PRMT 3, a Type I Protein Arginine N-Methyltransferase That Differs from PRMT1 in Its Oligomerization, Subcellular Localization, Substrate Specificity, and Regulation

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Methylation is one of the many post-translational modifications that modulate protein function. Although asymmetric $\text{N}^\text{G},\text{N}^\text{G}$-dimethylation of arginine residues in glycine-arginine-rich domains of eucaryotic proteins, catalyzed by type I protein arginine N-methyltransferases (PRMT), has been known for some time, members of this enzyme class have only recently been cloned. The first example of this type of enzyme, designated PRMT1, cloned because of its ability to interact with the mammalian TIS21 immediate-early protein, was then shown to have protein arginine methyltransferase activity. We have now isolated rat and human cDNA orthologues that encode proteins with substantial sequence similarity to PRMT1. A recombinant glutathione S-transferase (GST) fusion product of this new rat protein, named PRMT3, asymmetrically dimethylates arginine residues present both in the designed substrate GST-GAR and in substrate proteins present in hypomethylated extracts of a yeast rmt1 mutant that lacks type I arginine methyltransferase activity; PRMT3 is thus a functional type I protein arginine N-methyltransferase. However, rat PRMT1 and PRMT3 glutathione S-transferase fusion proteins have distinct enzyme specificities for substrates present in both hypomethylated rmt1 yeast extract and hypomethylated RAT1 embryo cell extract. TIS21 protein modulates the enzymatic activity of recombinant GST-PRMT1 fusion protein but not the activity of GST-PRMT3. Western blot analysis of gel filtration fractions suggests that PRMT3 is present as a monomer in RAT1 cell extracts. In contrast, PRMT1 is present in an oligomeric complex. Immunofluorescence analysis localized PRMT1 predominantly to the nucleus of RAT1 cells. In contrast, PRMT3 is predominantly cytoplasmic.

Protein function is often modulated by post-translational covalent modifications. One such modification is the N-methylation of the side chain of guanidino arginine residues (1–3). Type I protein arginine N-methyltransferase (PRMT) enzymes catalyze the formation of asymmetric $\text{N}^\text{G},\text{N}^\text{G}$-dimethylarginine residues in proteins by transferring methyl groups from S-adenosylmethionine (AdoMet) to the guanidino nitrogen atoms of arginine residues. These enzymes generally methylate arginines found in RGG consensus sequences in the context of GAR (glycine and arginine-rich) domains (1, 4–6). The first cDNA for a mammalian type I PRMT enzyme to be cloned, PRMT1, was identified by a yeast two-hybrid screen as a rat cDNA encoding a protein that interacts with the product of the mammalian TIS21 immediate-early gene (7). TIS21 (also known as PC3 and BTG2) is a member of a family proteins (TIS21, BTG1, BTG3, and TOB) thought to be involved in negative control of the cell cycle (8, 9). Association of recombinant TIS21 protein with a fusion protein between glutathione S-transferase and rat PRMT1, GST-PRMT1, modulates PRMT1 activity in vitro (7), suggesting that interaction between transiently induced TIS21 (10–14) and constitutively expressed PRMT1 (7) may modulate PRMT1 enzyme activity in vivo. Moreover, human PRMT1 was independently isolated as a protein that interacts with the intracellular domain of the interferon-α, β receptor (15). The cytoplasmic domain of this receptor is also a docking site for many signaling proteins such as tyrosine kinases, serine/threonine kinases, and STAT transcription factors (16). PRMT1 antisense oligonucleotides relieve interferon-β-induced growth inhibition (15). The interaction of PRMT1 with both the TIS21 immediate-early gene product and with a transmembrane receptor suggests a role for this enzyme in cell signaling. Human and rat PRMT1 are 96% identical at the amino acid level. Rmt1, the yeast PRMT1 homologue, is 45% identical to the human and rat PRMT1 proteins and is the predominant protein arginine methyltransferase activity in Saccharomyces cerevisiae, accounting for more than 85% of yeast PRMT activity (17, 18). Rmt1 is also a type I enzyme, catalyzing the formation of $\text{N}^\text{G},\text{N}^\text{G}$-dimethylarginine residues. Data base searches have identified a distinct human gene, HRMT1L1 (19), whose predicted open reading frame encodes a protein containing a potential protein arginine N-methyltransferase domain that has 33% of its amino acid residues identical to and 61% of its amino acid residues similar to human PRMT1.

The calculated molecular mass for the PRMT1 polypeptide, based on the translated cDNA sequence, is 40.5 kDa (7). However, protein arginine methyltransferase activity from several mammalian tissues and cell lines migrates on gel filtration columns at apparent sizes ranging between 150 and 500 kDa (4, 7, 20, 21), suggesting that PRMT1 is predominantly present as a component of a polypeptide complex. By using a yeast methionine; GST, glutathione S-transferase; GAR, glycine- and arginine-rich region; PAGE, polyacrylamide gel electrophoresis; PFA, paraformaldehyde; PBS, phosphate-buffered saline; NAR, N-terminal acidic amino acid-rich.
two-hybrid screen to identify proteins that interact with PRMT1, we have identified a previously unknown protein whose carboxyl-terminal 365 residues share substantial sequence similarity with PRMT1. This protein, which has protein arginine N-methyltransferase activity, has been named PRMT3. Although PRMT3 and PRMT1 are both type I protein arginine N-methyltransferases, they differ in their substrate specificities, oligomerization properties, interaction with TIS21, and subcellular localization.

**EXPERIMENTAL PROCEDURES**

**Yeast Two-hybrid Analysis to Identify Proteins That Interact with Rat PRMT1**—The rat PRMT1 cDNA was amplified by polymerase chain reaction (PCR), using pUC86-PRMT1 (7) as the template and the primers 5 ’CCCCGGGAATTCGAGCCGGGAGCGGCG3’ and 5 ’GGACGACTGAGCTCTCGGCGC3’. This cDNA was subcloned into pLexA(L)/PRMT1. pLexA(L) contains a leucine-selective marker and encodes a LexA fusion protein that will bind to the LexA operator sequence. A rat pPC86 cDNA library prepared from rat FAO hepatoma cell poly(A+) mRNA (7) was used as “prey” plasmids for the screen. These plasmids contain a tryptophan-selective marker and encode fusion proteins with the tryptophan synthetase alpha subunit sequence preceding the LexA factor activation domain.

**Yeast two-hybrid screening to identify proteins that interact with PRMT1 was performed as described previously (7).** Twenty-five cDNA clones showed positive interactions with PRMT1 in both histidine prototrophy and β-galactosidase assays. These 25 clones were separated into four groups by PCR amplification, restriction digestion analysis, and sequencing. Fifteen clones were identical to pUC86-PRMT1, 8 were identical to pPC86-PRMT3, and the other 2 were independent clones 4A and 7A. Clones 2A, 4A, and 7A were sequenced using the Ulex Deoxyterminator cycle sequencing kit and a 373 DNA sequencer (Perkin-Elmer).

Homology searches were performed using the BLAST algorithm, through the National Center for Biotechnology Information (22).

**FAO cDNA Library Screening for a cDNA Clone Containing the Entire Open Reading Frame of PRMT3**—Yeast two-hybrid screening analysis revealed that it is an incomplete clone, lacking the 5’-end region encoding the amino-terminal end of the protein. To recover a cDNA encoding the entire open reading frame, a rat FAO cDNA library in Lambda-Zap vectors was screened using a 700-base pair 5’ end fragment of 2A as a probe. A 2.4-kilobase pair cDNA insert was recovered in pBluescript SK– (23), precipitated with 1 ml of 10% (w/v) trichloroacetic acid.

Bovine serum albumin was used as the standard for both procedures.

**Preparation and Characterization of Rabbit Polyclonal Antibodies against PRMT1 and PRMT3—Polyclonal antibodies against PRMT1 and PRMT3 were raised in rabbits, using TrpE fusion proteins as antigens.** The cDNA for the TrpE-PRMT1 fusion protein was constructed as follows: cDNA of PRMT1 was PCR-amplified from pUC86-PRMT1, using the primers 5 ’CCCCCAGGAAATTCTAGGGAGCCGGAGGACG3’ and 5 ’GGACGACTGAGCTCTCGGCGC3’. The amplified fragment was digested with XbaI and NotI sites and inserted into pGEX(SN)-PRMT3 (90–528) and pGEX(SN)-PRMT1, in-frame, into pATH11. This resulted in the GST-PRMT3 (90–528) and GST-PRMT1 (90–528) fusion proteins, respectively.

**Preparation of GST fusion proteins**—pGST-CAR-GAR, utilizing BsmI and EcoRI restriction sites engineered into the PCR primers. The resulting construct, pGST-CAR, was digested with NheI and NotI to remove the carboxyl-terminal portion of fibrillarin. The 5’-overhangs remaining from the digest were filled in with the Klenow large fragment polymerase, and the plasmid was purified and introduced into Escherichia coli DH5a cells (Life Technologies, Inc.).

The multiple cloning site of pGEX-2T (Amersham Pharmacia Biotech) was modified to accept cDNA fragments at SalI and NotI sites and termed pGEX(SN). To make pGEX(SN)-PRMT3 (184–528), the DNA encoding the sequence between these amino acids of PRMT3 was amplified from pPC86-PRMT3, using primers 5’TGGGAGCCGACATATTGATGGATGGCGCC3’ and 5’TGACATCTCGACCTGAGGGG3’. The amplified fragment was digested with SalI and NotI and inserted into pGEX(SN) at the SalI/NotI sites. pGEX(SN)-PRMT3 was constructed by inserting the PRMT3 (90–528) DNA sequence from pPC86-PRMT3 (90–528) into pGEX(SN) at the SalI/NotI sites.

**Protein Concentration Determinations—**RAT1 cell lysate protein concentration was determined by the bicinchoninic acid assay (Pierce). Other protein samples were assayed using a modified Lowry procedure (23), after precipitation with 1 ml of 10% (w/v) trichloroacetic acid.

**Preparation of GST fusion proteins**—pGST-CAR-GAR, utilizing BsmI and EcoRI restriction sites engineered into the PCR primers. The resulting construct, pGST-CAR, was digested with NheI and NotI to remove the carboxyl-terminal portion of fibrillarin. The 5’-overhangs remaining from the digest were filled in with the Klenow large fragment polymerase, and the plasmid was purified and introduced into Escherichia coli DH5a cells (Life Technologies, Inc.).
permeabilized with 100% methanol for 15 min at 220 °C. The PFA-fixed cells were washed twice with PBS containing 0.1 M glycine and 0.1% Triton X-100 and then blocked with goat serum (1:20 dilution in PBS containing 0.2% Tween 20). For methanol fixation, cells were blocked with goat serum. After blocking, cells were incubated for 2 h in primary antibody dilutions (1:350 for anti-PRMT1, 1:200 for anti-PRMT3) in PBS containing 0.2% Tween 20 and goat serum diluted 1:50. Then cells were washed three times with PBS containing 0.2% Tween 20 and incubated in the secondary antibody solutions (1:100 diluted fluorescein isothiocyanate-labeled anti-rabbit IgG in PBS containing 0.2% Tween 20/and goat serum diluted 1:50). After 1 h, cells were washed four times in PBS containing 0.2% Tween 20 and mounted in fluoromount (Southern Biotechnology Associates, Birmingham, AL) and examined with a Zeiss fluorescence microscope.

To immunodeplete PRMT1 and PRMT3 antisera, GST-PRMT1 and GST-PRMT3-(90–528) were isolated with glutathione-Sepharose beads from 350-ml E. coli cultures. After blocking, cells were incubated for 2 h in primary antibody dilutions (1:350 for anti-PRMT1, 1:200 for anti-PRMT3) in PBS containing 0.2% Tween 20 and goat serum diluted 1:50. Then cells were washed three times with PBS containing 0.2% Tween 20 and incubated in the secondary antibody solutions (1:100 diluted fluorescein isothiocyanate-labeled anti-rabbit IgG in PBS containing 0.2% Tween 20/and goat serum diluted 1:50). After 1 h, cells were washed four times in PBS containing 0.2% Tween 20 and mounted in fluoromount (Southern Biotechnology Associates, Birmingham, AL) and examined with a Zeiss fluorescence microscope.

To immunodeplete PRMT1 and PRMT3 antisera, GST-PRMT1 and GST-PRMT3-(90–528) were isolated with glutathione-Sepharose beads from 350-ml E. coli cultures. The beads with the absorbed GST proteins were resuspended in 100 µL of PBS, and 10 µL of anti-PRMT1 or anti-PRMT3 antisera was added. The mixtures were incubated at 4 °C for 2 h. The supernatant fractions were recovered by passing the mixtures through 0.2-µm filters. Western blotting experiments demonstrated the specificity of immunodepletion.

Preparation of a Methylation-deficient Yeast Extract—Hypomethylated yeast extract from S. cerevisiae rmt1 strain JDG9100-2, lacking the major yeast type I protein arginine N-methyltransferase, Rmt1, was prepared as described previously (17).

Analysis of Methylated Polypeptides by SDS-PAGE and Fluorography—Specific conditions for the methylation reactions are described in the relevant figure legends. Reactions were terminated by the addition of an equal volume of SDS-containing sample buffer (30) and heating to 100 °C for 5 min. Samples were then subjected to SDS-PAGE (27), Coomassie Brilliant Blue R staining, and fluorography as described previously (7).

Western blot Analysis—Protein samples were subjected to SDS-PAGE and immunoblotting analysis as described previously (28).
RESULTS

Identification of Proteins That Interact with PRMT1—A yeast strain expressing the bait fusion protein LexA-PRMT1 was transformed with a cDNA library in which the GAL4 activation domain (GAL4AD) is fused to cDNAs from rat liver-derived FAO cells (7). Twenty-five positive cDNA plasmids were isolated and separated into four groups by PCR analysis, restriction digest analysis, and sequencing; PRMT1 (15 isolates), 2A (8 isolates), 4A (1 isolate), and 7A (1 isolate). Sequence analysis indicated that 4A is homologous to a yeast alcohol dehydrogenase, and 7A encodes a homologue of a glycosylphosphatidylinositol-anchored extracellular membrane protein involved in transcytosis in Madin-Darby canine kidney cells.

The Open Reading Frame Encoded by the cDNA from Which the 2A Clone Is Derived Shows Significant Homology to PRMT1 and Is Termed “PRMT3”—A BLAST search (22) of protein sequence data bases indicated that the predicted open reading frame encoded by the 2A clone is closely related to mammalian PRMT1 (7, 15) and yeast Rmt1 (17, 18) (Fig. 1). Northern analysis of RNA from RAT1 fibroblast cells suggested that 2A is a truncated portion of a 2.4-kilobase pair transcript (data not shown). By using clone 2A as a probe, a longer cDNA was cloned from a RAT1 cDNA library. This cDNA encodes an open reading frame of 528 amino acids.

Comparison of PRMT1 and the “2A” putative methyltransferase domain (amino acids 195 to 528) reveals 46% identity and 67% similarity at the amino acid level. The designation “PRMT2” already exists as a GenBankTM entry (U80213) for a cDNA that shares some sequence identity with PRMT1. This human sequence was named HRMT1L1 (19). We have, therefore, named the polypeptide encoded by the full-length 2A transcript “protein arginine methyltransferase 3” or PRMT3. The high degree of identity among the Rmt1, PRMT1, and PRMT3 sequences suggests that PRMT3 might also be a protein arginine N-methyltransferase.

pH 7.5. Samples were incubated for 40 min at 37 °C. A, reaction mixtures were then subjected to SDS-PAGE and fluorography. Two exposure times (2 and 7 days) are shown; the lane in which GST-PRMT3 was tested is shown at both exposure times. The arrows indicate the position of the molecular weight standards. B, the product from a reaction mixture containing GST-GAR and 2.07 μg of the GST-PRMT3 was analyzed for the presence of methylated arginine derivatives. Proteins were precipitated in 6 × 50-nm borosilicate vials with an equal volume (55 μl) of 25% (w/v) trichloroacetic acid in the presence of 30 μg of bovine serum albumin. The resulting pellet was washed with 2 volumes of acetone at −20 °C. The air-dried protein pellets were then hydrolyzed in vacuo at 110 °C for 20 h in a vapor-phase Waters Pico-Tag apparatus using 200 μl of 12 N HCl. The hydrolyzed material was reconstituted in 50 μl of a diluted citrate buffer (0.1 M Na+, containing 1% (v/v) thiodiglycol and 0.05% phenol at pH 2.2) and analyzed as described previously (17). Prior to loading on the column, the sample was diluted with an equal volume of the concentrated citrate loading buffer (0.2 M Na+, containing 2% (v/v) thiodiglycol and 0.1% phenol at pH 2.2) and nonradiolabeled standards of N6-monomethylarginine (MMA) and N6,N8-dimethylarginine (DMA) were added (1.0 μmol each, Sigma). The column (0.9 cm in diameter × 11 cm in length) was equilibrated and eluted isocratically from a 200-nl aliquot of the fractions 1.0 ml/min in citrate buffer (0.35 M Na+, pH 5.27) at 55 °C. One-minute fractions were collected and 3H radioactivity was determined by analyzing 200-nl aliquots of the fractions using the ninhydrin method (1). The column was regenerated between runs by washing with 0.2 M NaOH for 20 min and then re-equilibrating in the elution buffer. C, a reaction mixture containing GST-GAR and 10.6 μg of GST-PRMT3-(184–538) was analyzed as in B. In a control experiment, we determined that incubation of GST-GAR with [3H]AdoMet alone gives no 3H-methylated arginine derivatives (data not shown). The large peak of radioactivity near fraction 10 may represent unreacted [3H]AdoMet or its degradation products that were not completely removed by the acid precipitation step.
The amino-terminal 194-amino acid fragment of PRMT3, which does not resemble any known protein, is rich in acidic amino acid residues. It is, therefore, called the N-terminal acidic amino acid-rich (NAR) domain of PRMT3. The PRMT3 NAR domain contains two functional motifs, a putative C2H2 zinc finger motif (Cys46–His99) and a tyrosine phosphorylation consensus sequence (Tyr85–Phe93) similar to the STAT1 tyrosine phosphorylation site (29).

A BLAST search identified two human EST sequences (AA307385 and H38113) closely related to rat PRMT3 cDNA. Sequencing confirmed that AA307385 is the human PRMT3 orthologue but is missing the amino-terminal 10 amino acid residues (Fig. 1). At the amino acid level, human PRMT3 is 90% identical to rat PRMT3. Human PRMT3 contains the carboxyl-terminal putative methyltransferase domain and the amino-terminal NAR domain.

**GST-PRMT1 and GST-PRMT3 Fusion Proteins Methylate GST-GAR—**GST-GAR is a recombinant protein arginine methyltransferase substrate containing the first 148 amino acids of the human fibrillarin protein, fused in-frame to GST. The amino-terminal 194-amino acid fragment of PRMT3, GST-PRMT3-(184–528), has approximately 3-fold lower specific activity relative to GST-PRMT3, based on quantitation of the radioactive methylarginine peak areas in Fig. 2, when compared with the activity of the GST-PRMT3 (Fig. 2A).

The specific activity of GST-GAR methylation by PRMT1 and PRMT3 was determined by measuring the incorporation of [3H]AdoMet into the methylated product. The reaction mixtures (60 μl) contained 48 μg (6 μM) of GST-GAR, 17.6 μCi of [3H]AdoMet (0.9 μCi), and either 3.2 μg of GST-PRMT1 or 12 μg of GST-PRMT3 in 25 mM Tris-HCl, pH 7.5. Methylation reactions were performed at 37 °C. At each time point (10, 20, 30, and 60 min), 60-μl aliquots (containing 0.8 μg of GST-PRMT1 or 3 μg of GST-PRMT3) were withdrawn; the reactions were stopped by addition of SDS-PAGE sample buffer and heating at 95 °C for 4 min, and the samples were subjected to SDS-PAGE. The GST-PRMT1 and GST-PRMT3 samples were subjected to fluorography for 15 min and 15 h, respectively. Methylation of GST-GAR was quantitated by densitometric scanning.

Amino-terminal truncated version of PRMT3, GST-PRMT3-(184–528), was used to determine whether the PRMT3 amino-terminal extension, not present in Rmt1 or PRMT1, may play a regulatory role in PRMT3 enzymatic activity. The ability of GST-PRMT3-(184–528) to methylate GST-GAR is reduced when compared with the activity of the GST-PRMT3 (Fig. 2A). GST-PRMT3-(184–528) has approximately 3-fold lower specific activity relative to GST-PRMT3, based on quantitation of the radioactive methylarginine peak areas in Fig. 2, B and C, when normalized for the amounts of recombinant enzyme present.

**PRMT1 and PRMT3 Associate in Yeast Two-hybrid Interaction Analysis—**The recovery of PRMT1 and PRMT3 cDNAs from the yeast two-hybrid screening experiment, using PRMT1 as bait, suggested that PRMT1 forms both homo-oligomers with itself and hetero-oligomers with PRMT3. To test whether PRMT3 can form homo-oligomers, two bait plasmids, pBTM117-PRMT3-(90–528) and pBTM117-PRMT3-(214–528), in which regions of PRMT3 were fused to the LexA DNA binding domain, were constructed. PRMT3-(90–528) contains a transcription activation domain (Fig. 4C) and cannot, therefore, be used as bait in a yeast two-hybrid analysis. The combination of pBTM117-PRMT3-(214–528), which does not by itself activate transcription (Fig. 4C), and pGAD424-PRMT3-(90–528) (a fusion protein of the GAL4 activation domain and PRMT3-(90–528)) can activate β-galactosidase expression (Fig. 4A). Therefore, PRMT3 has the potential to form homo-oligomers.

An amino-terminal truncation of PRMT3, PRMT3-(90–528), was identified by yeast two-hybrid analysis as a protein interacting with PRMT1. To determine whether full-length PRMT3 can interact with PRMT1, pPC86-PRMT3-(90–528) and pPC86-PRMT3 (in which the respective PRMT3 sequences are fused to the GAL4 activation domain) were each transformed into yeast in combination with pLexA(L)-PRMT1.

**Comparison of specific activities of recombinant PRMT1 and PRMT3, using GST-GAR as substrate and [3H]AdoMet as methyl donor.** A and B, 240-μl reaction mixtures contained 48 μg (6 μM) of GST-GAR, 17.6 μCi of [3H]AdoMet (0.9 μCi), and either 3.2 μg of GST-PRMT1 or 12 μg of GST-PRMT3 in 25 mM Tris-HCl, pH 7.5. Methylation reactions were performed at 37 °C. At each time point (10, 20, 30, and 60 min), 60-μl aliquots (containing 0.8 μg of GST-PRMT1 or 3 μg of GST-PRMT3) were withdrawn; the reactions were stopped by addition of SDS-PAGE sample buffer and heating at 95 °C for 4 min, and the samples were subjected to SDS-PAGE. The GST-PRMT1 and GST-PRMT3 samples were subjected to fluorography for 15 min and 15 h, respectively. Methylation of GST-GAR was quantitated by densitometric scanning. The specific activity of GST-PRMT1 or GST-PRMT3 was determined by measuring the incorporation of [3H]AdoMet into the methylated product.
To Demonstrate Interactions between PRMT1 and PRMT3

To investigate whether PRMT1 and PRMT3 directly associate in mammalian cells and whether PRMT3 can form homo-oligomers in vivo, a protein extract from RAT1 embryo fibroblast cells was fractionated on a Sephacryl S300HR gel filtration column. Elution of PRMT proteins was determined by Western analysis and by enzyme activity assay.

PRMT3 antigen elutes from the Sephacryl column at the approximate position of a 37-kDa globular polypeptide (Fig. 5A), somewhat smaller than its calculated molecular mass of 59.4 kDa (Fig. 1) and its estimated size of 60 kDa in SDS-PAGE immunoblotting experiments with RAT1 extract (data not shown). However, PRMT3 antigen eluted as a 64-kDa species when using a Superdex S200 (Amersham Pharmacia Biotech) column (data not shown). Endogenous PRMT3 is, therefore, probably present in RAT1 cells as a monomer. PRMT1, with a predicted molecular mass of 40.5 kDa (7), elutes in a broad peak ranging between 200 and 440 kDa (Fig. 5). PRMT1 and PRMT3 do not, in RAT1 cells, form hetero-oligomers that can survive cell disruption and gel filtration.

GST-GAR methylation could only be detected where PRMT1 elutes (Fig. 5, A and C). A lower level of PRMT3 protein and a significantly lower specific activity of the PRMT3 enzyme for GST-GAR probably account for the lack of detectable enzyme activity eluting with PRMT3.

PRMT1 and PRMT3 Reside in Distinct Subcellular Compartments in RAT1 Cells—To localize endogenous PRMT1, RAT1 cells were cultured in chamber slides and stained with anti-PRMT1 or pre-immune serum after fixation and permeabilization by PFA and Triton X-100 (Fig. 6). PRMT1-specific staining appears predominantly in the nucleus, although the cell cytoplasm is faintly stained. To confirm that the staining is specific for PRMT1, anti-PRMT1 antiserum was immunodepleted by GST-PRMT1 or GST-PRMT3. PRMT1 reactivity was depleted by GST-PRMT1 but not by GST-PRMT3 (90–528) (data not shown). To confirm this subcellular localization result, we also performed immunofluorescence studies with RAT1 cells fixed and permeabilized by methanol fixation at −20 °C. These results also demonstrated that PRMT1 is found predominantly nuclear, with some PRMT1 antigen present in the cytoplasm (data not shown).

PRMT3 was immunolocalized primarily to the cytoplasm with anti-PRMT3 antiserum, using either PFA/Triton X-100 fixation (Fig. 7) or methanol fixation (data not shown). PRMT3 staining could be depleted by GST-PRMT3 (90–528) but not by GST-PRMT1 (data not shown). In summary, PRMT1 is predominantly nuclear, whereas PRMT3 is predominantly cytoplasmic.

Tissue Distribution of PRMT1 and PRMT3—We compared the expression of PRMT1 and PRMT3 mRNAs in common preparations of rat tissues. PRMT3 distribution closely resembles PRMT1 distribution (Fig. 8). Small variations in PRMT1 and PRMT3 expression are observable, however. For example, PRMT1:PRMT3 ratios are reversed for heart and small intestine.

PRMT3, Like PRMT1, Is Constitutively Expressed in Cells—We performed Northern analyses with total RNA from rat PC12 pheochromocytoma cells to determine whether PRMT3 message is constitutively expressed or is induced by ligand stimulation. Like PRMT1, PRMT3 mRNA is constitutively expressed in PC12 cells (Fig. 9). Forskolin induction of the c-fos gene illustrates induction of a primary response gene. The PRMT1 and PRMT3 probes each detect both messages; the PRMT1 probe shows slight cross-hybridization with PRMT3 message and vice versa (Fig. 9). The PRMT3 probe also identifies a third, higher molecular weight message, whose identity is unknown.

GST-PRMT1 and GST-PRMT3 Methylate Distinct Substrates in Hypomethylated Yeast Cell Extracts—A solubilized protein extract from yeast lacking RMT1, the major S. cerevisiae

Fig. 4. Yeast two-hybrid analyses of interactions between PRMT1, PRMT3, and TIS21. pLexAL/TIS21 and pLexAL-PRMT1 are two-hybrid bait plasmids that express TIS21 and PRMT1 fusion proteins linked to the LexA transcription factor DNA binding domain. PRMT1/TIS21 (90–528) and pBMTM117-PRMT3 (214–528) are bait plasmids that express fusion proteins between the LexA transcription factor DNA binding domain and amino-terminal truncations of PRMT3. The pPC86 and pGAD425 prey plasmids express fusions of the GAL4 transcription factor activation domain with the indicated regions of PRMT1 or PRMT3. The choice of plasmids used in the various two-hybrid analyses in A was determined by the genetic requirements necessary for the stable maintenance of the bait and prey plasmids. Yeast strain L40 was transformed with plasmids encoding the LexA DNA binding domain fusion proteins or the GAL4 transcription activator DNA binding domain alone (7). To determine whether TIS21 can also interact with protein extract from yeast in combination with the prey plasmids pPC86-PRMT3 or pPC86-PRMT3-(90–528). The interaction between TIS21 and PRMT1 was used as a positive control and the lack of interaction between TIS21 and PRMT1 as a negative control (7). TIS21 interacts only with PRMT1 and does not interact with PRMT3 or its amino-terminal truncated derivative (Fig. 4A).

Both combinations activate LexA-responsive lacZ (Fig. 4A) and HIS3 gene expression. Therefore the full-length PRMT3 protein can interact with PRMT1 in yeast two-hybrid analysis.

PRMT1 was originally isolated from a yeast two-hybrid screen with the TIS21 immediate-early gene product as the bait (7). To determine whether TIS21 can also interact with PRMT3, the bait plasmid pLexAL/TIS21 was transformed into yeast in combination with the prey plasmids pPC86-PRMT3 or pPC86-PRMT3-(90–528). The interaction between TIS21 and PRMT1 was used as a positive control and the lack of interaction between TIS21 and PRMT1 as a negative control (7). TIS21 interacts only with PRMT1 and does not interact with PRMT3 or its amino-terminal truncated derivative (Fig. 4A).

Gel Filtration Chromatography of RAT1 Cell Extracts Fails to Demonstrate Interactions between PRMT1 and PRMT3—To investigate whether PRMT1 and PRMT3 directly associate in yeast in combination with the prey plasmids pPC86-PRMT3, the bait plasmid pLexAL-PRMT1 was transformed into yeast in combination with the prey plasmids pPC86-PRMT3 (Fig. 4 with PRMT3 or its amino-terminal truncated derivative (7). To determine whether TIS21 can also interact with protein extract from yeast in combination with the prey plasmids pPC86-PRMT3 or pPC86-PRMT3-(90–528). The interaction between TIS21 and PRMT1 was used as a positive control and the lack of interaction between TIS21 and PRMT1 as a negative control (7). TIS21 interacts only with PRMT1 and does not interact with PRMT3 or its amino-terminal truncated derivative (Fig. 4A).

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Fig. 5. PRMT1 and PRMT3 proteins present in RAT1 cell extract are separated by gel filtration chromatography. RAT1 cell-soluble extract (2.2 ml, 8.8 mg of protein) was loaded onto a Sephacryl S300HR (Amersham Pharmacia Biotech) gel filtration column (63-cm column height × 2.6-cm inner diameter, 334-ml bed volume). The column was equilibrated and eluted in 25 mM Tris-HCl, 1 mM sodium EDTA, and 1 mM sodium EGTA, pH 7.5, at 4 °C, at a flow rate of 22 ml/h, and 3-ml fractions were collected. The main section of A shows that the total protein elution profile as absorbance at 280 nm (filled circles). Protein arginine N-methyltransferase activity was determined by incubating 21 μl of every other column fraction with 0.7 μg of GST-GAR and 0.92 μM (2.2 μCi) [3H]AdoMet in a final volume of 30 μl at 37 °C for 30 min. The reaction mixtures were then subjected to SDS-PAGE and fluorographic analysis (C), and GST-GAR methylation was quantitated by densitometry (A, open triangles). The relative concentrations of each protein were determined by densitometry. Arrows (A) indicate the column fraction containing the peak activity of each size marker enzyme, assayed as described in the Worthington enzyme manual (ferritin was quantitated by absorbance at 400 nm). The inset in A shows the peak elution positions of the protein standards, plotted against the logarithm of their molecular mass. The peaks of PRMT1 activity and PRMT3 protein are in bold type. Their native molecular masses (317 and 37 kDa, respectively) were approximated using the equation of the best curve fit. B shows Western blots of column fractions, using anti-PRMT1 (1:10,000 dilution) and anti-PRMT3 (1:5,000 dilution) antisera. C shows the protein arginine N-methyltransferase activity of column fractions, using GST-GAR as substrate.

Fig. 6. Immunofluorescence localization of PRMT1 in RAT1 cells. RAT1 cells were fixed with 2% PFA and then permeabilized with 0.1% Triton X-100 in 2% PFA. The fixed and permeabilized cells were stained and photographed as described under “Experimental Procedures” using anti-PRMT1 and pre-immune serum at a 1:350 dilution.
protein arginine N-methyltransferase (7), was utilized as a collection of hypomethylated substrates to assess the enzymatic specificity of PRMT1 and PRMT3. When \( rmt1 \) extract is incubated with GST-Rmt1 and radiolabeled [\( ^3H \)]AdoMet, polypeptide species of 55, 38, 35, and 33 kDa are labeled (Fig. 10A). In similar reactions with GST-PRMT1, polypeptides of 55, 38, 35, and 26 kDa are methylated, with the predominant species at 55 and 26 kDa. In contrast to the several substrates methylated when GST-Rmt1 and GST-PRMT1 are incubated with the \( rmt1 \) extract (Fig. 10A), only one 29-kDa polypeptide in the \( rmt1 \) extract is methylated by GST-PRMT3 (Fig. 10B). In control reactions containing [\( ^3H \)]AdoMet with \( rmt1 \) extract alone or with GST-PRMT3 enzymes alone, no protein methylation is observed (Fig. 10B).

TIS21 associates with PRMT1 in vitro and qualitatively and quantitatively modulates PRMT1 activity (7). Methylation of a 26-kDa GST-PRMT1 substrate present in the \( rmt1 \) yeast extract is suppressed when GST-TIS21 is included in the reaction (Fig. 10, compare lanes 2 and 3). In contrast, GST-TIS21 has no effect on GST-PRMT3 enzymes alone, no protein methylation is observed (Fig. 10B).

We considered the hypothesis that the amino-terminal NAR extension of PRMT3 may regulate PRMT3 enzyme activity and/or substrate specificity. To begin to determine the role of the amino-terminal domain of PRMT3, we used a GST-PRMT3-(184–528) construct that lacks the NAR domain but includes all of the conserved regions shared among methyltransferases. GST-PRMT3-(184–528) cannot methylate the 29-kDa polypeptide substrate in the yeast extract that is methylated by GST-PRMT3 (Fig. 10B; compare lanes 3 and 4). In contrast, GST-PRMT3-(184–528) fusion protein can methylate the GST-GAR substrate (Fig. 2, A and C).

**DISCUSSION**

Mammalian Cells Contain Multiple Type I Protein Arginine N-Methyltransferases—Type I protein arginine N-methyltransferases methylate protein arginine residues to form \( N^G \cdot N^G \)-dimethylarginine residues (asymmetric). In contrast, type II protein arginine methyltransferases catalyze the formation of \( N^G \cdot N^\gamma \)-dimethylarginine residues (symmetric) (1–3). Type II protein arginine N-methyltransferase activity has not been
purified to homogeneity, and the catalytic subunit has not been cloned. Both PRMT1, the catalytic subunit of a type I protein arginine methyltransferase from mammalian cells, and Rmt1, a type I protein arginine N-methyltransferase from S. cerevisiae, have recently been cloned and characterized (7, 15, 17, 18). Mutation of the RMT1 gene of S. cerevisiae eliminates all detectable N-G,N-G'-dimethylarginine residues present in proteins, suggesting that Rmt1 is the sole protein type I arginine N-methyltransferase present in this organism (17).

Katsanis et al. (19) recently identified a human gene, HRMT1L1 (PRMT2 in the GenBank™ data base), that is 33% identical in amino acid sequence with human PRMT1. Although we have not been able to demonstrate enzyme activity with a GST-HRMT1L1 fusion protein, the sequence similarities between HRMT1L1, PRMT1, and PRMT3 suggest that HRMT1L1 will also have enzyme activity on an appropriate substrate. Current data thus suggest that two mammalian genes, whose properties are summarized in Table I, encode demonstrated protein arginine N-methyltransferase catalytic subunits. EST data base searches suggest that these three genes may encompass the entire gene family.

**PRMT1 and PRMT3 Have Distinct Enzymatic Properties**—GST-PRMT1 and GST-PRMT3 both asymmetrically dimethylate arginine residues on GST-GAR. However, GST-PRMT3 has substantially lower activity (Figs. 2 and 3, Table I). Analysis of the protein arginine methyltransferase activity of RAT1 extracts suggests that the difference in specific activities of GST-PRMT1 and GST-PRMT3 is not a consequence of the GST fusion. Column fractions containing easily detectable levels of PRMT3 antigen have little or no detectable enzyme activity on GST-GAR, whereas fractions containing PRMT1 antigen have substantial enzyme activity (Fig. 5). In contrast, there exists at least one substrate, a 29-kDa protein present in hypomethylated yeast rmt1 extracts, that can be methylated by GST-PRMT3 but not by GST-PRMT1 (Fig. 10).

We anticipated that a subset of the hypomethylated proteins present in adenosine dialdehyde-treated RAT1 cell extracts would serve as GST-PRMT3 substrates. Although numerous hypomethylated substrates are present, as demonstrated by GST-PRMT1 methylation (7), none could be detectably methylated by GST-PRMT3 (data not shown). There are a number of possible reasons for the failure to detect GST-PRMT3 substrates in RAT1 cell extracts. The GST-PRMT3 fusion protein may not accurately reflect the substrate specificity of the native Rmt1 strain of S. cerevisiae was incubated with 0.75 µM (3.3 nM) [3H]AdoMet and either 0.84 µg of GST-Rmt1, 0.77 µg of GST-PRMT1, 0.77 µg of GST-PRMT1 together with 2.2 µg of GST-TIS21 protein, 2.07 µg of GST-PRMT3, or 10.6 µg of GST-PRMT3-(184–528) in a final volume of 55 µl containing 25 mM Tris-HCl, 1 mM sodium EDTA, 1 mM sodium EGTA at pH 7.5 for 40 min at 37 °C. The reaction mixtures were then subjected to SDS-PAGE and fluorography. B, rmt1 yeast extract (190 µg) was incubated with 1.65 µCi (0.46 µM) of [3H] AdoMet and 2.5 µg of either GST-PRMT3 (lane 3) or GST-PRMT3-(184–528) (lane 4) in a final volume of 45 µl in PBS for 40 min at 37 °C. Control reactions contained 1.65 µCi (0.46 µM) of [3H] AdoMet and 190 µg of rmt1 extract (lane 5), 2.5 µg of GST-PRMT3 (lane 1) or 2.5 µg of GST-PRMT3-(184–528) (lane 2). A is from a 2-day exposure; B is from an overnight (14 h) exposure. The arrows indicate the positions of polypeptide size standards.

**FIG. 10.** GST-PRMT3 methylates substrates distinct from those of GST-Rmt1 or GST-PRMT1 in a hypomethylated rmt1 yeast extract. A, soluble extract (190 µg of protein) from the rmt1 strain of S. cerevisiae was incubated with 0.75 µM (3.3 nM) [3H]AdoMet and either 0.84 µg of GST-Rmt1, 0.77 µg of GST-PRMT1, 0.77 µg of GST-PRMT1 together with 2.2 µg of GST-TIS21 protein, 2.07 µg of GST-PRMT3, or 10.6 µg of GST-PRMT3-(184–528) in a final volume of 55 µl containing 25 mM Tris-HCl, 1 mM sodium EDTA, 1 mM sodium EGTA at pH 7.5 for 40 min at 37 °C. The reaction mixtures were then subjected to SDS-PAGE and fluorography. B, rmt1 yeast extract (190 µg) was incubated with 1.65 µCi (0.46 µM) of [3H] AdoMet and 2.5 µg of either GST-PRMT3 (lane 3) or GST-PRMT3-(184–528) (lane 4) in a final volume of 45 µl in PBS for 40 min at 37 °C. Control reactions contained 1.65 µCi (0.46 µM) of [3H] AdoMet and 190 µg of rmt1 extract (lane 5), 2.5 µg of GST-PRMT3 (lane 1) or 2.5 µg of GST-PRMT3-(184–528) (lane 2). A is from a 2-day exposure; B is from an overnight (14 h) exposure. The arrows indicate the positions of polypeptide size standards.

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**Table I**

<table>
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<th>Relative activity on GST-GAR</th>
<th>Methylated arginine residue formed</th>
<th>Activity modulated by</th>
<th>Native molecular size of enzyme estimated by Sephacryl S300 gel filtration</th>
<th>Predominant intracellular location</th>
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<td>Rat PRMT1</td>
<td>Rat PRMT3</td>
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<td></td>
<td>100%</td>
<td>Monomethylarginine and asymmetric dimethylarginine</td>
<td>PRMT3 amino-terminal domain</td>
<td>~317 kDa</td>
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<td>Predominant intracellular location</td>
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<td>Nuclear</td>
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enzyme. Alternatively, PRMT3 may need to be activated in some as yet unidentified fashion. PRMT3 substrates might be denatured during the preparation of hypomethylated RAT1 extract or only be available under specific conditions. In the latter case, it is possible that amino-accepting sites would only be exposed to the PRMT3 enzyme when substrates have specific ligands bound or when segments of the polypeptide chain are partially unfolded, such as during or immediately after translation (35).

**PMRT1 and PMRT3 Are Present in RAT1 Cells in Different Subcellular Compartment**—Mammalian type I protein arginine methyltransferase enzyme activity has consistently been detected as a high molecular weight complex (4, 7, 20, 21). We consequently expected that PRMT3, the principal protein identified in a yeast two-hybrid screen for PRMT1-interacting proteins, would form hetero-oligomers with PRMT1. However, the PRMT1 and PRMT3 antigens are completely separated by gel filtration chromatography of RAT1 cell extracts. PRMT1 antigen is associated with the high molecular weight complex that demonstrates protein arginine methyltransferase activity. In contrast, PRMT3 protein chromatographs as an apparent monomer. The relatively low specific activity of PRMT3 on conventional type I protein arginine N-methyltransferase substrates explains why this isoform of the enzyme has not been detected in previous studies of protein arginine methyltransferase enzyme activity (1–3).

Since we isolated PRMT3 as a PRMT1-interacting protein in the yeast two-hybrid analysis, we were surprised to observe that PRMT1 is primarily nuclear and PRMT3 is primarily cytoplasmic in RAT1 cells. However, we investigated PRMT1 and PRMT3 localization in only one cell type, under a single physiological condition. If protein-protein interactions between PRMT1 and PRMT3 do occur in cells, it seems likely that these interactions are subject to regulatory events that may lead to altered subcellular distribution of at least a subpopulation of PRMT3 and/or PRMT1 molecules. Substantial precedent exists for ligand-induced alterations in subcellular distribution of enzymes (e.g. protein kinases) that result in altered protein-protein interactions. In this regard it is of interest that PRMT1 was also isolated as a protein that interacts with the cytoplasmic domain of the interferon-α, β receptor (15). This domain provides a docking site for many proteins involved in interferon signaling pathways, e.g. the JAK kinases and STAT transcription factors (16). It is, of course, possible that PRMT1 and PRMT3 do not form complexes in cells under any conditions and that the identification of PRMT3 by yeast two-hybrid analysis was a fortuitous artifact that resulted in the cloning of this second enzymatically active mammalian type I protein arginine N-methyltransferase.

**Mammalian Type I Protein Arginine N-Methyltransferases Each Have a Potential Regulatory Region That May Influence Their Enzyme Activities**—GST-PRMT1 methyltransferase activity is dramatically modulated by interaction with TIS21 protein; both quantitative activation and qualitative alterations in substrate specificity occur when GST-TIS21 is incubated with GST-PRMT1 (Ref. 7 and Fig. 10). In contrast, GST-TIS21 does not interact with GST-PRMT3 or modulate its methyltransferase activity. However, PRMT3 has an amino-terminal extension that is not shared with PRMT1. The tyrosine phosphorylation consensus sequence GFPXYGYK of the PRMT3 NAR region is similar to the JAK kinase substrate site GPKFYGYK present in STAT1 (29). Phosphorylation at this site is required for STAT1 dimerization and transport to the nucleus (29, 36). The PRMT3 amino-terminal region also contains a potential C2H2 zinc finger, a protein motif involved in both protein-protein (37–39) and protein-nucleic acid (40, 41) interactions. The activity of amino-terminal truncated GST-PRMT3-(184–528) was reduced for GST-GAR (Fig. 2) and eliminated for the 29-kDa substrate present in rmt1 yeast cell extract (Fig. 10), suggesting that the PRMT3 NAR region may play a regulatory role in PRMT3 enzymatic activity, subcellular localization, and/or protein-protein interactions.

**HRMT1L1(PRMT2)** also has an amino-terminal extension. Although this region of HRMT1L1 does not contain zinc finger or phosphorylation consensus sequences, it does contain a sequence that has 68% amino acid sequence similarity to the SRC SH3 domain. We suggest (i) that PRMT1, PRMT3, and HRMT1L1(PRMT2) each contains a catalytic methyltransferase domain and (ii) that each may be subject to distinct modes of protein-protein interaction and regulation of enzyme activity by interaction with TIS21 (PRMT1), by zinc-finger-mediated interactions and/or modifications at the tyrosine phosphorylation site (PRMT3), and by SH3-mediated protein-protein interactions with proline-rich regions of regulatory molecules (HRMT1L1).

Protein arginine methylation extends across a wide range of eucaryotic organisms (1). Substrates for these enzymes play roles in a number of important biological functions. However, the biochemical and biological consequences of this post-translational modification are not well understood. With the isolation of distinct enzymes with alternative substrate specificities, cellular distributions, and regulatory interactions, it should now be possible to carry out the molecular and cellular studies that will elucidate the roles of these enzymes.

**Acknowledgments**—We thank the members of the Herschman and Clarke labs for helpful discussions.

**REFERENCES**