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EFFECT OF DNA METHYLATION ON GENE EXPRESSION
FROM THE MAREK'S DISEASE VIRUS GENOME IN THE
LYMPHOBLASTOID CELL LINE, MDCC-MSB1

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Transcription from the latently infected Marek's disease virus (MDV) genome in lymphoblastoid cells is restricted to a portion of the viral genomes. However, it is not clear which factors or events are responsible for the transcriptional control of the MDV genome in lymphoblastoid cells. Since some latent viral genomes are highly methylated, the effect of DNA methylation on the repression of transcription from MDV DNA was examined in the lymphoblastoid cell line, MDCC-MSB1 (MSB-1).

Restriction endonuclease analysis with *Hpa* II and *Msp* I showed that latent MDV genomes in MSB-1 were highly methylated. Since both transcriptionally active and inactive regions of MDV DNA were methylated, other regulating factors may be also responsible for the transcriptional control of the MDV genome.

When MSB-1 cells were treated with the DNA demethylating agent, 5-azacytidine (5-AzC), latent MDV genomes were demethylated and the synthesis of mRNA from *Bam* HI-A, -B, -D, -H, -I₂ and-L regions of MDV DNA was enhanced. The mRNA from other regions was not detected.

When MDV DNA was digested with DNaseI of the nuclei prepared from MSB-1 cells treated with 5-AzC and hybridized with the MDV-*Bam* HI-H fragment, new bands appeared. Thus, a DNaseI hypersensitive site, which is especially seen in transcriptionally active regions, appeared in the *Bam* HI-H region by the treatment with 5-AzC. This result suggests that the chromatin structure of latent MDV genomes is changed by demethylation of DNA and transcriptional activity of the latent MDV genome is stimulated. Thus, DNA methylation may play an important role in regulating transcription from the latent MDV genome in MSB-1.