obvious that the surface structure of a virus determines pathogenicity.

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Functional and Structural Analysis of Pseudorabies Virus Early Protein 0

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Early protein 0 (EP0) of pseudorabies virus (PRV) has been identified to be a homolog of ICP0 of herpes simplex virus 1 (HSV-1). EP0 contains the RING finger domain near its amino terminus with homology to, besides of ICP0 of HSV-1, ORF61 of varicella-zoster virus, BICP0 of bovine herpesvirus 1, and EICP0 of equine herpesvirus 1 which belong to alphaherpesvirus. These ICP0 homologs are thought to be involved in transcriptional regulation, suggesting that EP0 may also have transcriptional regulatory activities. In the present study, the function, structure/function relationship of EP0, and regulatory mechanism of EP0 gene expression were analyzed by transient expression assays.

To characterize the function of EP0 in gene expression of PRV, a plasmid expressing EP0 was constructed. EP0 was detected by indirect immunofluorescence assay in the nuclei of the cells transfected with an EP0 expression plasmid as is the case in the cells infected with PRV. In transient expression assay, the effect of EP0 on transcription under the control of PRV immediate early (IE), thymidine kinase (TK), and glycoprotein X (gX) promoters was analyzed. In result, EP0 transactivated these promoters, indicating that EP0, like ICP0 of HSV-1, is a transactivating protein.

To map the functional domains on EP0 molecule, a series of truncated forms of the EP0 gene were constructed. The amino-terminal region containing the RING finger domain, amino

acids 1 to 84, and the region between amino acids 114 to 243 containing acidic amino acid sequences were required for the transactivation. Among the mutants constructed, interestingly, the mutant consisting amino acids 1 to 113 (dlC113) possessed a dominant-negative property. This mutant could inhibit transcription and a cell line stably transformed with this mutant gene showed resistance to PRV infection.

To analyse the reguratory mechanisms of EP0 gene expression, various fragment-chloramphenicol acetyltransferase constructs containing a series of deletions within the upstream region of the EP0 gene were constructed. It was shown that the EP0 gene was transcribed from the region between −170 and +43 relative to the transcription start site of the EP0 gene reported previously, although 5' end of EP0 mRNA was not identified. This region lacked a TATA element and contained an Inr element, the putative binding site for IE protein of PRV (IE180), and three consensus Sp1 binding sites as *cis*-reguratory elements. It was demonstrated that the EP0 gene might be transcribed from the TATA-less promoter, and that transcription from this promoter was activated by IE180. Analysis of deletion mutants of the promoter revealed that Sp1 binding sites were critical for the basal and IE180-mediated transcription.

Results obtained in this study suggest a possible mechanism for the enhancement of PRV replication by EP0 and that a dominant-negative mutant of EP0 may be applicable for the antiviral therapy. The mechanism could be explained as follows; EP0 in the virion is released in the infected cells, and transactivates the IE gene, resulting in enhancement of initiation of PRV infection. After this, IE180 expressed from the IE gene transactivate the early and late genes, leading efficient replication of PRV. The mechanism by which the mutant dlC113 inhibited the viral gene transcription and replication remains unknown, however, these findings are notable from standpoint of an antiviral therapy. If expression of this mutant gene can be controled, it will be very useful for the therapy.

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Antibacterial Activity of Plaunotol, a Cytoprotective Antiulcer Agent, against *Helicobacter pylori*

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Recently, some antiulcer agents have been reported to have antibacterial activity against *Helicobacter pylori*, which is highly associated with gastritis and peptic ulcers. *In vitro* activity of plaunotol, a cytoprotective antiulcer agent, against *H. pylori* was investigated. Plaunotol showed the most potent antibacterial activity against *H. pylori* among the cytoprotective antiulcer agents. Moreover, plaunotol had a strong bactericidal effect against this organism. This bactericidal effect resulted in a rapid reduction of culture turbidity, with an extensive loss of viability. In addition, cell lysis also occurred in gram-positive and some gram-negative bacteria.