

Reovirus Nonstructural Protein μ NS Binds to Core Particles but Does Not Inhibit Their Transcription and Capping Activities

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Received 23 August 1999/Accepted 22 March 2000

Previous studies provided evidence that nonstructural protein μ NS of mammalian reoviruses is present in particle assembly intermediates isolated from infected cells. Morgan and Zweerink (Virology 68:455–466, 1975) showed that a subset of these intermediates, which can synthesize the viral plus strand RNA transcripts in vitro, comprise core-like particles plus large amounts of μ NS. Given the possible role of μ NS in particle assembly and/or transcription implied by those findings, we tested whether recombinant μ NS can bind to cores in vitro. The μ NS protein bound to cores, but not to two particle forms, virions and intermediate subvirion particles, that contain additional outer-capsid proteins. Incubating cores with increasing amounts of μ NS resulted in particle complexes of progressively decreasing buoyant density, approaching the density of protein alone when very large amounts of μ NS were bound. Thus, the μ NS-core interaction did not exhibit saturation or a defined stoichiometry. Negative-stain electron microscopy of the μ NS-bound cores revealed that the cores were intact and linked together in large complexes by an amorphous density, which we ascribe to μ NS. The μ NS-core complexes retained the capacity to synthesize the viral plus strand transcripts as well as the capacity to add methylated caps to the 5' ends of the transcripts. In vitro competition assays showed that mixing μ NS with cores greatly reduced the formation of recoated cores by stoichiometric binding of outer-capsid proteins μ 1 and σ 3. These findings are consistent with the presence of μ NS in transcriptase particles as described previously and suggest that, by binding to cores in the infected cell, μ NS may block or delay outer-capsid assembly and allow continued transcription by these particles.

The infectious virion of mammalian orthoreoviruses (reoviruses), prototype members of the *Reoviridae* family, has a genome composed of 10 double-stranded RNA (dsRNA) segments surrounded by two concentric protein capsids. The virion can be proteolytically cleaved in vitro to generate the intermediate subvirion particle (ISVP), which lacks outer-capsid protein σ 3 and contains fragments of outer-capsid protein μ 1. Further proteolysis removes the μ 1 fragments and releases outer-capsid protein σ 1, yielding the core particle (reviewed in reference 34). When provided with substrates, the core is transcriptionally active in vitro, using the dsRNA genome segments as templates for synthesis of the 10 full-length plus strand transcripts (3, 24, 39). In addition, these transcripts are modified to have a cap 1 structure (^{m7}GpppG^{m2'}O) at their 5' ends by viral enzymes within the core (15, 37). The resulting capped transcripts, which are released from the core as they are synthesized (4), are competent for translation into the reovirus proteins (38). Three of these proteins, μ NS, σ NS, and σ 1s, are synthesized in infected cells but are not found in purified virions (36, 49). The functions of these “nonstructural” proteins are not well understood, but all members of the *Reoviridae* family encode such proteins suggesting that they play important roles during infections by these viruses (13).

μ NS (called μ 0 in older papers), an 80,000- M_r (80K) nonstructural protein, is encoded by the reovirus M3 genome segment (27, 32). M3 encodes another protein, μ NSC, whose M_r

is approximately 5,000 smaller than that of μ NS and that is recognized by μ NS-specific monoclonal antibodies (23). μ NSC is thought to be generated by translation initiation at a downstream start codon in the open reading frame that encodes μ NS, such that μ NSC lacks approximately 5,000 Da of sequences that are present at the amino (N) terminus of μ NS (28, 44). Both μ NS and μ NSC are present in cells infected with the prototype isolates of all three reovirus serotypes (23), are expressed to moderate levels throughout infection (17), and are present in the infected cell at a μ NS: μ NSC ratio of 1:1 to 4:1 (44). Whether the two proteins have functional differences has not yet been addressed. Because the activities of μ NSC have not been differentiated from those of μ NS, the two proteins are generally referred to as μ NS in this report.

Although the roles of μ NS in the reovirus life cycle remain poorly understood, previous observations suggest several possibilities. In one study, antibodies to μ NS coimmunoprecipitated the viral plus strand RNA transcripts soon after the transcripts were synthesized in infected cells (1). Through this RNA-protein interaction, μ NS may be involved in translation of the viral transcripts, packaging of the RNA segments into new reovirus particles, synthesis of the minus strand RNA, or recognition and sorting of the 10 distinct RNA segments prior to packaging (1). In other studies, μ NS was isolated from infected cells in association with different types of viral particles (30, 31, 50). These particles were believed to be assembly intermediates because they chased into virions later in infection (50). In one of these studies, newly assembled “transcriptase particles,” capable of synthesizing the viral plus strand transcripts in vitro, were isolated from cells and shown to comprise core-like particles plus large amounts of μ NS (30).

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The precise function of μ NS in these particles was unclear because cores are transcriptionally active in vitro in the absence of μ NS (3, 24, 39) and because transcriptionally active particles isolated from cells in other studies contained less or no μ NS (31, 40). Nevertheless, the findings of Morgan and Zweerink (30) suggest that μ NS may play a role in the regulation of reovirus transcription or particle assembly. Other observations concerning μ NS include its association with the cytoskeletal fraction from infected cells (29), possession of predicted α -helical coiled-coil motifs in the carboxyl (C)-terminal third of the μ NS sequence (28), and coimmunoprecipitation with σ NS using σ NS-specific antibodies (23). M3 was additionally identified as a genetic determinant of genome segment deletion during passage of reovirus at high multiplicity in culture (6). These results suggest that μ NS may be involved at several steps in the viral life cycle, but additional experiments should provide a better description of its roles.

To investigate the association of μ NS with viral particles and its possible involvement in transcription or assembly, we obtained μ NS protein from expression in insect cells using a recombinant baculovirus and studied its interactions with different types of reovirus particles. After demonstrating μ NS binding to cores, but not to virions or ISVPs, we determined various characteristics of the μ NS-bound cores (μ NS cores), including their continued transcription and capping activities. We also showed that μ NS can compete with outer-capsid proteins μ 1 and σ 3 for binding to cores. The results of these studies suggest several possible roles for μ NS cores in the reovirus life cycle, including a role in enhancing production of the viral plus strand transcripts by blocking or delaying outer-capsid assembly on these particles.

MATERIALS AND METHODS

Reagents. All enzymes were from New England Biolabs, Inc. (Beverly, Mass.), unless otherwise stated. All chemicals were from Sigma (St. Louis, Mo.) unless otherwise stated.

Construction of M3 recombinant baculoviruses. The type 3 Dearing (T3D) reovirus M3 genome segment was cloned by Cashdollar et al. (7) and subcloned into pUC8 by Wiener et al. (44). The clone was a generous gift from M. R. Rorer (Florida Atlantic University). For our work, we cut the T3D M3 gene from pUC8 using the *Pst*I and *Afl*III sites in the terminal nontranslated regions of T3D M3. The 5' overhang of the *Afl*III site was filled in using the Klenow fragment of DNA polymerase I (Pharmacia, Piscataway, N.J.). The T3D M3 gene fragment was then blunt end ligated to *Sma*I-cut pGEM4Z (Promega, Madison, Wis.) to generate pGEM4Z-M3(T3D). The T3D M3 gene was excised from pGEM4Z-M3(T3D) at the *Bam*HI and *Kpn*I sites and ligated to pFastBacI (Gibco-BRL, Gaithersburg, Md.) that had been cut with the same enzymes. The pFastBacI vector containing T3D M3 was transformed into DH10Bac cells (Gibco-BRL) following the manufacturer's instructions to produce a recombinant bacmid. The isolated bacmid was transfected into *Spodoptera frugiperda* (Sf21) cells (Invitrogen, Carlsbad, Calif.) to yield a progeny recombinant baculovirus containing the reovirus T3D M3 gene [M3(T3D)-bac]. The stock was then subjected to two serial passages in Sf21 cells to increase viral titer.

The type 1 Lang (T1L) M3 genome segment was reverse transcribed from transcripts and amplified by PCR as described previously (28). For PCR, a primer corresponding to the 29 5'-most nucleotides of the minus strand of the T3D M3 sequence (44) with extra sequence at the 5' end containing a *Bam*HI restriction site (5'-GCAGGGGATCC-3') and a primer corresponding to the 35 5'-most nucleotides of the plus strand from the T3D M3 sequence (44) with extra sequence at the 5' end containing a *Sal*I restriction site (5'-GCGGTCCGTCCAC-3') were used. The PCR-amplified T1L M3 gene was cut with *Bam*HI and *Sal*I and ligated to pGEM4Z that had been cut with the same enzymes, generating pGEM4Z-M3(T1L). The T1L M3 gene was excised from pGEM4Z-M3(T1L) at the *Kpn*I and *Sph*I sites and ligated to pFastBacI that had been cut with the same enzymes to yield pFastBacI-M3(T1L). The cloned T1L M3 gene was then sequenced and found to contain one nucleotide change at position 242 (G to A) that caused an amino acid change in the encoded protein sequence compared to the published sequence (28). To correct the nucleotide change at 242, part of M3 was removed from pFastBacI-M3(T1L)-G242A and swapped with PCR fragments containing an introduced restriction site. pFastBacI-M3(T1L)-G242A was cut in the multiple cloning site of the vector and at nucleotide 660 in the M3 gene with *Pst*I. The fragment consisting of the pFastBacI vector and nucleotides 661 to 2241 of T1L M3 was gel isolated. Reverse

transcripts from the T1L M3 genome segment were amplified by PCR with a primer at the 5' end containing extra sequence with a *Pst*I site (5'-AGGATCC TGACGCTAGCTAAAGTGACCGTGGTC-3') and an internal primer (5'-GC ACAATATCAACCCTGAC-3') as described previously (28). The PCR product was cut with *Pst*I and ligated to the gel-isolated pFastBacI and M3 fragment. The resulting pFastBacI-M3(T1L) was sequenced to ensure that the encoded amino acid sequence from the cloned T1L M3 gene matched the published sequence (28). A recombinant baculovirus containing the T1L M3 gene [M3(T1L)-bac] was constructed as described above for the T3D M3 gene.

Expression of recombinant μ NS. To express μ NS protein, 7.5×10^6 *Trichoplasia ni* cells (High Five, Invitrogen) were plated on a 100-mm-diameter dish, infected with M3(T3D)-bac at a multiplicity of infection (MOI) of 1, and incubated at 27°C. The cells were harvested at 52 h postinfection by being pelleted at $500 \times g$ for 10 min at 4°C, washed with phosphate-buffered saline (137 mM NaCl, 3 mM KCl, 8 mM Na_2HPO_4 , 1 mM KH_2PO_4), and repelleted. The cell pellet was resuspended in 500 μ l of lysis buffer (10 mM Tris [pH 7.5], 2.5 mM MgCl_2 , 100 mM NaCl , 0.5% Triton X-100, 5 μ g of leupeptin/ml, 1 mM phenylmethylsulfonyl fluoride, 1 mM dithiothreitol) and placed on ice for 30 min with mixing every 5 min. The insoluble fraction was removed by spinning the mixture at $500 \times g$ for 10 min at 4°C. The amount of μ NS expressed in the lysate varied from 0.3 to 0.8 μ g of μ NS per μ l of lysate as estimated from Coomassie blue-stained gels with bovine serum albumin standards. The μ NS protein used in the experiments described in this paper was T3D μ NS unless otherwise specified.

Production of μ NS polyclonal antibodies. To direct expression of μ NS with an N-terminal histidine tag, the T3D M3 gene was removed from pGEM4Z-M3(T3D) at the *Bam*HI and *Kpn*I sites and ligated to pRSETB (Invitrogen) that had been cut with the same enzymes. The plasmid was transformed into BL21-DE3 cells (Novagen, Madison, Wis.), and the histidine-tagged μ NS was expressed and purified following the protocol in the pET system manual (Novagen). In brief, expression was induced with isopropyl- β -D-thiogalactopyranoside (0.19 mg/ml), and the cells were grown at 37°C for 3 h. Intact cells were pelleted, resuspended, and lysed by sonication. The insoluble fraction containing μ NS was spun down and solubilized in 8 M urea. The histidine-tagged μ NS was purified with His-bind resin (Novagen) in column format. The eluent was dialyzed into phosphate-buffered saline and concentrated with polyethylene glycol. The antiserum was generated in a rabbit by the polyclonal antibody service in the animal care unit of the University of Wisconsin Medical School (Madison, Wis.).

Growth of reovirus and purification. Infections and purification of reovirus T1L and T3D virions were performed as described previously (14). ISVPs were prepared by digestion of particles with chymotrypsin as described previously (33). Reovirus cores were prepared by digestion as described for reoviruses T3D (25) and T1L (12). Cores were alternatively prepared using an expedited protocol as described previously (9). To obtain particles labeled with [^{35}S]methionine and [^{35}S]cysteine, 5 mCi of Easy Tag Express protein labeling mixture (Dupont, Wilmington, Del.) was added per 4×10^8 cells in spinner culture. All particles were purified using equilibrium centrifugation in CsCl density gradients, followed by dialysis into virion buffer (VB) (10 mM Tris [pH 7.5], 10 mM MgCl_2 , 150 mM NaCl) and storage at 4°C. The concentrations of virions and cores were determined using $1.0 A_{260} = 2.1 \times 10^{12}$ virions/ml (42) and $1.0 A_{260} = 4.2 \times 10^{12}$ cores/ml (10).

SDS-PAGE and immunoblot analysis. Samples were subjected to sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) in 10% polyacrylamide gels as described previously (18). Proteins were visualized by staining with Coomassie brilliant blue R-250 (Coomassie blue). Gels with radiolabeled proteins were dried onto filter paper and visualized by phosphorimaging (Molecular Dynamics, Sunnyvale, Calif.). To estimate relative amounts of reovirus proteins from Coomassie blue-stained gels, gels were scanned with a laser densitometer (Molecular Dynamics) and volume-based intensities of the protein bands were determined using the ImageQuant program (Molecular Dynamics). For immunoblots, protein samples were subjected to SDS-PAGE and transferred to nitrocellulose (Bio-Rad, Hercules, Calif.) at 4°C for 1 h at 100 V in transfer buffer (25 mM Tris, 192 mM glycine, pH 8.3). Binding of the primary antibody was detected with alkaline phosphatase-coupled goat anti-rabbit or goat anti-mouse immunoglobulin (Bio-Rad) and colorimetric reagents *p*-nitroblue tetrazolium chloride and 5-bromo-4-chloro-3-indolylphosphate *p*-toluidine salt (Bio-Rad).

Incubation of μ NS lysate with reovirus particles and gradient fractionation. The buffer conditions for binding were 10 mM Tris, 100 to 120 mM NaCl, 3 to 6 mM MgCl_2 , and 0.3 to 0.5% Triton X-100. Fifty microliters of insect cell lysate containing μ NS was mixed with 2×10^{12} particles (cores, ISVPs, or virions) in VB. For the lysate-alone gradients, 50 μ l of insect cell lysate containing μ NS was mixed with VB. For the particle-alone gradients, 2×10^{12} particles in VB were mixed with lysis buffer. Samples were incubated for 1 h at 37°C, except for ISVPs, which were incubated at room temperature due to instability at 37°C. The samples were layered onto preformed 3.5-ml CsCl density gradients (1.26 to 1.47 g/cm 3 for cores and 1.2 to 1.45 g/cm 3 for ISVPs and virions) in an SW60 tube and spun in a Beckman ultracentrifuge for 2 h at 50,000 rpm at 5°C. The gradients were fractionated with a peristaltic pump into 200- μ l fractions. The optical density at 280 nm (OD_{280}) and refractive index of each fraction were determined. The density of each fraction was determined based on its refractive index.

Identification of proteins bound to reovirus particles. Cores, virions, or ISVPs (10^{12}) were mixed with 140 μ l of insect cell lysate containing μ NS as described

above except that all samples were incubated at room temperature. After centrifugation, the particle bands were visualized by light scattering and were harvested by puncturing the bottom of the tube, except for μ NS cores, which were harvested with a Pasteur pipette from the top of the gradient. Samples were dialyzed into VB prior to analysis by SDS-PAGE and immunoblotting.

μ NS-expressing recombinant baculovirus and protein expression. The recombinant baculovirus expressing the T1L σ NS protein was previously described (18). *T. ni* cells were infected with recombinant baculovirus as described previously (18). Cell lysate was prepared as described above for μ NS.

RNase A treatment of μ NS cores and μ NS lysate. μ NS cores (approximately 2×10^{12}) purified on a CsCl gradient and dialyzed into VB were treated with 20 μ g of RNase A for 2 h at 37°C and then purified on another CsCl gradient. Untreated μ NS cores were analyzed in parallel as a control. μ NS lysate (50 μ l) was treated with 4 μ g of RNase A for 30 min at 25°C and then incubated with 2×10^{12} cores for 1 h at 25°C. Untreated μ NS lysate was also analyzed in parallel as a control. The samples were layered on CsCl gradients and spun to equilibrium. Particles were removed from the gradients with a Pasteur pipette and analyzed by SDS-PAGE.

Gradients with different amounts of μ NS. Cores (10^{12}) in 20 μ l of VB were mixed with twofold-increasing amounts of insect cell lysate containing μ NS (4.3, 8.5, 17, 34, 68, and 140 μ l) and brought to a final volume of 170 μ l with lysis buffer. Cores (10^{12}) in 20 μ l of VB were mixed with 150 μ l of lysis buffer or 140 μ l of lysate from insect cells infected with wild-type baculovirus and 10 μ l of lysis buffer. For the lysate-alone sample, 140 μ l of insect cell lysate containing μ NS was mixed with 30 μ l of lysis buffer. The samples were incubated at room temperature for 1 h and then layered onto preformed 3.5-ml CsCl gradients (1.31 to 1.50 g/cm³) in an SW60 tube. The samples were spun at 50,000 rpm for 2 h at 5°C and visualized with a high-intensity lamp.

Negative-stain electron microscopy (EM). Samples were negatively stained with 1% uranyl acetate and viewed with a Philips 120 transmission electron microscope at 100 kV as described previously (8).

Sucrose gradient velocity sedimentation of lysate containing μ NS. Insect cell lysate containing μ NS (150 μ l) was layered on a preformed 11-ml sucrose gradient (5 to 20%) in an SW41 tube and spun in a Beckman ultracentrifuge at 40,000 rpm for 15 h at 5°C. An additional gradient contained 2 mg of each marker, gamma globulin (7S) and thyroglobulin (19S). The gradients were fractionated with a piston gradient fractionator (BioComp Instruments, Inc., New Brunswick, Canada) into 26 equal fractions. The positions of the markers were determined by OD₂₆₀. Samples from the gradient of μ NS lysate were analyzed by immunoblotting.

Transcription and methylation assay. T3D cores were mixed with various amounts of μ NS lysate, incubated for 1 h at room temperature, purified on CsCl gradients, and dialyzed into VB. Cores were also incubated with lysate from wild-type baculovirus-infected cells (the same amount of lysate used to make μ NS cores with 980 molecules of μ NS per core) and purified on CsCl gradients. μ NS cores for transcription reactions were made with [³⁵S]methionine- and [³⁵S]cysteine-labeled T3D cores. The amount of μ NS per core was determined from densitometry of Coomassie blue-stained gels. Transcription reactions and transcription/methylation reactions were performed as described previously (26). The aggregated nature of μ NS cores led to variability of particle input, so transcription activity was expressed as a ratio of the ³²P incorporated into trichloroacetic acid (TCA)-precipitable counts to ³⁵S in the TCA-precipitable counts to standardize the amount of RNA synthesized to the number of ³⁵S-labeled cores in each reaction mixture. Methylation activity was expressed as a ratio of ³H incorporated into TCA-precipitable counts to ³²P incorporated into TCA-precipitable counts to standardize for differences in transcription activity.

μ NS and μ 1- σ 3 competition for core binding. The baculovirus to express T1L μ 1 and σ 3 proteins was previously described (9). μ 1- and σ 3-containing lysate (μ 1- σ 3 lysate) was prepared as described for μ NS. T3D cores (5×10^{10}) were mixed with 25 μ l of lysis buffer, with 20 μ l of μ 1- σ 3 lysate and 5 μ l of lysis buffer, or with 5 μ l of μ NS lysate and 20 μ l of lysis buffer as controls for the positions of the resulting particles, cores, re-coated cores and μ NS cores, respectively. T3D cores (5×10^{10}) were mixed with 5 μ l of μ NS lysate and incubated for 1 h at 37°C, and then 20 μ l of μ 1- σ 3 lysate was added, followed by incubation for 2 h at 37°C. T3D cores (5×10^{10}) were mixed with 20 μ l of μ 1- σ 3 lysate and incubated at 37°C for 2 h, and then 5 μ l of μ NS lysate was added, followed by incubation for 1 h at 37°C. The amount of μ 1- σ 3 lysate added was sufficient to recoat cores completely as demonstrated previously (9). The amount of μ NS lysate was chosen to add approximately the same amount of μ 1 and μ NS to each sample as estimated from Coomassie blue-stained gels of lysate. After incubation at 37°C, the samples were layered on performed 5.4-ml CsCl density gradients (1.30 to 1.40 g/cm³) in an SW50 tube and spun in a Beckman ultracentrifuge at 40,000 rpm for 2 h 45 min at 5°C. Fractions were TCA precipitated by adding 30 μ g of bovine serum albumin as a carrier and 900 μ l of cold TCA. Samples were incubated on ice for 20 min and spun for 15 min at 16,000 \times g in a microcentrifuge. The supernatant was removed, and the pellet was washed with 500 μ l of 70% ethanol, allowed to air dry, resuspended in 20 μ l of 1 \times Laemmli sample buffer (125 mM Tris [pH 8.0], 2% β -mercaptoethanol, 1% SDS, 0.1% bromophenol blue), and incubated at 100°C for 5 min. Samples were analyzed by immunoblotting. μ NS, μ 1, and the core λ proteins were detected using polyclonal antiserum specific to μ NS, polyclonal antiserum specific to reovirus core proteins

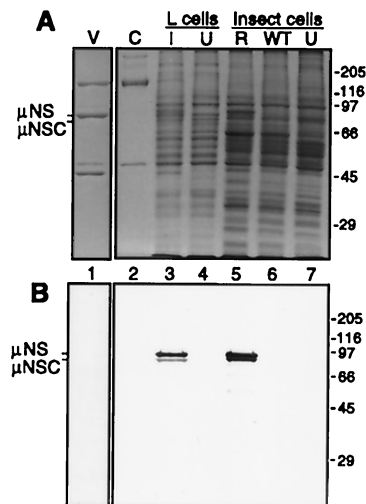


FIG. 1. SDS-PAGE and immunoblot analysis of μ NS expression. Murine L cells were infected with T3D reovirus at an MOI of 40 and harvested at 24 h postinfection. Insect cells were infected with M3(T3D)-bac at an MOI of 1 and harvested at 52 h postinfection. (A) An SDS-polyacrylamide gel was loaded with 5×10^{10} reovirus virions (V), 5×10^{10} reovirus cores (C), cytoplasmic lysate of 8.8×10^4 L cells infected with reovirus (I), cytoplasmic lysate of 8.8×10^4 uninfected L cells (U), cytoplasmic lysate of 2.8×10^4 insect cells infected with M3(T3D)-bac (R), cytoplasmic lysate of 3.9×10^4 insect cells infected with wild-type baculovirus (WT), and cytoplasmic lysate of 2.3×10^4 uninfected insect cells (U). (B) An identically loaded gel was analyzed by immunoblotting with a polyclonal antiserum specific to μ NS. The positions of μ NS and μ NSC from infected L cells are indicated to the left, and those of molecular mass markers (kilodaltons) are indicated to the right of each panel.

(S. Noble and M. L. Nibert, unpublished data), and a monoclonal antibody specific to μ 1, 10H2 (43).

Computer software. Images for the figures were scaled uniformly and adjusted for optimal brightness and contrast in Photoshop 4.0 (Adobe System, San Jose, Calif.). All figures were produced in Illustrator 7.0 (Adobe).

RESULTS

Reovirus μ NS protein is expressed to high levels in insect cells. To obtain large amounts of μ NS for study, we generated recombinant baculovirus M3(T3D)-bac containing the entire coding region of the T3D reovirus M3 genome segment under transcriptional control of the baculovirus polyhedrin promoter. Insect cells infected with this virus produced a prominent protein doublet with a size of approximately 80K in SDS-polyacrylamide gels, similar to those of the μ NS and μ NSC proteins from reovirus-infected L cells (Fig. 1A). The doublet is found mostly in the cytoplasmic fraction of lysed insect cells (data not shown). Both the 80K doublet from M3(T3D)-bac-infected cells and μ NS and μ NSC from reovirus-infected cells were recognized in immunoblots by a polyclonal antiserum that we raised against μ NS expressed in *Escherichia coli* (Fig. 1B). These proteins were also recognized in immunoblots by a monoclonal antibody to μ NS (23) (data not shown). The ratio of the two proteins in the doublet varied with each preparation (data not shown). Experiments are in progress to determine whether the lower protein in this doublet has the same origin as μ NSC from reovirus-infected cells (44) or may instead represent a breakdown product of μ NS. In the subsequent text, we refer to both proteins in the 80K doublet from M3(T3D)-bac-infected cells as μ NS. A recombinant baculovirus [M3(T1L)-bac] containing the T1L M3 gene was also constructed and directed expression of an 80K doublet, recognized by the polyclonal μ NS antiserum, to levels as high as those for the T3D protein (data not shown).

Density of cores, but not virions and ISVPs, is decreased after incubation with insect cell lysate containing μ NS. Based on the observation from Morgan and Zweerink (30) that transcriptase particles from reovirus-infected cells represent core-like particles plus μ NS protein, we tested the capacity of μ NS from M3(T3D)-bac-infected insect cells to bind reovirus cores as well as other particle types. In initial experiments, lysate from insect cells expressing μ NS (μ NS lysate) was mixed with purified T3D cores, T1L ISVPs, or T3D virions. T3D ISVPs were not tested because of their instability at high concentrations. As controls, cores, ISVPs, and virions without insect cell lysate and μ NS lysate without cores were analyzed separately. After a period of incubation, a floccular precipitate became visible in the cores-plus- μ NS sample, but not in the other samples (data not shown). To separate the reovirus particles and particle-bound proteins from nonbound proteins, the samples were subjected to equilibrium centrifugation in CsCl density gradients. Following centrifugation, virus particles and/or other abundant proteins formed visible bands in the gradients (data not shown). The virions-plus- μ NS and ISVPs-plus- μ NS gradients contained well-defined bands near the positions of virions and ISVPs observed in the gradients with each of those particles alone ($\rho \approx 1.36$ and 1.38 g/cm³, respectively). In the cores-plus- μ NS gradient, however, the core band was absent from its expected position, and instead a flocculent white band was seen at a higher position (lower density) than that of cores in the gradient with cores alone ($\rho \approx 1.43$ g/cm³). A second prominent band was observed at the top of the cores-plus- μ NS, ISVPs-plus- μ NS, and virions-plus- μ NS gradients, at the same position as the band in the gradient with μ NS lysate alone ($\rho \approx 1.30$ g/cm³). The loss of the core band and the appearance of a new band at lower density suggested that the RNA-to-protein ratio of the particles had been lowered by the binding of a lysate protein(s) to the cores.

To provide better documentation of the preceding results, the gradients were fractionated and the fractions were analyzed for absorbance at 280 nm and buoyant density. The strong absorbance seen at the top of all gradients was attributable to Triton X-100 in the lysis buffer (data not shown). The gradient profile of μ NS lysate alone showed a peak of absorbance near the expected density of protein alone, 1.30 g/cm³, and that of cores alone showed a peak of strong absorbance near the expected density of cores, 1.43 g/cm³ (Fig. 2A). In contrast, the gradient profile of cores plus μ NS lacked an absorbance peak at the expected density for cores but exhibited a strong absorbance peak at a lower density, near 1.39 g/cm³ (Fig. 2A), in agreement with the qualitative results described above. Cores were found to migrate near the expected density of 1.43 g/cm³ after incubation with insect cell lysate that lacked μ NS, either from uninfected cells or from wild-type baculovirus-infected cells (data not shown). In contrast to what was found for cores, strong absorbance peaks near the densities expected for virions and ISVPs, 1.36 and 1.38 g/cm³, respectively, were noted for these particles in either the presence or absence of μ NS lysate (Fig. 2B and C). Taken together, these data indicate that μ NS-containing lysate altered the density of reovirus cores, but not those of virions and ISVPs, and that lysate which lacked μ NS did not alter the density of cores.

μ NS binds cores but not virions or ISVPs. To determine if a specific lysate protein was interacting with cores, experiments similar to those described above were performed with an increased amount of μ NS lysate to allow for detection of particle-bound protein by Coomassie blue staining. The prominent bands in the CsCl gradients were collected and analyzed by SDS-PAGE. The sample collected from the gradient of cores plus μ NS contained both core proteins and an additional pro-

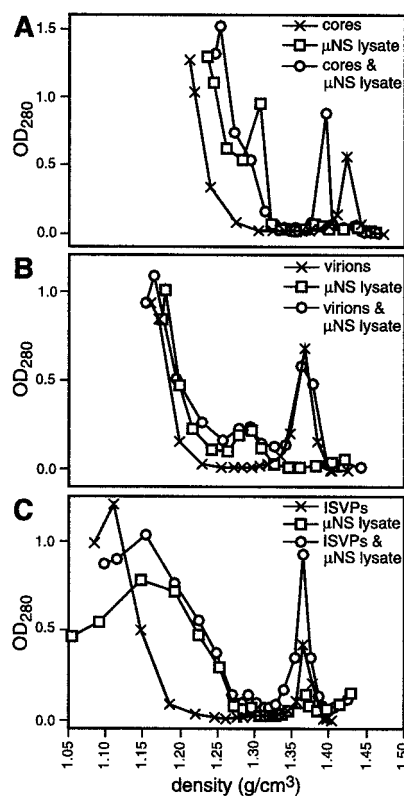


FIG. 2. Analysis of reovirus particle density shifts in the presence of lysate containing μ NS. Reovirus cores (A), virions (B), and ISVPs (C) (2×10^{12}) were incubated with 50μ l of buffer or insect cell lysate containing μ NS. Lysate was also incubated alone. Samples were subjected to equilibrium centrifugation in CsCl density gradients and fractionated. The buoyant density and OD₂₈₀ were determined for each fraction. The strong absorbance seen at the top of the gradient (lowest density) is due to detergent in the lysis buffer.

tein of approximately 80K (Fig. 3A, lane 2). This protein was not present in the samples collected from gradients of cores alone or of cores plus wild-type baculovirus lysate (Fig. 3A, lanes 1 and 3). Samples isolated from gradients containing virions and ISVPs, whether previously incubated with μ NS lysate or not, contained only proteins present in the respective virus particles (Fig. 3A, lanes 4 through 7). Immunoblot analysis of the gradient-isolated material confirmed that μ NS was present as an 80K protein doublet comigrating with cores (Fig. 3B, lane 2). μ NS and cores comigrated in gradients after incubation at temperatures from 4 to 37°C and with core concentrations between 1.8×10^{12} and 2.4×10^{13} cores/ml (data not shown). At all ratios of cores to μ NS lysate tested to date, both proteins in the μ NS doublet bound to cores (data not shown). No detectable μ NS comigrated with virions or ISVPs (Fig. 3B, lanes 5 and 6). Similar results were obtained for T3D μ NS binding to reovirus T1L particles: the μ NS doublet bound to cores but not to virions (data not shown). Thus, the capacity to interact with cores was not specific to the strain or serotype of the virus particles. Moreover, the T1L μ NS protein doublet was shown to bind to T1L and T3D cores but not to T1L and T3D virions or T1L ISVPs (data not shown), demonstrating that the selectivity of μ NS binding to cores was not specific to the strain or serotype of the virus from which μ NS was derived.

To determine whether similar results might be obtained with σ NS, the other major nonstructural protein of reovirus, cores and insect cell lysate containing σ NS were mixed and then

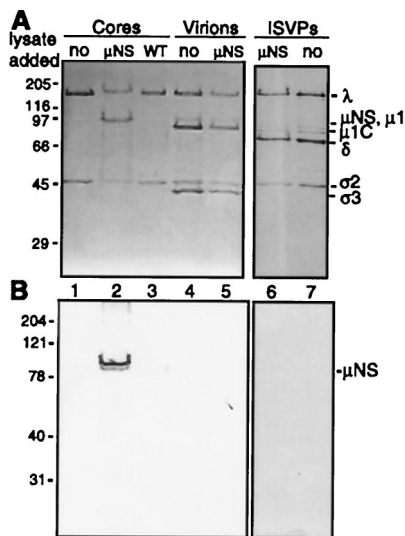


FIG. 3. SDS-PAGE and immunoblot analysis of μ NS binding to reovirus particles. Reovirus cores, virions, or ISVPs (2×10^{12}) were incubated in the presence and absence of μ NS lysate. Cores were also incubated with wild-type baculovirus lysate. Samples were subjected to equilibrium centrifugation in CsCl density gradients. (A) Particle bands isolated from CsCl density gradients were analyzed by SDS-PAGE with 5×10^{10} particles loaded per lane. Samples (lanes): no, no lysate added; μ NS, μ NS lysate added; WT, wild-type baculovirus lysate added. (B) An identically loaded gel was subjected to immunoblot analysis with a polyclonal antiserum generated against μ NS. For both panels, molecular mass markers (kilodaltons) are on the left and protein mobilities are on the right.

subjected to equilibrium centrifugation in a CsCl density gradient. The appearance and migration of the core band were unchanged in the presence of σ NS. In addition, no σ NS was detected in the harvested core band by immunoblot analysis with polyclonal antiserum to σ NS (18) (data not shown). Thus, σ NS and μ NS have different capacities to bind to cores.

Because μ NS may bind RNA (1) and because cores produce RNA transcripts, we performed additional experiments to address the possibility that RNA may serve as a required intermediate for μ NS binding to cores. Gradient-purified μ NS cores were treated with RNase A and then purified in another CsCl gradient. This treatment was not sufficient to disrupt the μ NS-core interaction (data not shown). μ NS lysate was also treated with RNase A prior to incubation with cores, and this treatment did not prevent μ NS cores from forming (data not shown). These findings suggest that μ NS associates with cores via protein-protein interactions and not through a single-stranded RNA intermediate.

Density of μ NS-core complexes changes with the amount of μ NS. To determine if μ NS forms a defined layer on the outside of the core similar to the outer-capsid proteins μ 1 and σ 3 in virions (9), we investigated whether μ NS binding to cores is saturable. Equal numbers of cores were incubated with increasing volumes of μ NS lysate. The mixtures were then analyzed in CsCl density gradients to determine their buoyant densities. As controls, cores alone, μ NS lysate alone, and cores mixed with wild-type baculovirus lysate were also analyzed. Following centrifugation to equilibrium, the abundant proteins were visualized by direct observation. μ NS cores generated with different volumes of μ NS lysate were found at different positions in the separate gradients and, therefore, exhibited different buoyant densities. As the volume of added μ NS lysate was increased in gradients 5 through 7 (Fig. 4), the buoyant densities of μ NS cores continuously decreased. The complexes formed with smaller amounts of μ NS lysate in gradients 3 and

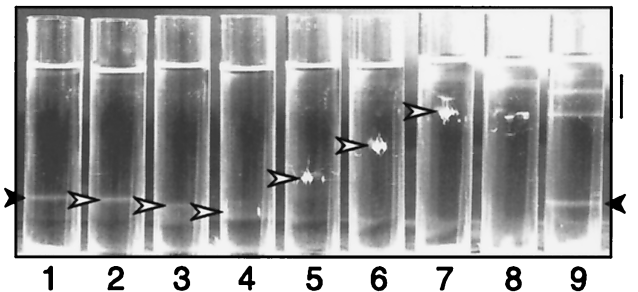


FIG. 4. CsCl density gradients of cores incubated with increasing amounts of lysate containing μ NS. Cores (10^{12}) were incubated alone (gradient 1); with 4.3 (μ l) (gradient 2), 8.5 (μ l) (gradient 3), 17 (μ l) (gradient 4), 34 (μ l) (gradient 5), 68 (μ l) (gradient 6), or 140 (μ l) (gradient 7) of μ NS lysate; or with 140 (μ l) of wild-type baculovirus lysate (gradient 9). μ NS lysate (140 μ l) was incubated alone (gradient 8). The samples were subjected to equilibrium centrifugation in CsCl density gradients and visualized with a high-intensity light. Solid arrowheads, bands of cores; open arrowheads, complexes of μ NS cores; line, position of bands from the lysate alone.

4 (Fig. 4), appeared to migrate at a slightly higher density than cores alone in this experiment. This may have been due either to a small increase in the density of the complexes or to slight inconsistencies in the way the different gradients were formed. The complexes formed using the largest lysate volume (Fig. 4, gradient 7) migrated close to the position of the protein alone in the gradient of μ NS lysate alone (Fig. 4, gradient 8). After isolation of the μ NS-core complexes from the gradients, SDS-PAGE analysis showed that increasing amounts of μ NS were bound to the cores, corresponding to the increase in added lysate (data not shown). As in previous experiments, migration of the core band was unchanged after incubation with wild-type baculovirus lysate (Fig. 4, gradient 9). The overall trend of decreasing buoyant density of complexes with increasing μ NS, with the density ultimately approaching that of protein alone, suggested that the binding of μ NS to cores is not saturable. The progressively larger amounts of μ NS bound to a fixed number of cores may reflect the capacity of μ NS molecules to self-associate.

Negative-stain EM of μ NS cores reveals cores linked together in large complexes. To investigate the morphology of μ NS cores, the complexes from the gradients in Fig. 4 were examined by negative-stain EM. Micrographs of μ NS cores from gradients 5 and 6 revealed intact cores embedded within large complexes (Fig. 5A and B). Cores, the appearance of which is well defined (8, 42), are shown for comparison (Fig. 5B, inset). The cores in the μ NS core samples were linked together by an amorphous density which we attribute to μ NS. The large complexes and amorphous density surrounding the cores were not present in samples containing either cores alone or cores that had been mixed with wild-type baculovirus-infected cell lysates before gradient isolation (Fig. 5B, inset, and data not shown). μ NS cores from other gradients exhibited similar morphology (data not shown). Notably, the cores in samples with smaller amounts of μ NS were also linked together in complexes (data not shown). Since nonphysiological cysteine bond formation between μ NS molecules was one possible explanation for the observations, in a subsequent experiment 1 mM dithiothreitol was added to the lysis buffer, the core-binding reaction mixture, and the CsCl gradient; however, the presence of this reducing agent did not affect the aggregated nature of μ NS cores (data not shown). In sum, these data provide evidence that (i) μ NS bound to cores such that a regularly structured outer capsid of protein was not formed and (ii) the intact particles were linked together.

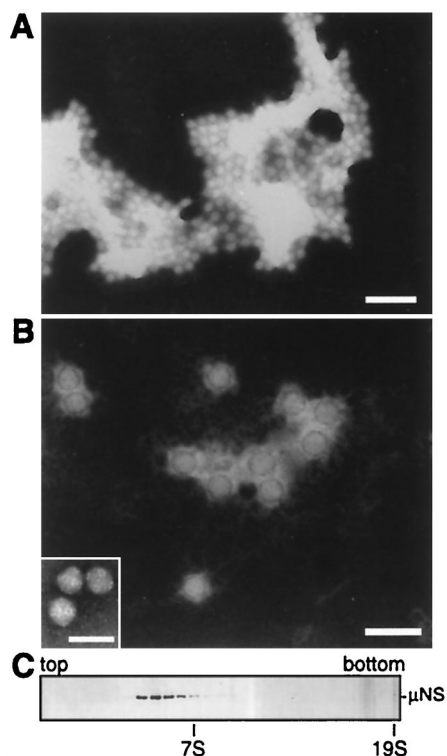


FIG. 5. Negative-stain EM of μ NS cores and velocity sedimentation analysis of μ NS lysate. μ NS cores were purified on a CsCl gradient, dialyzed into VB, stained with uranyl acetate, and viewed by EM. (A) μ NS cores viewed at low resolution. Bar, 200 nm. (B) μ NS cores viewed at higher resolution. The inset provides an image of cores for comparison. Bars, 100 nm. (C) μ NS lysate was subjected to velocity sedimentation on a sucrose gradient. The gradient was fractionated and subjected to immunoblot analysis with polyclonal antiserum specific to μ NS. Markers (7S and 19S) were analyzed on a parallel gradient, and the positions were determined by OD₂₆₀. The positions of the 7S and 19S markers and the top and bottom of the gradient are indicated. The 19S marker was pelleted at the bottom of the gradient with the centrifugation conditions used in this experiment. The position of μ NS is indicated to the right.

μ NS may have been present in the lysate as large complexes before binding to cores. We could not test this by visualization with EM because the lysate contained too many proteins and other contaminants. Instead, we analyzed μ NS lysate by velocity sedimentation in sucrose gradients to estimate the size of μ NS complexes present in the lysate prior to incubation with cores. μ NS sedimented as a single peak near the 7S marker (Fig. 5C). The 19S marker was pelleted under these sedimentation conditions. The predicted S values for a globular 80-kDa protein are 4.7 for a monomer, 7.4 for a dimer, and 9.7 for a trimer (47). Thus, μ NS in the lysate appears to be a monomer or small oligomer that forms large complexes only when incubated with cores.

μ NS cores retain transcriptional activity. If the μ NS-core complexes formed *in vitro* are similar to transcriptase particles isolated from reovirus-infected cells (30), the complexes should be transcriptionally active. The transcriptional activities of μ NS cores containing different amounts of bound μ NS were therefore tested and compared to that of cores. Cores mixed with wild-type baculovirus-infected lysate and then gradient purified were included as a control to address whether cellular factors from the lysate could affect the transcriptional activity of cores. Because the aggregated nature of μ NS cores made them difficult to aliquot consistently, the transcriptional activity of each sample was standardized to the number of input par-

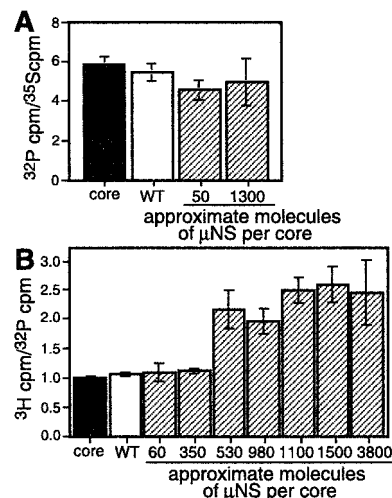


FIG. 6. Analysis of μ NS cores for transcription and methylation activities. (A) Standard transcription reactions were performed in triplicate with purified ^{35}S -labeled cores (core), purified ^{35}S -labeled cores previously mixed with wild-type baculovirus lysate (WT), and purified ^{35}S -labeled cores with two different amounts of μ NS bound. The approximate amount of μ NS per core was determined by densitometry. The mean transcriptional activity \pm standard deviation is reported as TCA-precipitable ^{32}P counts relative to ^{35}S counts to normalize for particle input. (B) Methylation activity was monitored using standard transcription reaction mixtures containing the methyl donor [^3H]SAM. Activity is expressed as TCA-precipitable ^3H counts normalized to the amount of transcription with TCA-precipitable ^{32}P counts. These results are from four separate experiments with three separately prepared μ NS core samples. The average activity of cores in each experiment was normalized to one, and the other samples were scaled appropriately. Cores mixed with wild-type baculovirus lysate and purified (WT), μ NS cores with 350 molecules of μ NS per core, and μ NS cores with 980 molecules of μ NS per core were assayed once in triplicate. The other samples of μ NS cores were assayed twice in triplicate.

ticles by use of cores labeled with [^{35}S]methionine and [^{35}S]cysteine. Transcriptional activity was expressed as the ratio of ^{32}P incorporated into acid-precipitable counts to the ^{35}S counts in each reaction mixture. Results of a representative experiment are shown in Fig. 6A. μ NS cores containing approximately 50 or 1,300 μ NS molecules per core were slightly less active at transcription than either the original cores or cores mixed with wild-type baculovirus-infected lysate prior to purification. In four different experiments, the transcriptional activities of μ NS cores ranged from 46 to 84% (mean, 66% \pm 13%) of that of cores. The transcripts from cores and μ NS cores were indistinguishable when separated on denaturing gels (data not shown). To verify that μ NS remained bound to cores during transcription, transcription reaction mixtures containing μ NS cores were layered on CsCl density gradients, spun to equilibrium, and fractionated. μ NS continued to comigrate with cores in this experiment (data not shown), suggesting that it remained bound to cores. In sum, the results indicate that the binding of μ NS to cores did not inhibit the core transcriptional activity as assembly of outer-capsid proteins is believed to do (2, 11, 21, 46; D. L. Farsetta, K. Chandran, and M. L. Nibert, unpublished data).

μ NS cores may have elevated transcript 5'-end capping activities. To evaluate the effects of μ NS on the capping of the viral transcripts, μ NS cores and cores were quantitatively compared for 5' cap methylation. RNA methylation activity was assayed in a standard transcription assay mixture containing [α - ^{32}P]GTP and the methyl donor *S*-adenosyl-L-[methyl- ^3H]methionine ([^3H]SAM). In addition to assaying cap methylation, this approach indirectly assesses the RNA triphos-

phatase and guanylyltransferase capping activities of particles since these reactions must precede methylation (15). Methylation activity was expressed as a ratio of acid-precipitable ^3H counts to acid-precipitable ^{32}P counts to adjust for any differences in transcription activity between samples. The activities of μNS cores with approximately 60 or 350 molecules of μNS bound per core and of cores mixed with wild-type baculovirus-infected lysate and then purified were similar to that of cores (Fig. 6B). However, when more μNS molecules were bound per core (530 to 3,800 molecules of μNS), the methylation activity was increased to approximately twofold that of cores (Fig. 6B). To test if the increased methylation activity was due to a contaminating methylase or nonspecific trapping of [^3H]SAM when such large amounts of μNS were bound to cores, we repeated the assay using μNS cores containing either 60 or 980 molecules of μNS under conditions that are not permissive for full-length transcript production: in the presence of GTP only at 45°C, ATP only at 45°C, or all four nucleotides at 4°C. None of these conditions supported detectable methylation activity with either preparation of μNS cores or cores alone (data not shown). Thus, we conclude that the methylation increase observed with higher levels of μNS per core was dependent on transcript production, suggesting that it was due to an increase in transcript capping.

μNS incubation with cores greatly decreases the efficiency of recoated core formation. To test if μNS can inhibit the binding of the outer-capsid proteins to cores, we mixed μNS lysate and lysate containing $\mu 1$ and $\sigma 3$ ($\mu 1$ - $\sigma 3$ lysate) with cores in vitro. Relative amounts of the two lysates were chosen to provide approximately the same amount of μNS and $\mu 1$ for binding to the core surface. Cores were incubated alone, with μNS lysate, or with $\mu 1$ - $\sigma 3$ lysate to provide controls for the positions of the resulting particles, cores, μNS cores, and recoated cores, respectively, in CsCl gradients. Cores were incubated with both μNS lysate and $\mu 1$ - $\sigma 3$ lysate together, with μNS lysate first then with $\mu 1$ - $\sigma 3$ lysate, or with $\mu 1$ - $\sigma 3$ lysate first then with μNS lysate to see if the incubation of μNS with cores during or before the addition of $\mu 1$ and $\sigma 3$ would affect the formation of recoated cores. The samples were layered on CsCl density gradients, spun to equilibrium, fractionated, and subjected to immunoblot analysis. Cores alone migrated to the bottom of the gradient (Fig. 7A), whereas recoated cores migrated into the lower half of the gradient (Fig. 7B). Note that some core proteins and $\mu 1$ remained trapped at the top of the gradient, migrating with protein alone (Fig. 7B). μNS cores migrated only into the upper half of the gradient (Fig. 7C), near protein alone at the top of the gradient. When cores were incubated first with $\mu 1$ - $\sigma 3$ lysate, allowing the formation of recoated cores before μNS lysate was added, both the core proteins and $\mu 1$ were detected in the lower half of the gradient at the position of recoated cores (Fig. 7D). In addition, no μNS was detected in the fractions containing core proteins and $\mu 1$ at the position of recoated cores, confirming that recoated cores had been formed. This agrees with the result that μNS does not bind to virions (Fig. 3). When cores were incubated first with μNS lysate, allowing the formation of μNS cores before $\mu 1$ - $\sigma 3$ lysate was added, little or no core proteins or $\mu 1$ was detected in the lower half of the gradient (Fig. 7E), suggesting that the formation of recoated cores was greatly reduced by prior formation of μNS cores. When $\mu 1$ - $\sigma 3$ lysate and μNS lysate were mixed prior to addition of cores, little or no core proteins or $\mu 1$ was detected in the lower half of the gradient (Fig. 7F), suggesting that formation of recoated cores was greatly reduced by simultaneous incubation with μNS . From these results, we conclude that the incubation of μNS with cores greatly reduces

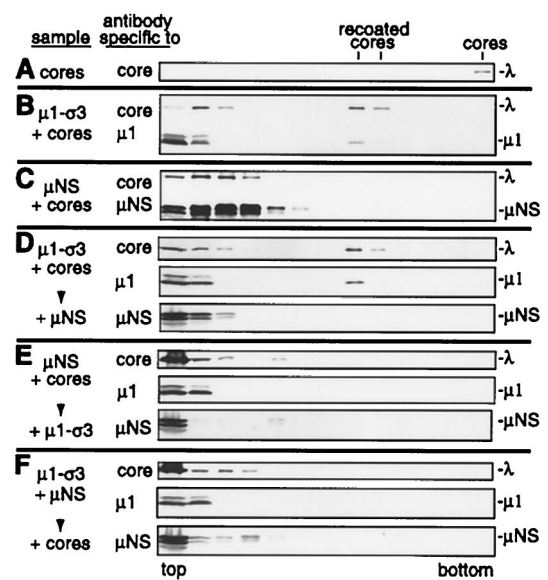


FIG. 7. Incubation of cores with μNS lysate and/or $\mu 1$ and $\sigma 3$ lysate. Cores were incubated alone or with combinations of lysate containing μNS or $\mu 1$ and $\sigma 3$. Samples were layered on CsCl density gradients and spun to equilibrium. Gradients were fractionated, and the fractions were subjected to immunoblot analysis. (A) Cores incubated with lysis buffer. (B) Cores incubated with $\mu 1$ and $\sigma 3$ lysate. (C) Cores incubated with μNS lysate. (D) Cores incubated with $\mu 1$ and $\sigma 3$ lysate followed by addition of μNS lysate and further incubation. (E) Cores incubated with μNS lysate followed by addition of $\mu 1$ and $\sigma 3$ lysate and further incubation. (F) $\mu 1$ and $\sigma 3$ lysate and μNS lysate mixed, followed by addition of cores and incubation. Antibodies used in the immunoblots are listed to the left, and proteins are labeled on the right. The top and bottom of the gradients are labeled below. The positions of recoated cores and cores are labeled at the top.

the capacity of $\mu 1$ and $\sigma 3$ to bind to cores in a manner conducive to recoated core formation.

DISCUSSION

μNS cores are similar to transcriptase particles. The μNS -coated cores that we formed in vitro from purified cores and recombinant μNS protein share a number of characteristics with the transcriptase particles previously isolated from reovirus-infected cells (30). (i) They have similar protein compositions, including μNS in place of outer-capsid proteins. (ii) They have a complete dsRNA genome (30, 31), in contrast to "replicate" particles isolated from infected cells, which contained little or no μNS and were in the process of converting single-stranded RNA to dsRNA (30, 31). (iii) They are capable of synthesizing the viral plus strand transcripts, although the transcription activity of μNS cores was slightly lower than the activity of cores in this study (Fig. 6A). The activity of transcriptase particles was not quantitatively compared to that of cores in the previous study (30). The μNS cores that we generated in vitro also exhibit mRNA capping activities (Fig. 6B), whereas the capping activities of transcriptase particles were not tested in the previous study (30).

Transcriptase particles isolated from infected cells by another group were inactive for capping of transcripts (40). Gel electrophoresis indicated that these particles did not contain μNS , but they were extracted with Freon prior to electrophoresis, which may have removed μNS (40). Additionally, late transcripts isolated from infected cells by these investigators were uncapped (41), leading to a hypothesis that the presence of μNS may inactivate the capping activities of cores (48). We did not find this to be the case with in vitro-assembled μNS cores;

instead, cap methylation was enhanced to twofold that of cores when μ NS cores had 530 or more molecules of μ NS per core (Fig. 6B). While these data do not directly refute the idea that "late" transcripts are uncapped, they suggest that binding of μ NS to cores is not sufficient to result in uncapped transcript production.

The addition of cap 1 structures to reovirus transcripts can approach 100% efficiency in vitro under appropriate conditions: high GTP concentration (0.5 mM), addition of SAM, and inclusion of pyrophosphatase (16). Reaction mixtures that lack pyrophosphatase but contain SAM and a high concentration of GTP have been previously reported to allow cap 1 formation on only 50 to 75% of the transcripts while the remaining transcripts contain diphosphorylated uncapped 5' ends (5, 15). The reaction conditions used in this study (SAM, high GTP concentration, no pyrophosphatase) were thus similar to the latter conditions and allowed us to detect either an increase or decrease in capping activities by μ NS cores. Further studies are required to determine which enzymatic activity(ies) in capping is elevated in μ NS cores and what is the mechanism of the increased activity.

μ NS core large-complex formation. The interaction of recombinant μ NS with cores links them together within large complexes, as viewed by negative-stain EM. μ NS binding to cores could produce such aggregates if μ NS were present in insect cell lysate as large oligomers formed solely from μ NS- μ NS interactions; these large oligomers could bind to many cores, yielding large complexes. However, this seems unlikely since μ NS sediments as a monomer or small oligomer in velocity gradients (Fig. 5C), suggesting that formation of large complexes is specific to the interaction with cores. If μ NS is a monomer or small oligomer, it could link cores together by the binding of one μ NS molecule to multiple core particles or by the oligomeric association of μ NS molecules bound to different core particles. Once all of the μ NS binding sites on the cores are occupied, additional μ NS might be added to the complexes by μ NS- μ NS interactions so that the binding of μ NS to cores is not saturable. Further studies on the oligomeric status of μ NS and the localization of the μ NS binding site(s) for cores may provide insight into the formation of the μ NS-core complexes.

Possible role(s) of μ NS-core interaction. In the infected cell, the interaction of the nonstructural protein μ NS with the reovirus core may function in steps as diverse as regulation of outer-capsid assembly, virus particle assembly, and RNA translation or sorting. The binding of μ NS to newly formed cores within infected cells could prevent the assembly of outer-capsid proteins, as suggested by in vitro findings in this study (Fig. 7), allowing those particles to continue synthesizing viral plus strand transcripts. Prevention of outer-capsid assembly onto certain cores may be required in the cell because assembly of the outer-capsid proteins is believed to shut off transcription by the enclosed core-like particles (2, 11, 21, 46; D. L. Farsetta, K. Chandran, and M. L. Nibert, unpublished data) and because the outer-capsid proteins are present throughout infection in high levels (17). It has been calculated that secondary transcriptase particles (newly formed particles within infected cells) produce 95% of the reovirus mRNA in infected cells (19, 20, 22). μ NS could bind a subset of newly assembled cores, sequestering them away from outer-capsid proteins and dedicating them to produce mRNA. Alternatively, μ NS cores could be formed only transiently on the assembly pathway from core to virion, but long enough to allow more transcript production than would occur in the absence of μ NS.

The μ NS-core interaction could be involved in other ways in reovirus particle assembly. It is possible that μ NS might be

required for directing assembly of the outer-capsid proteins onto the core. However, recent work demonstrated that the reovirus outer-capsid proteins can assemble on cores in vitro in the absence of μ NS (9; K. Chandran and M. L. Nibert, unpublished data) (Fig. 7), indicating that μ NS is not strictly required for outer-capsid assembly. Furthermore, the results from mixing cores with μ NS, μ 1, and σ 3 in vitro suggest that μ NS prevents outer-capsid assembly (Fig. 7). μ NS might also function during the assembly of cores. However, assembly of core-like particles containing σ 2, λ 1, and λ 2 has been shown to occur in the absence of μ NS (45; J. Kim, S. Noble, and M. L. Nibert, unpublished data), suggesting that μ NS is not strictly required for assembling the protein components of cores, although it might be needed to get RNA inside the particle (see next paragraph). Characterization of μ NS-bound particles from reovirus-infected cells may provide further evidence for μ NS involvement in assembly.

Yet another possibility is that μ NS is closely associated with the transcriptase particles in infected cells in order to bind the plus strand RNA transcripts soon after synthesis, as reported previously (1). Through RNA interactions, μ NS may assist either in sorting and packaging the 10 different viral transcripts or during minus strand synthesis in the early steps of progeny particle assembly. It may also serve a function in protein translation from these transcripts. For example, μ NS may be similar to the rotavirus nonstructural protein NSP3, which interacts with eIF4GI and is believed to enhance translation of the rotavirus transcripts (35). Experiments investigating μ NS-RNA interactions should allow these hypotheses to be tested.

ACKNOWLEDGMENTS

We are grateful to M. R. Roner for supplying the T3D M3 clone and monoclonal antibodies to μ NS and to K. L. Tyler and H. W. Virgin IV for supplying the μ 1 monoclonal antibody. Special thanks to Wai-Ming Lee for assistance with RNA denaturing gels. We thank A. L. Gillian and K. Chandran for baculovirus stocks for expression of reovirus proteins σ NS, μ 1, and σ 3; S. J. Harrison for technical assistance; J. Lugus and C. Chapman for laboratory support; the other members of our laboratory for helpful discussions; and D. L. Farsetta, A. L. Gillian, and C. L. Luongo for reviews of a preliminary manuscript. We also thank L. C. Vanderploeg from the Biochemistry Media Lab for photographing gradients and C. Nicolet and colleagues in the DNA sequencing facility at the UW Biotechnology Center for DNA sequencing.

This work was supported by NIH grant R29 AI39533, a USDA Hatch grant awarded through the College of Agricultural and Life Sciences, and a grant to the Institute for Molecular Virology from the Lucille P. Markey Charitable Trust. M.L.N. received additional support as a Shaw Scientist from the Milwaukee Foundation. T.J.B. received additional support from predoctoral fellowships from the Wisconsin Alumni Research Foundation and NIH grant T32 GM07215 to the Molecular Biosciences Training Grant (University of Wisconsin-Madison).

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