Marek's disease (MD) is a lymphoproliferative disease causing a serious threat in poultry production. Field strains of Marek's disease virus (MDVs) are continuously re-emerging, causing great economical losses to the poultry industry worldwide in spite of the intensive vaccination and restrictive management policy used. Histopathological and molecular characterizations of MDVs are essential for monitoring the changes of viruses and evaluating the effectiveness of existing vaccines. During 2016, 190 visceral tumor tissues representing 30 vaccinated chicken flocks from Gifu prefecture, Japan were analyzed. Pathological examination revealed presence of lymphoproliferative lesions in visceral organs. Polymerase chain reaction (PCR) screening of tissue specimens using specific primers for Avian leucosis virus (ALV), Reticuloendotheliosis Virus (REV), and MDV were positive only for MDV. The PCR products of meq, Pp38, vIL-8, and glycoprotein (gL) MDV genes were sequenced and used for homology, phylogenetic, and similarity level analysis with the published reference of MDVs in the database. The results revealed high similarity between the field isolates, vv and vv+ strains of MDV from the USA and China. Several point mutations in nucleotide sequence of the field isolates and their deduced amino acid sequences were detected in that genes. The present molecular analyses indicated that nucleotides and amino acids changes could be valuable criteria for differentiation and determination of the
pathogenicity and oncogenicity of MDVs according to The Avian Disease and Oncology Laboratory (ADOL) pathotyping in vivo studies. Furthermore, the results suggest that development of a new vaccine must be considered to overcome this devastating avian oncogenic viral disease.