

Our theory may also give an account of the non-metastatic and multicentric de novo occurrence characteristics of HCC, which would be the result of persistent HCV infection.

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## Accumulation of LANA at nuclear matrix fraction is important for Kaposi's sarcoma-associated herpesvirus replication in latency

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### ABSTRACT

The Kaposi's sarcoma-associated herpesvirus (KSHV) genome replicates once per cell cycle, and the number of viral genome is maintained in the latency. The host cell-cycle-dependent replication of the viral genome is a fundamental process to critically keep the number of the genome. Here we show that the cellular pre-replication complex (pre-RC), the viral replication origin (ori-P) in a unit of the terminal repeat of the KSHV genome, and a viral replication factor, latency-associated nuclear antigen (LANA) accumulate at the nuclear matrix fraction in the G1 phase. We found not only that LANA itself was localized mainly to the nuclear matrix fraction but also that TR region of the KSHV genome existed together in the G1 phase. The localization of LANA at the nuclear matrix could be determined by structural consequence of the full length of LANA. Furthermore, transient replication assay revealed that the LANA's nuclear matrix localization was a pre-requisite for the efficient viral genome replication in the latency. Since LANA has been shown to bind the LANA binding sites (LBS) of the ori-P, these results suggest that LANA should recruit the ori-P to the nuclear matrix, where the complete pre-RC then forms on the ori-P, during the G1 phase. Thus, the nuclear matrix accumulation of cellular and viral replication factors is likely to be a key process for the initiation of replication of KSHV in the latency.

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### 1. Introduction

Kaposi's sarcoma-associated herpesvirus (KSHV) is a gamma-herpesvirus associated with Kaposi's sarcoma (Boshoff and Weiss, 2001; Chang et al., 1994; Chang and Moore, 1996) primary effusion lymphomas (PEL), and multicentric Castlemann's disease (Cesarman et al., 1995; Chang et al., 1994; Chang and Moore, 1996). Like all other herpesviruses, KSHV displays both latent and lytic infection. In fact, in most KSHV-infected cells, the virus is in the latent state, and the viral genome replicates according to the cell cycle, maintaining a constant number of viral genomes. Thus, the viral genome has to replicate once per cell cycle in the host cells and segregate accurately into the two daughter cells. In the latent phase, only a limited set of viral genes is expressed and among them, latency-associated nuclear antigen (LANA), one of the major latent proteins, is essential for the episomal maintenance and the replication of KSHV genome in latency (Ballestas et al., 1999; Cotter and Robertson, 1999; Hu et al., 2002).

Replication of KSHV genome is thought to be executed using host replication machinery. This includes the pre-replication complex (pre-RC), which contains ORC1–6 (ORCs), Ccd6, Cdt1, MCM1–7

(MCMs), and other factors and is set up on a replication origin prior to initiation (Bell, 2002; DePamphilis, 2003; Ohsaki et al., 2004). Previous studies have demonstrated that the viral terminal repeat region and LANA play key roles in the latent replication of KSHV (Fejer et al., 2003; Hu et al., 2002; Stedman et al., 2004; Verma et al., 2006). An interaction between LANA and ORCs has been reported to be detected by GST-ORC pull-down, immunoprecipitation followed by immunoblotting, and ChIP assays (Lim et al., 2002; Verma et al., 2006). It is, however, still unclear, how LANA is involved in the KSHV genome replication and how one viral replication origin (ori-P), which consists of LANA binding sites (LBS) and a 32-bp GC-rich segment among multiple copies of them is determined and how components of the pre-RC are specifically recruited to the ori-P region in the latency. In their model, LANA binds to the LBS in the ori-P and recruits ORCs there by direct interaction between LANA and ORCs. N-terminal deletion of LANA, which is supposed to maintain binding activity to LBS and ORCs, cannot support the viral replication (Garber et al., 2001; Lim et al., 2002; Verma et al., 2006).

As for Epstein-Barr virus (EBV), it also replicates dependent on cell cycle in latency. In this case, EBNA1 binds with its ori-P and recruits ORCs by directly binding ORCs (Chaudhuri et al., 2001; Dhar et al., 2001; Ritzi et al., 2003; Schepers et al., 2001; Sugden, 2002). And also, it was reported that nuclear matrix had a function for EBV replication in the latency and the lytic replication (Mattia et

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al., 1999). The detail, however, remains to be elucidated (Sugden, 2002).

Recently, the importance of nuclear matrix as the site of replication factory has been realized (Anachkova et al., 2005; Jackson and Cook, 1995), and many nuclear matrix-associated proteins have been identified (Mika and Rost, 2005; Radichev et al., 2005). It is well-known that chromatin is arranged into repeating loop domains of 50–200 kb in the interphase nucleus (Cook and Brazell, 1975; Pardoll et al., 1980; Vogelstein et al., 1980). These chromatin loops are anchored to the nuclear matrix by scaffold/matrix attachment regions (S/MARs), which bind to specific components on the nuclear matrix. It is proposed that the organization of chromatin into higher-order structure is mediated by clustering of these repeating loops. This higher-order clustering of loop domains is thought to be a fundamental feature of the functional units of chromatin in the cell nucleus. Consistent with this concept, DNA replication foci have been visualized in the nucleus of cell preparations that preserve the nuclear matrix structures (Berezney et al., 1995; Nakayasu and Berezney, 1989; Neri et al., 1992). Similarly, transcription sites in the cell nucleus are proposed to be composed of clusters of transcriptional units attached to the nuclear matrix as a transcriptosome (Cook, 1999; Jackson and Cook, 1995; Wei et al., 1999).

In this study, we demonstrated that LANA, the ori-P, and the pre-RCs were associated with the nuclear matrix and that the nuclear matrix accumulation of LANA was likely to be a key process for the initiation of replication of KSHV in the latency, suggesting that the nuclear matrix is important for the replication initiation site for the KSHV genome. Our findings suggest a model in which the ori-P is recruited to the nuclear matrix region by LANA, which accumulates there on its own, via LANA-binding sites within the TR. The LANA-bound ori-P is then ready for pre-RC placement. This model does not necessarily require LANA to interact with the pre-RC components directly, since the cellular pre-RCs itself accumulates at the nuclear matrix (Jenke et al., 2004; Radichev et al., 2005), though it does not explain necessity of GC-rich 32 bp replicator (RE) for the viral replication in the latency.

## 2. Materials and methods

### 2.1. Plasmids

pGEX-hORC1 (a gift from Dr. Hiroyoshi Ariga, Hokkaido Univ.) (Takayama et al., 2000) was digested with BamHI and Sall and inserted into the BglIII/Sall site of the pEGFP-C1 vector (Clontech) to construct the pEGFP-ORC1. As for V5 tagged expression vectors, the full length of LANA ORF (vFL), and v $\Delta$ CBS, in which a chromosome binding site up to 106aa was deleted, and v $\Delta$ N, in which N-terminal amino acids up to 496aa was deleted, and vDBD1, which contained a DNA binding domain of LANA from 922aa to 1162aa as described elsewhere (Sakakibara et al., 2004), were fused with the V5 tag at C-terminus of each construct. EGFP tagged expression vectors, gFL, which contained the full length of LANA, and gN, which contained N-terminal 273aa of LANA, were fused with EGFP at N-terminus. gN-DBD contained the N-terminal 273aa plus C-terminal part from 922aa to 1162aa in frame and EGFP was fused with its N-terminus in this construct. gL321 contained N-terminal 107aa of LANA, and EGFP was fused to the C-terminus in this case. BSII-TR6 is a plasmid containing six TR units in the XbaI site of the pBluescript II vector (Stratagene).

### 2.2. Cells

BC3, a KSHV-positive and EBV-negative primary effusion lymphoma cell line, was grown in RPMI 1640 (Nissui, Tokyo, Japan)

supplemented with 10 i.u. per milliliter penicillin G, 10  $\mu$ g per milliliter streptomycin, and 20% heat-inactivated fetal bovine serum (FBS). BJAB, a KSHV-negative and EBV-negative Burkitt lymphoma cell line, was grown under the same conditions, with 10% heat-inactivated FBS.

A human embryonic kidney cell line HEK293 was grown in Dulbecco's modified Eagle's medium (DMEM) (Nissui, Tokyo, Japan) with the same supplements as used for the BJAB cells. 293LANA cells, which were obtained by introducing a retroviral vector, pHyTc-LANA, which constitutively expresses LANA, into HEK293 cells (Sakakibara et al., 2004), were cultured under the same conditions as the HEK293 cells, except that 0.2 mg/ml hygromycin B (Wako Pure Chemicals, Osaka, Japan) was added. 293hyg cells were obtained by introducing the parental pHyTc vector and cultured as the 293LANA cells. All cells were cultured in a 5% CO<sub>2</sub> atmosphere.

GFP-ORC1/BC3 cells were generated by introducing pEGFP-ORC1, in which an EGFP gene was followed by the full-length *orc1* gene in the pEGFP-C1 vector (Clontech) (see below), with TransFectin<sup>®</sup> (BioRad) according to the manufacturer's instructions, and cultured for 2 days. Two days after transfection, the cells were exposed to 500  $\mu$ g/ml G418, cultured for 7 more days, and individual G418-resistant colonies were obtained in RPMI medium containing 0.15% methylcellulose and the same supplements as above. Isolation was repeated at least three times to obtain a completely single clone, and several independent clones were established.

### 2.3. Cell fractionation

Cells were fractionated as described (Belgrader et al., 1991; Payraastre et al., 1992; Radichev et al., 2005; Reyes et al., 1997). Briefly,  $2 \times 10^6$  cells were harvested and suspended in 200  $\mu$ l CSK buffer (100 mM NaCl, 300 mM Sucrose, 3 mM MgCl<sub>2</sub>, 10 mM PIPES [pH 6.8], 0.5% Triton X-100, protease inhibitor cocktail [Sigma Cat # P8340], 0.5 mM dithiothreitol [DTT]). After centrifugation at 10,000  $\times$  g for 5 min at 4°C, the supernatant (the nucleocytoplasmic fraction; Sup1) was separated from the pellet, which was re-suspended in 200  $\mu$ l CSK buffer and treated with 50 U/ml DNase I at 37°C for 4 h. Ammonium sulfate was then added to this suspension to a final concentration of 0.25 M, and the sample was spun at 10,000  $\times$  g for 5 min at 4°C. The supernatant from this centrifugation contained the chromatin (Sup2). The pellet was further extracted with 200  $\mu$ l 2 M NaCl in CSK buffer for 5 min at 4°C, and then subjected to centrifugation at 10,000  $\times$  g for 5 min. The supernatant fraction was collected and considered to contain histones and the other DNA (Sup3), and the pellet was considered to be the nuclear matrix-containing fraction. The pellet was finally solubilized in 200  $\mu$ l 8 M Urea buffer (Sup4). For Western blotting, ten percent of each fraction (20  $\mu$ l) was separated on an SDS-PAGE and subjected to the analysis. Each protein was probed with a respective specific antibody followed by appropriate secondary antibodies conjugated with horseradish peroxidase (HRP). The chemiluminescence image was taken as pictures with a lumino-image analyzer (LAS-3000<sup>®</sup>, Fujifilm, Co) and the band intensity was analyzed with Quantity One (BioRad). For PCR analysis of the associated DNA, each fraction was diluted in ten-fold volume of nuclear lysis buffer (Promega), and 0.2 mg/ml proteinase K and 0.1 mg/ml RNase A were added, and the mixture was incubated at 56°C overnight. After a phenol-chloroform-isoamyl alcohol (25:24:1) extraction, the aqueous phase was precipitated with ethanol, and the precipitated DNA was suspended in TE (10 mM Tris-HCl [pH 7.6], 1 mM EDTA). The concentration was measured with a spectrophotometer (DU640, Beckman) and the final DNA concentration was adjusted to 10 ng/ $\mu$ l. PCR was

performed using primers: 5'-CCTGTCCCGCGCGGGCCCG-3' and 5'-GGCGCCCCCTCCCTCGTGC-3' for TR as described (Sakakibara et al., 2004), and 5'-AGAAAGTGATAAAAAGAATAAAC-3' and 5'-GGAGCTGTTAGAACACTTCTGG-3' for ORF57 region, respectively.

#### 2.4. Indirect immunofluorescence assay (IFA)

BC3, BJAB, and BC3/GFP-ORC1 cells were harvested and washed with phosphate buffered saline (PBS). To prepare cells that preserved the nuclear matrix structure, the cells were permeabilized with ice-cold CSK buffer for 5 min and then attached to a glass slide using the Cytospin 3 system (Shandon). The dried and spread cells on the slides were treated with 50 u/ml DNaseI in CSK buffer at 37 °C for 15 min in a humidified box, and then with 0.25 M (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub> in the buffer, to stop the reaction. Next, the cells were treated with 2 M NaCl in the CSK buffer for 5 min at RT and then fixed with 4% paraformaldehyde in PBS (4% PFA-PBS). After being washed three times for 5 min each with PBS containing 0.1% Tween 20 (Sigma, cat#: P9416) (PBS-T) and then dried, the cells were incubated with the first antibodies overnight at room temperature (RT). After another round of PBS-T washes, the cells were incubated with the secondary antibodies. The secondary antibodies used in this experiment were goat anti-mouse IgG Fab fragment antibodies conjugated either with Alexa<sup>®</sup> 488 or 546 and goat anti-rabbit IgG Fab fragment antibodies conjugated either with Alexa<sup>®</sup> 488 or 546 dependent on the first antibodies. In cases where the DNA was preserved, it was counter-stained with 4',6'-diamino-2-phenylindole (DAPI) (Molecular Probes).

To visualize LANA and its mutants in transfected cells, 2 days after transfection of the expression vectors, the cells were fixed in 4% PFA-PBS and permeabilized with PBS containing 0.1% Triton X-100 for 30 min. EGFP tagged proteins were detected with its fluorescence and V5 tagged ones were probed with an anti-V5 antibody (Nakalaitesq) followed by secondary antibodies conjugated with Alexa<sup>®</sup> 488 mentioned above. DNA was counterstained with DAPI.

#### 2.5. Cell synchronization and fluorescence-activated cell sorting (FACS) analysis

Mimosine (200 μM) (Calbiochem) was used to synchronize the BC3 and BJAB cells. Fourteen hours later, the cells were released into ordinary medium. They were harvested 0, 3, and 9 h later, washed with PBS, and then fixed with 70% ethanol at 4 °C overnight. The cells were then treated with 50 mM sodium citrate containing 100 μg/ml RNaseA, incubated at 37 °C for 2 h, suspended in 500 μl FACS flow solution containing 125 μg/ml propidium iodide (Nakalaitesq), and analyzed by flow cytometry (FACSCalibur, Becton Dickinson).

#### 2.6. Transfection

In a transient replication assay, HEK293 cells (2 × 10<sup>6</sup> per 3 cm dish) were transfected with 1 μg either LANA or its deletion mutant expression vectors with 1 μg BSH-TR6 using Superfect<sup>®</sup> (Qiagen). Forty-eight hours post-transfection, the cells were harvested and the Hirt DNA was prepared. The DNA was digested either with XhoI or XhoI plus DpnI and subjected to Southern blotting analysis with a TR fragment as a probe.

#### 2.7. Antibodies

Goat polyclonal antibodies against ORC1 (Abcam, ab10876), ORC4 (Abcam, ab9641), and Cdt1 (Abcam, ab14676) were purchased from Abcam (Cambridge, UK). Rabbit polyclonal antibodies against Histone H2B (-371) and H2A (-146) were purchased from

Upstate (New York, USA). Mouse monoclonal antibodies against Mcm7 (4B4), ORC2 (3B7), and GFP (RQ2) were purchased from MBL (Nagoya, Japan), an anti-Mcm5 antibody (CRCT5.1) was from Cosmo Bio (Tokyo, Japan), an anti-NuMA antibody (Ab-2) was from Oncogene (San Diego, USA), an anti-CDC6 antibody (C0224) was from Sigma (Saint Luis, USA), an anti-V5 antibody (V5005) was from nakarai tesque (Kyoto, Japan) and a rat monoclonal antibody against LANA (LN53) was from Advanced Biotechnologies Incorporated (ABi,) (Columbia, USA).

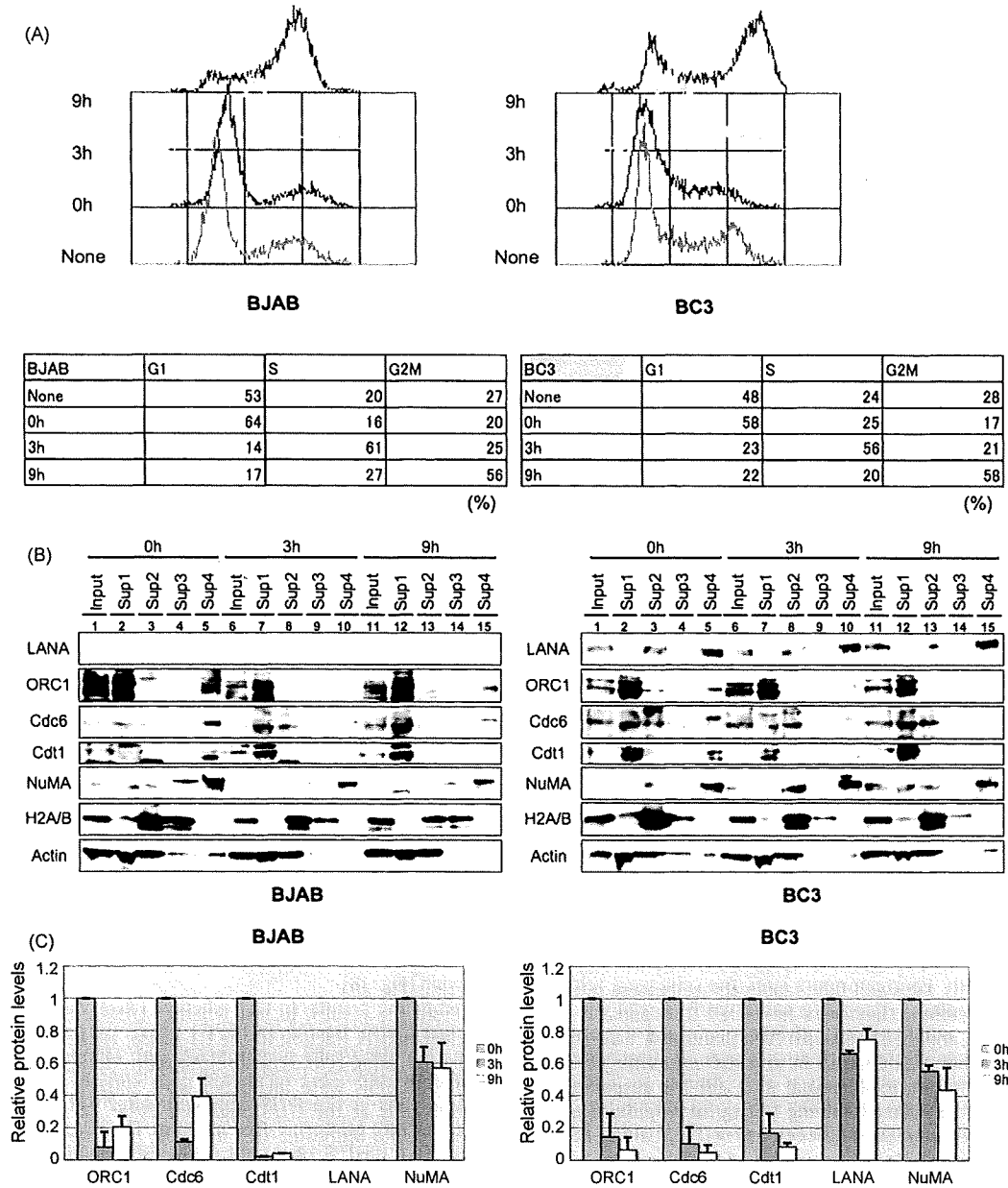
### 3. Results

#### 3.1. LANA and pre-RC components are localized in the nuclear matrix fraction in G1 phase

ORC1, a component of pre-RC, must be present to complete the pre-RC formation. ORC1 joins the ORC2-6 complex on the replication origin only during the G1 phase, and thereafter it is released from chromatin during the G1-to-S transition; it is then ubiquitinated and degraded (Li and DePamphilis, 2002; Ohta et al., 2003). ORC1 is reported to enter the sub-nuclear insoluble fraction called nuclear matrix and to join the ORC2-6 complex bound to replication origins in the late G1 phase, to initiate origin replication firing (Ohta et al., 2003). Thus, a proper time and place are required for ORC1 to execute its key role in replication origin activity.

Since previous study reported that LANA interacts with all kinds of ORCs (Lim et al., 2002; Verma et al., 2006), we also tried many times to show the physical interaction of them with immunoprecipitation followed by immunoblot, but failed. Then, we constructed a plasmid expressing GFP-tagged ORC1 (GFP-ORC1) to more easily detect ORC1 biochemically and histologically. We transfected BC3 cells with this plasmid, and established several stable cell lines expressing GFP-ORC1 (GFP-ORC1/BC3) and observed that GFP-ORC1 was colocalized with LANA (Fig. 2C, and see below). We thought that ORC1 and the other pre-RC components present at the active replication origin might be hard to be solubilized. To test the nuclear localization of the pre-RC, we performed a cell fractionation experiment and detected the GFP-ORC1 in the nuclear matrix fraction (Fig. 2B).

From the results, to test whether LANA was localized to the nuclear matrix fraction in the G1 phase, we performed cell fractionation using cells synchronized with Mimosine (Fig. 1A). BC3 and BJAB cells were incubated with 200 μM Mimosine, which arrests cells at the G1/S boundary. After 14 h, then they were released into Mimosine-free medium, harvested at the indicated times (G1 [0H], S [3H], and G2/M [9H]), and fractionated into nucleocytoplasmic (Sup1), chromatin (Sup2), histones containing the other DNA (Sup3), and nuclear matrix fractions (Sup4). Immediately after the release, about 58% of BC3 cells and 64% of BJAB cells were in the G1 phase (G1 [0H]); 3 h later, 56% of BC3 cells and 61% of BJAB cells had entered the S phase (S [3H]); 9 h after release, 58% of the BC3 and 56% of BJAB cells had entered the G2/M phase (G2/M [9H]), respectively (Fig. 1A). Cell fractionation followed by Western blotting analysis was carried out under these conditions (Fig. 1B), and we detected several replication factors in the fractions. In both of BC3 and BJAB cells, ORC1, Cdc6, and Cdt1 were in the nuclear matrix fraction in the G1 phase, and in the S phase at obviously lower levels (lanes 1–4 of BJAB and BC3 panels in Fig. 1B). LANA seemed to be enriched at the nuclear matrix throughout the cell cycle. Some extra bands of ORC1 and Cdt1 in the nucleocytoplasmic fraction may have been modified or degraded forms of these proteins (Fig. 1B). The change in protein level at the nuclear matrix fraction in each phase was calculated by normal-

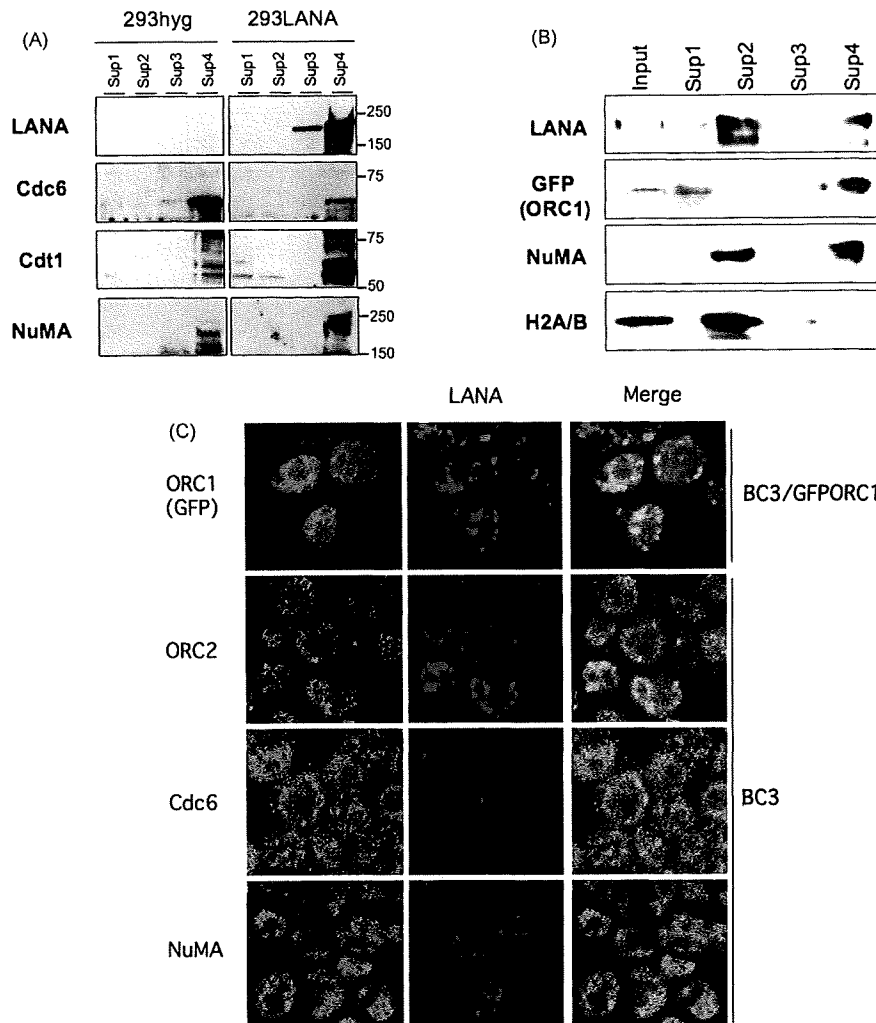


**Fig. 1.** LANA and pre-RC components are present in the nuclear matrix fraction in a cell-cycle-dependent manner. (A) BC3 and BJAB cells were arrested by incubation in the 200  $\mu$ M mimosine containing culture medium for 14 h and then released into medium without mimosine. Cells were harvested 0, 3, and 9 h after release and analyzed by FACS. The population of each phase was analyzed by the FACSCalibur system (Beckton–Dickinson) and is shown below. (B) Western blotting analysis of the cell fractions. Samples containing  $1 \times 10^6$  cells of each phase shown in (A) were fractionated as described in Section 2. Ten percent of each fraction (20  $\mu$ l) was separated by SDS-PAGE and analyzed by Western blotting with the specific antibodies indicated on the left. In Input, 2.5% of each fraction was combined and analyzed in the same way. This experiment was repeated several times and a typical result is represented. (C) Accumulation pattern of ORC1, CDC6, Cdt1, LANA and NuMA in the Sup 4 fraction (nuclear matrix) was graphed. The band intensity of ORC1, CDC6, Cdt1, LANA and NuMA in the Sup 4 lane and that of actin in the input lane at 0, 3, and 9 h after release of mimosine, respectively, was analyzed with a Quantity One<sup>®</sup> software (BioRad). Each Sup 4 band intensity to that of actin in the input lane at each time point after release of mimosine, respectively, was set at 1. Average from three experiments was calculated and shown with the standard deviation.

izing the values to the signal of actin in input lane at each time point after release (Fig. 1C). In the S phase, the level of LANA in the nuclear matrix fraction decreased marginally compared to that in the G1 phase. The level of NuMA also marginally decreased in the S and the G2/M phase. Because NuMA plays different roles, one of which is to regulate centrosome function, during the cell cycle, therefore the modification and/or the localization of NuMA

changes. In contrast, the levels of pre-RC components drastically decreased in the S phase (lane 10 of BJAB and BC3 panels in Fig. 1B and C).

Nuclear matrix mitotic apparatus (Numazaki et al., 1998), which is one of the nuclear matrix components and has an important role in the formation of the spindle pole (Gehrmlich et al., 2004) in the G2/M phase, was mainly present in the nuclear matrix fraction



**Fig. 2.** LANA self-associates with the nuclear matrix fraction and colocalizes with host pre-RC components. (A) One million 293hyg or 293LANA cells were harvested and fractionated. Ten percent of each fraction was separated on 10% SDS-PAGE and subjected to Western blotting analysis. (B) One million GFP-ORC1/BC3 cells were harvested and fractionated and subjected to Western blotting analysis as in (A). (C) Colocalization analysis of LANA and pre-RC components by immunofluorescent analysis. BC3 and GFP-ORC1/BC3 cells were permeabilized with ice-cold CSK buffer for 5 min, then placed on a glass slide and prepared to preserve the nuclear matrix. Components of the Pre-RC such as Cdc6, Cdt1, and a nuclear matrix protein, NuMA were detected with specific antibodies against them. ORC1 was detected with an anti-GFP antibody in GFP-ORC1/BC3 cells. LANA is shown in red and others are shown in green. Pictures were taken with a laser confocal microscopy (Radiance<sup>®</sup> 2000, BioRad). The original magnification was 10 × 40. Note that most of the cells in the ordinary culture are in the G1 phase and most of proteins outside of nuclear matrix were depleted in this treatment.

(lanes 5, 10, and 15 of BJAB and BC3 panels in Fig. 1B), which confirmed that cell fractionation was appropriately performed, though core histones, H2A and H2B, were mainly detected in the chromatin fraction in our condition probably due to somewhat severe DNase I treatment (Fig. 1B).

### 3.2. LANA localizes to the nuclear matrix fraction in the absence of other viral factors

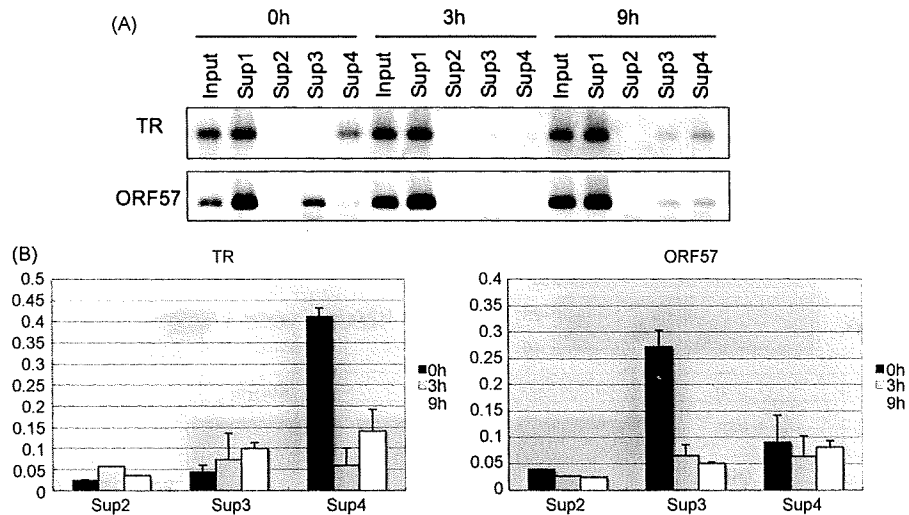
The above data showed that LANA was preferentially located in the nuclear matrix fraction throughout the cell cycle in KSHV-infected cells. The next question was whether LANA was recruited there by the other component, such as the viral genome. To answer this question, we performed cell fractionation in HEK293 cells stably expressing LANA (Fig. 2A). The results showed that LANA was localized mainly to the nuclear matrix fraction, and the nuclear matrix localization of Cdt1, Cdc6 and NuMA was consistent with

the experiment using BC3 and BJAB cells. These results indicated that LANA localized to the nuclear matrix fraction by itself, in the absence of other viral components. In the GFP-ORC1/BC3 cells, the similar results were obtained in the cell fractionation experiment (Fig. 2B). From this finding we predicted that the TR region would be recruited to the nuclear matrix by LANA, thereby allowing the KSHV genome to initiate replication at the nuclear matrix, with the complete pre-RC. If this is the case, the TR including the ori-P should also be present in the nuclear matrix region (see below).

### 3.3. LANA colocalizes with pre-RC components at the nuclear matrix

To demonstrate LANA's association with the pre-RC at the nuclear matrix, we carried out an immunofluorescence assay of nuclear matrix preparations using a confocal fluorescence





**Fig. 3.** The TR region (ori-P) is present in the nuclear matrix in a cell-cycle-dependent manner. DNA from fractions of the BC3 cells prepared in Fig. 1C was extracted as described in Section 2. The amount of DNA was measured by spectrophotometer (DU640, Beckman) and was adjusted to 10 ng/ $\mu$ l. Input DNA was prepared as a mixture of equal volume of the sup 1, 2, 3, and 4 fractions adjusted to 10 ng/ $\mu$ l. PCR was performed using 30 cycles for the TR and 40 cycles for ORF57, using 10 ng of each DNA. (A) The amplified samples were separated on the 2% agarose gel and visualized with ethidium bromide staining. (B) The band intensity was measured with a FX laser scanner (BioRad) and a QuantityOne<sup>®</sup> (BioRad) software. The data was calculated as the band intensity to that of the input, which was a mixed sample of all four fractions.

microscopy (BioRad Radiance<sup>®</sup> 2000). In this case, the cells were in the ordinary culture condition and most of the cells were in the G1 phase (data not shown). Cells were treated to preserve the nuclear matrix structure (see Section 2), and then stained for LANA, ORC2, GFP-ORC1, and NuMA using specific antibodies against them. No DNA was stained with DAPI, showing that most of the DNA integrity was destroyed and the nuclear matrix preparation was done well (data not shown). As shown in Fig. 2C, LANA was localized to the perinuclear region in a dotted pattern. The co-localization of LANA with components of the pre-RC, such as ORC1, ORC2, and Cdc6, was observed mainly at the perinuclear region. NuMA, a nuclear matrix protein, was also observed in the perinuclear region and co-localized with LANA, although it was stained more diffusely than LANA. These results suggested that LANA was co-localized with pre-RC components at the nuclear matrix.

#### 3.4. The TR region is predominantly located in the nuclear matrix fraction in a cell-cycle-dependent manner

As described above, if LANA accumulated in the nuclear matrix region without being recruited by other viral components and co-localized with the pre-RC, the viral replication origin should also go to the same region to replicate, since LANA binds to the LBS within the TR and supports the replication. Fraction-associated DNA was extracted from the cells synchronized with mimosine as in Fig. 1A. All the cellular materials were exposed to DNase I except for the nucleo-cytoplasmic fraction (Sup1), which was the DNase I pre-treatment fraction. The DNA resistant to DNase I treatment in each fraction was then treated with proteinase K followed by phenol-chloroform-isoamyl alcohol extraction and ethanol precipitation. The DNA concentration was adjusted to 10 ng/ $\mu$ l, and 10 ng of the DNA of each fraction was subjected to PCR. The results showed the TR region containing ori-P was present in the nuclear matrix fraction (Sup4), especially during the G1 phase (Fig. 3A and B). The ORF57 region was analyzed as a control, but it was barely detectable in the nuclear matrix fraction

(Sup4) at any phase (Fig. 3A and B) and was consistently detected in the histone-DNA fraction (Sup3) in the G1 phase, although it is unclear why the sequence around ORF57 was detected in the fraction in the G1 phase. Even if the condition used in this experiment was not informative for quantitative analysis, it might be still suggestive for that TR region was detected in Sup4 at the G1 phase. Thus, remarkable difference in accumulation profile of TR and ORF57 region in the G1 phase suggests that the ori-P uniquely resides at the nuclear matrix but not all of the viral genome. Thus, the viral genome around the TR region predominantly existed in the nuclear matrix, especially during the G1 phase.

#### 3.5. The nuclear matrix localization of LANA might be determined by the whole structural consequence

We thus elucidated that LANA was predominantly present at the nuclear matrix and TR containing ori-P was also recruited there. Then, we tested whether the localization of LANA and ori-P coincidentally happened or not. Firstly, we made several deletion mutants of LANA to determine which region of the LANA open reading frame was a minimum requirement to accumulate in the nuclear matrix fraction (Fig. 4A). As shown in Fig. 4B, only the full length of LANA was accumulated in the nuclear matrix fraction (Sup4). Either the N-terminal or the C-terminal part was not enough to nuclear matrix localization and neither was the N-terminal plus C-terminal part. In IFA (Fig. 4C), N-terminally deleted LANA ( $\Delta$ CBS and  $\Delta$ N) was localized in the cytoplasm. Further deletion up to 921aa ( $\Delta$ DBD) restored its nuclear localization, but still not in the nuclear matrix fraction (Fig. 4B). We observed similar localization gFL, gN and gN-DBD in the other cell lines such as Vero and HuH7 cells. Thus, strong nuclear localization signal should be in the N-terminus (1-106aa) and in the C-terminus (922-1162aa), but they were not enough for localization at nuclear matrix fraction. Therefore, our data suggest that not a typical signal but the structural consequence of the whole protein could be a determinant for LANA's localization at nuclear matrix.

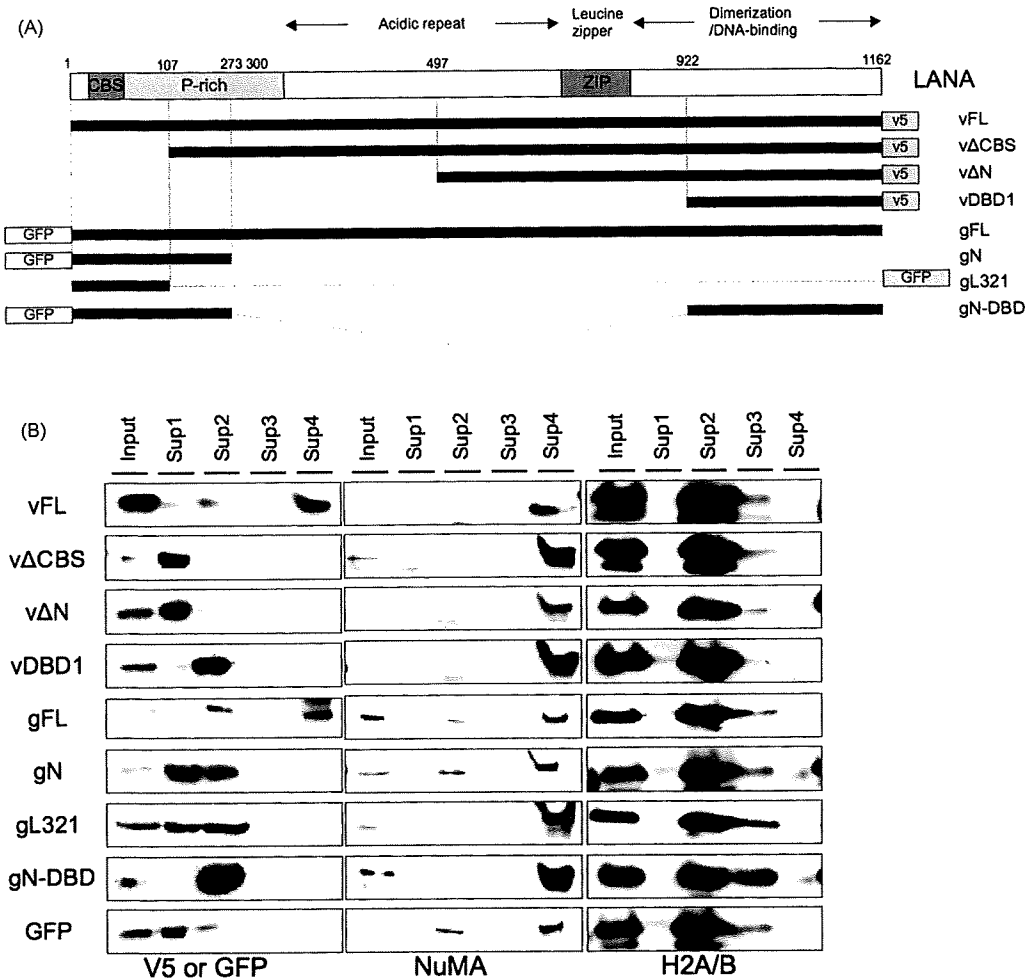
### 3.6. Viral replication in the latency is dependent on nuclear matrix localization of LANA

Next, we investigated the relationship between the nuclear matrix localization and the replication in a transient replication assay. A TR-containing plasmid was transfected to HEK293 cells with various LANA deletion mutants shown in Fig. 4A and the Hirt DNA was collected 48 h post-transfection and subjected to Southern blotting analysis with or without Dpn I (Fig. 4D). The results showed that decrease in the nuclear matrix localization of LANA led to drastic reduction of the replication of ori-P containing plasmid, even though some constructs (vDBD and gN-DBD) showed nuclear localization and retained LBS-binding activity (Garber et

al., 2001; Komatsu et al., 2004). Thus, nuclear matrix localization of LANA could be a pre-requisite condition for KSHV replication in the latency.

### 4. Discussion

The KSHV genome exists as an episome in latently infected cells and maintains this condition while replicating in concert with the cell cycle. KSHV replication in latency seems to be mainly dependent on the cellular replication machinery and two viral factors, LANA and ori-P. In case of de novo infection, it probably takes a time to establish latency and start host cell cycle dependent viral replication, since the viral particles does not contain LANA (Bechtel



**Fig. 4.** Nuclear localization of LANA is required for ori-P mediated viral replication. (A) Schematic presentation of LANA expression constructs. Two full-length LANA expression vector was constructed. One was tagged at the C-terminus with a V5 epitope (vFL) and another was at the N-terminus with a GFP ORF (gFL). N-terminally deleted mutants tagged at C-terminus with a V5 epitope were vΔCBS, vΔN, and vDBD, and in each construct, N-terminal 106aa, 464aa, and 921aa were deleted, respectively. gN contained GFP tagged N-terminal 273aa of LANA and gL321 did N-terminal 107aa followed by a GFP ORF, and gN-DBD did N-terminal 273aa plus C-terminal 922 to 1162aa. (B) Cell fractionation experiment of the LANA mutants. Each expression vectors including a GFP expression vector were transfected into HEK293 cells and 2 days post-transfection, the cells were harvested and subjected to cell fractionation. The expression of LANA mutants was tested with an anti-V5 antibody or an anti-GFP antibody. Cellular fractionation was assured by checking localization of NuMA and Histone H2A/B (H2A/B). In input lane, 2.5% (5 μl) of each fraction was combined and analyzed. (C) Cellular localization of LANA mutants. Transfected cells as in (B) were also subjected to IFA. LANA and its mutants were detected either by GFP or an anti-V5 antibody shown in green. Counterstained DNA was shown in red. (D) Ori-P mediated transient replication assay with LANA mutants. The Six-mer of TR containing plasmid (BSII-TR6) was transfected into HEK 293 cells with LANA expression constructs shown in (A). Forty-eight hours post-transfection, the cells were harvested and Hirt DNA was prepared. The DNA was digested with BglIII completely and nine-tenth of the aliquot was further digested with DpnI. (upper panel) DpnI resistant DNA was detected with a TR fragment as a probe along with the sample without DpnI digestion (transfection control). A typical autoradiography is shown. (lower panel) Replication efficiency was calculated by setting the band intensity of DpnI (+)/(–) in case of vFL expression at 1 from three Southern blotting analyses as shown in the upper panel. The experiment was performed three times and the data are shown as the average with the standard deviation.

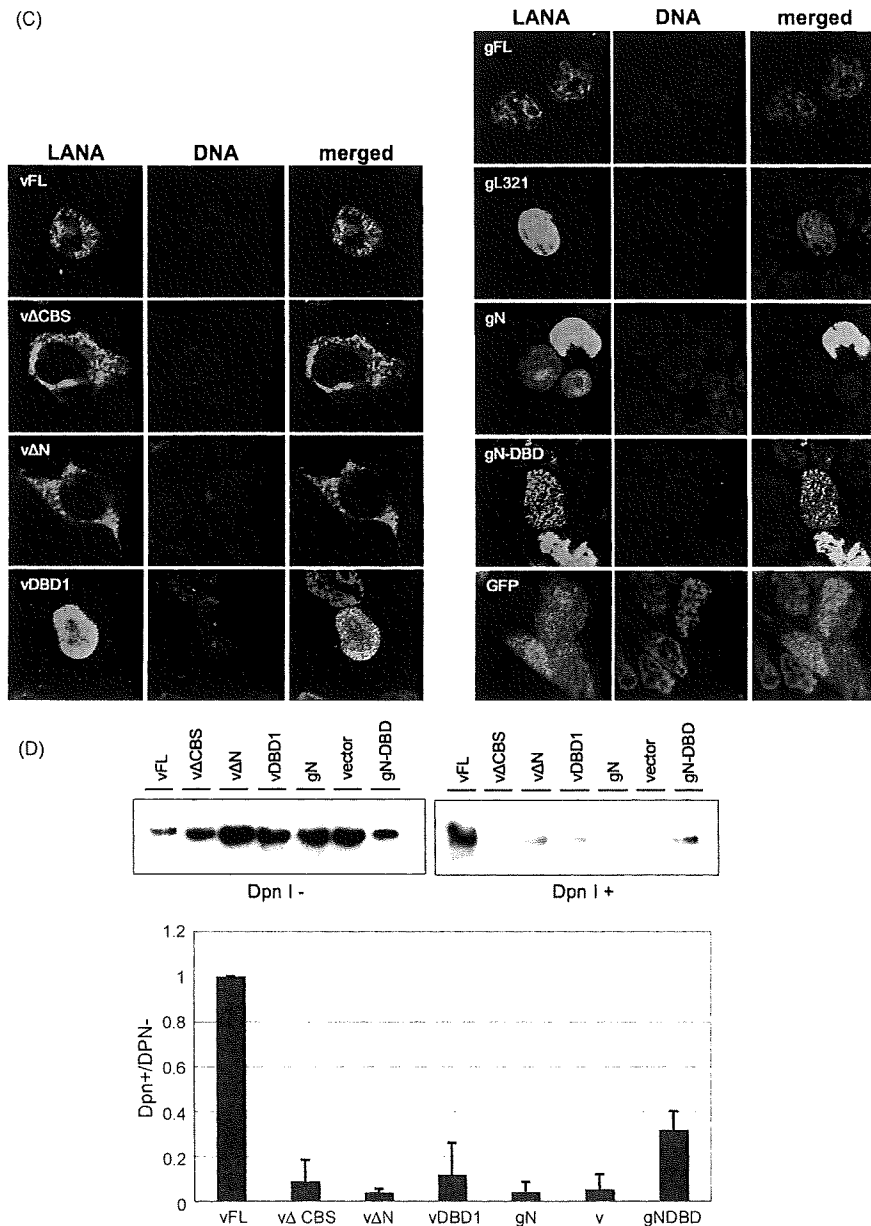
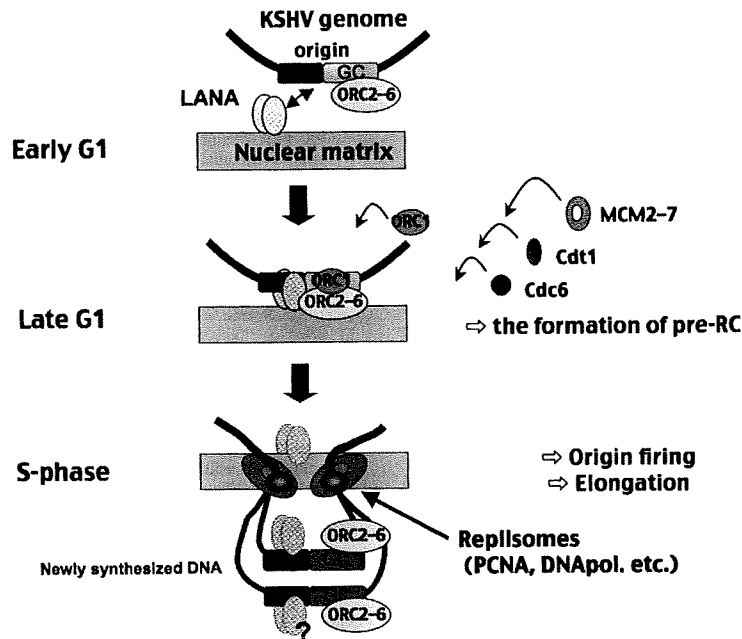


Fig. 4. (Continued).

et al., 2003, 2005; Grundhoff and Ganem, 2004; Lagunoff et al., 2002).

To initiate the genome replication, a complete pre-RC must be formed on the replication origin (DePamphilis, 2003; Sun et al., 2002). For completion of the pre-RC, ORC1 is finally recruited to the ORC2-6 complex (Bell, 2002; DePamphilis, 2003). Although some reports showed that ORC1 as well as ORC2-6 interacted directly with LANA *in vitro* or *in vivo* (Lim et al., 2002; Verma et al., 2006), we could not confirm these results. Cell fractionation experiments (Fig. 1) showed that LANA and pre-RC components including ORC1, Cdc6, and Cdt1 were present together in the nuclear matrix fraction, which is a specialized part of nucleus in terms of resistance to

DNaseI treatment and high salt condition, at the G1 phase, and at reduced levels in the S phase, even though only about 50-60% of the population was in the S phase. The ORC1 signal in the nuclear matrix in the G2/M phase could result from the remaining G1 phase population, or this fraction of ORC1 might function in the G2/M phase, consistent with the recent observation that not only ORC2-6 but also a portion of the ORC1 binds chromatin throughout the cell cycle (Laman et al., 2001; McNairn et al., 2005; Okuno et al., 2001). The release of the ORC1 from chromatin is believed to be modified by ubiquitination for its degradation (Li and DePamphilis, 2002), but it is also reported that the role of ubiquitination of ORC1 during the S-to-M transition does not result just in the destruction but also in its



**Fig. 5.** A suggestive model for replication of the KSHV genome at the nuclear matrix. LANA associates with the nuclear matrix in itself and recruits the ori-P of KSHV genome to the nuclear matrix region by binding to the LBS. The complete pre-RC is formed on the nuclear matrix in the late G1 phase. In the S phase, the components of the pre-RC except for ORC2-6 are released from the origin by ubiquitination or phosphorylation. The replisome including PCNA, DNA polymerases, etc., is recruited to the nuclear matrix and kept there, and the origin DNA is unwound, and elongation is initiated. The replicated DNA is immediately released from the nuclear matrix region. The majority of LANA is thought to stay at the nuclear matrix from our analysis, though it is needed further to elucidate how and where replicated KSHV DNA is localized.

sequestration from the origin, to prevent its re-replication with the ORC-chromatin sites (Anachkova et al., 2005; Li and DePamphilis, 2002).

Experiments with BC3 cells expressing GFP-ORC1 suggested that some specialized ORC1 kept its intact form at nuclear matrix region. Such experiments also gave us a hint that nuclear matrix localization of LANA could be an important condition in terms of LANA-dependent viral replication in the latency, because it has been discussed about nuclear matrix localization of cellular replication machinery (Anachkova et al., 2005; Cook, 1999; Kitamura et al., 2006; Radichev et al., 2006).

Therefore, it was not surprising that we were unable to detect the interaction between LANA and ORC1 by immunoprecipitation assay, since pre-RC components such as ORC1, Cdc6, and Cdt1 localized to the nuclear matrix fraction, which is very insoluble with an ordinary buffer as mentioned and LANA was almost exclusively present at the nuclear matrix throughout the cell cycle. We showed that LANA and pre-RC components were present in the nuclear matrix fraction and the co-localization of LANA with pre-RC components and with NuMA, by IFA. It was reported that LANA and NuMA interacted each other and LANA might be recruited by NuMA in the nuclear matrix, though it is still unclear because gN-DBD, which retains the interacting region to NuMA, was fractionated into the chromatin fraction but not into the nuclear matrix fraction (Si et al., 2008). Although it is not clear either how much the fraction components vary cells from cells, NuMA might function to keep the virus genomes at a constant number. Different from Kaposi's sarcoma cell lines, PEL cell lines could have a special reason keeping the viral genome, which is partly because PEL requires KSHV function to be alive (Chen and Lagunoff, 2005; Ueda et al., 2006). Further investigation is required to confirm that these factors are directly associated with the nuclear matrix components.

On the other hand, some investigators have suggested that the origin of replication is associated with the nuclear matrix and that this association is cell-cycle dependent (Djeliova et al., 2001; Radichev et al., 2005), leading them to propose a model for formation of the pre-RC at the nuclear matrix (Anachkova et al., 2005). Our experiment confirmed these previous reports, and in case of KSHV genome, it was thought that LANA had an essential role for the recruitment of ori-P to the nuclear matrix since non-nuclear matrix-associated LANA mutants did not support the viral replication in a transient replication assay and the less effectiveness might be dependent on the loss of interaction with NuMA (Si et al., 2008), even though such mutants maintained the binding activity to the LBS (Garber et al., 2001; Hu et al., 2002; Kelley-Clarke et al., 2007; Komatsu et al., 2004).

ORC2-6 is known to bind to chromatin throughout the cell cycle, but ORC1 and MCMs are recruited to the origin only in the late G1 phase (Blow and Dutta, 2005; DePamphilis et al., 2006), and we showed that LANA constantly existed in the nuclear matrix region. Such data suggest that the cellular replication machinery for complete pre-RC formation probably functions for activation of the viral ori-P in the presence of LANA in a cell-cycle-dependent manner. In such a sense, an indirect action by LANA such as the interaction with histone acetyltransferase binding to ORC1 (HBO1) might be important to establish the ori-P activity (Stedman et al., 2004).

Furthermore, for the KSHV replication in latency, recent studies showed that the minimal replicator consists of LBS1/2 and a downstream 32-bp GC-rich segment (nt 539-610 in GenBank accession No. 75699) (Hu and Renne, 2005). Our experiment further confirmed that one of the two LANA-binding sites and the 32-bp GC-rich downstream segment were required and sufficient for the replication, independent of their orientation, though the orientation might affect the efficiency (our personal communication and the similar result by Hu et al. [page 29 in the Abstract of "the

10th International Workshop on Kaposi's Sarcoma Associated Herpesvirus (KSHV) and Related Agents", August 1-5, Portland, OR). Neither the LBS-binding sites nor the GC-rich segment alone was sufficient for the viral ori-P activity. The requirement of the 32-bp GC-rich segment remains to be elucidated; if LANA recruits ORCs by its binding activity with them, the LBS-binding sites should be sufficient to initiate replication, because the DNA-binding activity of ORCs is not sequence specific, although it has a preferred sequence (Vashee et al., 2003), and the GC-rich segment is rather unusual as a replicator. Thus, further investigation is needed to elucidate how the LBS and 32-bp GC-rich downstream segment function in viral replication in latency.

It has been demonstrated by live-cell imaging that DNA replication of chromosomal loci occurs at replication factories where the bulk of DNA synthesis takes place (Leonhardt et al., 2000). Such a replisome in the S phase is associated with replication factories, and the replicated DNA separates from there (Cook, 1999). We demonstrated that not only LANA and the pre-RC, but also the TR region of the KSHV genome preferentially localized to the nuclear matrix fraction, especially in the G1 phase. The DNA in the nuclear matrix fraction was resistant to DNase I treatment and also to high salt condition, thus the detection of the TR region in this assay was very suggestive of a strong association of ori-P with a nuclear matrix component occurring in the G1 phase.

Taken together, these experiments suggest that a viral latent protein, LANA, recruits the viral latent origin to the nuclear matrix through its binding activity to the LBS, which leads to the formation of the complete pre-RC on the GC-rich segment to initiate viral replication in a cell-cycle-dependent manner (Fig. 5). This process could not be necessarily achieved by the direct interaction between LANA and ORCs, and at least, such a recruitment factor for ORCs have not been identified in case of host genome replication system. Needless to say, further experiments will be needed to show whether the GC-rich segment is in fact required for the pre-RC placement. Moreover, elucidation of the fundamental mechanism of KSHV genome replication in latency may shed light on how the mammalian replication origin is determined.

## Acknowledgements

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# ヘルペスウイルス学のエッセンス

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現在8つのヒトヘルペスウイルスが同定されているが、最初に分離された単純疱疹ヘルペスウイルスから考えると、その研究の歴史は90年に及ぶ。その結果、慢性感染症に関わる本ウイルスの実態が少しずつ分かりつつある。ひとたびヒトに侵入すると、潜伏感染状態を樹立し、感染細胞内でゲノムの一部として振る舞い、子孫存続の機会を待ち続ける。その過程で宿主との相互作用の結果、多彩な病態に関与している。どのような機構でそれぞれの病態が惹起されるのか、いまだ不明の点も多く、今後の研究展開が期待される。そして研究成果に基づいた、より効果的なウイルス制御法が開発されることを願う。

**Key Words:** ヘルペスウイルス, 潜伏感染,  $\alpha$ ヘルペスウイルス,  $\beta$ ヘルペスウイルス,  $\gamma$ ヘルペスウイルス

## I はじめに

“Herpes”とはギリシャ語で“這う”を意味する言葉で、這うようにして広がる皮膚疾患に用いられていたと思われる。口唇ヘルペスの疾患としての認識は紀元前100年くらいにはあったと思われるが<sup>1)</sup>、20世紀初期に口唇ヘルペスからウイルスが分離され、ヘルペスウイルス属の確立に至った。この時点で研究が開始されたと考え、ヘルペスウイルス研究は90年の歴史を持つ。

ヘルペスウイルスはヒトに潜伏感染するDNAウイルスの代表格である。ヒト染色体には組み込まれないepisome (ウイルスに特化してviromeという言い方も使われ始めている)として機能し、水平感染によってヒト界に伝播・維持されている。本稿では8つのヘルペスウイルス<sup>1)</sup>について、その特徴を総論的に解説したい。

## II 疫学

ヒトに感染するヘルペスウイルスの感染率は地域性・民族により若干の差があるものと考えられ

るが、本ウイルスの感染率は群を抜いて高い。水疱瘡ウイルス (varicella zoster virus : VZV)<sup>2)</sup>、ヒトヘルペスウイルス6 (human herpesvirus 6 : HHV-6)<sup>3)</sup>、ヒトヘルペスウイルス7 (human herpesvirus 7 : HHV-7)<sup>3)</sup>、サイトメガロウイルス (cytomegalovirus : CMV)<sup>4)</sup>やエプスタイン・バーウイルス (Epstein-Barr virus : EBV)<sup>5)</sup>は、ヒト成人での感染率は80%以上であると考えられている。単純疱疹ヘルペスウイルス1型 (herpes simplex virus : HSV-1)<sup>6)</sup>で50~70%、単純疱疹ヘルペスウイルス2型 (herpes simplex virus 2 : HSV-2)<sup>6)</sup>が20~50%、カポジ肉腫関連ヘルペスウイルス (Kaposi's sarcoma-associated herpesvirus : KSHV)<sup>7)</sup>が2~60%と言われている。KSHVの感染率は地域差が大きいと思われるが、ポリオーマBK (polyoma virus BK, 72~98%)、ポリオーマJC (polyoma JC, 72~98%)、アデノ随伴ウイルス (adeno-associated virus : AAV, 60~90%)を除くと、ヘルペスウイルスはヒト界に広く蔓延し潜伏感染状態を樹立する代表格で、潜伏感染した細胞

The essence of herpesvirology

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においてゲノムの一部として振る舞うことになる<sup>8)</sup>。

### Ⅲ 感染経路・様式

8つのヘルペスウイルスの感染様式にはそれ程違いはなく、基本的には salivary shedding (唾液拡散)、感染局所との粘膜接触感染がおもな感染様式であると思われる。HSV-1, CMV, EBV, HHV-6 および HHV-7, KSHV は唾液発散による感染が主流で、幼少期に、特に両親との緊密な接触により感染が成立するものと思われる。この時期の感染はほとんど不顕性で、そのまま潜伏感染状態となりウイルス保因者となる。

一方、VZV は一般に幼児期の流行時期に感染を受ける。HSV-2 はウイルス学的には HSV-1 に酷似するが、感染組織は性器を中心とすることが多く、また KSHV も男性同性愛者にカポジ肉腫 (Kaposi's sarcoma : KS) が多くみられることから、性行為感染症としての側面も持つ。

### Ⅳ 潜伏感染と溶解感染

ヘルペスウイルスの最大の特徴のひとつは潜伏感染を樹立することであり、慢性感染症を惹き起こす多くのウイルスが持続感染状態になることと対比される。潜伏感染と持続感染の違いは、ウイルスを産生し続けているかどうかである。個体の中でウイルスを産生し続けながら感染状態を維持する持続感染では、免疫監視機構をいかに調節して回避するかが感染持続の鍵となる。一方、潜伏感染はウイルス自体がその遺伝子発現を極限状態まで落として、いわばステルス (stealth) 状態にな

ることで免疫監視機構を回避し、娘ウイルスを産生して子孫を残す機会を待っていると考えられる。

潜伏感染を樹立する組織・細胞は各ヘルペスウイルスにより異なる。一般的には、 $\alpha$ ヘルペスウイルス (HSV-1 および HSV-2, VZV) は感覚神経系の神経節神経細胞に、 $\beta$ ヘルペスウイルス (CMV, HHV-6 および HHV-7) は血球系に、 $\gamma$ ヘルペスウイルス (EBV, KSHV) は B リンパ球に潜伏感染するとされている。

娘ウイルスを産生する生活環を溶解感染と呼ぶ。本生活環では 100 個前後存在するウイルス遺伝子すべてが順序よく発現して、最終的には爆発的な娘ウイルス産生に至る。潜伏感染状態に何らかの刺激が入ると、溶解感染が誘導 (再活性化) されることがある。HSV-1 では日光 (UV) など、EBV では IgG (免疫グロブリン G) の結合、KSHV ではある種のサイトカインやフォルボールエステルなど、薬剤が誘導の起因になる。

### Ⅴ ウイルス粒子構造・ウイルスゲノム・遺伝子

ヘルペスウイルス粒子は、外側に脂質二重膜からなる膜粒子 (envelope : 120nm 前後)、内部にキャプシッド (capsid : 70nm 前後) を内包し、その内部にゲノムがある。粒子としての最大の特徴は、膜粒子とキャプシッドのあいだにテグメント (tegument) という構造があることである。

ヘルペスウイルスは 120 ~ 230kb の直鎖状二本鎖 DNA ゲノムを持つ。直鎖状のゲノムは感染後に末端で結合し、環状ゲノムとなる。基本的なエレメントとしては、ユニーク領域、反復配列領

VZV (varicella zoster virus)

HHV-6 (human herpesvirus 6 ; ヒトヘルペスウイルス 6)

HHV-7 (human herpesvirus 7 ; ヒトヘルペスウイルス 7)

CMV (cytomegalovirus ; サイトメガトウイルス)

EBV (Epstein-Barr virus ; エプスタイン・バーウイルス)

HSV-1 (herpes simplex virus ; 単純疱疹ヘルペスウイルス 1 型)

HSV-2 (herpes simplex virus 2 ; 単純疱疹ヘルペスウイルス 2 型)

KSHV (Kaposi's sarcoma-associated herpesvirus ; カポジ肉腫関連ヘルペスウイルス)

AAV (ade-no-associated virus ; アデノ随伴ウイルス) KS (Kaposi's sarcoma ; カポジ肉腫)

IgG (免疫グロブリン G)



域、溶解感染の複製 origin として機能する配列 (ori-Lyt) などがある。潜伏感染で機能する複製 origin (ori-P) は細胞分裂に呼応して、複製・分配・維持する機構を持つ  $\gamma$  ヘルペスウイルスだけに知られている。

ヘルペスウイルスの基本的なエレメントのひとつであるユニーク領域にある 100 ~ 150 個ほどの遺伝子は、前初期 (immediate early : IE,  $\alpha$ ) 遺伝子, 初期 (early : E,  $\beta$ ) 遺伝子, 後期 (late : L,  $\gamma$ ) 遺伝子に大別される。IE 系遺伝子の多くは転写制御系遺伝子であり、HSV-1 では、 $\alpha 4$  (ICP4),  $U_{L54}$  (ICP27),  $\alpha 47$  (ICP47) など複数の遺伝子が IE とされている。EBV や KSHV では真の IE 遺伝子はひとつ (それぞれ *zta* と *rtA*) であり、それが発現すると溶解感染の回路が始動する。E 系遺伝子群は複製に直接関わるポリメラーゼなどの遺伝子が含まれる。複製に直接関わらないものの、溶解感染の完遂を助ける多くの副遺伝子 (accessory gene) もこの中に含まれることが多い。KSHV では、*v-bcl-2*, *v-il-6*, *v-mip*, *v-gPCR*, *v-irf* や *k1*, *k15* などの宿主から取り込んだと思われる機能性遺伝子や、トランスフォーメーションに関わるとされる遺伝子がこの中に含まれている<sup>9)</sup>。L 系遺伝子群は粒子構成タンパク遺伝子をコードしている。

## VI 潜伏感染における遺伝子発現制御と複製機構

潜伏感染と溶解感染ではまったく異なった遺伝子発現制御機構が働いているものと考えられる。HSV-1 潜伏感染ではごく限られた領域のみが活性化していて、LAP (LAT promoter) を利用して 8.3kb 超、2.0kb とその 1.45kb の3つの LAT (latency-associated transcript) 遺伝子のみが発現する。ただ、LAT 遺伝子が潜伏感染にどのように機能しているのかについては報告がまちまちで、一定の見解がない。この領域の欠損変異株も

潜伏感染を樹立できるという報告もある。また、タンパクをコードしているのかも未解決の問題のひとつである。

限局した領域のみが活性化していることは KSHV にも当てはまる。KSHV の潜伏感染では、*lana*, *v-cylin*, *v-flip*, *k12* 遺伝子と、*lana-2* と呼ばれる *v-irf* ホモログのひとつが発現している。前者4遺伝子はひとつの発現領域を形成して、17個の miRNA もこの領域で発現している。ヘルペスウイルスゲノム内のひしめく遺伝子の中でみられるこのような制御はきわめて緻密である。

EBV では少し状況が異なっている。EBV には3つの基本的な潜伏感染の型 (latency I [バーキットリンパ腫], latency II [鼻咽頭がん], latency III [lymphoblastoid cell line : LCL と一部のバーキットリンパ腫]) があり、発現している遺伝子に若干の違いがある。共通しているのは、*EBNA1*, *EBERs* と *BARTs* である。*EBNA1* の発現に関わるプロモーターが、latency I と latency II では Qp, III では Wp と Cp といった違いもあるが、ゲノムの半分~それを超えた領域で転写が行われている。

潜伏感染におけるウイルスゲノム複製については、EBV と KSHV で研究が進んでいる。EBV の ori-P は family of repeats (FR) と dyad symmetry (DS) から構成され、ウイルス側因子 EBNA1 の結合配列が存在している。DS が複製の開始に、FR は複製したゲノムの分配維持に機能していると考えられている<sup>10)</sup>。KSHV の ori-P はゲノムの末端反復配列 (terminal repeats : TR) 内にあり、ウイルス因子 LANA の結合配列とそれに続く 32bp の GC に富んだ配列で構成される<sup>11)</sup>。EBNA1 や LANA が細胞周期依存性に、宿主複製開始前複合体 (pre-replication complex : pre-RC) を複製開始領域に呼び寄せる機構が提唱されている<sup>12)</sup>。

LCL (lymphoblastoid cell line)

FR (family of repeats)

DS (dyad symmetry)

TR (terminal repeats ; 末端反復配列)

pre-RC (pre-replication complex ; 宿主複製開始前複合体)

VII 疾患特性

HSV-1 および HSV-2 の関わる疾患はそれぞれ、頭頸部（三叉神経領域）、臀部～会陰部（仙骨神経領域）を中心とする水疱様疾患として、カポ

ジ水痘様発疹症、口唇ヘルペス、顔面ヘルペス、性器ヘルペスが、初感染、再感染、再活性化により発症する。また、HSV は神経細胞に親和性・増幅性が高く、中枢神経系に侵入し脳炎などを起こすと、多くの場合、生命に関わるほど重症化する。

表 ヒトヘルペスウイルスの特徴

ウイルス	α β γ	ゲノム サイズ (kb)	ウイルス 保有率 (%)	潜伏感染場所 (臓器/組織・ 細胞)	急性病態	慢性病態	
						正常人	免疫不全者
herpes simplex virus 1 (HSV-1)	α	152	50 ~ 70	感覚新神経節 神経細胞	咽頭炎 角膜炎 脳炎	口唇ヘルペス 角膜炎 脳炎	左記疾患の重症化 肺炎 肝炎
herpes simplex virus 2 (HSV-2)	α	155	20 ~ 50	感覚新神経節 神経細胞	性器 ヘルペス	性器ヘルペス 脳炎	左記疾患の重症化
varicella zoster virus (VZV)	α	125	> 90	感覚新神経節 神経細胞・星状 細胞・リンパ球	水痘	带状疱疹	左記疾患の重症化 (全身性) 肺炎 肝炎
Epstein-Barr virus (EBV)	γ	172	80 ~ 90	咽頭粘膜細胞 B リンパ球	伝染性単核症	バーキットリンパ腫 非ホジキンリンパ腫 鼻咽頭がん 胃がん	左記疾患に準ずる リンパ球増殖症
cytomegalovirus (CMV)	β	230/236	80 ~ 90	骨髄単核球	伝染性単核症	まれ	血管炎 肺炎 網膜炎 肝炎・胃腸炎 髄膜脳炎
human herpesvirus 6 (HHV-6A, HHV-6B)	β	A: 159/170 B: 162/168	> 90	リンパ球?	突発性発疹	?	髄膜脳炎?
human herpesvirus 7 (HHV-7)	β	145	> 90	リンパ球?	突発性発疹	?	?
Kaposi's sarcoma-associated herpesvirus (KSHV)	γ	170/210	2 ~ 60	内皮細胞 B リンパ球	?	カポジ肉腫 キャッスルマン病	カポジ肉腫 キャッスルマン病 原発性滲出性リンパ腫

(文献8より一部改変)

IM (infectious mononucleosis ; 伝染性単核症)

PTLD (posttransplant lymphoproliferative disease ; 移植後リンパ球増殖症)

PEL (primary effusion lymphoma)

MCD (multicentric Castleman's disease ; 多中心性キャッスルマン病)

ACV (acyclovir ; アシクロビル)

VCV (valacyclovir ; バラシクロビル)

GCV (gancyclovir ; ガンシクロビル)

VZVの関わる疾患は水痘と帯状疱疹である。水痘は初感染で帯状疱疹は再活性化で発症する。

EBVの感染は幼少期に不顕性感染で終わることが多いが、思春期以降の初感染は伝染性単核症(infectious mononucleosis: IM)として顕性化することがある。潜伏感染から発症する疾患として重要なものは、バーキットリンパ腫、鼻咽頭がんなど腫瘍性疾患で、近年、胃がんの発生にも関わっていることが報告されている。移植後リンパ球増殖症(posttransplant lymphoproliferative disease: PTLD)にも深く関わっているとされる。KSHVもカポジ肉腫(KS), primary effusion lymphoma (PEL)といった腫瘍や、多中心性キャッスルマン病(multicentric Castleman's disease: MCD)という腫瘍性疾患ときわめて深く関わっている。ただ、バーキットリンパ腫や鼻咽頭がんでは地域性が異なったり、発症年齢に差があったり、EBV単独の疾患ではないのかもしれない。KSHVが関わる腫瘍・腫瘍性疾患はAIDS(acquired immunodeficiency syndrome)病態下で発症することが多く、本ウイルスの腫瘍発生能力は免疫監視機構から免れることが重要であると思われる。

CMVでもっとも問題になるのは、妊娠初期の母親の初感染で聴力障害(~17%)が報告されている。思春期以降の水平・初感染で単核症が発症することがあるが、EBVによるIMに比し、症状は軽く発熱・倦怠感で終わることが多い。免疫不全状態では網膜炎や間質性肺炎など多彩な病態に絡んでいると考えられている。

HHV-6とHHV-7は初感染で突発性発疹の原因ウイルスとして知られる。唾液を介した親からの乳児期の感染によると思われるが、詳細は不明である。

## VIII 治療法

抗ヘルペスウイルス剤としてはAra-A, IDUなどの核酸アナログが用いられてきたが、ヘルペスウイルス感染症の治療を本質的に変えたのはアシクロビル(acyclovir: ACV)の出現である。ACVはグアノシンの核酸アナログで、ヘルペスウイル

スのコードするチミジンキナーゼでモノリン酸化が起こることで活性化され、GMPキナーゼ、NDPキナーゼにより最終的に三リン酸化されてウイルスのDNAポリメラーゼによるDNA合成に利用され、DNA鎖合成終結核酸として機能する感染細胞特異的に作用するプロドラッグである<sup>13)</sup>。その誘導体のバラシクロビル(valacyclovir: VCV)も使用されている。CMV感染症に対しては最近、ガンシクロビル(gancyclovir: GCV)が使用されているが、他のヘルペスウイルスに臨床効果の確認された薬剤はまだない。

## IX おわりに

ヒトに感染する8つのヘルペスウイルスのこれまでの研究の成果をもとに概説し、それぞれのヘルペスウイルスの特徴を表にまとめた。限られた紙面でヘルペスウイルス学を論ずるのはいささか無理な感があるが、ヒト体内に潜んでいる本ウイルスが細胞形質や疾患発生にどのように絡んでいるのか謎は多い。これからさらに研究が進み、共通点や相違点が明確となり、治療法の開発に応用されることを願っている。

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# Hepatocyte Growth Factor Protects Auditory Hair Cells From Aminoglycosides

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**Objectives/Hypothesis:** To examine the effect of hepatocyte growth factor (HGF) for protection of auditory hair cells against aminoglycosides and its molecular mechanisms.

**Study Design:** Experimental study.

**Methods:** We quantitatively assessed protective effects of HGF on mouse cochlear hair cells against neomycin toxicity using explant culture systems. To understand mechanisms of hair cell protection by HGF, we examined the expression of c-Met, HGF receptor, and 4-hydroxynonenal (a lipid peroxidation marker) in the cochlea by means of immunohistochemistry and Western blotting.

**Results:** The application of HGF to cochlear explant cultures significantly reduced the hair cell loss induced by neomycin. Immunohistochemistry showed c-Met expression in normal auditory hair cells, and its increase in response to neomycin-induced damage. Immunostaining for 4-hydroxynonenal suggested that HGF acted by attenuating the lipid peroxidation of auditory epithelia induced by neomycin.

**Conclusions:** These findings demonstrate that a functional HGF/c-Met coupling is present in the cochlea, and HGF application exerts protective effects on hair cells, indicating the potential of HGF as a therapeutic agent for sensorineural hearing loss.

**Key Words:** Cochlea, protection, c-Met, growth factor, hearing loss, 4-hydroxynonenal.

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## INTRODUCTION

Hepatocyte growth factor (HGF), which was initially identified and purified as a multifunctional protein in hepatocytes,<sup>1</sup> exerts its activities, such as mitogenic, morphogenic, angiogenic, and antiapoptotic activities, in various types of cells,<sup>2,3</sup> including neuronal cells. HGF, and its receptor c-Met, are expressed in various regions of the brain and peripheral neurons.<sup>2–4</sup> A functional coupling between HGF and c-Met has been reported to play important roles in the development and the maintenance of the nervous system.<sup>5,6</sup> Previous studies have revealed that HGF gene transfer with hemagglutinating virus of Japan envelope (HVJ-E) prevents postischemic delayed neuronal death in the hippocampus.<sup>2,7</sup> Kitamura et al. also delivered the HGF gene to the injured spinal cords using herpes simplex virus-1.<sup>8</sup> Altogether, these studies suggest that HGF functions as a neurotrophic factor to maintain the physiological structure and function of the nervous system.

Several studies indicated a therapeutic potential of HGF for inner ear disorders. Previously, Oshima et al. reported that HGF gene delivery into the cerebrospinal fluid with HVJ-E vector promotes functional recovery after aminoglycoside-induced hearing loss.<sup>9</sup> Recently, we have demonstrated that local application of recombinant human HGF protein into the cochlea using gelatin hydrogels,<sup>10</sup> which enables sustained delivery of growth factors, rescues auditory hair cells from noise-induced damage.

However, actual mechanism of HGF action to the hair cells is not yet clearly described. The present study aimed to explore the molecular mechanism of HGF effect and examine the potential of HGF. We used cochlear explant culture systems and tested the capability of HGF for protection of auditory hair cells against aminoglycoside toxicity. In addition, to explore the HGF signaling mechanism on the auditory epithelium, we examined the expression of the c-Met receptor and monitored the changes in lipid oxidation in auditory epithelia damaged by neomycin.

## MATERIALS AND METHODS

### Animals

ICR mice (Japan SLC, Hamamatsu, Japan) were used in this study. The Animal Research Committee, Graduate School

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