

It is generally difficult to visualize intracellular microstructures and perform antigenic protein localizations using immunogold electron microscopy due to the low resolution and contrast of micrographs. In order to overcome this difficulty, we applied a silver-intensified immunogold labeling method in our experiment (Figs. 5B and C). Using this method, antigen-reactive immunogold particles approximately 20 nm in diameter were observed. Specific immunolabeling of core and E1 protein was detected in the ER or on the ER membranes. Intense immunopositive reactions were also seen on the virus-like particles observed in cytoplasmic vesicles and on ER membranes; however, no such immunolabeling was observed when normal mouse serum was used as a first antibody (data not shown). These results confirm the ultrastructural observations of conventional TEM and suggest that the formation of HCV particles is achieved by budding of the putative core particles at the ER membrane.

Infectivity of HCV-LPs depends on E2 glycoprotein

To determine whether HCV-LPs released from RCYM1 cells cultured in the TGP system are infectious, we inoculated naive Huh-7.5.1 cells (Zhong et al., 2005), which are HCV-negative Huh-7.5 (Blight et al., 2002)-derived cells, with a culture supernatant of RCYM1 spheroids. HCV RNAs in the cells at

days 0, 1, 2, 3, and 7 postinoculation were determined by real-time RT-PCR. Fig. 6A shows the kinetics of HCV RNA after the inoculation of HCV-LPs. HCV RNA levels in the infected Huh-7.5.1 cells fluctuated at the indicated times, reaching 10^3 – 10^4 copies/ μ g of cellular RNA at days 1–7. Immunofluorescence staining 4 days postinoculation revealed that approximately 1% of cells were positive for NS5A protein (Fig. 6B). In contrast, no NS5A-positive cells were detected when the cell supernatant sample obtained from 5 to 15 cell cultured in TGP was used to inoculate Huh-7.5.1 cells (data not shown). These results suggest that HCV-LPs released from TGP-cultured RCYM1 cells are infectious.

To further determine whether viral envelope proteins mediate infection by HCV-LPs, we preincubated HCV-LPs with the anti-E2 monoclonal antibody AP33, which demonstrates potent neutralization of infectivity against HCV pseudoparticles carrying E1 and E2 proteins representative of the major genotypes 1 through 6 (Owsianka et al., 2005), or with patient sera with high titers of HCV neutralization of binding (NOB) antibodies (Ishii et al., 1998), or with anti-FLAG antibody (Fig. 6C). NOB antibodies have the ability to neutralize the binding of E2 protein to human cells (Rosa et al., 1996), and NOB3 and NOB4 were sera obtained from patients who recovered naturally from chronic hepatitis C (Ishii et al., 1998). Intracellular HCV RNA levels were decreased by 43%, 28%,

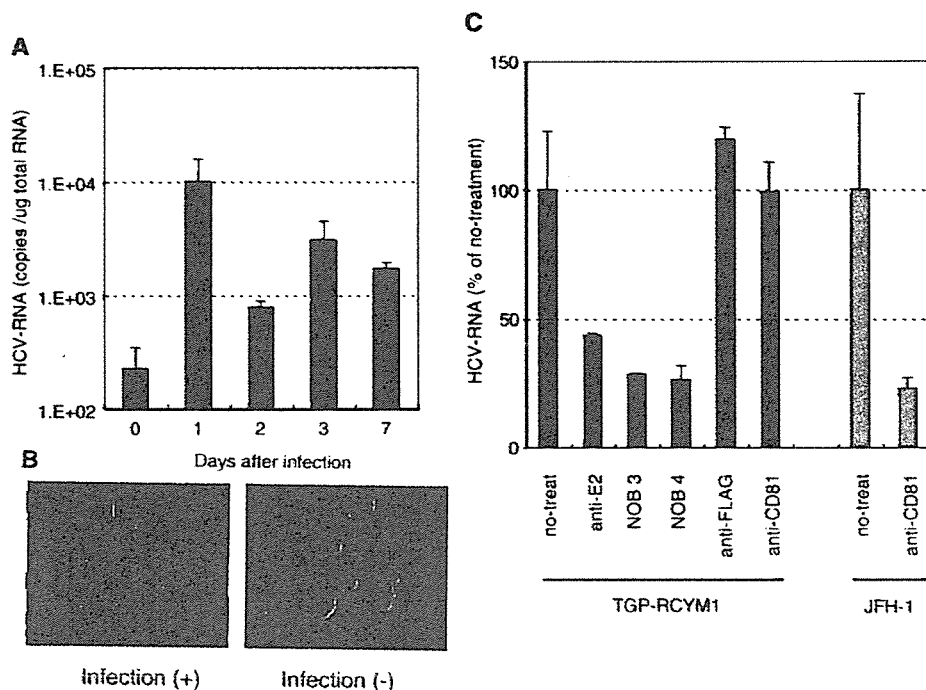


Fig. 6. Infectivity of HCV-LPs secreted from TGP-cultured RCYM1 cells and neutralization of the infection. (A) Kinetics of HCV RNA after the infection of HCV-LPs. Huh-7.5.1 cells were infected with HCV-LPs and harvested at days 0, 1, 2, 3, and 7. HCV RNAs in the cells were determined by real-time RT-PCR. (B) Huh-7.5.1 cells infected with HCV-LPs (upper panel) or without infection (lower panel) were cultured for 4 days, followed by immunostaining with anti-NS5A antibody. Nuclei were counterstained with 4',6-diamidino-2-phenylindole (DAPI). (C) Huh-7.5.1 cells were infected with HCV-LPs after pretreatment with anti-E2 antibody AP33, neutralization of binding (NOB) antibodies, or anti-FLAG antibody. Anti-human CD81 antibody was preincubated with Huh-7.5.1 cells prior to the infection. Huh-7.5.1 cells were infected with HCV-LPs derived from TGP-cultured RCYM1 cells or JFH1 virus and incubated for 4 days; HCV RNAs in the cells were determined by real-time RT-PCR. The inhibition rate is given as the percentage of the no-treatment controls. Average values with standard deviations in triplicate samples are shown. Closed bars, HCV-LPs secreted from TGP-cultured RCYM1 cells; shaded bars, JFH1 virus.

and 26% in the presence of AP33, NOB3, and NOB4, respectively. No reduction of viral RNA in infected cells was observed following treatment with anti-FLAG antibody. Thus, the present results suggest that viral envelope proteins play a crucial role in the infectivity of HCV-LPs produced by RCYM1 cells cultured in TGP. We further tested anti-CD81 antibody for inhibition of the virus infection in our system. As shown in Fig. 6C, pretreatment of the cells with the anti-CD81 antibody resulted in no inhibition of the intracellular HCV RNA level in the infected cells. In contrast, under the same condition of treatment, the antibody efficiently inhibited the infection of JFH-1 virus, which was produced from the HCV JFH-1 molecular clone as previously described (Wakita et al., 2005; Zhong et al., 2005), suggesting that CD81 has no or little, if any, need for the infection of HCV produced in our system.

Potential use of the TGP culture system for HCV production and evaluation of antiviral agents

In a recent report, Lindenbach et al. (2005) found that a cell culture system supporting complete replication of an HCV genotype 2a clone is useful for the evaluation of antiviral drugs. However, to date this complete HCV culture system has not been extended to genotype 1b, which is more frequently detected in patients with hepatitis C and is the most difficult to treat.

We show here the potential utility of the TGP culture of RCYM1 cells for evaluating anti-HCV drugs (Fig. 7). Intracellular HCV RNA levels in TGP-cultured RCYM1 cell spheroids were reduced by 90% after 3 days of culture with 100 IU/ml of IFN- α (Fig. 7A). Likewise, the extracellular HCV particle level, which was calculated using the HCV RNA copy number of the 1.18 g/ml supernatant fraction, was reduced by 89% by IFN- α treatment (Fig. 7B). Moreover, the production of HCV particles was inhibited by treatment with 100 μ M RBV to the same degree (85%) as intracellular HCV RNA (Fig. 7B).

The level of HCV RNA detected in the 1.04 g/ml fraction of the culture supernatant of the untreated group was approximately one fourteenth of that in the 1.18 g/ml fraction, and the level increased with the addition of IFN- α or RBV (Fig. 7B). Although the mechanism underlying this increase is unknown, a similar phenomenon was observed when several highly cytotoxic agents were evaluated using TGP-RCYM1 cultures (data not shown). It is therefore likely that some cellular proteins associated with HCV RNA are released into the culture supernatant as a result of cell death caused by the moderate cytotoxic effects of IFN and RBV.

Collectively, these results demonstrate that the HCV production model based on TGP culture is useful for evaluating HCV particle production and the inhibitory effects of anti-HCV drugs.

Discussion

In the present report, we describe that HCV-LPs are assembled and released from Huh-7 cells harboring a dicistronic genome-length Con1 HCV RNA in two independent 3D culture systems. The HCV-LPs closely resemble virus-like particles detected in the sera of patients with hepatitis C in terms of both particle size and morphology. The HCV-LPs released into the culture supernatant have a buoyant density of approximately 1.18 g/ml, which is much higher than that of putative HCV particles isolated from patient sera reported previously (Andre et al., 2002; Kanto et al., 1994; Nakajima et al., 1996; Trestart et al., 1998) and slightly higher than the average density of virus particles produced with the JFH-1 isolate (Wakita et al., 2005). One possible explanation is that the HCV particles are highly bound to lipids and low-density lipoproteins in patient sera. In agreement with a recent report (Wakita et al., 2005), our EM examination demonstrated that HCV-LPs are 50–60 nm in diameter and are composed of core-like particles with a diameter of approximately 30 nm that are surrounded by ER-derived E1/

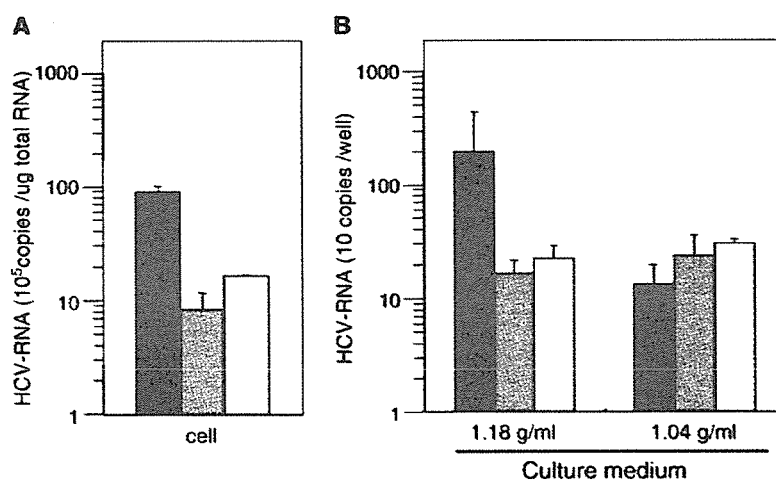


Fig. 7. Inhibition of HCV-LP production by IFN and RBV. TGP-cultured RCYM1 cells were treated with 100 IU/ml IFN- α or 100 μ M RBV, and HCV RNAs in the cells (A) and in the culture media (B) were then determined. Culture media from each sample were fractionated by sucrose gradient centrifugation and HCV-LP positive (1.18 g/ml) and negative (1.04 g/ml) fractions were assayed. Average values with standard deviations in triplicate samples are shown. Closed bars, no-treatment control; shaded bars, IFN- α ; open bars, RBV.

E2 proteins. These particles are observed at the ER membranes and in dilated cisternae of the ER, suggesting that the interaction of the ER membrane containing HCV envelope proteins with the viral core protein drives the budding process of HCV particles into the ER lumen.

Although studies on the ultrastructure and morphogenesis of HCV-LPs have been conducted using recombinant viral vectors carrying HCV structural protein genes (Baumert et al., 1998; Blanchard et al., 2002, 2003), the present study provides the first visual evidence of assembly and budding of HCV particles in a heterologous expression system in which a full-length viral genome is replicating and the viral particles are secreted into the culture medium. We also demonstrated that the HCV-LPs produced in our 3D culture system are infectious and that their infection is prevented by the monoclonal antibody AP33 directed against E2 (Owsianka et al., 2005) as well as by NOB antibodies (Ishii et al., 1998), which are sera of patients naturally resolving from chronic hepatitis C and exhibiting neutralizing activity. This result is consistent with the recent demonstration that E2 is required for the infectivity of JFH-1 virus (Wakita et al., 2005). It has been shown that CD81 interacts with E2 (Pileri et al., 1998) and that anti-CD81 antibodies or a soluble CD81 fragment block the infection of Huh-7 cells with either pseudotyped retroviral particles, JFH-1 virus or J6/JFH1 chimera (Lindenbach et al., 2005; Netski et al., 2005; Wakita et al., 2005; Zhong et al., 2005). Inconsistent with these studies, however, we found that anti-CD81 antibody did not inhibit the virus infection in our system. Although CD81 is considered to represent an important component in HCV entry, there are several other candidate cellular receptors for HCV (Bartosch and Cosset, 2006) and a study has demonstrated that *in vitro* binding of HCV to hepatoma cell lines was not inhibited by the anti-CD81 antibody (Sasaki et al., 2003).

In a previous report (Aizaki et al., 2003), we describe the production and release of infectious HCV particles from a human hepatocellular carcinoma-derived cell line, FLC4, using RFB culture in two experiments: inoculation of cells with infectious plasma from an HCV carrier and transfection of cells with viral RNA transcribed from the full-length cDNA of genotype 1a, which is known to infect chimpanzees. These findings prompted us to use the RFB system to create a culture model of HCV production based on genome-length dicistronic viral RNA, which has not been found to produce viral particles in standard monolayer cultures. As expected, HCV-LPs were produced and secreted into the medium during RFB culture of RCYM1 cells, whereas virus production was not observed in the conventional monolayer culture of RCYM1 cells. The presence of the viral envelope protein(s) on the HCV-LPs obtained in the RFB culture was strongly suggested from their density analysis with and without NP40 treatment.

We also created another 3D environment supportive of RCYM1 culture using TGP, a chemically synthesized biocompatible polymer which has a sol-gel transition temperature, thus enabling us to culture cells three-dimensionally in the gel phase at 37 °C and to harvest them in the sol phase at 4 °C, without enzyme digestion (Yoshioka et al., 1994). In contrast to other matrix gels made from conventional natural polymers and

developed for 3D culture, including matrigel (Kleinman et al., 1986), collagen gel (Lawler et al., 1983), and soft agar, TGP has several advantages that allow us to investigate the functional characteristics of epithelial cells, their tissue-like morphology, and their potential clinical applications. The use of 3D culture materials other than TGP requires treatment with appropriate digestive enzymes or heating to collect cells grown as spheroids from the culture media, and the matrices may damage the cultured cells to some extent. Thus, it is difficult to keep the viable cells in a functionally and structurally intact. In addition, because matrigel and collagen gel are made from animal or tumor tissue, the possibility that certain pathogens or unidentified factors might influence cell function cannot be excluded. In the present study, we found that Huh-7 and RCYM1 cells formed an organized structure of spheroids after 7–10 days of culture in TGP, and that HCV-LPs were assembled and released from RCYM1 spheroids, as observed in RFB culture. It can be ruled out that HCV-LPs, RNA, and core protein detected in the TGP culture supernatant are released by damaged and/or broken cells because neither digestive enzymes nor heating is used in the culture procedures and no cell damage has been observed in the cultures.

It remains to be clarified why HCV particles were produced from Huh-7 cells harboring the genome-length dicistronic HCV RNA more efficiently in the 3D cultures than in the monolayer cultures. However, this might be related to the fact that directional protein transport in hepatocytes occurs more readily in 3D culture. EM examination demonstrated that, in the RFB and TGP culture systems, human hepatoma cells, such as Huh-7, FLC4, and FLC5 cells, self-assemble into spheroids with possible polarized morphology in which microvilli develop on the cell surface and channels resembling bile canaliculi and junction structures are created in the intercellular spaces (Aizaki et al., 2003; Iwahori et al., 2003). In contrast, human hepatoma cells adhere when grown on a plastic surface, growing as a flat monolayer without exhibiting the characteristics of polarized epithelium. In general, the interaction of viruses with polarized epithelia in the host is one of the key steps in the viral life cycle. A variety of viruses, especially enveloped viruses, mature and bud from distinct membrane domains of the host cells (Compans, 1995; Garoff et al., 1998; Schmitt and Lamb, 2004; Takimoto and Portner, 2004). For example, several respiratory viruses, such as influenza virus, parainfluenza virus, rhinovirus, and respiratory syncytial virus, are released preferentially from the apical surface. Conversely, other viruses egress from the basolateral membrane; these include vesicular stomatitis virus, Semliki Forest virus, vaccinia virus, and certain retroviruses. Thus, it is likely that more organized intracellular trafficking pathways exist in the 3D culture of Huh-7-derived cells, thereby driving the assembly and release of HCV.

The efficient production of HCV in 3D cultures could also be due to the reduction of HCV RNA replication and/or translation in 3D cultures as compared to those in monolayer cultures. RNA replication and/or translation of HCV replicons in Huh-7 cells are highly dependent on host cell growth (Pietschmann et al., 2001). In the present study, we found that the slow growth of spheroids resulted in reduced expression of HCV protein and

viral RNA in 3D-cultured RCYM1 cells compared to that in monolayer cultures containing similar cell numbers. The doubling time of cells grown in TGP or RFB culture was approximately twice that observed in monolayer culture. Although it is possible that amino acid substitutions of culture-adaptive mutations contribute to interference with virus production, another possibility might be that in cases of certain HCV clones, higher expression of the viral proteins leads to their misfolding, thereby precluding the formation of virus particles.

Complete cell culture systems for HCV have recently been developed (Lindenbach et al., 2005; Wakita et al., 2005; Zhong et al., 2005) using a genotype 2a isolate, JFH-1, obtained from a Japanese patient with fulminant hepatitis (Date et al., 2004; Kato et al., 2001, 2003). Unlike many other HCV isolates, JFH-1-based subgenomic replicons do not require culture-adaptive mutations for efficient RNA replication (Kato et al., 2003). Transfection of Huh-7 cells with the full-length JFH-1 genome or a chimeric genome using JFH-1 and J6 results in the efficient production of infectious HCV (Lindenbach et al., 2005; Wakita et al., 2005; Zhong et al., 2005). This newly established HCV culture system is undoubtedly useful for a variety of HCV studies; however, these systems rely on the JFH-1 replicase (NS3 to 5B) and little is known about the reasons that this particular isolate permits efficient HCV production. Virus yield in the 3D systems presented here is significantly lower than that in systems based on JFH-1; it seems that 0.1–1 copies of HCV RNA/cell/day are generated and assembled into viral particles. The ratio of viral RNA to the core protein in these fractions is approximately 10^5 RNA copies/1 fmol of the core. Although only moderate production of HCV particles is observed in 3D culture of RCYM1 cells, this is the first study to demonstrate the production of infectious HCV particles derived from genotype 1b, which is highly prevalent worldwide and is thought to present a higher risk of developing hepatocellular carcinoma and/or cirrhosis than infections with other HCV types (Bruno et al., 1997; Silini et al., 1996). The findings of the present study may also suggest that an extremely high efficiency of viral replication, such as that observed in the case of JFH-1 isolate, is not needed to produce HCV particles in 3D cultures of Huh-7 cells. Heller et al. (2005) report HCV virion production in a culture transfected with the genomic cDNA of genotype 1b; however, the infectivity of the virus particles remains to be determined. More recently, it was shown that chimeric HCV containing structural proteins of genotypes 1a, 1b, or 3a was produced from fusion of the core to the p7 or NS2 region with downstream nonstructural regions of JFH1 clone, but that intergenotypic chimeras frequently yielded lower titers of infectious HCV compared to JFH1 or J6/JFH1 chimera (Pietschmann et al., personal communication). The 3D culture system described in the present study might be a helpful method of increasing the efficiency of assembly and release of intergenotypic chimeric HCV.

In summary, we found that the expression of dicistronic genome-length Con1 HCV RNA of genotype 1b in 3D-cultured Huh-7 cells yields infectious virus particles, and we demonstrated the usefulness for producing HCV particles of two 3D culture systems based on RFB and TGP, in which

human hepatoma cells can assemble into spheroids with potentially polarized morphology. HCV morphogenesis occurs in a complex cellular environment in which host factors may either enhance or reduce the assembly and budding process. The culture system described here will allow us to further study viral morphogenesis and the biophysical properties of HCV particles, and it provides a new tool for the future development of anti-HCV drugs.

Materials and methods

Cell lines bearing dicistronic HCV RNAs

To generate a stable cell line harboring genome-length dicistronic HCV RNA, we electroporated 10^7 Huh-7 cells with 50 μ g of the RNA transcribed from a plasmid pFKI389neo/core-3'/NK5.1 (Pietschmann et al., 2002). The cells were maintained in Dulbecco's modified Eagle's medium with 10% fetal bovine serum and 0.5 mg/ml G418 (Promega). After stringent selection for 3 weeks, a fast-growing clone was isolated and designated as RCYM1. A Huh-7-derived cell line, 5–15, harboring a subgenomic replicon (Lohmann et al., 1999) was also used.

3D cell cultures

The RFB system (Able, Japan) was manipulated as described previously (Aizaki et al., 2003) with minor modifications. Briefly, the RFB column, being filled with 4 ml of porous carrier beads made from polyvinyl alcohol, seeded with 1×10^7 of RCYM1 or 5–15 cells. The cells were cultured in ASF104 medium (Ajinomoto, Japan) supplemented with 4 g/l of D-glucose, 2% fetal calf serum, and 0.5 mg/ml of G418 (Promega). TGP (Mebiol Gel MB-10; Mebiol, Japan) was supplied as a lyophilized form and its aqueous solution was prepared before use as previously described (Hishikawa et al., 2004; Nagaya et al., 2004; Yoshioka et al., 1994). Briefly, TGP in a flask was dissolved in 10 ml of the culture medium and was maintained at 4 °C overnight. To prepare HCV particles, we suspended 5×10^6 cells of RCYM1 in 10 ml of TGP solution and aliquots were poured into a multi-well plate. Upon warming to 37 °C, the TGP solution quickly turned into a gel form, and 3 volumes of the culture medium were added to cover the gel. To recover spheroid cells and the culture supernatant after cultivation, we subjected the cultured plate to a temperature of 4 °C for 10 min to dissolve the gel. In order to separate spheroid cells from the culture medium, we subsequently centrifuged the TGP culture diluted with the overlaid culture medium at $1000 \times g$ for 5 min.

Sucrose density gradient centrifugation

The culture medium collected from the RFB or TGP was centrifuged at $8000 \times g$ for 50 min to remove all cellular debris, after which the supernatant was centrifuged at 25,000 rpm at 4 °C for 4 h with an SW28 rotor (Beckman). The precipitant was suspended in 1 ml of TNE buffer [10 mM Tris-HCl (pH 7.8), 1 mM EDTA, 100 mM NaCl] and was then layered on top of continuous 10–60% (wt/vol) sucrose gradient in TNE buffer,

followed by centrifugation at 35,000 rpm at 4 °C for 14 h with an SW41E rotor (Beckman). Fractions (1 ml each) were collected from the top of the tube (12 fractions in total). The density of each fraction was determined by the weight of 100 µl of the fraction. For NP40 treatment, 0.5 ml of the TNE-suspended sample as described above was supplemented with 10 µl of RNase inhibitor (Takara, Japan) and 5 µl of 1M DTT, which was diluted by adding NP40 solution to a final concentration of 0.2%. After incubation at 4 °C for 20 min, the sample was fractionated by discontinuous 10–60% sucrose gradient centrifugation.

Quantitation of HCV RNA and core protein

Total RNA was extracted from cells and from the culture medium using TRIZOL (Invitrogen) and a QIAamp Viral RNA Mini spin column (Qiagen), respectively. Real-time RT-PCR was performed using TaqMan EZ RT-PCR Core Reagents (PE Applied Biosystems), as described previously (Aizaki et al., 2004; Suzuki et al., 2005). HCV core antigen within cells and culture medium was measured by immunoassay (Ortho HCV-Core ELISA Kit; Ortho-Clinical Diagnostics), following the manufacturer's instructions.

Western blot analysis

The protein concentration of cells recovered from monolayer or 3D cultures was determined by BCA Protein Assay Kit (Pierce). Aliquots of samples were analyzed by sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS–PAGE) and transferred to polyvinylidene difluoride membranes (Immobilon; Millipore, Japan) using a semidry blotter. After overnight incubation at 4 °C in blocking buffer (Dainippon Pharmaceuticals, Japan) with 0.2% Tween 20, the membranes were incubated with appropriately diluted anti-HCV core (Anogen) and anti-NSSA (Austral Biologicals) monoclonal antibody, followed by incubation with horseradish peroxidase conjugated anti-mouse immunoglobulin G (Cell Signaling). The blots were then washed and developed with enhanced SuperSignal West Pico Chemiluminescent Substrate (Pierce).

Immunocytochemistry

For NSSA staining, infected cells cultured on collagen-coated coverslips were washed with phosphate buffered saline (PBS) and fixed with 4% paraformaldehyde at 4 °C for 30 min, followed by permeabilization with PBS containing 0.2% TritonX-100. After preincubation with BlockAce (Dainippon Pharmaceuticals), the samples were stained using mouse anti-NSSA antibody and rhodamine-conjugated goat anti-mouse IgG (ICN Pharmaceuticals) as the first and second antibodies, respectively.

Electron microscopy

To visualize HCV-LPs secreted into the medium, we concentrated and adsorbed sucrose density fractions prepared

as described above onto carbon-coated grids for 1 min. The grids were stained with 1% uranyl acetate for 1 min and examined under a Hitachi H-7600 transmission electron microscope. To prepare thin sections of HCV-LPs, we prefixed precipitated HCV-LPs in 2% glutaraldehyde–0.1 M cacodylate buffer at 4 °C overnight, followed by three rounds of washing with 0.1 M cacodylate buffer. The samples were then postfixed in 2% osmium tetroxide at 4 °C for 2 h, dehydrated in a graded series of ethanol solutions followed by propylene oxide, and embedded in a mixture of EPON 812, dodecyl succinic anhydride (DDSA), methyl nadic anhydride (MNA), and 2,4,6-tri (dimethylaminomethyl) phenol (DMP-30) at 60 °C for 2 days. Thin sections (80 nm) were stained with uranyl acetate and lead citrate. For electron microscopy of RCYM1 cells cultured in TGP, the cells were prefixed in 2% glutaraldehyde–0.1 M cacodylate buffer at 4 °C for 1 h and washed three times with 0.1 M cacodylate buffer, followed by postfixation in 2% osmium tetroxide for 3 h. After dehydration in a graded series of ethanol solutions and propylene oxide, the cells were embedded in a mixture of Epoxy 812, DDSA, MNA, and DMP-30 at 60 °C for 2 days. Thin sections (60–80 nm) were stained with 2% uranyl acetate.

Immunoelectron microscopy

HCV-LP samples were adsorbed on formvar-carbon grids and then floated for 30 min on a drop of BlockAce. Diluted anti-E2 mouse antibody was then applied for 1 h. After three rounds of washing, diluted anti-mouse IgG conjugated with 5-nm gold particles was applied for 1 h, and the grids were then stained with 1% uranyl acetate. In order to perform immunoelectron microscopy of TGP cultures using silver-intensified immunogold labeling, we fixed the cells in 4% paraformaldehyde–0.1% glutaraldehyde with 0.15 M HEPES buffer at 4 °C, followed by incubation with either anti-core rabbit antibody or anti-E1 mouse antibody overnight. After several washings, anti-rabbit or anti-mouse secondary antibody coupled with 1.4-nm-diameter gold particles (Nanoprobes) was applied overnight. The samples were then washed and fixed in 2% glutaraldehyde in 0.1 M sodium cacodylate buffer (pH 7.4) for 3 h, followed by enlargement of the gold particles with an HQ-Silver Enhancement Kit (Nanoprobes). For double staining with anti-E1 and anti-core antibodies, the cells were fixed in 7% paraformaldehyde–0.25 M sucrose in 0.03% picric acid–0.05 M cacodylate buffer at pH 7.4. Ten-nanometer gold particle-coupled anti-rabbit and 5-nm gold particle-coupled anti-mouse antibodies were used as secondary antibodies.

Assays for the infectivity of HCV-LPs and neutralization of the infection

Cell supernatant from 3D-cultured RCYM1 cells was centrifuged at 8000 × g for 50 min to remove all cellular debris, after which the supernatant was centrifuged at 25,000 rpm at 4 °C for 4 h with an SW28 rotor. The precipitant was suspended in 0.2–0.5 ml of ASF104 medium and the aliquot containing approximately 1×10^5 HCV RNA copies was used as each inoculum. Huh-7.5.1

cells (provided by Dr. F. V. Chisari, The Scripps Research Institute) (Zhong et al., 2005), which were seeded at a density of 10^4 cells/well in a 48-well plate 24 h before infection. The inocula were incubated for 3 h, followed by 3 rounds of washing with PBS and the addition of complete medium. For the kinetics assay, cells were harvested 0, 1, 2, 3, and 7 days after infection and the amount of intracellular HCV RNA was quantified as described above. Infection with HCV-LP was determined after 4 days by immunofluorescence staining for HCV NS5A. In the neutralization assay, the HCV-LP samples were incubated with the anti-E2 antibody AP33 (Owsianka et al., 2005) at 10 μ g/ml (kindly provided by Dr. A. H. Patel, University of Glasgow, UK), with the human sera with high titers of NOB antibodies NOB3 and NOB4 (Ishii et al., 1998), or with anti-FLAG antibody (Sigma) at 10 μ g/ml for 1 h at 37 °C prior to infection. Anti-human CD81 antibody (BD Pharmingen) at 10 μ g/ml was preincubated with Huh-7.5.1 cells for 1 h at 37 °C, followed by being washed with PBS three times. HCV-LP derived from TGP-cultured RCYM1 cells or JFH1 virus was incubated with these cells, as mentioned above. JFH1 virus was prepared from pJFH1 (Wakita et al., 2005), which contains the full-length cDNA of JFH1 isolate and was kindly provided by T. Wakita (Tokyo Metropolitan Institute for Neuroscience, Japan), as described (Wakita et al., 2005). The cells were harvested 4 days after infection and neutralizing activity was assessed by quantifying the amount of intracellular HCV RNA as described above.

Assay for anti-HCV-LP production

At the initiation of the 3D culture of RCYM1 cells (5×10^5 in 1 ml TGP), 100 IU/ml IFN- α (Sumiferon 300; Sumitomo Pharmaceuticals, Japan), or 100 μ M RBV (MP Biomedicals, Germany) were added and the cells were cultured for 5 days. Culture media were harvested and fractionated by sucrose density centrifugation as described above. Total RNAs were extracted from aliquots of 1.18 g/ml (HCV-LP positive) and 1.04 g/ml (HCV-LP-negative) fractions, followed by quantification of viral RNA.

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Induction of protective immunity against severe acute respiratory syndrome coronavirus (SARS-CoV) infection using highly attenuated recombinant vaccinia virus DIs

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Abstract

SARS-coronavirus (SARS-CoV) has recently been identified as the causative agent of SARS. We constructed a series of recombinant DIs (rDIs), a highly attenuated vaccinia strain, expressing a gene encoding four structural proteins (E, M, N and S) of SARS-CoV individually or simultaneously. These rDIs elicited SARS-CoV-specific serum IgG antibody and T-cell responses in vaccinated mice following intranasal or subcutaneous administration. Mice that were subcutaneously vaccinated with rDIs expressing S protein with or without other structural proteins induced a high level of serum neutralizing IgG antibodies and demonstrated marked protective immunity against SARS-CoV challenge in the absence of a mucosal IgA response. These results indicate that the potent immune response elicited by subcutaneous injection of rDIs containing S is able to control mucosal infection by SARS-CoV. Thus, replication-deficient DI constructs hold promise for the development of a safe and potent SARS vaccine.

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Introduction

Severe acute respiratory syndrome (SARS) has become a priority for healthcare agencies around the world given its communicability, associated mortality, and the potential for pandemic spread. As of 31 July 2003, 8,098 SARS cases had been identified worldwide, resulting in 774 deaths and a mortality rate of about 9.6% (World Health Organization statistics). SARS is now known to result from infection with a novel coronavirus (SARS-CoV) (Drosten et al., 2003; Ksiazek et al., 2003; Peiris et al., 2003). Evidence that SARS-CoV is the

etiologic agent of SARS follows an experimental infection of macaques (*Macaca fascicularis*), fulfilling Koch's postulates (Fouchier et al., 2003). The clinical manifestations of SARS are hardly distinct from other common respiratory viral infections, including influenza. Because influenza epidemics might occur simultaneously with the eventual re-emergence of SARS, an effective SARS vaccine is urgently required, as well as more sensitive diagnostic tests specific for SARS.

Structural characterization of SARS-CoV and characterization of its complete RNA genome (Marra et al., 2003; Rota et al., 2003; Ruan et al., 2003) have provided us with the opportunity to develop a SARS vaccine. Like other coronaviruses, SARS-CoV is a plus-stranded RNA virus with a 30-kb genome encoding replicase gene products and the 4 structural proteins: i.e., spike (S), envelope (E), membrane (M), and nucleocapsid

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(N) (Marra et al., 2003; Rota et al., 2003). The S protein is thought to be involved in receptor binding, while the E protein has a role in viral assembly, the M protein is important for virus budding, and the N protein has a role in viral RNA packaging (for review, see reference (Holmes, 2003)). Recently, angiotensin-converting enzyme 2 (ACE2) has been identified as a cellular receptor for SARS-CoV (Li et al., 2003). Thus, the first step of infection likely involves binding of S protein to the ACE2 receptor. In a model of MHV infection, S protein is known to contain important virus-neutralizing epitopes that elicit neutralizing antibody responses in mice (Collins et al., 1982). Therefore, the S protein of coronavirus might be manipulated to induce immunity. However, S, M, and N proteins are also known to contribute to the host immune response (Anton et al., 1996; Jackwood and Hilt, 1995). A DNA vaccine encoding the S glycoprotein of the SARS-CoV induces T cell and neutralizing antibody responses, as well as protective immunity, in a mouse model (Yang et al., 2004). Vaccination with a plasmid expressing N protein is capable of generating strong N-specific humoral and T-cell-mediated immune responses in vaccinated C57BL/6 mice (Kim et al., 2004; Zhao et al., 2005; Zhu et al., 2004). In addition, N-specific CD8⁺ T cells provide protective immunity against some coronaviruses (Collisson et al., 2000; Seo et al., 1997).

The DIs strain is a highly restricted host range mutant of the vaccinia virus isolated by successive 1-day egg passage of the DIE vaccinia strain, an authorized strain for smallpox vaccine and actually used in Japan until 1981. DIs does not replicate and is not pathogenic in mice, guinea pigs or rabbits. Furthermore, the DIs does not replicate in various mammalian cell lines (Tagaya et al., 1961). Recently, we established a system for foreign gene expression by inserting target genes into this strain, after which expression of (i) bacteriophage T7 polymerase, and (ii) the full-length HIV-1_{NL4.32} *gag* gene, was observed (Ishii et al., 2002), thus demonstrating the usefulness of this system.

In the present study, we constructed a recombinant vaccinia virus DIs expressing one or more SARS-CoV structural proteins (E, M, N, and S, or a combination of E, M, and S (E/M/S), or E, M, N and S (E/M/N/S)). These rDIs vaccines were administered to mice either subcutaneously or intranasally, and the humoral and cellular immunity against SARS-CoV in vaccinated mice were analyzed. We demonstrated here that replication-deficient DIs constructs expressing S protein alone or in combination with other components, but not N alone, elicited strong protective immune responses against SARS-CoV infection.

Results

Expression of SARS-CoV structural proteins by rDIs

The structures of transfer vectors used in this study (pDIsSARS-E, pDIsSARS-M, pDIsSARS-N, pDIsSARS-S, pDIsSARS-E/M, pDIsSARS-E/M/S and pDIsSARS-E/M/N/S) were summarized in Fig. 1. Expression of SARS-CoV N and S proteins in chick embryo fibroblast (CEF) cells infected

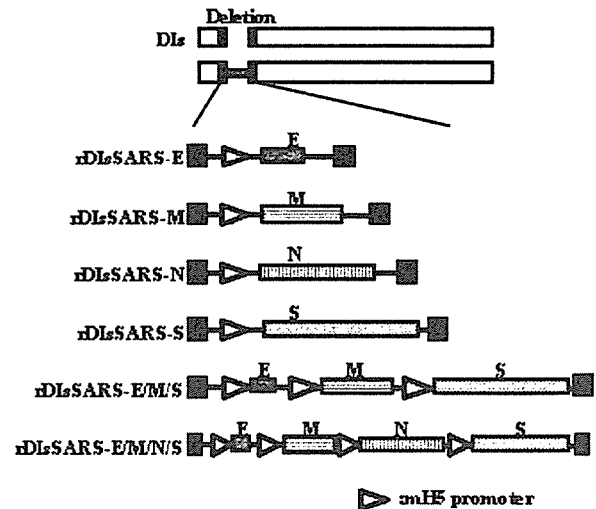


Fig. 1. Schematic diagram of rDIs constructs expressing SARS-CoV structural proteins. DNA fragments encoding E, M, N and S proteins were inserted into the location of the 15.4 kb deletion in DIs using the vaccinia virus transfer vector pDIs_{gptmH5}. Six rDIs constructs are shown.

with rDIsSARS was detected by Western blotting using monoclonal antibodies (Fig. 2A) (Ohnishi et al., 2005). Purified SARS-CoV virion was used as a positive control (Fig. 2A, lane PC). A robust signal was detected at 50 kDa, corresponding to the N protein of SARS-CoV, as predicted by its genomic size (Marra et al., 2003; Rota et al., 2003). A band approaching 200 kDa likely corresponds to the S protein, which is known to be heavily glycosylated (Fig. 2A). Our results are consistent with data reported by Xiao et al. (2003) who expressed the full-length S glycoprotein of SARS-CoV Tor2 strain in 293 cells and demonstrated a protein approaching 180–200 kDa by SDS gel electrophoresis. Concerning the M protein, only a smear band in the stacking gel was detected using a polyclonal antibody against synthetic peptide of the M protein (Mizutani et al., 2004), presumably because it formed large oligomers with SDS-resistance in cells (Fig. 2A). Similar result was mentioned by the analysis of the M protein of SARS-CoV (Buchholz et al., 2004) and infectious bronchitis virus (Weisz et al., 1993).

The subcellular localization of S, M, and N proteins was analyzed by immunofluorescence staining. Cells infected with rDIsSARS-M demonstrated M proteins primarily co-localized with the Golgi marker GM-130 (Fig. 2B), which is consistent with the results of the recent study (Nal et al., 2005). Individually expressed SARS-CoV N protein could be detected partially with Golgi apparatus, but remained principally localized to the cytoplasm (Fig. 2B). Overexpressed recombinant SARS-S glycoprotein could be detected partially with Golgi apparatus, but also be detected throughout the cytoplasm (Fig. 2B). These results indicate that cells infected with rDIsSARS expressed significant levels of SARS-CoV proteins under the control of mH5 promoter with an expected post-translational processing (Nal et al., 2005; You et al., 2005).

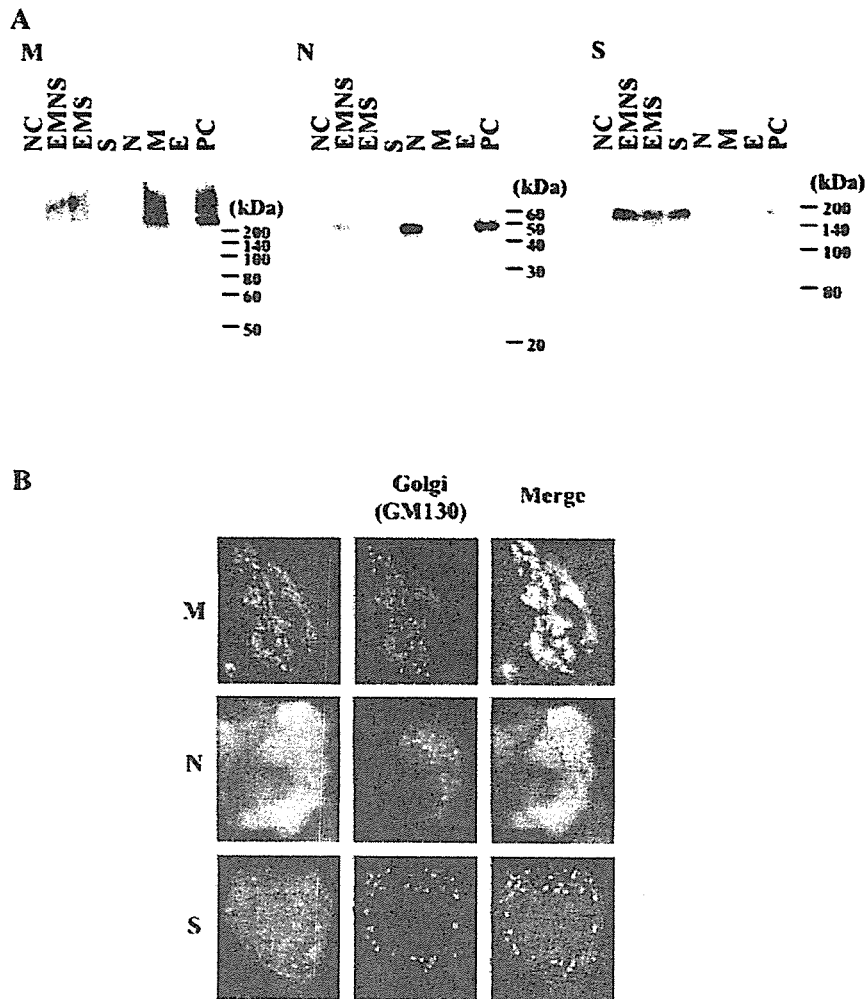


Fig. 2. Western blot analysis and indirect immunofluorescence analysis. (A) CEF cells were infected with rDIs constructs expressing SARS-CoV structural proteins (M, N and S, respectively). Purified SARS-CoV virion (0.5 μ g) was used as a positive control. SARS-CoV proteins were detected using monoclonal antibodies (N and S) or polyclonal antibodies (M). Detection of bound antibodies was done with horseradish peroxidase-conjugated goat anti-mouse or anti-rabbit antibody, and visualized by chemiluminescence. (B) CEF cells were infected with rDIs constructs expressing SARS-CoV structural proteins (M, N and S, respectively). To detect SARS-CoV proteins, the cells were incubated with rabbit polyclonal antibodies against these proteins. The cells were further incubated with FITC-conjugated goat anti-rabbit IgG. To analyze subcellular localization of these proteins, monoclonal antibody against GM-130 (Golgi marker) and rhodamine-conjugated goat anti-mouse IgG were used. SARS proteins are shown in green. Golgi apparatus is shown in red and co-localization, where it occurs, is shown in yellow.

rDIsSARS induces serum IgG antibody responses specific for SARS-CoV

To examine the anti-SARS-CoV response in mice after inoculation with rDIsSARS, four mice in each group were subcutaneously or intranasally inoculated three times with 10 pfu of rDIsSARS-N, rDIsSARS-M, rDIsSARS-S, rDIsSARS-E/M/S or rDIsSARS-E/M/N/S. Ten days after the final inoculation, vaccinated mice were observed to have high levels of anti-SARS-CoV IgG antibodies in their sera (Fig. 3).

In order to prove effective vaccination, we next examined whether neutralizing antibodies against SARS-CoV were elicited in these mice. Neutralizing antibodies against

SARS-CoV were induced in mice following subcutaneous or intranasal injection of rDIsSARS-S, rDIsSARS-E/M/S, or rDIsSARS-E/M/N/S, but not in mice immunized with rDIsSARS-N or rDIsSARS-M. These results of ELISA data were incorporated into Fig. 3 by depicting the neutralization positive serum as closed circles. Thus, our results, consistent with others (Bisht et al., 2004; Buchholz et al., 2004; Yang et al., 2004), indicate that the S protein is a prerequisite for eliciting a sufficient IgG antibody response for neutralization. Similar neutralizing activity was obtained in mice receiving S alone or in combination with other components. Therefore, we expected that the rDIsSARS expressing E/M/N/S proteins in combination could be the best vaccine candidate among others.

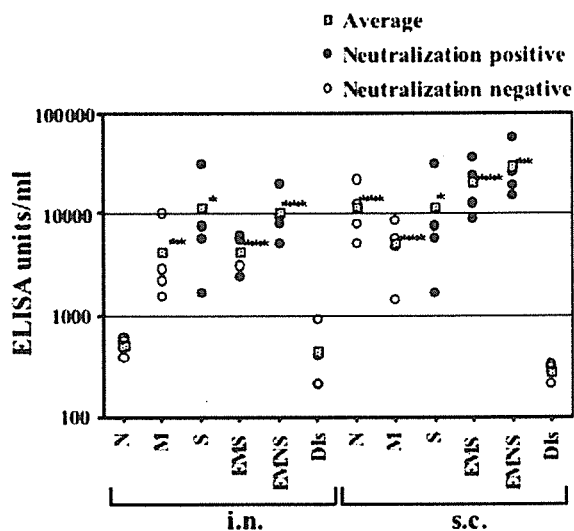


Fig. 3. Detection of anti-SARS-CoV IgG in vaccinated mice. IgG antibody levels against SARS-CoV were determined as described in Materials and methods. SARS-CoV-specific IgG titers were calculated as follows: SARS-specific IgG titer (ELISA units/ml) = (the unit value obtained for wells coated with virus-infected cell lysate) – (the unit value obtained for wells coated with non-infected cell lysate). * $P < 0.1$, ** $P < 0.05$, *** $P < 0.01$ vs. DIs-administered group. The data for neutralizing sera are represented by closed circles and the data for non-neutralizing sera are represented by open circles.

Intranasal inoculation of rDIsSARS expressing E/M/N/S induces SARS-CoV-specific IgA in nasal mucosa and a high level of mucosal IgG in parallel with that of serum IgG

Mucosal IgA response is believed to be crucial for the protective immunity against various pathogens (Meeusen et al., 2004). We, next, examined mucosal immunity in the respiratory tracts of mice inoculated with rDIsSARS either subcutaneously or intranasally. The level of anti-SARS-CoV IgA within nasal wash fluid of vaccinated mice was determined by enzyme-linked immunosorbent assay (ELISA). As shown in Fig. 4A, substantial levels of anti-SARS-CoV IgA were detected only in mice received intranasal inoculation of rDIsSARS-E/M/N/S, compared to those inoculated with parental DIs ($P = 0.0010$). The level of IgA detected in intranasally rDIsSARS-E/M/N/S-inoculated mice was similar to that observed following intranasal immunization with UV-inactivated, purified SARS-CoV virion (positive control). On the other hand, subcutaneous injection of all forms of rDIsSARS produced only slightly higher levels of IgA than those observed in DIs-injected control mice. Therefore, the results indicated that the subcutaneous route of injection is inefficient, especially when mucosal IgA response is required.

Since neutralizing activity was, nevertheless, detected in the nasal washes of mice following subcutaneous immunization (data not shown), we also measured anti-SARS-CoV IgG levels in the nasal washes of these mice (Fig. 4B). High levels of IgG were detected in the nasal washes of mice following nasal immunization, which were observed to correspond well with IgG levels in the serum (Fig. 4C). A similar trend was observed in mice following subcutaneous immunization, despite at a

lower level than in mice immunized intranasally. These results suggest that neutralizing IgG antibodies are capable of reaching the mucosal surface if plasma levels are high enough.

Protection of rDIsSARS-immunized mice from nasal SARS-CoV challenge is achieved without mucosal IgA response

The level of protection against SARS-CoV challenge in mice following inoculation with rDIsSARS is a critical issue for the vaccine development. We inoculated three times with 10 pfu of rDIsSARS-N, rDIsSARS-E/M/S or rDIsSARS-E/M/N/S into four mice in each group either subcutaneously or intranasally. One week after final inoculation, the mice were challenged intranasally with 10^4 tissue culture 50% infectious dose (TCID₅₀) of SARS-CoV. The results were shown in Fig. 4D. In mice inoculated with saline, 10^3 TCID₅₀/ml of SARS-CoV were recovered from lung wash fluid on day 3. In contrast, titers of SARS-CoV from the lungs of mice subcutaneously immunized with rDIsSARS-E/M/S or rDIsSARS-E/M/N/S were below the limits of detection. The same was true for mice intranasally immunized with rDIsSARS-E/M/N/S, whereas the virus was recovered in mice similarly immunized with rDIsSARS-E/M/S. Taken into consideration of a relatively low or marginal level of mucosal IgA antibody in mice intranasally immunized with rDIsSARS-E/M/N/S or rDIsSARS-E/M/S, or even no IgA response by subcutaneous route as described above, it was suggested that mucosal IgG antibody, but not IgA antibody, likely contributed to the protective immunity, especially in mice simultaneously immunized with recombinant rDIsSARS-E/M/N/S.

On the other hand, titers of SARS-CoV from the lung wash fluid of mice intranasally or subcutaneously immunized with rDIsSARS-N, were similar or slightly lower than the titers of negative controls, suggesting that intranasal or subcutaneous administration of rDIsSARS-N does not protect mice from SARS-CoV challenge, which is highly reflected by the non-neutralizing nature of anti-SARS-CoV N antibodies.

Cellular immunity induced by rDIsSARS

Although now we know that the systemic neutralizing IgG antibody against SARS-CoV S protein is a major component of protective immunity, T cell responses are also important to protect hosts from various viral infection. In a previous study of coronaviruses, S protein was shown to play an important role in viral pathogenesis, as well as induction of protective immunity (Holmes, 2003). In order to assess the ability of rDIsSARS to induce SARS-CoV S-specific T cells, T cells from axillary lymph nodes (ALN), superficial cervical lymph nodes (CLN) and spleens of mice subcutaneously immunized with rDIsSARS-S or DIs were isolated and stimulated *in vitro* with UV-inactivated, purified SARS-CoV virion. Culture supernatant was collected 4 days later, and the levels of interferon- γ (IFN- γ), interleukin (IL)-2, IL-4, IL-5 and tumor necrosis factor- α (TNF- α) were measured. T cells in ALN produced the greatest cytokine levels (Fig. 5, and data not shown). This is not surprising in light of the subcutaneous route of immunization.

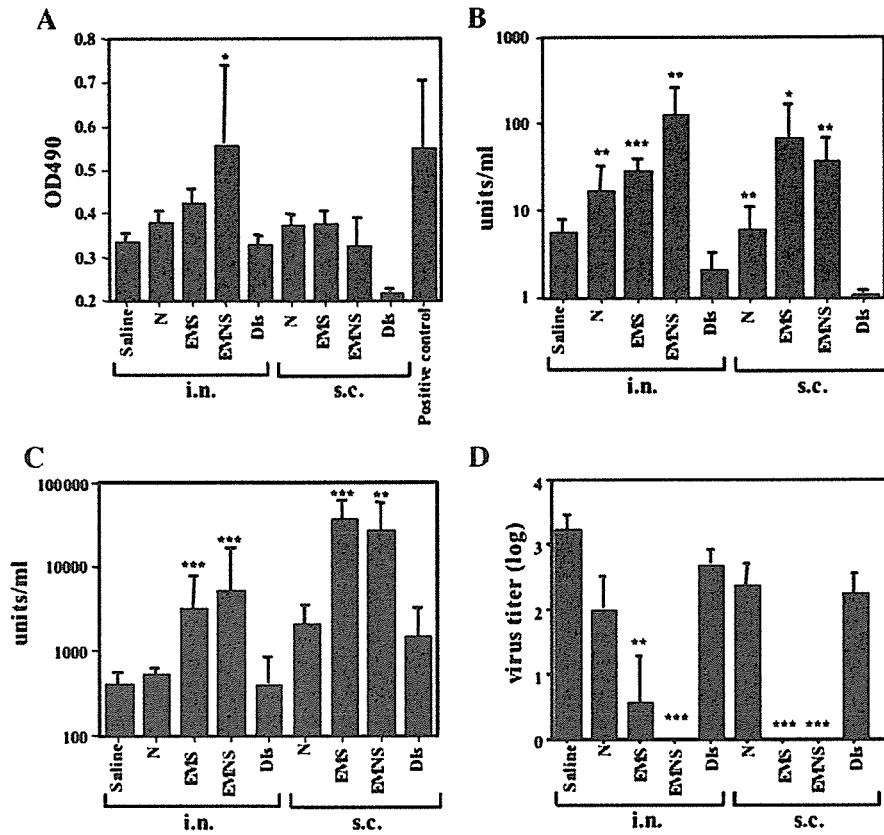


Fig. 4. Mucosally secreted anti-SARS-CoV IgG, but not IgA, antibodies are protective from nasal SARS-CoV challenge in vaccinated mice. The levels of IgA and IgG antibodies against SARS-CoV were determined as described in Materials and methods. (A) Titers of anti-SARS-CoV IgA in the nasal washings of vaccinated mice. Error bars represent the mean \pm SD. (B) Titers of anti-SARS-CoV IgG in the nasal washings of vaccinated mice. Error bars represent the mean \pm SD. (C) Titers of anti-SARS-CoV IgG in the sera of vaccinated mice. Error bars represent the mean \pm SD. (D) The titers of SARS-CoV in the lungs of vaccinated mice challenged 1 week later with 10^4 TCID₅₀ of SARS-CoV. Virus titers are expressed as log₁₀TCID₅₀. Error bars represent the mean \pm SD. **P* < 0.1, ***P* < 0.05, ****P* < 0.01 vs. DIs-administered group.

Notably, mice immunized with rDIsSARS-S produced a high level of IFN- γ upon in vitro stimulation with UV-inactivated, purified SARS-CoV virion. The production of TNF- α , an inflammatory cytokine, was significantly elevated in T cells in

ALN of rDIsSARS-S immunized mice after in vitro stimulation with virion antigens. However, TNF- α production was observed also in mice immunized with parental DIs without in vitro stimulation with virion antigens. Since T cells from the

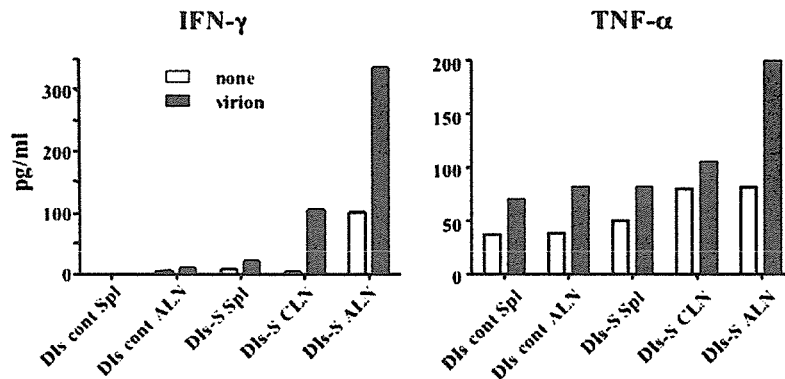


Fig. 5. In vitro response of SARS-CoV-specific T cells in mice subcutaneously immunized with rDIsSARS-S. CLN, ALN and spleens were obtained from mice 1 week after the third vaccination of either DIs control or rDIsSARS-S. After preparation of single cell suspensions, T cells were purified and cultivated with irradiated and T-cell depleted normal BALB/c mouse splenocytes as APCs in the presence or absence of 10 μ g/ml of purified UV-irradiated SARS-CoV virion. Four days later, IFN- γ and TNF- α concentrations in the culture supernatant were measured.

lymph nodes of naïve mice did not produce cytokines even after in vitro stimulation with virion antigens (data not shown), it is possible that injection of DIs induces mild local inflammation, even when viral proliferation does not occur at the injection site. The pattern of IL-2, IL-5 and IL-4 production were similar to that of IFN- γ , and the maximum level of these cytokines in ALN T cells from rDIsSARS-S-immunized mice were 254, 227 and 88 ng/ml, respectively.

Next, we analyzed the antigenic epitopes of SARS-CoV-specific T cells in the spleen. We carried out IFN- γ enzyme-linked immunospot (ELISPOT) analysis using four 20-mer peptides corresponding to the ACE2 binding region of the S protein selected using the SYFPEITHI score (S44-47), as well as overlapping 20-mer peptides pool covering a whole N protein. When the splenic T cells of mice were analyzed following intranasal or subcutaneous immunization with the most potent vaccine, rDIsSARS-E/M/N/S, a high level of reactivity against S46 was observed especially in the T cells of subcutaneously immunized mice (Fig. 6A). Zhi et al. recently identified a CD4⁺ T cell epitope, known as NYNYKYRYL, in BALB/c mice (Zhi et al., 2005). S46 contains this sequence, thus, these IFN- γ -producing T cells are likely CD4⁺ T cells. To detect N-specific T cells, mice subcutaneously or intranasally immunized with rDIsSARS-N were analyzed by ELISPOT. In this case, ten peptides were pooled from amino-terminus of N protein, resulting in 5 pools of peptides. We thus detected N-reactive T cells capable of recognizing the first 10 peptides pool (Fig. 6B), and observed a greater proportion of N-specific T cells following nasal immunization than subcutaneous immunization. These results indicate that S- and N-specific T cells are generated systemically by rDIs.

In order to elucidate whether or not SARS-CoV-specific CD8⁺ T cells were induced by immunization with the rDIs, the splenic T cells of mice subcutaneously or intranasally immunized with rDIsSARS-E/M/N/S were further analyzed by ELISPOT using a stably S-expressing A20.2J B cell S6.2

clone, as an antigen presenting cells (APC). Expression of S protein on the S6.2 clone was confirmed by FACS analysis using anti-SARS S monoclonal antibody (Fig. 7A). An empty vector transfectant, BOS-5, was used as a negative control APC. Subcutaneous and intranasal immunization with the most potent rDIsSARS-E/M/N/S generated a significant level of S-specific T cells (Fig. 7B), and a dramatic decrease in S-specific T cells was observed following partial depletion of CD8⁺ T cells (Fig. 7C). Therefore, rDIsSARS-E/M/N/S was able to induce both SARS-CoV-reactive CD4⁺ and CD8⁺ T cells.

Histopathological findings

The immunogenicity of rDIs expressing SARS-CoV structural proteins was further evaluated by histopathological and immunohistochemical analysis of lung tissue in mice, the primary infection site of SARS-CoV (Fig. 8). Slight migration of inflammatory cells and mild disruption of the bronchial epithelium were detected in lung tissue of mock-vaccinated mice. SARS-CoV antigens were diffusely observed within the bronchial and alveolar epithelium. In contrast, significant lymphocytic infiltration into peribronchial sites, with little to no detection of SARS-CoV antigens, was observed in mice intranasally immunized with rDIsSARS-E/M/S or rDIsSARS-E/M/N/S (Fig. 8). The infiltrating lymphocytes were found to be CD3-positive T-cells, as determined by immunohistochemistry with anti-CD3 antibody (Fig. 8). On the other hand, intranasal or subcutaneous immunization by only N-expressing DIs induced neither T-cell infiltration nor protective immunity against SARS-CoV, despite of the induction of N-specific antibodies and T cells. These results suggest that marked induction of T-cell response in mice immunized with rDIsSARS-E/M/S and rDIsSARS-E/M/N/S help to eliminate SARS-CoV from the lung tissue. On the other hand, intranasal or subcutaneous immunization by only N-expressing DIs did not induce protective immunity against SARS-CoV, despite of the

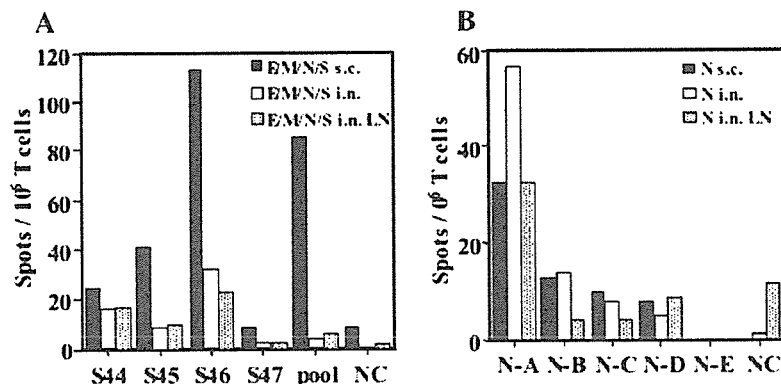


Fig. 6. Detection of SARS-CoV-specific T cells elicited by rDIsSARS-E/M/N/S or rDIsSARS-N vaccination. Splenic and lymph node (LN) T cells of mice s.c. or i.n. immunized with recombinant rDIsSARS-E/M/N/S (A) or rDIsSARS-N (B) were separated using a MACS system (Miltenyi Biotec), and IFN- γ ELISPOT analysis was performed. (A) T cells (5×10^5 cells) from mice immunized with rDIsSARS-E/M/N/S were cultured with irradiated A20.2J B cells (1×10^4), in triplicate, in a 96-well membrane plates coated with IFN- γ capture antibody in the absence or presence of 5 μ M of S peptides (S44–S47). The numbers of IFN- γ spot-forming cells were then counted and are depicted. (B) T cells from mice immunized with rDIsSARS-N and A20.2J B cells were cultured as described in A. N protein (422 amino acids) was divided into 5 parts by 100 amino acids (A, B, C, D and E) and 10 peptides each of pooled 20-mer overlapping peptides specific to the each stretch of N sequence were used as an antigen.

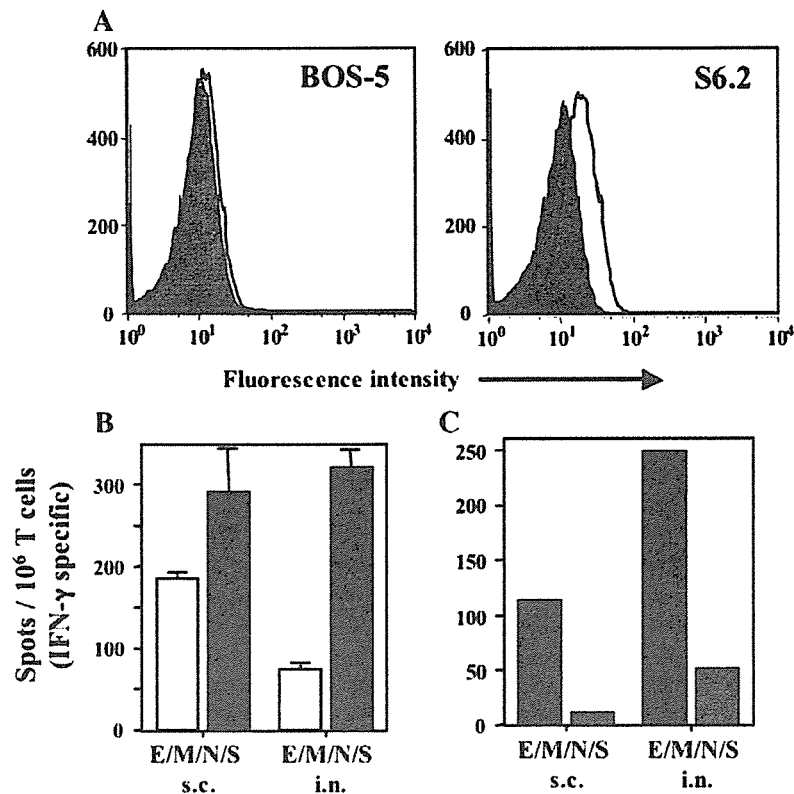


Fig. 7. Detection of SARS-CoV S-specific CD8⁺ T cells in mice immunized with rDisSARS-E/M/N/S. (A) A20.2J B cell clone expressing S (S6.2) or empty vector (BOS-5) was stained with biotinylated anti-SARS-CoV S monoclonal antibody (solid line) or control IgG (shaded line), followed by the incubation with streptavidin-APC, and then analyzed by FACScalibur. A histogram of APC fluorescence of gated live cells (PI negative) is depicted. (B) Splenic T cells from mice immunized s.c. or i.n. with recombinant rDisSARS-E/M/N/S were purified and IFN- γ ELISPOT analysis was carried out using γ -irradiated S6.2 and BOS-5 as APCs. The number of T cells reactive for BOS-5 control (white column) and S6.2 (black column) cells are shown. Error bars represent the mean \pm SD. (C) Using the same splenic T cells as in panel B, CD8⁺ T cells were partially removed using anti-CD8 mAb-coated magnetic beads (Miltenyi Biotec), and the number of T cells reactive for BOS-5 and S6.2 cells were counted by ELISPOT. The number of BOS-5-reactive T cells was subtracted and the number of S-specific T cells is depicted. Black columns: total T cells; grey columns: partially CD8-depleted T cells.

induction of N-specific antibodies and T cells. Thus, rDIs expressing the S protein, along with other membrane components (E/M and E/M/N), are capable of inducing strong immunity of both humoral and cellular arms and are fully competent to clear SARS-CoV infection.

Discussion

The DIs strain, which replicates well in CEF cells but not in most mammalian cells, was isolated from the DIE strain of the vaccinia virus during serial 1-day egg passage, and it is characterized by the induction of tiny pocks on chicken chorioallantoic membrane (Tagaya et al., 1961; Kitamura et al., 1967; Ishii et al., 2002). The DIs-derived recombinant viruses express high levels of viral and inserted genes, even in non-permissive cell lines without any cytopathic effects (Ishii et al., 2002). In earlier studies, MVA strain of vaccinia virus, which is also replication-incompetent in most mammal cells, was used to express a variety of foreign genes and some of these recombinant viruses were studied as candidate vaccine vectors and appeared to be more effective than many replication-competent vaccinia virus vaccines (Sutter and Moss, 1992;

Sutter et al., 1994; Belyakov et al., 1998; Nam et al., 1999; Stittelaar et al., 2000). rDIs does not replicate nor produce infectious virions in most mammalian cells, therefore the DIs strain has a safety advantage when used as a recombinant vaccine vector as for MVA. Recently, a recombinant DIs, rDIsSIVGag, expressing a full-length gag gene of SIV, was developed, and demonstrated to have a potential for use as an HIV/AIDS vaccine (Someya et al., 2004).

Attempts at vaccine development against SARS-CoV are ongoing by a number of organizations using various techniques (see review, Groneberg et al., 2005). DNA vaccines (Kim et al., 2004; Yang et al., 2004; Zhu et al., 2004; Zhao et al., 2005) and viral vectors such as vaccinia virus (Bisht et al., 2004; Weingartl et al., 2004), parainfluenza virus (Bukreyev et al., 2004), adenovirus (Zakhartchouk et al., 2005) and rhabdoviruses (Faber et al., 2005; Kapadia et al., 2005) are used as recombinant vaccines. Yang et al. (2004) showed that viral replication was reduced by more than six orders of magnitude in the lungs of mice vaccinated with these S plasmid DNA expression vectors, and protection was mediated by a humoral but not a T-cell-dependent immune mechanism. Bisht et al. (2004) showed that inoculation of BALB/c mice with a

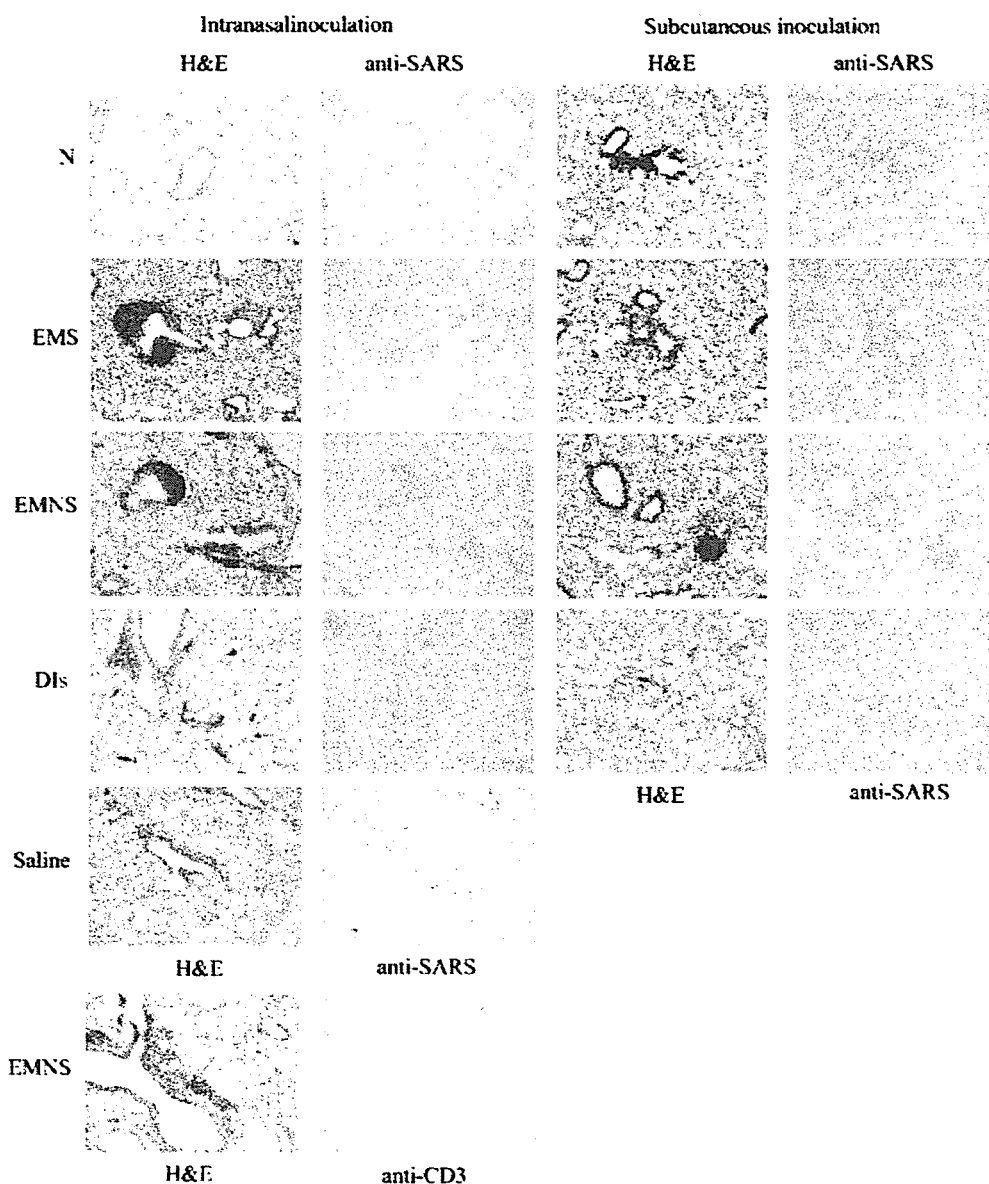


Fig. 8. Histopathology and immunohistochemistry. Lung specimen of mice immunized with rDIs expressing structural proteins of SARS-CoV and challenged with SARS-CoV. Mice were immunized i.n. or s.c. with DIs. rDIsSARS-N, rDIsSARS-E/M/S, rDIsSARS-E/M/N/S or saline. Mice were challenged with SARS-CoV 2 weeks after the final vaccination. Lungs were harvested 3 days after the challenge. The section was stained with hematoxylin and eosin (H&E) or immunohistochemically stained with anti-SARS-CoV antibody or anti-CD3 antibody.

recombinant MVA expressing SARS-CoV S protein elicited serum antibodies to SARS-CoV S protein and protective immunity against SARS-CoV infection. Previous studies demonstrated passive transfer of serum from immunized mice conferred protection against SARS-CoV in the respiratory tract following inoculation with either SARS CoV or recombinant MVA expressing S protein (Bisht et al., 2004; Subbarao et al., 2004). These results suggest that S protein is a crucial antigen in generating protective immunity. We observed that intranasal or subcutaneous inoculation of BALB/c mice with rDIs expressing S protein (rDIsSARS-S, rDIsSARS-E/M/S or rDIsSARS-E/M/N/S) produced serum antibodies capable of recognizing the

SARS-CoV virion by ELISA, also capable of neutralizing SARS-CoV in vitro. The subcutaneous route appears to elicit stronger immunity than intranasal immunization with respect to the level of anti-SARS-CoV IgG antibody produced. Important finding here is that although the mucosal IgA antibody response was induced only in mice intranasally immunized with rDIsSARS-E/M/N/S, the mice administered with rDIsSARS-E/M/N/S by either route elicited strong protective immunity. Therefore, the protection was achieved in the absence of a mucosal IgA response in mice subcutaneously immunized with rDIsSARS-E/M/N/S. Thus, our results clearly show that mucosal infection might be prevented in the presence of a

high level of neutralizing serum IgG antibody. Control mice vaccinated with DIs not expressing envelope proteins were not protected, indicating that the effect was specific for the expressed envelope proteins of SARS-CoV and was not due to enhanced nonspecific immunity.

A recent report suggests that a combination of three adenovirus vector expressing SARS-S, -M and -N protein is capable of eliciting neutralizing antibodies in serum and N-specific T cell responses in rhesus macaques (Gao et al., 2003). However, in this report, the relationship between these immune responses and actual protection was not presented. In another study, the importance of SARS-CoV structural proteins in generating protective immunity was investigated by expressing them individually and in combination using a recombinant parainfluenza virus (PIV) type 3 vector. The expression of S with the two other putative virion envelope proteins, M and E protein, did not augment the neutralizing antibody response. In the absence of S, expression of M and E, or the nucleocapsid protein N, did not induce a detectable serum SARS-CoV-neutralizing antibody response (Buchholz et al., 2004). Our results were consistent with this in that expression of M or N proteins by administration of DIs harboring SARS-CoV M or N gene singly did not induce a neutralizing antibody response, although anti-SARS-CoV antibodies were detected by ELISA.

Recent studies have shown that vaccination with a plasmid expressing N protein can elicit SARS-CoV nucleocapsid-specific humoral and cellular immune responses (Kim et al., 2004; Zhu et al., 2004; Zhao et al., 2005). They showed that linkage of N protein to calreticulin, Ca²⁺-binding protein known to enhance immune response, in a DNA vaccine resulted in the significant enhancement of the humoral and cellular immune responses to N protein in vaccinated mice. They also showed that the N protein-specific DNA vaccine elicited partial protection against N protein expressing vaccinia virus challenge. However, the efficacy of N-specific cellular immune responses in protection of SARS-CoV infection is not clear. Although we here showed that N protein expression by rDIs was capable of eliciting N-specific humoral and cellular immunity, vaccination with rDIsSARS-N failed to elicit a neutralizing antibody response against SARS-CoV infection *in vitro*, and failed to confer full protection in vaccinated mice against SARS-CoV challenge, suggesting that SARS-CoV N protein-specific antibodies and CTLs were not sufficient to provide full protection against SARS-CoV infection.

Histopathological analysis of lung tissues in the present study revealed a marked lymphocytic infiltration in peribronchial sites in mice immunized intranasally or subcutaneously with recombinant vaccinia virus DIs expressing E/M/S or E/M/N/S. Almost no SARS-CoV antigens were detected in these areas upon immunohistochemical analysis. The infiltrating lymphocytes were shown to be CD3 positive T-cells. This is the first evidence of induction of protective immunity against SARS-CoV associated with marked infiltration of T cells at a SARS-CoV infection site. We were able to detect SARS-CoV S-specific CD8⁺ T cells in the spleen of these immunized mice by INF- γ ELISPOT. Thus, these results suggest that T

cell induction in mice immunized with rDIsSARS-E/M/S and rDIsSARS-E/M/N/S might provide additional help to completely eliminate SARS-CoV in the lung. Of note, Weingartl et al. (2004) reported a low level of neutralizing antibody response in ferrets (*Mustela putorius furo*) immunized with a recombinant MVA expressing SARS-CoV S protein. They also showed that there are more rapid and vigorous neutralizing antibody responses in immunized ferrets, compared to control animals after challenge with SARS-CoV. However, SARS-CoV infection and spreading in the immunized ferrets is not prevented. Moreover, upon infection with SARS-CoV, strong inflammatory responses were noted in ferrets immunized with either recombinant MVA expressing SARS-CoV S or N protein, suggesting that vaccination with the recombinant MVA expressing SARS-CoV S or N protein may, in some case, lead to enhanced pathology during SARS-CoV infection (Czub et al., 2005; Weingartl et al., 2004). It was also reported that antibodies that neutralized most human SARS-CoV S enhanced entry mediated by the civet virus S, suggesting the possibility that such kind of vaccines might enhance viral infection (Yang et al., 2005). Although we observed no such pathology in rDIs-immunized mice after virus challenge, the potential for widespread tissue damage following administration of SARS-CoV proteins should be carefully investigated. In addition, further studies are required to clarify whether the recruited T-cells indeed play an important role in clearance of SARS-CoV from sites of infection.

In this study, we constructed rDIs containing genes encoding four structural proteins of SARS-CoV that were individually or simultaneously expressed. Intranasal or subcutaneous inoculation of BALB/c 3T3 mice with rDIs expressing S protein with or without other structural proteins elicited a high level of neutralizing antibodies against SARS-CoV and protective immunity, in the lungs of mice after intranasal challenge. Furthermore, both cellular and mucosal immunity against SARS-CoV structural proteins were also induced following administration of the rDIs. Therefore, the replication-deficient DIs strain is a feasible, safe and effective SARS vaccine vector.

Materials and methods

Cells

CEF cells and Vero E6 cells were grown in Dulbecco's modified essential medium (DMEM) supplemented with 10% fetal bovine serum (FCS), 1% penicillin-streptomycin and L-glutamine (GIBCO BRL/Life Technologies, Gaithersburg, MD). A20.2J murine B cells were maintained in RPMI1640 supplemented with 10% FCS, 50 μ M β -mercaptoethanol, L-glutamine and antibiotics.

Plasmid DNA constructs and DNA preparation

cDNA encoding SARS-CoV structural proteins were generated by reverse transcription of SARS-CoV HKU39849

(Accession No. AY278491) using superscriptII (Invitrogen Corp., Carlsbad, CA), followed by amplification using expand high fidelity PCR system (Roche diagnostics), as described previously (Ohnishi et al., 2005). These DNA fragments encoding E, M, N and S proteins were cloned into the vaccinia virus transfer vector pDisgptmH5, which also harbored *E. coli* xanthine-guanine phosphoribosyltransferase, under control of a vaccinia virus p7.5 promoter in the cloning site of pUc/DIs (Ishii et al., 2002), to generate pDisSARS-E, pDisSARS-M, pDisSARS-N, and pDisSARS-S, respectively. To construct transfer vectors to generate rDIs expressing E/M, E/M/S, or E/M/N/S, DNA fragments encoding M, N and S proteins controlled by the mH5 promoter of the vaccinia virus (Wyatt et al., 1996) were inserted into pDisSARS-E *Sma*I, *Nor*I and *Sac*I sites, respectively, thus generating pDisSARS-E/M, pDisSARS-E/M/S and pDisSARS-E/M/N/S (Fig. 1). A plasmid expressing S driven by the EF-1 α promoter was constructed using pEF-BOS-bst (Yoshizawa et al., 2001), and designated pEF-S-bst.

Generation of recombinant vaccinia virus

Recombinant forms of DIs were obtained by hypoxanthine-guanine phosphoribosyltransferase selection (Falkner and Moss, 1988). Monolayers of CEF cells in 6-well plates were pre-incubated with DMEM containing 10% FCS, 25 μ g/ml of micophenoic acid (MPA), 250 μ g/ml of xanthine and 15 μ g/ml of hypoxanthine. Infection was performed onto CEF cells grown in 8 cm dishes with DIs at a multiplicity of infection (moi) of 1.0. Transfection was performed using 20 μ g of each DIs transfer vector and Lipofectamine (GIBCO BRL/Life Technologies). rDIs expressing SARS-CoV structural proteins were selected following four consecutive rounds of plaque purification of CEF cells in 6-well plates pre-incubated with DMEM containing 10% FCS, 25 μ g/ml of MPA, 250 μ g/ml of xanthine, and 15 μ g/ml of hypoxanthine. Resultant rDIs expressing SARS-CoV structural proteins were designated as rDIsSARS-E, rDIsSARS-M, rDIsSARS-N, rDIsSARS-S, rDIsSARS-E/M, rDIsSARS-E/M/S and rDIsSARS-E/M/N/S, respectively, and subsequently maintained in CEF cells for use in further studies.

Western blot analysis

CEF cells infected with rDIs constructs harboring ORFs of SARS-CoV structural proteins were fractionated by SDS-PAGE under reduced conditions. Purified SARS-CoV virion (0.5 μ g) was used as a positive control. The proteins were then transferred to an Immobilon-P PVDF membrane (MILLIPORE, Bedford, MA) and incubated with monoclonal antibodies against N or S proteins (Ohnishi et al., 2005) or polyclonal antibody against M protein (Mizutani et al., 2004). After washing, the membrane was reacted with HRP-conjugated Fab fragment of anti-mouse or rabbit IgG (H + L) (1:20,000, Santa Cruz Biotechnology, Santa Cruz, CA), followed by visualization of the bands using chemiluminescent reagents (Pierce, Rockford, IL).

Indirect immunofluorescence analysis

CEF cells were infected with rDIs expressing SARS-CoV structural proteins. After 48 h of incubation, the cells were washed with PBS and fixed with 3% paraformaldehyde in PBS for 20 min at room temperature. The fixed cells were then permeabilized with 0.2% Triton X-100 for 3 min at room temperature, and then blocked with a non-fat milk solution, Block Ace (Yukijirushi Co., Tokyo, Japan). The cells were incubated with polyclonal antibodies against M, N or S proteins (Mizutani et al., 2004) for 60 min at 37 °C. The cells were further incubated with fluorescein isothiocyanate (FITC)-conjugated goat anti-rabbit IgG (TAGO, Burlingame, CA) diluted to 1:500 in PBS to detect SARS-CoV M, N or S proteins. To analyze the subcellular localization of SARS structural proteins, anti-GM-130 monoclonal antibody (BD Biosciences, Mississauga, ON, Canada) and rhodamine-conjugated goat anti-mouse IgG (TAGO) were used to stain the Golgi apparatus.

Vaccination

Animal studies were carried out under a protocol approved by the Animal Care and Use Committee of the National Institute of Infectious Diseases, Japan. Five- to 6-week-old female BALB/c mice were purchased from Japan SLC (Hamamatsu, Japan) and immunized with 10⁶ pfu of rDIs, either subcutaneously (s.c.) or intranasally (i.n.). After 2 and 6 weeks, identical titers of recombinant virus were re-administered. One week later, the mice were intranasally challenged with 10⁴ TCID₅₀ of SARS-CoV in 20 μ l of saline as previously described (Subbarao et al., 2004). Three days later, serum, nasal wash fluid and bronchoalveolar wash fluid were collected to measure viral titers and antibodies against SARS-CoV from mice that were sacrificed under anesthesia with chloroform.

Detection of SARS-CoV specific IgA and IgG antibodies

IgA and IgG titers against SARS-CoV were determined by ELISA, as previously described (Takasuka et al., 2004). Briefly, microtiter plates (Dynatech, Chantilly, VA) were coated overnight at 4 °C with SARS-CoV-infected or mock-infected Vero E6 cell lysate samples previously treated with 1% NP40, followed by UV-inactivation. The plates were blocked with 1% OVA in PBS–0.05% Tween 20, and then incubated with serially diluted sera (1:10–1:25⁵) for 1 h at room temperature. The plates were then incubated with either peroxidase-conjugated anti-mouse IgG (1:2000, Zymed, South San Francisco, CA) or IgA (1:2000, Southern Biotechnology, Birmingham, AL) antibody. The plates were washed three times with PBS–Tween at each step. The substrate mixture (o-phenylenediamine (Zymed) and hydrogen peroxide) was added to each well, and the absorbance of each well was read at 490 nm using a model 680 microplate reader (Bio-Rad, Hercules, CA). To provide a standard for IgG detection, serum was obtained from a hyper-immunized mouse and the OD_{490nm} value of 100 ELISA units/ml of standard serum was around three in every assay.

Each SARS-CoV-specific IgG titer was calculated by subtracting the optical density of wells coated with non-infected cell lysate from the optical density of wells coated with virus-infected cell lysate. As a positive control to induce SARS-CoV-specific IgA, mice were immunized intranasally with UV-inactivated purified SARS-CoV together with 3 µg of poly(I:C) (Ichinohe et al., 2005).

SARS-CoV neutralizing assay

Sera collected from vaccinated mice were inactivated by incubation at 56 °C for 30 min. The serially diluted mice sera (up to five-fold) were incubated with 100 TCID₅₀ of SARS-CoV for 1 h, then the mixtures were added to a Vero E6 cell culture grown to confluence in 96-well microtiter plates. After 48 h, the cells were fixed with 10% formaldehyde and stained with crystal violet to visualize the cytopathic effects of the virus (Storch, 2001). Neutralization antibody titers were expressed as the minimal dilution of sera capable of inhibiting viral cytopathic effects.

Analysis of the SARS-CoV-specific T-cell response

CLN, ALN and spleens were obtained from mice 1 week after their third vaccination. Following preparation of a single cell suspension, T cells were purified using a Pan T cell isolation kit and a magnetic cell sort system (MACS: Miltenyi Biotec, Bergisch Gladbach, Germany). To prepare APC, normal BALB/c mouse splenocytes were depleted of Thy-1⁺ T cells by MACS and irradiated at 2000 cGy. Purified T cells (1×10^6) were cultured with APC (5×10^6) in the presence or absence of UV-irradiated, purified SARS-CoV virion at 10 µg/ml. Four days after cultivation, cytokine concentrations within culture supernatant were measured by flow cytometry using a mouse Th1/Th2 cytokine cytometric bead array kit (Becton Dickinson, San Jose, CA).

Generation of a stable S-transfectant

A20.2J murine B cells were transfected with either pEF-Sbst or pEF-BOS-bst by electroporation at 960 µF and 310 V using a GenePulser (BioRad Laboratories, Hercules, CA). After selection using blasticidine S (Invitrogen), followed by limiting dilution cloning, S6.2 and BOS-5 clones were obtained. To detect S protein expression in S6.2 cells, the cells were stained with biotinylated anti-S monoclonal antibody (Ohnishi et al., 2005) or control antibody, followed by the incubation with APC-streptavidin (e-Bioscience Inc., San Diego, CA), after which they were analyzed by FACScalibur (BD Bioscience) using the Cell Quest II program. Propidium Iodide was used to exclude dead cells. The data were re-analyzed and depicted using Flowjo software (Tree Star Inc., San Carlos, CA).

ELISPOT assay

Spleen T cells of mice immunized with rDisSARS-N or rDisSARS-E/M/N/S were separated using a MACS system

(Miltenyi Biotec, Auburn, CA). To enrich CD4⁺ T cells in the T cell fraction, CD8⁺ T cells were partially removed using anti-CD8 mAb-coated magnetic beads (Miltenyi Biotec). This procedure reduced the number of CD8⁺ T cells to less than one third. Overlapping 20-mer peptides covering the whole N sequences of SARS-CoV were obtained from Sigma-Aldrich Japan. S peptides S44 (S331–350), S45 (S381–400), S46 (S431–450), and S47 (S481–500) corresponding to the ACE2 binding region of the S protein were selectively produced based on a web-site program by SYFPEITHI (<http://syfpeithi.de/>). A20.2J murine B cells irradiated at 2000 cGy were used as APCs with peptides corresponding to either S or N proteins. In some experiments, A20.2J cells stably transfected with pEF-S or the empty vector pEF-BOS were used.

ELISPOT assays were performed according to the methods outlined by DIACLONE research (Besancon, France). In brief, 96-well flat-bottom plates (Maxisoap Nunc plates, Nunc, Rochester, NY) were coated with anti-IFN-γ capture antibody for one h at 37 °C. The plates were then washed with PBS containing 0.05% Tween 20 (PBST), and blocked with PBS containing 2% bovine serum albumin overnight at 4 °C. Freshly isolated splenic T cells (5×10^5) and APCs (1×10^4) were added to the plates in the presence or absence of 5 µM of N or S peptides and incubated for 16 h at 37 °C in 5% CO₂ on the anti-IFN-γ-coated plates, followed by a lysis with ice-cold deionized water. After the plates were washed, biotinylated detection antibody was added, then the plates were further incubated for 1 h at 37 °C. The plates were washed three times with PBST, then 50 µl/well of Streptavidin-alkaline phosphatase-conjugated anti-biotin immunoglobulin G solution was added, followed by incubation for 1 h at 37 °C. After washing with PBST, substrate mix (50 µl/well) was added, and the plates were allowed to develop over 4 h at 37 °C. The wells were imaged and the number of spot-forming cells SFC counted using a KS ELISPOT compact system (Carl Zeiss, Jena, Germany).

Histopathology and immunohistochemistry

Lung tissue from the mice was fixed in 10% buffered formalin and embedded in paraffin. Paraffin block sections were stained with hematoxylin and eosin (H&E). SARS-CoV antigens were immunohistochemically detected using a labeled-streptavidin-biotin complex staining system (DakoCytomation Co. Japan, Kyoto, Japan). Rabbit polyclonal antibodies raised against UV-inactivated, purified SARS-CoV were used as a primary antibody. A catalyzed signal amplification method (Dako) was also used to detect SARS-CoV antigens with enhanced sensitivity. Lung sections from mice vaccinated with rDisSARS-E/M/N/S and infected with SARS Co-V were stained with anti-CD3 antibody. (Santa Cruz Biotechnology)

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