Abstract. The survival motor neuron (SMN) protein, the protein product of the spinal muscular atrophy (SMA) disease gene, plays a role in the assembly and regeneration of small nuclear ribonucleoproteins (snRNPs) and spliceosomes. By nanoelectrospray mass spectrometry, we identified RNA helicase A (RHA) as an SMN complex–associated protein. RHA is a DEAH box RNA helicase which binds RNA polymerase II (pol II) and reportedly functions in transcription. SMN interacts with RHA in vitro, and this interaction is impaired in mutant SMNs found in SMA patients. Coimmunoprecipitation demonstrated that the SMN complex is associated with pol II, snRNPs, and RHA in vivo. In vitro experiments suggest that RHA mediates the association of SMN with the COOH-terminal domain of pol II. Moreover, transfection of cells with a dominant negative mutant of SMN, SMN ΔN27, causes accumulation of pol II, snRNPs, and RHA in nuclear structures that contain the known markers of gems and coiled bodies, and inhibits RNA pol I and pol II transcription in vivo. These findings indicate a functional as well as physical association of the SMN complex with pol II and suggest a role for the SMN complex in the assembly of the pol II transcription/processing machinery.

Key words: survival motor neuron • RNA helicase A • RNA polymerase II • nuclear bodies • transcriptosome

Introduction

Spinal muscular atrophy (SMA) is an autosomal recessive disease and the most common genetic cause of infant death (Pearn, 1980). SMA is characterized by degeneration of motor neurons in the anterior horn of the spinal cord, resulting in muscular weakness and atrophy (for review see Melki, 1997). The survival motor neuron (SMN) gene is the SMA determining gene (Lefebvre et al., 1995). In humans, the SMN gene is duplicated as an inverted repeat on chromosome 5, and only deletions or mutations in the telomeric copy, SMN1, result in SMA (for review see Burghes, 1997). The centromeric copy, SMN2, does not protect from SMA because, as a result of a single nucleotide difference from SMN1, it produces mostly a nonfunctional truncated form of SMN lacking the COOH-terminal domain of pol II. Moreover, transfection of cells with a dominant negative mutant of SMN, SMN ΔN27, causes accumulation of pol II, snRNPs, and RHA in nuclear structures that contain the known markers of gems and coiled bodies, and inhibits RNA pol I and pol II transcription in vivo. These findings indicate a functional as well as physical association of the SMN complex with pol II and suggest a role for the SMN complex in the assembly of the pol II transcription/processing machinery.

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Abbreviations used in this paper: BRCA1, breast cancer gene 1; Bru, bromouridine; CBP, cAMP response element binding protein; CTD, COOH-terminal domain; G/CB, nuclear accumulation containing gem and coiled (cajal) body-specific marker; GST, glutathione S-transferase; hnRNP, heterogeneous nuclear RNP; IGC, interchromatin granule cluster; pol, polymerase; RHA, RNA helicase A; RNP, ribonucleoprotein; Sm, Smith antigen; snRNP, small nuclear RNP; SMA, spinal muscular atrophy; SMN, survival motor neuron; SR, serine- and arginine-rich; TBP, TATA box binding protein.
The pathway of spliceosomal snRNP assembly and function in higher eukaryotes requires a cytoplasmic phase where the snRNPs are exported from the nucleus, bind a common set of proteins to form the Sm core and, after 5′ cap hypermethylation and 3′ end maturation, are imported into the nucleus where snRNPs function in pre-mRNA splicing (Mattaj and De Robertis, 1985; Mattaj, 1986; Luhrmann et al., 1990). Experiments in Xenopus laevis oocytes and in mammalian cells have demonstrated a key function for the SMN complex in the cytoplasmic assembly of snRNPs (Fischer et al., 1997; Pellizzoni et al., 1998; Buhler et al., 1999). In addition, SMN functions in the nucleus in pre-mRNA splicing, a function which likely involves the reorganization of splicing components after rounds of splicing (Pellizzoni et al., 1998; Meister et al., 2000). SMN forms large oligomers, and this is essential for its activity, since a defect in SMN oligomerization correlates with SMA (Lorson et al., 1998; Pellizzoni et al., 1999). SMN oligomerization is necessary for efficient interaction with Sm proteins whereas SMN mutants found in SMA patients are deficient in both splicing reactivation activity and interaction with Sm proteins and with Gemin3 (Pellizzoni et al., 1998, 1999; Charroux et al., 1999; Friesen and Dreyfuss, 2000).

Here, we report the identification by nanoelectrospray mass spectrometry of RNA helicase A (RHA) as an SMN complex-interacting protein. In vitro, SMN interacts with RHA and this interaction is impaired for SMN mutants found in SMA patients. In vivo, the SMN complex is associated with RNA polymerase II (pol II), snRNPs, and RHA in a large complex. In the nucleus, the COOH-terminal domain (CTD) of pol II physically and functionally couples transcription, splicing, and polyadenylation (Steinmetz, 1990). Experiments in mammalian cells have demonstrated a key function for the SMN complex in transcription, possibly for assembly of the key components of the mRNA transcription/processing machinery before their association with genes.

**Materials and Methods**

**DNA Constructs**

The cDNA encoding SMN was described previously (Liu and Dreyfuss, 1996). Plasmids expressing myc-tagged SMN wild-type and SMNΔN27 proteins under the control of the cytomegalovirus promoter were described previously (Pellizzoni et al., 1998). The RHA cDNA was a kind gift of Dr. Chee-Gun Lee (UMDNJ, New Jersey Medical School, Newark, NJ; Lee and Hurwitz, 1993).

**Antibodies**

Antibodies used in these experiments were as follows: mouse IgG1 monoclonal anti-SMN (2B1; Liu and Dreyfuss, 1996); mouse IgG1 monoclonal anti-Gemin2 (2E17; Liu et al., 1997); mouse IgG1 monoclonal anti-Gemin3 (1G9; Charroux et al., 1999); mouse IgG1 monoclonal anti-Gemin4 (22C10; Charroux et al., 2000); mouse IgG1 monoclonal antibromouridine (BrU) (Sigma-Aldrich); mouse IgG1 monoclonal anti-SC35 (Fu and Maniatis, 1990); mouse IgG2 monoclonal anti-Sm (Y12; Lerner et al., 1981); mouse IgG1 monoclonal anti-nectin 9E10; affinity-purified rabbit polyclonal anti-nectin 9E10 epitope (A-14; Santa Cruz Biotechnology, Inc.); mouse IgG monoclonal anti-pol II (H5; Bregman et al., 1995; BabCo); mouse IgG2a monoclonal anti-pol II (6WG16; Thompson et al., 1989; BabCo); mouse IgG2a monoclonal anti-heterogeneous (hn)RNP A1 (4B10; Pinol-Roma et al., 1988); mouse IgG2b monoclonal anti-hnRNP C1/C2 (2B12; Dreyfuss et al., 1984); mouse IgG1 monoclonal anti-U2B + (4G3; Habets et al., 1989; Cappe); mouse IgG2a monoclonal anti-TFIIB (Transduction laboratories); rabbit polyclonal anti-TATA box binding protein (TBP; Kato et al., 1994); and rabbit polyclonal anti-RHA (Nakajima et al., 1997).

**Cell Culture and Treatments**

HeLa cells were cultured in DMEM (GIBCO BRL) supplemented with 10% FBS (GIBCO BRL). HeLa cells, plated on glass coverslips, were transfected by the standard calcium phosphate method. After overnight incubation with DNA, cells were washed and fresh medium was added. Transfected cells were fixed and processed by immunofluorescence staining after an additional 24–36 h of incubation. Transfection efficiencies of myc-SMN wild-type and myc-SMNΔN27 plasmids were similar. Western blot analysis of lysates from transfected cells showed single bands of the expected size corresponding to myc-SMN wild-type and myc-SMNΔN27 proteins, the expression level of both proteins was approximately 10-fold over the endogenous SMN level (data not shown).

For in situ detection of sites of transcription, HeLa cells grown on glass coverslips were incubated for 1 h in culture medium containing 2 mM BrU (Sigma-Aldrich), washed briefly three times with PBS, fixed, and processed for immunofluorescence staining with anti-BrU monoclonal antibodies. RNase and DNase treatments were performed before immunofluorescence staining at room temperature in PBS containing 200 µg/ml RNase A and 100 µg/ml DNase I, respectively. To inhibit pol II or both pol I and pol II, HeLa cells were incubated for 3 h in the presence of either 0.04 or 5 µg/ml actinomycin D, respectively, before addition of BrU. To inhibit pol II activity, α-amanitin (50 µg/ml) was added to the culture medium 4 h before the addition of BrU.

**Immunofluorescence Microscopy**

Cells grown on glass coverslips were briefly washed with PBS, fixed in 2% formaldehyde/PBS for 20 min at room temperature, permeabilized either in acetone (5 min) at −20°C or in 0.5% Triton X-100 for 5 min at room temperature. Cells were blocked in PBS containing 3% BSA for 1 h at room temperature. Double-label immunofluorescence experiments were performed by separate sequential incubations of each primary antibody followed by incubation with its specific secondary antibody coupled to FITC or Texas red diluted in PBS–3% BSA. All incubations were at room temperature for 1 h. Laser confocal fluorescence microscopy was performed with a Leica TCS four-dimensional (Germany) confocal microscope. Images from each channel were recorded separately and then merged.

**Immunoprecipitation Experiments**

Immunoprecipitations were carried out using HeLa cell nucleolarplasm extract prepared in the presence of 0.5% Triton X-100 as described previously (Pinol-Roma et al., 1988). Immunoblotting was performed as described previously (Liu et al., 1997).

**Protein Microsequencing by Mass Spectrometry**

The p130 protein was coimmunoprecipitated from total HeLa cell extract prepared in the presence of 0.5% Triton X-100 as described previously (Pinol-Roma et al., 1988). Immunoblotting was performed as described previously (Liu et al., 1997).

**Recombinant Proteins Production**

His-tagged SMN wild-type and mutant proteins cloned into pET28 and pET29b(+)-expressed from a single one-dimensional Coomassie-stained polyacrylamide gel and in gel digested with trypsin as described previously (Shevchenko et al., 1996). Tryptic peptides were recovered from gel pieces by extraction with 5% formic acid and acetonitrile. The combined extracts were pooled, dried in a speed vac, and peptides were sequenced by nanoelectrospray tandem mass spectrometry (nano-ES MS/MS) as described in Wilm et al. (1996). The sequencing was performed on a PE-Sciex QSTAR instrument equipped with an ion source from Protana. Comprehensive protein and EST databases were searched using the Protana Software suite. No limitations on protein molecular weight and species of origin were imposed.
p15A origin of replication was kindly provided by Dr. Greg Van Duyne (University of Pennsylvania, Philadelphia, PA). GST–Gemin2 and histagged SMN wild-type or mutant proteins were coexpressed by cotransformation of the respective plasmids into Escherichia coli BL21(DE3) followed by induction with 1 mM IPTG at 17°C for 15 h. The recombinant proteins were purified by affinity chromatography on glutathione-Sepharose beads (Pharmacia) according to the manufacturer’s instructions. The plasmid encoding the GST–CTD fusion protein was a generous gift of Dr. James Manley (Department of Biological Sciences, Columbia University, New York, NY). GST–CTD was produced in E. coli BL21(DE3) and purified as described above.

In Vitro Protein-binding Assay
The SMN full length (1–1279) and the SMNΔRGG COOH-terminal deletion (1–1106) proteins were produced by in vitro–coupled transcription/translation (Promega) in the presence of [35S]methionine (Amersham Pharmacia Biotech) using the RHA cDNA, either undigested or digested with Bgl II, respectively. Purified GST, GST–Gemin2, or GST–Gemin2/SMN proteins (2 µg) bound to 25 µl of glutathione-Sepharose beads were incubated with in vitro–translated product proteins in 1 ml of binding buffer (50 mM Tris-HCl, pH 7.5, 200 mM NaCl, 2 mM EDTA, 0.1% NP-40, 2 µg/ml leupeptin, pepstatin A, and aprotinin). After incubation for 1 h at 4°C, the beads were pelleted, washed five times with 1 ml of binding buffer, and boiled in SDS-PAGE sample buffer. The eluted proteins were analyzed by SDS-PAGE, and the signal was enhanced by treatment with Amplify solution (Amersham Pharmacia Biotech). Purified GST or GST–CTD bound to glutathione-Sepharose beads was incubated with either HeLa nuclear extract prepared according to Dignam et al. (1983), or [35S]methionine-labeled in vitro–translated proteins in buffer D containing 0.025% NP-40 at 4°C. After five washes with the same buffer, bound proteins were eluted by boiling in SDS-PAGE, sample buffer, separated by SDS-PAGE and analyzed by Western blotting or autoradiography.

Results
Identification of RHA as an SMN-interacting Protein
We have recently identified two novel components of the SMN complex by a combination of coimmunoprecipitation and mass spectrometry (Charroux et al., 1999, 2000). Immunoprecipitations from [35S]methionine-labeled HeLa cell lysates with antibodies against components of the SMN complex revealed the presence of additional proteins whose identity is not yet known (Liu et al., 1997; Charroux et al., 1999, 2000). Here, we employed the same strategy to identify a novel SMN complex-interacting protein. Fig. 1 A shows the proteins that specifically coimmunopurify with anti-Gemin3 antibodies compared with antitransportin antibodies as a control. In addition to the known components of the SMN complex (SMN, Gemin2, Gemin3, and Gemin4), there are protein bands of ∼175, 130, and 95 kD. These bands were excised from the gel and digested with trypsin. The resulting peptides were sequenced by nano-electrospray mass spectrometry as described in Materials and Methods. In this paper, we report the identification of the 130-kD protein and experiments that led us to propose a role for the SMN complex in transcription. Databases search with several peptides revealed that p130 is identical to RHA, an essential ATP-dependent RNA helicase of the DEAH family (Lee and Hurwitz, 1993; Lee et al., 1998).

Because RHA contains an RGG box at the COOH terminus and SMN has been found to interact with some arginine- and glycine-rich domains (Liu and Dreyfuss, 1996; Friesen and Dreyfuss, 2000), we tested whether RHA can bind SMN in vitro. Fig. 1 B shows that in vitro–translated RHA binds efficiently to purified recombinant GST–SMN but not to GST–Gemin2 or GST alone. We also tested the ability of SMN mutants, expressed and purified as GST–Gemin2/SMN complexes, to bind RHA in vitro (Fig. 1 C). SMN interaction with RHA is impaired by either a single point mutation (SMNY272C) or a deletion of the amino acids encoded by exon 7 (SMNΔEx7) as found in some SMA patients. In contrast, the binding of SMNΔN27 to RHA is indistinguishable from that of SMN wild-type. Furthermore, the RGG-rich COOH-terminal domain of RHA, which is not required for its interactions with pol II and with transcriptional coactivators (Nakajima et al., 1997; Anderson et al., 1998), is necessary for interaction with SMN (Fig. 1, C and D).

Figure 1. Identification of RHA as a novel SMN-interacting protein. (A) Coimmunoprecipitation experiments with anti-Gemin3 (11G9) or antitransportin (19D9) monoclonal antibodies were carried out from total HeLa cell extract. The immunoprecipitates (IP) were analyzed by SDS-PAGE and Coomassie blue staining. The band corresponding to the p130 protein coimmunoprecipitated with anti-Gemin3 antibodies was excised and identified by nanoelectrospray tandem mass spectrometry as described in Materials and Methods. Molecular weight markers, heavy (Ig h.c.) and light (Ig l.c.) chains of immunoglobulins, and the bands corresponding to the components of the SMN complex are indicated. (B) SMN interacts with RHA in vitro. In vitro–translated [35S]methionine-labeled RHA full length (RHA) was incubated with either GST, GST–Gemin2, or GST–SMN as indicated. 10% of the input is shown. (C) The SMN interaction with RHA is impaired by SMN mutations found in SMA patients and requires the RGG-rich domain of RHA. In vitro–translated [35S]methionine-labeled RHA full-length (RHA) or a COOH terminus deletion lacking the RGG domain (RHAΔRGG) were incubated with the indicated GST–Gemin2/SMN complexes containing either wild-type (wt) or mutant his-SMN proteins coexpressed and purified as described in Materials and Methods. 10% of the input is shown. (D) Schematic representation of the structure of RHA and the domains involved in the interaction with pol II, BRCA1, CBP, and SMN.

RHA full-length (RHA) or a COOH terminus deletion lacking the RGG domain (RHAΔRGG) were incubated with the indicated GST–Gemin2/SMN complexes containing either wild-type (wt) or mutant his-SMN proteins coexpressed and purified as described in Materials and Methods. 10% of the input is shown. (D) Schematic representation of the structure of RHA and the domains involved in the interaction with pol II, BRCA1, CBP, and SMN.
Association of the SMN Complex with Pol II, snRNPs, and RHA

We further examined the association between RHA and the SMN complex in vivo by coimmunoprecipitation experiments. Anti-RHA antibodies specifically coimmunoprecipitate SMN, Gemin2, Gemin3, and Gemin4 in addition to snRNPs and both hyperphosphorylated (pol IIo) and hypophosphorylated (pol IIa) pol II (Fig. 2). The general transcription factors TBP and transcription factor IIB are also detected in the RHA immunoprecipitate. None of these proteins are detectable in immunoprecipitates using a rabbit preimmune serum, and the abundant hnRNP A1 is not detected in the RHA immunoprecipitate. Fractionation of an HeLa nuclear extract by sucrose gradient centrifugation indicates that >30% of nuclear SMN, Gemin2, Gemin3, and Gemin4 cofractionate with RHA, snRNPs, and pol II as a large complex (Paushkin, S., and G. Dreyfuss, unpublished results). These results demonstrate that a large nuclear complex exists which contains pol II, snRNPs, RHA, and components of the SMN complex.

The CTD of pol II plays a key role in coupling transcription and pre-mRNA processing by interacting directly with components of the RNA processing machinery (for review see Steinmetz, 1997). To ask if the SMN complex can bind pol II CTD, we employed an approach similar to the one used to demonstrate the physical interaction of polyadenylation factors with pol II CTD (McCracken et al., 1997). We investigated whether pol II CTD can associate with the SMN complex by pull-down experiments from HeLa nuclear extract using GST–CTD. Fig. 3 A shows that SMN, Gemin2, Gemin3, and Gemin4 specifically associate with pol II CTD. The interaction of the SMN complex is not influenced by the phosphorylation state of the CTD (data not shown).

RHA has been suggested to function in transcription as a direct molecular link between pol II and transcriptional co-activators including cAMP response element binding protein (CBP)/p300 and breast cancer gene 1 (BRCA1; Nakajima et al., 1997; Anderson et al., 1998). We addressed the possibility that RHA may play a similar role in the association of SMN with pol II CTD. To do so, we incubated GST–CTD with in vitro–translated [35S]methionine-labeled SMN in the presence or absence of similarly produced RHA and found that RHA stimulates the binding of SMN to pol II CTD (Fig. 3 B). Although these interactions may be mediated by additional components in the reticulocyte lysate or in the nuclear extract, the data strongly suggest that the SMN complex associates with pol II and that RHA promotes this association possibly by stabilizing or acting as a bridging factor between pol II CTD and SMN.

Pol IIa Accumulates in the G/CBs

Previous transfection experiments in HeLa cells with SMNΔN27 showed that this dominant negative SMN mutant blocks snRNP assembly in the cytoplasm, causes a profound rearrangement of snRNPs in the nucleus, and inhibits pre-mRNA splicing in vitro (Pellizzoni et al., 1998). To address further the possible involvement of the SMN complex in transcription, we examined the subcellular localization of pol II in cells expressing SMNΔN27. Consistent with previous reports (Bregman et al., 1995), pol IIa shows a diffuse nucleoplasmic punctate distribution excluding nucleoli, and this is also the case in cells transfected with SMN wild-type (Fig. 4, A–C). However, in cells transfected with SMNΔN27, pol IIa is reorganized and accumulates in large nuclear aggregates which contain gem- and CB-specific markers (G/CBs [Fig. 4, D–F]). For brevity, we shall refer to these merged accumulations as G/CBs. The CTD of pol II undergoes extensive phosphorylation in vivo and pol IIo...
shows a speckled nucleoplasmic distribution more evident by confocal than by standard epifluorescence microscopy (Bregman et al., 1995; Zeng et al., 1997). The pattern of pol IIo distribution in cells transfected with SMN wild type, similar to untransfected cells, shows little or no localization in gems (Fig. 4, G–I). Surprisingly, on transfection with SMNΔN27, pol IIo is excluded from the large G/CBs, the diffuse nucleoplasmic pool appears reduced, and most of pol IIo is localized in interchromatin granule clusters (IGCs) around the G/CBs (Fig. 4, J–L; see Fig. 6, G–I).

**RHA, TBP, and snRNPs Accumulate in the G/CBs**

Next, we examined the effect of SMNΔN27 expression on the localization of RHA. RHA shows a nucleoplasmic distribution in untransfected HeLa cells and in cells transfected with SMN wild-type and with no evident colocalization with the G/CBs (Fig. 5, A–C). However, in cells transfected with SMNΔN27, RHA becomes relocalized in the nucleus and accumulates in the large G/CBs (Fig. 5, D–F). We also examined additional components of the pol II transcription/processing machinery such as TBP, poly-pyridimidine tract binding protein-associated splicing factor, and polyadenylation factors CstF64 and CPSF160, and found them to be similarly reorganized (Fig. 5, G–I; and data not shown). This reorganization of pol II, RHA, and TBP is restricted to the nuclear SMNΔN27-containing aggregates, whereas Sm proteins of spliceosomal snRNPs also accumulate in the cytoplasmic aggregates (Fig. 5, J–L), consistent with a role of the SMN complex in cytoplasmic snRNP assembly (Pellizzoni et al., 1998). In summary,
several key components of the transcription and pre-mRNA processing machineries are strongly affected by SMNΔN27 expression and accumulate in the G/CBs.

**Specificity of the Accumulation of Transcription and Pre-mRNA Processing Components in G/CBs**

To assess the specificity of the accumulation in G/CBs of the components described above, we examined the effect of SMNΔN27 expression on hnRNP and serine- and arginine-rich (SR) proteins, two classes of protein that are both well characterized and intimately involved in the process of mRNA biogenesis. HnRNP proteins are very abundant nuclear RNA-binding proteins which interact with pre-mRNAs as they emerge from the transcription complex, modulate most of the posttranscriptional processes, and accompany the spliced mRNA to the cytoplasm (Dreyfuss et al., 1993). Fig. 6, A–F, shows that neither hnRNP A1 nor hnRNP C1/C2 proteins are reorganized by expression of SMNΔN27, and they are excluded from the G/CBs. Similarly, the essential splicing factor SC35, which is also a marker of IGCs (Spector, 1993), does not accumulate in the G/CBs (Fig. 6, G–I). Staining with another monoclonal antibody that reacts with the entire class of SR proteins shows a similar exclusion (Zahler et al., 1992; data not shown). Together these results demonstrate the specificity of the relocalization of components to G/CBs observed by expression of SMNΔN27. Nevertheless, SMNΔN27 expression alters the distribution of SC35. IGCs are found closely associated with the periphery of G/CBs, lose inter-
connections with the surrounding nucleoplasm, and round up their contour in a way that resembles what is observed when transcription is inhibited by drugs or heat shock (Figs. 4 and 6; Zeng et al., 1997).

Expression of SMNΔN27 Inhibits Transcription In Vivo

Because of the strong effects of SMNΔN27, we were interested to determine whether transcription of pre-mRNAs in these cells is affected. The current methods for in situ detection of nascent RNA transcripts rely on microinjection of BrU triphosphate into living cells or run-on transcription in permeabilized cells followed by indirect immunofluorescence microscopy (Jackson et al., 1993; Wansink et al., 1993). By analogy with early experiments using \[^3\text{H}\]uridine incorporation for in vivo labeling of RNA (Fakan and Bernhard, 1971), we developed a simple method that avoids microinjection to detect transcriptional activity in living cells in situ (Fig. 7). An in situ method was necessary because only a fraction of the cells are transfected with SMNΔN27. We found that the addition of BrU to the culture medium results in its efficient uptake and incorporation into nascent RNA by the cells. Fig. 7 A shows the results of labeling HeLa cells for 1 h with 2 mM BrU followed by cell fixation and staining with anti-BrU antibodies. Pol II transcription sites are visible as anti-BrU reactive dots scattered throughout the nucleoplasm. Noticeably, nucleolar labeling, which is not readily detected by the methods of BrU triphosphate microinjection and run-on transcription in permeabilized cells (Jackson et al., 1993; Wansink et al., 1993), is also very intense. Higher concentrations of BrU do not increase the intensity of the signal but the intensity does increase proportional to the time of incubation (data not shown). The sensitivity of the staining to RNase treatment demonstrates that BrU was incorporated into RNA (Fig. 7 B). Although BrU may also be used as a thymidine analogue and become incorporated into DNA (Eidinoff et al., 1959), the staining we observed is resistant to DNase digestion, demonstrating that DNA incorporation does not significantly contribute to the signal detected (Fig. 7 C). Treatment with low concentrations of actinomycin D selectively inhibits transcription by pol I in the nucleolus (Fig. 7 D), whereas higher concentrations inhibit both pol I and pol II activities (Fig. 7 E). Extranucleolar incorporation is also strongly reduced by treatment with α-amanitin concentrations that inhibit pol II (Fig. 7 F). This method is rapid, simple, sensitive, and less invasive than previous methods, and is therefore probably more reflective of physiological transcription.

Using this method, we examined the transcriptional activity of cells transfected with SMN wild type or SMNΔN27.
Cells transfected with SMN wild-type, similar to untransfected cells, show high levels of transcription both in the nucleoplasm and in the nucleolus. No significant coincidence between SMN (or gem) staining with the sites of transcription was observed (Fig. 8, A–C). Strikingly, expression of SMN<sup>DN27</sup> strongly inhibits transcription both in the nucleoplasm and in the nucleolus, corresponding to pol II and pol I activities, respectively (Fig. 8, D–F). A reduction in the nucleoplasmic pool of pol II due to the accumulation of pol II in the GCBS provides a likely explanation for the inhibition of transcription upon expression of SMN<sup>DN27</sup>.

Discussion

We have identified RHA as a novel SMN-interacting protein and showed that this interaction is defective in SMN mutants found in some SMA patients. Coimmunoprecipitation and pull-down experiments demonstrated the physical association of the SMN complex with pol II, snRNPs, and RHA in vivo and in vitro. Importantly, the SMN complex binds pol II CTD, and RHA at least in part mediates this interaction. Thus, RHA likely plays a role in the association between the SMN complex and pol II possibly similar, but not mutually exclusive, to its role in bridging CBP and BRCA1 to pol II (Nakajima et al., 1997; Anderson et al., 1998). We further demonstrated that expression of SMN<sup>DN27</sup> brings about a profound rearrangement of pol II, RHA, snRNPs, TBP and polyadenylation factors, all of which specifically accumulate in enlarged GCBS. This reorganization is accompanied by the inhibition of both pol I and pol II transcription, as detected in vivo by the BrU labeling method we have developed. These findings indicate a physical as well as a functional interaction between the SMN complex and components of the pol II transcription/processing machinery. Previous studies have indicated the presence of additional proteins associated with the SMN complex and the possibility that multiple SMN complexes may exist in vivo (Liu et al., 1997; Charroux et al., 1999, 2000; Meister et al., 2000). The observations that RHA does not localize to gems and is not found in all SMN complexes suggest that RHA is not a core component of the SMN complex such as Gemin2, Gemin3, and Gemin4. Similar to Sm proteins of spliceosomal snRNPs, we consider RHA as a possible substrate of SMN complex function.

The structure and organization of the nucleus are highly dynamic (Lamond and Earnshaw, 1998; Misteli and Spector, 1998; Lewis and Tollervey, 2000). Actively transcribing genes are found throughout the nucleus, and pol II transcriptional activity is not restricted to specific regions.

**Figure 7.** A rapid method for the in situ detection of transcription. (A) Indirect immunofluorescence detection of nascent RNA by laser confocal microscopy using anti-BrU antibodies on HeLa cells labeled in the presence 2 mM BrU as described in Materials and Methods. (B) Effect of RNase A treatment before immunostaining. (C) Effect of DNase I treatment before immunostaining. (D–E) Effect of low (0.04 μg/ml) or high (5 μg/ml) doses of actinomycin D (ActD) on BrU incorporation into RNA. (F) Effect of α-amanitin (50 μg/ml) on BrU incorporation into RNA. Dashed lines demarcate the nucleus. Bars, 5 μm.
A Role for SMN in Transcription

Jackson et al., 1993; Wansink et al., 1993). Since the initial observations of cotranscriptional splicing in vivo, considerable evidence has accumulated that most pre-mRNA processing steps take place coordinately at sites of transcription (Beyer and Osheim, 1988; Bauren and Wieslander, 1994). Physical and functional interactions between the transcriptional apparatus and the capping, splicing and polyadenylation machineries have recently been demonstrated, and pol II appears to be a key factor in coordinating all the major pre-mRNA processing events through its CTD (for review see Steinmetz, 1997; Neugebauer and Roth, 1997; Corden and Patturajan, 1998; Bentley, 1999; Hirose and Manley, 2000). Pol II CTD has been shown to associate with the capping enzyme, snRNPs, splicing and polyadenylation factors, possibly forming a large complex for which the terms “mRNA factory” or “transcriptosome” have been used (Halle and Meisterernst, 1996; McCracken et al., 1997; Corden and Patturajan, 1998). Recently, a role for CBs in the assembly of transcriptosomes has been suggested (Gall et al., 1999).

Our findings are consistent with the possibility that the assembly of transcriptosomes is a process that is extrinsic to, and precedes, binding of the polymerase complex to gene promoter elements. Most importantly, we propose that the SMN complex plays a central role in the pathway of transcriptosome assembly. The physical association of the SMN complex with components of the pol II transcription/processing machinery in untransfected cells indicates that they interact under normal conditions, and expression of SMN\(\Delta N27\) likely blocks this pathway. Although no dominant-negative mutations have been reported in SMA patients, possibly because they would result in embryonic lethality, a point mutation in exon 1 has been identified in three unrelated SMA patients (Parsons et al., 1998). This suggests that the amino acid sequence encoded by exon 1, which is deleted in SMN\(\Delta N27\), is important for SMN function and SMA. Moreover, we recently identified a dominant-negative mutant of Gemin2 that displays a phenotype similar to SMN\(\Delta N27\) (Pellizzoni, L., and G. Dreyfuss, manuscript in preparation). The observation that expression of mutants of two different proteins of the SMN complex with components of the pol II transcription/processing machinery, and the inhibition of transcription in vivo argues that these effects result from disruption of a genuine pathway that requires SMN functions in normal cells.

Pol II CTD undergoes cycles of phosphorylation and dephosphorylation that modulate its association with processing factors and its activity in transcription (Dhamus, 1996). Pol IIa binds to the preinitiation complex on promoter elements, and CTD phosphorylation is believed to trigger release from the promoter and initiation of transcription (Lu et al., 1991; Akoulitchev et al., 1995). Pol IIo drives elongation and pre-mRNA processing events and is released from the gene upon termination of transcription (O’Brien et al., 1994). After their release from sites of transcription, pol II and several components of the transcription and pre-mRNA processing machineries seem to follow a common pathway in the nucleus (Zeng et al., 1997). A pool of both pol II isoforms exists in the nucleoplasm that is not engaged in active transcription and may represent the fraction of pol II undergoing recycling or regeneration between rounds of transcription (Kim et al., 1997; Zeng et al., 1997). Dephosphorylation of pol II CTD is one of the steps required for pol II recycling (Cho et al., 1999). The observation that the SMN complex associates with both pol II isoforms but only pol IIa accumulates in the G/CBs upon SMN\(\Delta N27\) expression, suggests that pol II CTD dephosphorylation may take place in association with components of the SMN complex and that SMN\(\Delta N27\) blocks the pathway downstream of this event.

hnRNP and SR proteins represent indirect markers of pre-mRNA distribution in the nucleus, and these abundant RNA-binding proteins do not accumulate in G/CBs (Fig. 6). Moreover, hnRNP proteins do not coimmunoprecipitate with the SMN complex (Fig. 2; data not shown).
These results suggest that the SMN complex associates with transcriptosomes components that are not bound to pre-mRNAs. It is tempting to speculate that pol II and transcriptosomes components associate with the SMN complex after their dissociation from transcribing genes and before being recruited for a new round of transcription.

TPB is a general transcription factor common to all three RNA polymerases (Hernandez, 1993; Rigby, 1993). TPB accumulates in the G/CBs upon expression of SMNAN27, and likely as a consequence pol I transcription in the nucleolus is strongly inhibited. Similar to the case of pol II, RNA polymerase I holoenzyme as a transcriptionally competent large multisubunit complex has been identified, and the possibility that it may be preassembled in CBs has been suggested (Seither et al., 1998; Gall et al., 1999). By extension of what we have observed here for components of pol II transcriptosomes, the SMN complex may interact with components of the pol I transcription machinery and also play a role in the assembly of a class I transcriptosome. Experiments are underway to assess this possibility.

Our findings suggest a critical role for the SMN complex in several aspects of mRNA biogenesis. Neurons are likely to be particularly sensitive to defects in mRNA metabolism as neuronal differentiation and maintenance require highly active and finely regulated pre-mRNA transcription and processing activities (Tanabe and Jessell, 1996; Grabowski, 1998). It is conceivable that the drastic reduction in SMN in motor neurons of SMA patients leads to an impaired capacity to produce mRNAs, and thus leads to neuronal degeneration.

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