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CLONING AND CHARACTERIZATION OF cDNAS MAPPED ON
THE SHORT UNIQUE SEGMENT AND SHORT INVERTED
REPEATS OF MAREK'S DISEASE VIRAL DNA

Seiki KOJIMA

*Department of Radiation Biology,
Faculty of Veterinary Medicine,
Hokkaido University, Sapporo 060, Japan*

The short unique segment (Us) and short inverted repeats (IRs) of Marek's disease virus (MDV), which correspond to the BamHI-A fragment of MDV DNA, code for multiple species of RNA. Thirteen cDNA clones were isolated and mapped on the region above. To determine in detail the location of these clones, cDNAs were hybridized with sub-fragments of BamHI-A which were digested with BglII, SmaI, EcoRI, HindIII, PstI, Sall or XhoI. From the hybridization pattern of each cDNA with the sub-fragments of BamHI-A, it was suggested that 6 cDNAs mapped on the IRs, 5 cDNAs mapped on the border region of IRs and Us, and 2 cDNAs mapped on the Us. Since the expression of the MDV genome is thought to be well-controlled after infection, it could be classified into three classes: immediate early (IE) RNA present in cycloheximide-treated infected cells, early RNA present in phosphonoacetic acid-treated infected cells and late RNA. When the cDNAs were classified by Northern blot hybridization, the 3 cDNAs which mapped on IRs were suggested to correspond to IE RNA. Subsequently, 4 cDNAs were partially sequenced with the dideoxy method. Predicted amino acid sequences for these clones were compared to other herpesvirus sequences which have been registered in the NBRF amino acid data base. Three clones of herpesvirus genes were listed with weak homology scores. It was further indicated that the 178 bp direct repeat was included in the DNA sequence of a cDNA (mapped on IRs). It was suggested that this cDNA was important to elucidate the biological meaning of the 178 bp direct repeat.