### p250GAP, a Novel Brain-enriched GTPase-activating Protein for Rho Family GTPases, Is Involved in the *N*-Methyl-D-aspartate Receptor Signaling

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*N*-Methyl-D-aspartate (NMDA) receptors regulate structural plasticity by modulating actin organization within dendritic spines. Herein, we report identification and characterization of p250GAP, a novel GTPase-activating protein for Rho family proteins that interacts with the GluR $\epsilon$ 2 (NR2B) subunit of NMDA receptors in vivo. The p250GAP mRNA was enriched in brain, with high expression in cortex, corpus striatum, hippocampus, and thalamus. Within neurons, p250GAP was highly concentrated in the postsynaptic density and colocalized with the GluR $\epsilon$ 2 (NR2B) subunit of NMDA receptors and with postsynaptic density-95. p250GAP promoted GTP hydrolysis of Cdc42 and RhoA in vitro and in vivo. When overexpressed in neuroblastoma cells, p250GAP suppressed the activities of Rho family proteins, which resulted in alteration of neurite outgrowth. Finally, NMDA receptor stimulation led to dephosphorylation and redistribution of p250GAP in hippocampal slices. Together, p250GAP is likely to be involved in NMDA receptor activity-dependent actin reorganization in dendritic spines.

#### INTRODUCTION

The adaptive properties of brain circuitry require dynamism of neuronal connectivity that includes conversion of transient events into long-lasting changes in synaptic transmission. *N*-methyl-D-aspartate (NMDA) receptors are involved in the experience-dependent plasticity (Feldman and Knud-

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Abbreviations used: BAP, bacterial alkaline phosphatase; GAP, GTPase activating protein; GEF, guanine nucleotide exchange factor; GDI, guanine nucleotide dissociation inhibitor; GluR, glutamate receptor; CRIB, Cdc42/Rac-interactive binding domain GST, glutathione S-transferase mAb, monoclonal antibody NMDA, N-methyl-D-aspartate PSD, postsynaptic density RBD, Rho-binding domain SH3, src homology 3.

sen, 1998; Fischer *et al.*, 2000; Lendvai *et al.*, 2000). NMDA receptors in postnatal and adult brains modulate synaptic plasticity by regulating their localization, voltage-controlled Ca<sup>2+</sup> influx, downstream signaling events, and morphological changes of dendritic spines (Kennedy, 2000; Scannevin and Huganir, 2000; Sheng and Pak, 2000; Hering and Sheng, 2001; Yuste and Bonhoeffer, 2001). These functions are likely to reside in complex formations of NMDA receptors with various proteins, including scaffolding proteins, kinases, phosphatases, cytoskeletal proteins, and other signaling molecules (Husi *et al.*, 2000). Through cooperation of these molecules, NMDA receptors mediate long-lasting changes in synaptic strength (Kennedy, 2000; Scannevin and Huganir, 2000; Sheng and Pak, 2000; Hering and Sheng, 2001; Yuste and Bonhoeffer, 2001).

Members of the Rho family of small GTPases, including RhoA, Rac1, and Cdc42, are critical regulators of actin cytoskeleton organization (Ridley and Hall, 1992; Nobes and Hall, 1995; Van Aelst and D'Souza-Schorey, 1997; Hall, 1998). As such, these proteins regulate a variety of cellular

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processes, including migration, adhesion, and morphological change. RhoA regulates formation of focal adhesions and subsequent assembly of stress fibers. Rac1 regulates formation of membrane lamellae, and Cdc42 triggers outgrowth of peripheral spike-like protrusions called filopodia (Ridley and Hall, 1992; Nobes and Hall, 1995; Van Aelst and D'Souza-Schorey, 1997; Hall, 1998). Like Ras GTPases, Rho family GTPases cycle in a tightly regulated manner between a GDP-bound inactive state and a GTP-bound active state. This cycling is regulated by the action of three major classes of proteins: guanine nucleotide exchange factors (GEFs), guanine nucleotide dissociation inhibitors (GDIs), and GTPase-activating proteins (GAPs). GEFs stimulate the replacement of GDP by GTP, which results in activation of the substrate GTPases. In contrast, GAPs stimulate the relatively weak intrinsic GTP-hydrolyzing activity of their substrate GTPases, thereby inactivating them. GDIs block dissociation of GDP from the GTPases (Lamarche and Hall, 1994; Whitehead et al., 1997; Sasaki and Takai, 1998).

Dendritic spines are actin rich, and their shape and motility are influenced by the actin cytoskeleton (Matus et al., 1982; Kaech et al., 1997; Fiala et al., 1998; Hering and Sheng, 2001). Rho family GTPases are thought to regulate turnover of dendritic spines (Luo et al., 1996; Threadgill et al., 1997; Ruchhoeft et al., 1999; Lee et al., 2000; Wong et al., 2000). For example, constitutively active Rac1 disrupts the morphology of dendritic spines in pyramidal neurons (Nakayama et al., 2000; Tashiro et al., 2000). Dominant negative Rac1 and constitutively active RhoA cause a progressive reduction in spine number (Nakayama et al., 2000; Tashiro et al., 2000). Stimuli that induce long-term potentiation result in alteration of spine size, increase of synaptic surface area, and perforation of postsynaptic density (Sorra and Harris, 1998; Engert and Bonhoeffer, 1999; Maletic-Savatic et al., 1999; Toni et al., 1999). Application of NMDA receptor antagonist blocks these changes, indicating that dendritic spine density and morphology are influenced by NMDA receptor activity (Engert and Bonhoeffer, 1999; Maletic-Savatic et al., 1999; Toni et al., 1999). Conversely, actin cytoskeleton is involved in NMDA receptor channel properties, NMDA receptor-mediated long-term potentiation, and NMDA receptor localization (Rosenmund and Westbrook, 1993; Allison et al., 1998; Kim and Lisman, 1999). Intriguingly, some actin binding proteins and regulators of the actin cytoskeleton, such as α-Actinin, Cortactin, Vinculin, Spectrin, and Kalirin-7, interact directly or indirectly with NMDA receptors, providing a potential link between the NMDA receptor and actin filaments (Wyszynski et al., 1998; Husi et al., 2000; Penzes et al., 2001). Thus, the signaling pathways that link NMDA receptors to the postsynaptic actin cytoskeleton are apparently important for synaptic plasticity; however, the underlying mechanism is poorly understood.

Herein, we report identification and characterization of p250GAP, a novel brain-enriched GAP for Rho family GTPases. p250GAP is the first GAP for Rho family GTPases shown to be enriched in the NMDA receptor complex. We provide evidence suggesting that p250GAP links NMDA receptor activity to actin reorganization.

### MATERIALS AND METHODS

#### Plasmids

The human p250GAP cDNA (KIAA 0712, GenBank/EMBL/DDBJ accession no. AB018255) clone was obtained from the Kazusa DNA Research Institute (Chiba, Japan). A GAP inactive mutant (R58I) of p250GAP was generated by polymerase chain reaction. The FLAGtagged and Myc-tagged p250GAP expression plasmids were constructed in the pME18S vector (Takeuchi et al., 1993). For preparation of glutathione S-transferase (GST)-fusion proteins in Escherichia coli BL21 (Nakazawa et al., 2001), p250GAP cDNA fragments encoding, respectively, amino acids 1055-1738, 1055-1371, 1371-1738, 1552-1738, and 1371-1518 were cloned in-frame into pGEX plasmids (Amersham Biosciences, Piscataway, NJ). For production of the GAP domain of p250GAP fused to GST (GST-GAP), the wild-type and R58I mutant of p250GAP cDNA fragments encoding amino acids 1–263 were cloned in-frame into pGEX plasmids. The expression plasmid pME-GluR $\epsilon$ 2 (NR2B) was described previously (Nakazawa et al., 2001). The expression plasmids pEF-BOSMycWT-RhoA, pEFBOSMycWT-Cdc42, pEFBOSMycWT-Rac1, pEFBOSMycN19RhoA, and pEFBOSMycN17Cdc42 were kindly provided by Y. Takai (Osaka University, Osaka, Japan). The plasmid for GST-Cdc42/Rac-interactive binding domain of Pak (GST-CRIB) was kindly provided by C. Sasakawa (University of Tokyo, Tokyo, Japan). The plasmid for GST-Rho binding domain of Rhotekin (GST-RBD) (Reid et al., 1996) was constructed by reverse transcription-polymerase chain reaction. The constructs were verified by dideoxynucleotide sequencing.

#### Antibodies

Polyclonal antibodies against p250GAP and postsynaptic density (PSD)-95 were raised by immunizing rabbits with a glutathione *S*-transferase (GST) protein fused with human p250GAP (amino acids 1401–1738) and human PSD-95 (amino acids 1–45), respectively. Anti-GluR $\epsilon$ 2 (NR2B) monoclonal antibody (mAb), anti-PY mAb (RC20AP), anti-RhoA mAb, and anti-Rac1 mAb were purchased from Transduction Laboratories (Lexington, KY). Anti-Synaptophysin mAb, anti-FLAG mAb (M2), and anti-FLAG antibodies were from Sigma-Aldrich (St. Louis, MO). Anti-MAP2 mAb was from Leinco Technology (Ballwin, MO). Anti-extracellular signal-regulated kinase (ERK) antibodies, anti-Myc mAb (9E10), and anti-Cdc42 antibodies were from Santa Cruz Biotechnology (Santa Cruz, CA). Anti-phospho-ERK antibodies were from Cell Signaling Technology (Beverly, MA). Anti-GluR $\epsilon$ 2 (NR2B) antibodies were from Chemicon International (Temecula, CA).

#### Yeast Two-Hybrid Screening

Yeast two-hybrid screening was conducted with a human adult brain cDNA library (BD Biosciences Clontech, Palo Alto, CA) as described previously (James *et al.*, 1996). The cytoplasmic region of GluR $\epsilon$ 2 (NR2B) (amino acids 900-1482) was used as a bait.

#### Cell Culture and DNA Transfection

Neuro-2A cells (IFO 50081) were purchased from Health Science Research Resources Bank (Osaka, Japan). Human embryonic kidney (HEK)293T cells and Neuro-2A cells were cultured as described previously (Brouns *et al.*, 2001; Nakazawa *et al.*, 2001). HEK293T cells were transfected using calcium phosphate precipitation (Nakazawa *et al.*, 2001). Two days later, the cells were harvested for protein preparation. Neuro-2A cells were plated on glass coverslips in six-well plates and transfected with plasmid DNAs (1 µg/well) by using FuGene 6 (Roche Diagnostics, Indianapolis, IN).

#### Preparation of Lysates, Immunoprecipitation, and Immunoblotting

Lysates of HEK293T cells, whole telencephalons, and hippocampal slices were prepared as described previously (Nakazawa *et al.*, 2001). In brief, HEK293T cells expressing GluR $\epsilon$ 2 (NR2B) were lysed in TNE buffer [1% (wt/vol) Nonidet P-40, 50 mM Tris-Cl, pH 8.0, 120 mM NaCl, 5 mM EDTA, 0.2 mM Na<sub>3</sub>VO<sub>4</sub> with aprotinin at 50 U/ml] and the cleared lysates were incubated at 4°C for 1 h GST fusion proteins immobilized on glutathione-Sepharose 4B. Bound proteins were separated by centrifugation and washed with TNE buffer. Immunoprecipitation and immunoblotting were performed as described previously (Nakazawa *et al.*, 2001).

#### Northern Blot Analysis and In Situ Hybridization

Northern blot analysis was carried out as described previously (Yoshida *et al.*, 2000). In situ hybridization was performed with  $\alpha$ -<sup>35</sup>S-UTP-labeled cRNA probe (Yoshida *et al.*, 2000). A partial mouse cDNA fragment (corresponding to nucleotides 5130–5569 in human p250GAP cDNA) was obtained by reverse-transcription-polymerase chain reaction and cloned into pBluescript II KS+ (Stratagene, La Jolla, CA). After verification of the sequence, the cRNA for GAP was prepared by in vitro transcription and used as a probe.

#### Preparation of PSD Fraction

Synaptosome and PSD (one Triton X-100 extraction) of adult mouse telencephalon were prepared as described previously (Carlin *et al.*, 1980).

#### Immunocytochemistry

Neuro-2A cells and hippocampal neurons were fixed with methanol for 10 min at  $-20^{\circ}$ C, blocked with 5% normal goat serum and then incubated with appropriate antibodies. The primary antibodies were visualized using goat anti-mouse or anti-rabbit IgG conjugated to fluorescein isothiocyanate (Sigma-Aldrich), Cy3 (KPL, Gaithersburg, MD; and Jackson Immunoresearch Laboratories, West Grove, PA), or Alexa 488 (Molecular Probes, Eugene, OR).

#### **RhoGAP** Assay

In vitro RhoGAP assay was carried out as described previously (Lamarche-Vane and Hall, 1998). In brief, recombinant RhoA, Rac1, and Cdc42 (100 ng) were preloaded with [ $\gamma$ -<sup>32</sup>P]GTP (10  $\mu$ Ci, 6000 Ci/mmol) in 30  $\mu \bar{l}$  of 20 mM Tris-Cl, pH 7.5, 25 mM NaCl, 0.1 mM dithiothreitol, and 5 mM EDTA for 10 min at 30°C. After the addition of MgCl<sub>2</sub> (20 mM at final concentration), the preloaded GTPases (20 nM at final concentration) were diluted with 20 mM Tris-Cl, pH 7.5, 0.1 mM dithiothreitol, 1 mM GTP, 0.86 mg/ml bovine serum albumin, and 10 nM GST or GST-GAP domain. The mixture (30 µl) was incubated at room temperature, and 10-µl samples were removed at 0, 3, and 6 min, diluted in ice-cold wash buffer (50 mM Tris-Cl, pH 7.5, 50 mM NaCl, 5 mM MgCl<sub>2</sub>), and filtered through nitrocellulose filters. Filters were washed with the wash buffer, dried, and counted. The RhoGAP activity of p250GAP in vivo was analyzed as described previously (Yamaguchi et al., 2001). Briefly, HEK293T cells were transfected with the expression plasmids for Myc-tagged RhoA, Cdc42, or Rac1 together with or without FLAG-tagged wild-type or R58I mutant of p250GAP. The cells were lysed for 5 min with the ice-cold lysis buffer (50 mM Tris-Cl, pH 7.4, 100 mM NaCl, 2 mM MgCl<sub>2</sub>, 1% Nonidet P-40, 10% glycerol for Cdc42 and Rac1; 50 mM Tris-Cl, pH 7.4, 150 mM NaCl, 30 mM MgCl<sub>2</sub>, 0.1% Triton X-100, 10% glycerol for RhoA), and then the lysates were centrifuged for 5 min at  $10,000 \times g$ . The supernatants were incubated with 20 µg of GST-CRIB for Cdc42 and Rac1 for 30 min, or 40 µg of GST-RBD for RhoA for 60 min. After washing the beads with the lysis buffer, the bound proteins were resolved on

SDS-PAGE, and subjected to immunoblotting with anti-Myc mAb. To analyze the GAP activity of endogenous p250GAP in brain, the p250GAP immunoprecipitates from brain lysates were incubated with extracts of HEK293T cells transiently transfected with plasmids encoding Myc-tagged RhoA, Cdc42, or Rac1. GTP-loaded RhoA, Cdc42, or Rac1 was then collected from the lysates by using GST-CRIB or GST-RBD immobilized on glutathione-Sepharose. After washing the beads with the lysis buffer, the bound proteins were resolved on SDS-PAGE, and subjected to immunoblotting with anti-Myc mAb.

#### Pharmacological Treatment of Hippocampal Slices

Mouse hippocampal slices were prepared as described previously (Nakazawa et al., 2001). Slices were submerged beneath continuously perfusing artificial cerebrospinal fluid (119 mM NaCl, 2.5 mM KCl, 1.3 mM MgSO<sub>4</sub>, 2.5 mM CaCl<sub>2</sub>, 1.0 mM NaH<sub>2</sub>PO<sub>4</sub>, 26.2 mM NaHCO<sub>3</sub>, 11 mM glucose) that had been saturated with 95% O<sub>2</sub> and 5% CO<sub>2</sub>. Slices were then treated with or without 50  $\mu$ M NMDA (Sigma-Aldrich) for 5 min in the presence or absence of a selective NMDA receptor antagonist DL-APV (Tocris Cookson, Ballwin, MO). Then, the slices were frozen in liquid N<sub>2</sub>. The TNE buffersoluble slice lysates were prepared as described above. The whole slice lysates were prepared by boiling in SDS-PAGE sample buffer (65 mM Tris-Cl, pH 6.8, 5% 2-mercaptoethanol, 3% SDS, 10% glycerol, 1 mg/ml bromophenol blue). The lysates were subjected to immunoblotting with antibodies against p250GAP, PSD-95, ERK, and phospho-ERK. For quantification, immunoreacted protein bands were analyzed with NIH Image software. The intensity of the band of p250GAP was indicated relative to that of PSD-95.

#### **Phosphatase Treatment**

Slice lysates (40  $\mu$ g of protein) and p250GAP immunoprecipitated from slice lysates were incubated with bacterial alkaline phosphatase (Takara, Kyoto, Japan) at 100 U/ml for 3 h (Nakazawa *et al.*, 2001).

#### RESULTS

#### p250GAP Is Isolated as a GluR $\epsilon$ 2 (NR2B) Subunitinteracting Protein

To clarify the glutamate receptor-mediated signaling pathways, we screened for molecules that interact with the GluR $\epsilon$ 2 (NR2B) subunit of the NMDA receptor. We carried out yeast two-hybrid screening by using the cytoplasmic region of GluR $\epsilon$ 2 (NR2B) as a bait. We obtained 23 candidate clones from a cDNA library of  $5.0 \times 10^6$  individual clones prepared from human adult brain. Database searches showed that one of the clones was a partial cDNA of the KIAA0712 clone identified by the Kazusa DNA Research Institute (Figure 1A). KIAA0712 contains a predicted open reading frame of 5217 base pairs that encodes a polypeptide of 1738 amino acids. Sequence analysis of KIAA0712 revealed that the KIAA0712-encoded protein contained a RhoGAP-like domain at its amino terminus (Figure 1A). Because an apparent molecular size of the protein, as was determined by its electrophoretic mobility, was 250 kDa, the protein was termed p250GAP. As shown in Figure 1B, the RhoGAP homology domain encompassed ~160 amino acids. The predicted amino acid sequence of p250GAP was 27 and 26% identical with that of p190RhoGAP and p50RhoGAP, respectively (Figure 1B). p250GAP contained several proline-rich sequences that may serve as SH3 binding sites (Figure 1A).

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А

			1.2		
1	MKSRPTKQKL	KQRGILKERV	FGCDLGEHLL	NSGFEVPQVL	QSCTAFIERY
51	GIVDGIYRLS	GVASNIQRLR	HEFDSEHVPD	LTKEPYVQDI	HSVGSLCKLY
101	FRELPNPLLT	YQLYEKFSDA	VSAATDEERL	IKIHDVIQQL	PPPHYRTLEF
151	LMRHLSLLAD	YCSITNMHAK	NLAIVWAPNL	LRSKQIESAC	FSGTAAFMEV
201	RIQSVVVEFI	LNHVDVLFSG	RISMAMQEGA	ASLSRPKSLL	VSSPSTKLLT
251	LEEAQARTQA	QVNSPIVTEN	KYIEVGEGPA	ALQGKFHTII	EFPLERKRPQ
01	NKMKKSPVGS	WRSFFNLGKS	SSVSKRKLQR	NESEPSEMKA	MALKGGRAEG
51	TLRSAKSEES	LTSLHAVDGD	SKLFRPRRPR	SSSDALSASF	NGEMLGNRCN
01	SYDNLPHDNE	SEEEGGLLHI	PALMSPHSAE	DVDLSPPDIG	VASLDFDPMS
51	FQCSPPKAES	ECLESGASFL	DSPGYSKDKP	SANKKDAETG	SSQCQTPGST
01	ASSEPVSPLQ	EKLSPFFTLD	LSPTEDKSSK	PSSFTEKVVY	AFSPKIGRKL
51	SKSPSMSISE	PISVTLPPRV	SEVIGTVSNT	TAQNASSSTW	DKCVEERDAT
501	NRSPTQIVKM	KTNETVAQEA	YESEVQPLDQ	VAAEEVELPG	KEDQSVSSSQ
51	SKAVASGQTQ	TGAVTHDPPQ	DSVPVSSVSL	IPPPPPPKNV	ARMLALALAE
701	SAQQASTQSL	KRPGTSQAGY	TNYGDIAVAT	TEDNLSSSYS	AVALDKAYFQ
51	TDRPAEQFHL	QNNAPGNCDH	PLPETTATGD	PTHSNTTESG	EQHHQVDLTG
01	NOPHOAYLSG	DPEKARITSV	PLDSEKSDDH	VSFPEDQSGK	NSMPTVSFLD
51	QDQSPPRFYS	GDQPPSYLGA	SVDKLHHPLE	FADKSPTPPN	LPSDKIYPPS
01	GSPEENTSTA	TMTYMTTTPA	TAQMSTKEAS	WDVAEQPTTA	DFAAATLORT
51	HRTNRPLPPP	PSQRSAEQPP	VVGQVQAATN	IGLNNSHKVQ	GVVPVPERPP
.001	EPRAMDDPAS	AFISDSGAAA	AQCPMATAVQ	PGLPEKVRDG	ARVPLLHLRA
.051	ESVPAHPCGF	PAPLPPTRMM	ESKMIAAIHS	SSADATSSSN	YHSFVTASST
101	SVDDALPLPL	PVPQPKHASQ	KTVYSSFARP	DVTTEPFGPD	NCLHFNMTPN
151	CQYRPQSVPP	HHNKLEQHQV	YGARSEPPAS	MGLRYNTYVA	PGRNASGHHS
1201	KPCSRVEYVS	SLSSSVRNTC	YPEDIPPYPT	IRRVQSLHAP	PSSMIRSVPI
251	SRTEVPPDDE	PAYCPRPLYQ	YKPYQSSQAR	SDYHVTQLQP	YFENGRVHYR
1301	YSPYSSSSSS	YYSPDGALCD	VDAYGTVQLR	PLHRLPNRDF	AFYNPRLQGK
1351	SLYSYAGLAP	RPRANVTGYF	SPNDHNVVSM	PPAADVKHTY	TSWDLEDMEK
L401	YRMQSIRRES	RARQKVKGPV	MSQYDNMTPA	VQDDLGGIYV	IHLRSKSDPG
451	KTGLLSVAEG	KESRHAAKAI	SPEGEDRFYR	RHPEAEMDRA	HHHGGHGSTQ
1501	PEKPSLPQKQ	SSLRSRKLPD	MGCSLPEHRA	HQEASHRQFC	ESKNGPPYPQ
1551	GAGQLDYGSK	GIPDTSEPVS	YHNSGVKYAA	SGQESLRLNH	KEVRLSKEME
1601	RPWVRQPSAP	EKHSRDCYKE	EEHLTQSIVP	PPKPERSHSL	KLHHTQNVER
1651	DPSVLYQYQP	HGKRQSSVTV	VSQYDNLEDY	HSLPQHQRGV	FGGGGMGTYV
1701	PPGFPHPOSR		FLPAELSLOH	DEMOTIVADA	

В			
p250GAP	22	CCIIGHHILNSGFEVECVIQSCTAFTERYCI-VIGIYRISCVASNIQFIRHEFDSHVFD GVFLTT-VVTPEKPIPIFIERCIEVIEATGISTEGIYRVSCNKSEMESLORCFDQLHNLD	
p190RhoGAP p50RhoGAP	1260 252	GVENTT-VVTPERPIETFIERGIETERATEGISTEGINAVSERRSEMESEDORDDULAID GWEN-QHIQEKNPEQEPIPIVIRETVAYLQAHANITEGIRRSANIVQVVREVQQKYNMGLPVD	
p250GAP	81	TKERYVODIRSKOSLORINGER PER PER PER PER VSAATIER IKINDU IKODE PP	143
p190RhoGAP	1319	laekdft vntvægamksfeseled plvæysmoidiver hkundreckih ælkevikkfere	1379
p50RhoGAP	313	FDCY-NELHLFRVILKTELRELFEPI-TFDLYPHVNGFLNIDES-ORVFATLCVLCTLFFE	370
p250GAP	144	HYRTIEFIMFHISLLADYCSITNMHAKNLAI-WWAPNLLK	182
p190RhoGAP	1380	NHEVFKYVISHINRVSHNNKVNIMISENISIOFW-FIIMR	1418
p50RhoGAP	371	NYQVIRFITAFI VQI <mark>S</mark> AHSDQ <b>NKMI</b> NT <u>NLA</u> VVI - G <b>PNII</b> W	409

Figure 1. Sequence of human p250GAP. (A) Protein sequence and domain structure of p250GAP. The RhoGAP domain is boxed, proline-rich sequences are double underlined, and the cDNA sequence obtained by two-hybrid screening (amino acids 1056–1738) is underlined. (B) Homology between RhoGAP domains of p250GAP, p190RhoGAP, and p50RhoGAP. Identical residues are highlighted in black, and the predicted critical residues for GAP activity are marked with asterisks.

To demonstrate that p250GAP interacts with GluR $\epsilon$ 2 (NR2B) in mammalian cells as well, HEK293T cells were transfected with an expression plasmid encoding FLAG-tagged p250GAP together with or without a GluR $\epsilon$ 2 (NR2B) plasmid. Then the lysates of the transfectants were subjected to a coimmunoprecipitation experiment. As shown in Figure 2A, GluR $\epsilon$ 2 (NR2B) was readily detectable in anti-FLAG immunoprecipitates. Coimmunoprecipitation of GluR $\epsilon$ 2 (NR2B) with anti-FLAG antibody was dependent on expression of p250GAP (Figure 2A). This finding indicates that p250GAP and GluR $\epsilon$ 2 (NR2B) do indeed interact with each other in mammalian cells, when they are coexpressed. To identify the regions of p250GAP that interact with GluR $\epsilon$ 2 (NR2B), various regions of p250GAP were produced as bacterial fusion proteins linked to GST. The GST fusion proteins

immobilized on glutathione-Sepharose were incubated with lysates of HEK293T cells expressing GluR $\epsilon$ 2 (NR2B), and then GluR $\epsilon$ 2 (NR2B) bound to the fusion protein were examined (Figure 2B). As shown in Figure 2B, the GST fusion proteins, GST-1, -3, and -5, but not GST-2 and -4, precipitated GluR $\epsilon$ 2 (NR2B). Therefore, the sequence of amino acid residues 1371–1518 in p250GAP contained the GluR $\epsilon$ 2 (NR2B) association site. We further performed coimmunoprecipitation experiments by using mouse brain extracts. Incubation of brain lysates with anti-p250GAP antibodies resulted in coprecipitation of GluR $\epsilon$ 2 (NR2B) with p250GAP (Figure 2C). p250GAP and GluR $\epsilon$ 2 (NR2B) were not coimmunoprecipitated with preimmune serum or antibodies preabsorbed with immunogen (Figure 2C). The data suggested that p250GAP interacted with GluR $\epsilon$ 2 (NR2B) in brain.

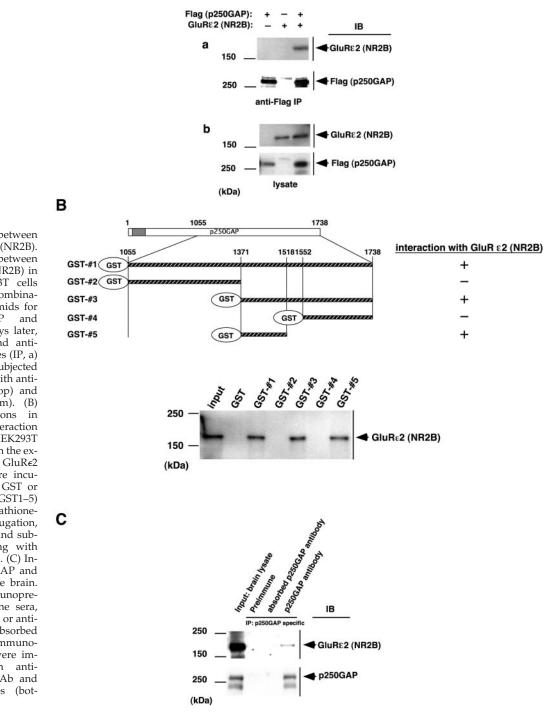
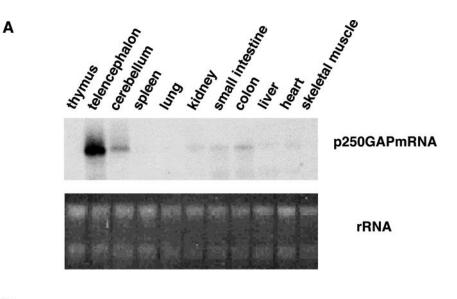


Figure 2. Interaction between p250GAP and GluR $\epsilon$ 2 (NR2B). (A) Interaction between p250GAP and GluRe2 (NR2B) in HEK293T cells. HEK293T cells were transfected with combinations of expression plasmids for FLAG-tagged p250GAP and GluR $\epsilon$ 2 (NR2B). Two days later, the cells were lysed and anti-FLAG immunoprecipitates (IP, a) and cell lysates (b) were subjected to immunoblotting (IB) with anti-GluRe2 (NR2B) mAb (top) and anti-FLAG mAb (bottom). (B) Mapping of the regions in p250GAP required for interaction with GluRe2 (NR2B). HEK293T cells were transfected with the expression plasmid for  $GluR\epsilon 2$ (NR2B). The lysates were incubated with 1  $\mu$ g of the GST or GST-fusion proteins (GST1–5) immobilized on glutathione-Sepharose. After centrifugation, the beads were washed and subjected to immunoblotting with anti-GluRe2 (NR2B) mAb. (C) Interaction between p250GAP and GluR $\epsilon$ 2 (NR2B) in mouse brain. Brain lysates were immunoprecipitated with preimmune sera, anti-p250GAP antibodies, or antip250GAP antibodies preabsorbed with immunogen. The immunoprecipitates and input were immunoblotted (IB) with anti-GluRe2 (NR2B) (top) mAb and anti-p250GAP antibodies (bottom).

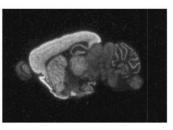
*Expression of p250GAP mRNA Is Enriched in Brain* To gain insights into possible function of p250GAP, we examined tissue distribution of the p250GAP mRNA expression. Northern blot analysis of RNAs from adult mouse tissues showed that the p250GAP mRNA was expressed at high levels in telencephalon and at low levels in cerebellum,

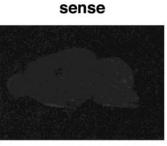
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colon, small intestine, and kidney (Figure 3A). Furthermore, in situ hybridization analysis showed that the level of p250GAP mRNA was high in cortex, corpus striatum, hippocampus, and thalamus of adult mouse brain (Figure 3, B and C). The expression pattern was very similar to that of GluR $\epsilon$ 2 (NR2B) (Watanabe *et al.*, 1992). p250GAP mRNA

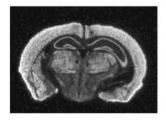


B antisense



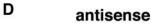


C antisense





sense





sense



**Figure 3.** Expression pattern of p250GAP. (A) Northern blot analysis. A blot with RNAs from adult mouse tissues was probed with a fragment of mouse p250GAP cDNA. The amounts and quality of RNAs were verified by EtBr staining. (B–D) In situ hybridization of p250GAP mRNA in mouse tissue sections. A parasagittal section of adult brain (B), a coronal section of adult brain (C), or a sagittal section of E18.5 embryo (D) was hybridized with an  $\alpha$ -<sup>35</sup>S-UTP–labeled mouse p250GAP cRNA probe.

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was also expressed at a high level in developing brain and at low levels in small intestine and kidney (Figure 3D).

## p250GAP Is Concentrated in the Postsynaptic Density

We visualized p250GAP in 20-d-old cultured primary hippocampal neurons with antibodies against MAP2, p250GAP, and GluR $\epsilon$ 2 (NR2B). The cultured primary neurons have mature synapses with fully differentiated PSDs. p250GAP was strikingly abundant in punctate structures arrayed along dendrites (Figure 4A). As p250GAP associates with GluR $\epsilon$ 2 (NR2B) in vivo (Figure 2C), p250GAP was colocalized with GluR $\epsilon$ 2 (NR2B) at the spine (Figure 4B). In addition, exogenous p250GAP expressed using Sindbis virus-mediated expression system colocalized with PSD-95 (our unpublished data). These results provided further evidence that p250GAP was localized at the dendritic spines and was associated with GluR $\epsilon$ 2 (NR2B) in vivo. Consistently, Western blot of subcellular fractions from mouse forebrain with antibodies against p250GAP, GluR $\epsilon$ 2 (NR2B), PSD-95, RhoA, Cdc42, Rac1, and Synaptophysin revealed that p250GAP, GluRe2 (NR2B), and PSD-95 were all enriched in the isolated PSD fraction (Figure 4C). Furthermore, the data revealed that RhoA and Rac1 were present in the PSD fraction. In contrast, Cdc42 was hardly detectable in the PSD fraction (Figure 4C).

#### p250GAP Is a GAP for Cdc42 and RhoA

To determine whether p250GAP encodes a functional GAP activity toward Rho GTPases, amino acids 1–263 of wild-type and R58I mutant of p250GAP were bacterially expressed in Arg-58 of p250GAP corresponds to the conserved amino acid of RhoGAPs, which is known to be required for GAP activity (Barrett *et al.*, 1997; Li *et al.*, 1997). GAP assay with [ $\gamma$ -<sup>32</sup>P]GTP-loaded Rho family proteins revealed that the RhoGAP-like domain of p250GAP was active on RhoA and Cdc42, but hardly on Rac1 (Figure 5A)

Next, the ability of p250GAP to regulate the GTP-loaded states of RhoA, Cdc42, and Rac1 in cells was tested. Because Rho GTPases bind downstream effectors when in the GTPbound state, a GST fusion protein containing the CRIB of Pak and the RBD of Rhotekin can be used to assay the levels of active Cdc42, active Rac1, and active RhoA, respectively. HEK293T cells were transiently transfected with plasmids encoding FLAG-tagged wild-type and R58I mutant of p250GAP together with Myc-tagged RhoA, Cdc42, or Rac1. GTP-loaded RhoA, Cdc42, or Rac1 was then collected from the cell lysates by GST-CRIB or GST-RBD. Simultaneous expression of wild-type p250GAP clearly reduced the amount of GTP-loaded Cdc42 and GTP-loaded RhoA, whereas expression of p250GAP had little effect on the GTPloaded status of Rac1 (Figure 5B). Apparently, GAP activity of p250GAP R58I mutant toward RhoA and Cdc42 was less than that of wild-type p250GAP. We then tested the ability of endogenous p250GAP to regulate the GTP-loaded states of Rho family GTPases. The anti-p250GAP immunoprecipitates from mouse brain lysates were incubated with extracts of HEK293T cells transiently transfected with plasmids encoding Myc-tagged RhoA, Cdc42, or Rac1. GTP-loaded RhoA, Cdc42, or Rac1 was then collected from the reaction mixtures with GST-CRIB or GST-RBD. Incubation of wildtype p250GAP immunoprecipitates with extracts from RhoA, Cdc42, or Rac1 expressing HEK293T cells clearly reduced GTP-Cdc42 and GTP-RhoA but not GTP-Rac1 (Figure 5C). These results suggest that p250GAP promotes GTP hydrolysis on RhoA and Cdc42 in vivo.

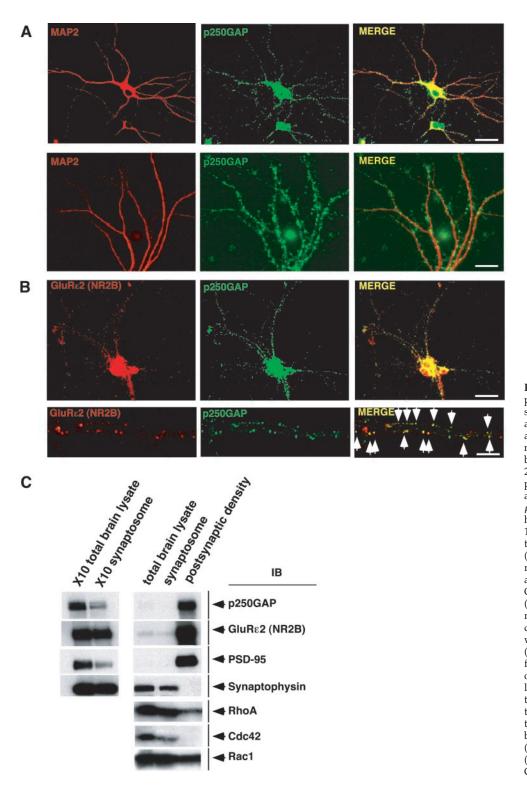
# p250GAP Regulates Neurite Outgrowth in Neuroblastoma Cells

Rho family GTPases regulate neurite outgrowth in Neuro-2A neuroblastoma cells (Brouns et al., 2001). To establish the biological significance of p250GAP in neuronal cells, we examined the effect of p250GAP expression on neurite outgrowth of Neuro-2A cells. Neuro-2A cells were transiently transfected with plasmid encoding wild-type p250GAP, R58I mutant of p250GAP, mutationally inactive Cdc42 (N17Cdc42), or mutationally inactive RhoA (N19RhoA). The mock-transfected cells undergo neuronal differentiation associated with extensive neurite outgrowth after serum withdrawal (Figure 6Aa, Ab) (Brouns et al., 2001). Without serum, expression of N17Cdc42 suppressed neurite outgrowth in Neuro-2A cells (Figure 6Ac, Ad). Expression of wild-type p250GAP also suppressed neurite outgrowth under this condition (Figure 6Ae, Af). The ratio of total neurite length of cells transfected with N17Cdc42 and wild-type p250GAP to that of mock-transfected cells were  $9.5 \pm 5.4$  and  $13.4 \pm 2.9\%$  (mean  $\pm$  SEM) (p <0.01), respectively (Figure 6C). Neuro-2A cells also undergo neuronal differentiation associated with extensive neurite outgrowth upon Rho inactivation by C3 transferase (Brouns *et al.*, 2001). In agreement with this, expression of N19RhoA induced extensive neurite outgrowth in the presence of serum (Figure 6Bk, Bl). Expression of wild-type p250GAP also induced extensive neurite outgrowth under this condition (Figure 6Bm, Bn). The ratio of total neurite length of cells transfected with N19RhoA and wild-type p250GAP to that of mocktransfected cells were 975  $\pm$  70.0 and 942  $\pm$  37.5% (mean  $\pm$ SEM) (p < 0.01), respectively (Figure 6D). Expression of R58I mutant of p250GAP had no effect on these morphological changes (Fig 6Ag, Ah, Bo, Bp), suggesting that these effects were completely dependent on the GAP function of p250GAP. These results suggest that RhoA and Cdc42 serve as physiological substrates for p250GAP in neuronal cells.

#### NMDA Receptor Stimulation Leads to Redistribution of p250GAP in Hippocampal Slices

Association of p250GAP with NMDA receptor led us to investigate whether NMDA receptor activity modulates p250GAP behavior. Hippocampal slices were stimulated with NMDA, and TNE buffer-soluble or whole slice lysates (see MATERIALS AND METHODS) were subjected to immunoblot analysis with antibodies against p250GAP, PSD-95, phospho-ERK, and ERK. As shown in Figure 7, A and B, NMDA stimulation led to a significant decrease in the level of p250GAP in TNE buffer-soluble fraction. Levels of PSD-95 and ERK were little affected by the NMDA treatment (Figure 7, A and B). Phosphorylation of ERK was increased upon NMDA receptor stimulation (Figure 7, A and C) as described previously (English and Sweatt, 1996). The ratio of the level of p250GAP in the TNE buffer-soluble fraction of NMDA stimulated slices to that of mock-stimulated slices was  $0.54 \pm 0.006$  (mean  $\pm$  SEM) (p < 0.0001) (Figure 7B). The

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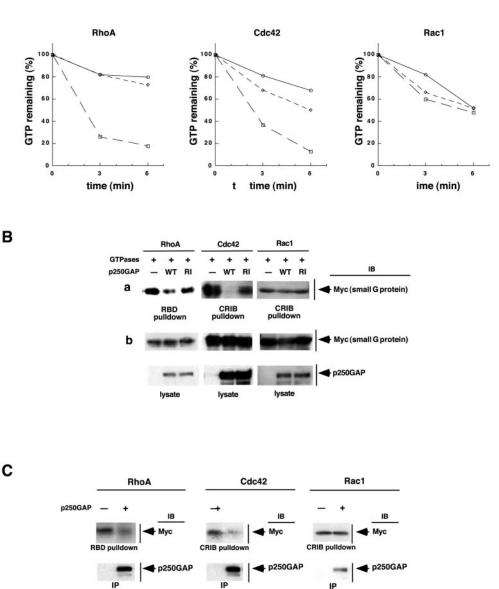


4. Enrichment Figure of p250GAP in postsynaptic density. (A) Localization of p250GAP at punctate structures arrayed along dendrites. Hippocampal neurons were dissociated at embryonic day 17.5, cultured for 20 d, and stained with antip250GAP antibodies (green) and anti-MAP2 mAb (red). Bars, 25  $\mu$ m (top). Lower panels show higher magnification images. Bar, 10 µm (bottom). (B) Colocalization of p250GAP with GluR $\epsilon$ 2 (NR2B). The hippocampal neurons were stained with antibodies against p250GAP (green) and GluR $\epsilon$ 2 (NR2B) (red). Bars, 25  $\mu$ m (top). Lower panels show higher magnification images. Arrows indicate colocalization of p250GAP with GluR $\epsilon$ 2 (NR2B). Bars, 5  $\mu$ m. (C) p250GAP in isolated PSD fraction. A sample of 50  $\mu$ g (left) or 5  $\mu$ g (right) of mouse forebrain lysates and synaptosomes, and the PSD extracted once with Triton X-100 (5 µg), were subjected to immunoblotting (IB) with antibodies against p250GAP, GluRe2 (NR2B), PSD-95, Synaptophysin (a presynaptic marker), RhoA, Cdc42, and Rac1.

decrease in p250GAP was completely blocked by application of a selective NMDA receptor antagonist DL-2-amino-5-phosphonovalerate (DL-APV) (Figure 7, A and B). On the other hand, the levels of p250GAP in whole slice lysates of NMDA-stimulated slices and in mock-stimulated slices were unchanged (Figure 7, C and D). These results suggest that NMDA receptor stimulation leads to redistribution of p250GAP in hippocampal neurons.

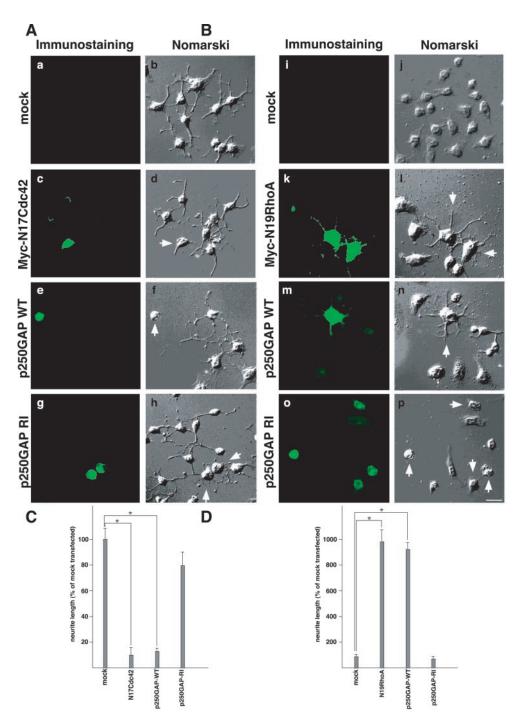
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Figure 5. Characterization of GAP activity of p250GAP. (A) GAP activity of recombinant GAP domain of p250GAP. Equal concentrations (10 nM) of recombinant GST (circle), GST-GAP domain of wild-type p250GAP (square), and R58I mutant of p250GAP (diamond) were added to in vitro GAP assay with 20 nM  $[\gamma^{-32}P]$ GTP-loaded RhoA, Cdc42, or Rac1. (B) GAP activity of p250GAP in HEK293T cells was analyzed by Rho GTPase effector pulldown assays. HEK293T cells were transiently transfected with expression plasmids for Myctagged RhoA, Cdc42, or Rac1 together with or without (-) FLAG-tagged wild-type (WT) or R58I mutant (RI) of p250GAP. Lysates of the cells were pulled down by GST-CRIB (for Cdc42 and Rac1) or GST-RBD (for RhoA) immobilized on glutathione-Sepharose. Levels of GTPloaded RhoA, Cdc42, and Rac1 were analyzed by immunoblotting with anti-Myc mAb (a). Whole-cell lysates were verified by immunoblotting with anti-Myc mAb (b, top) and antip250GAP antibodies (b, bottom). (C) GAP activity of endogenous p250GAP in mouse brain. Lysates of HEK293T cells expressing Myc-tagged RhoA, Cdc42, or Rac1 were incubated with (+) or without (-) p250GAP immunoprecipitates from brain lysates (IP). GTP-loaded RhoA, Cdc42, or Rac1 in the lysates was then collected by GST-CRIB or GST-RBD and detected by anti-Myc mAb (top). p250GAP immunoprecipitates were verified by antip250GAP antibodies (bottom). All experiments were repeated more than three times.



#### NMDA Receptor Stimulation Leads to Dephosphorylation of p250GAP in Hippocampal Slices

As shown in Figure 7A, NMDA stimulation led to not only a significant decrease in the level of p250GAP in TNE buffersoluble fraction but also an increase in its migration on SDS-PAGE. When the proteins in the lysate of unstimulated slices were treated with bacterial alkaline phosphatase (BAP), migration of p250GAP on SDS-PAGE increased to resemble that of p250GAP derived from NMDA-stimulated slices (Figure 7A). The migrations of PSD-95 and ERK were little changed by BAP treatment. These suggest that p250GAP is a phospho-protein and is subjected to dephosphorylation after NMDA stimulation. It was possible that p250GAP is tyrosine-phosphorylated in hippocampal slices, because p250GAP expressed together with kinase active Fyn in HEK293T cells becomes tyrosine-phosphorylated (our unpublished data). To examine whether p250GAP is tyrosinephosphorylated in brain and tyrosine-dephosphorylated after NMDA stimulation, equal amounts of p250GAP were immunoprecipitated from mock- and NMDA-stimulated hippocampal slices and subjected to immunoblotting with an anti-pY antibody. The anti-pY immunoreactivity clearly decreased upon NMDA-stimulation (Figures 7E), suggesting that p250GAP is tyrosine-dephosphorylated after the NMDA receptor stimulation. The ratio of the tyrosine-phosphorylation level of p250GAP in the NMDA-stimulated slices to that of mock-stimulated slices was  $0.39 \pm 0.05$ 



genesis in Neuro-2A cells by overexpression of p250GAP. (A) Suppression of neuritogenesis after serum withdrawal by overexpression of wild-type p250GAP. Neuro-2A cells were transiently transfected with expression plasmids for mock (Aa and antibody), Myc-tagged N17Cdc42 inactive mutant (Ac and Ad), FLAGtagged wild-type (WT) p250GAP (Ae and Af), or R58I mutant (RI) of p250GAP (Ag and Ah). (B) Induction of neuritogenesis by overexpression of wild-type p250GAP in the presence of serum. Neuro-2A cells were transiently transfected with an expression plasmid for mock (Bi and Bj), Myc-tagged N19RhoA inactive mutant (Bk and Bl), FLAGtagged wild-type (WT) p250GAP (Bm and Bn), and R58I mutant (RI) of p250GAP (Bo and Bp). (A and B) The cells were fixed and viewed using a Nomarski microscope (antibody, Ad, Af, Ah, Bj, Bl, Bn, and Bp). Exogenous expression of the proteins was confirmed by anti-Myc mAb or anti-FLAG antibodies staining (Aa, Ac, Ae, Ag, Bi, Bk, Bm, and Bo). Bar, 20 µm. (C and D) The neurite length of 20 cells was calculated using TI workbench software (kindly provided by T. Inoue, University of Tokyo). Results were shown as the mean from three independent experiments. Values are mean ± SEM, \*p < 0.01, mock transfected versus N17Cdc42, N19RhoA, wild-type (WT) p250GAP, or RI mutant of p250GAP (Student's t test).

Figure 6. Regulation of neurito-

(mean  $\pm$  SEM) (p < 0.01) (Figure 7F). Unlike the results shown in Figure 7A, immunoblotting of the anti-p250GAP immunoprecipitates from the TNE-solubilized lysates with anti-p250GAP detected similar amounts of p250GAP regardless of NMDA stimulation (Figure 7E). This was most likely due to low efficiency of immunoprecipitation with the anti-p250GAP antibodies that were used in the experiments. NMDA-induced dephosphorylation of p250GAP on residues other that tyrosine is under investigation.

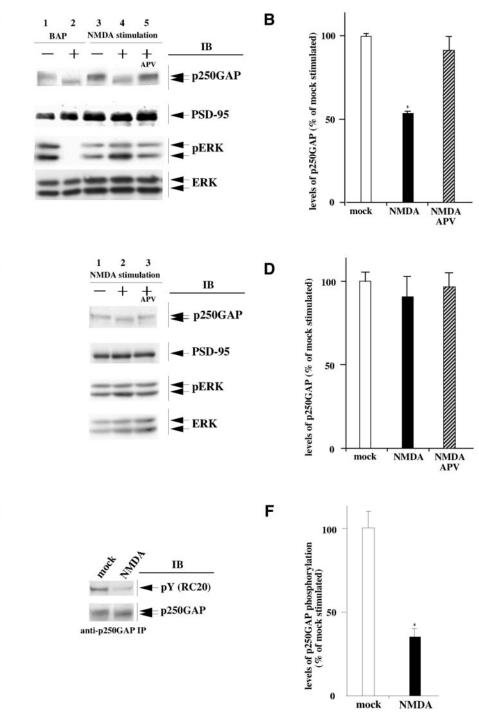
#### DISCUSSION

Recent data suggest that NMDA receptors regulate actin reorganization in dendritic spines (Engert and Bonhoeffer, 1999; Maletic-Savatic *et al.*, 1999; Toni *et al.*, 1999). However, the signaling pathways that link NMDA receptor activity to the postsynaptic actin cytoskeleton are poorly understood. We identified a novel GAP for Rho family GTPases, termed p250GAP, and showed that it interacts Α

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Figure 7. Redistribution and dephosphorylation of p250GAP after NMDA receptor stimulation in hippocampal slices. (A and C) Redistribution of p250GAP after NMDA receptor stimulation. Shown are representative blots of TNE buffer-soluble (A) or whole (C) lysates with antibodies against p250GAP, PSD-95, phospho-ERK, and ERK. The samples were prepared from mouse hippocampal slices that were mock stimulated (lane 3 in A and lane 1 in C), or stimulated with 50  $\mu$ M NMDA for 5 min, in the absence (lane 4 in A and lane2 in C) or presence (lane 5 in A and lane 3 in C) of 100  $\mu$ M DL-APV. In parallel experiments, the lysates of mockstimulated slices were treated with (lane 2 in A) or without (lane 1 in A) BAP and were subjected to immunoblotting with antibodies against p250GAP, PSD-95, phospho-ERK, and ERK. (B and D) Quantification of the p250GAP level. Results were shown as the mean from three independent experiments. Values are mean ± SEM, \*p < 0.0001, mock stimulated versus NMDA stimulation (Student's t test). (E) Dephosphorylation of p250GAP after NMDA receptor stimulation. The antip250GAP immunoprecipitates from mock-stimulated or NMDA stimulated slices were blotted with anti-pY mAb (RC20) (top) and then with anti-p250GAP antibodies (bottom). (F) Quantification of p250GAP phosphorylation level. The Student's t test value (0.39  $\pm$  0.05: mean  $\pm$  SEM, \*p < 0.01) was from three independent experiments.



with the GluR $\epsilon$ 2 (NR2B) subunit of the NMDA receptor. p250GAP was targeted to dendritic spines and highly concentrated in PSD (Figures 2 and 4). Because the PSD-95/NMDA receptor complex is tightly associated with the PSD (Allison *et al.*, 1998), this complex can provide rigid structural support for the recruitment of other PSD proteins. It is therefore possible that the recruitment of

p250GAP to dendritic spines is mediated by a direct interaction with NMDA receptor complex. We also showed that the NMDA receptor activity could regulate p250GAP behavior (Figure 7, further discussed below). To our knowledge, p250GAP is the first GAP for the Rho family GTPases whose behavior is modulated by NMDA receptor activity. p250GAP promoted GTP hydrolysis on both Cdc42 and RhoA in vitro and in vivo (Figures 5 and 6), suggesting that activities of Cdc42 and RhoA are regulated by p250GAP. Nevertheless, we assume that p250GAP targets RhoA but not Cdc42 in dendritic spines, because the amount of Cdc42 in PSD was under detectable level (Figure 4C). Rho family GTPases play a central role in dendritic spine plasticity (Luo *et al.*, 1996; Threadgill *et al.*, 1997; Ruchhoeft *et al.*, 1999; Lee *et al.*, 2000; Nakayama *et al.*, 2000; Tashiro *et al.*, 2000; Wong *et al.*, 2000; Hering and Sheng, 2001). We assume that p250GAP might be involved in morphological rearrangements of dendritic spines through regulation of the RhoA activity.

NMDA receptor-mediated synaptic activity modulates spine morphology, spine turnover, and synaptic transmission (Fischer et al., 1998; Halpain et al., 1998; Sorra and Harris, 1998; Engert and Bonhoeffer, 1999; Maletic-Savatic et al., 1999; Okabe et al., 1999; Parnass et al., 1999; Toni et al., 1999; Yuste and Bonhoeffer, 2001). In these processes, NMDA receptors must transduce highly localized signals to the actin cytoskeleton specifically in the region of the dendritic spines where they are activated. Because p250GAP interacts directly with NMDA receptors (Figure 2), NMDA receptors would be able to modulate p250GAP behavior to elicit spatially restricted activation of RhoA only at the site where they are activated. In fact, we showed that NMDA stimulation induces changes in the extractability of p250GAP (Figure 7, A-D). Moreover, we preliminarily observed changes in the immunostaining pattern of virally expressed GFP-tagged p250GAP in response to NMDA receptor stimulation (our unpublished data). Redistribution of p250GAP upon NMDA receptor stimulation may be one of the mechanisms of functional modulation of p250GAP. Intriguingly, p250GAP is a phospho-protein and can be phosphorylated by Fyn and CaMKII (Figure 7E; our unpublished data). When NMDA receptors were strongly stimulated, p250GAP was tyrosine-dephosphorylated (Figure 7E). Dephosphorylation of p250GAP may affect its interaction with proteins in the PSD, such as NMDA receptors, scaffold proteins, and cytoskeletal proteins.

Reduction of the level of NMDA receptor-associated p250GAP upon NMDA stimulation would result in activation of RhoA to alter local cytoskeletal arrangements in stimulated dendritic spines. Stimulation of cultured hippocampal neurons with 50  $\mu$ M NMDA for 5 min results in rapid and extensive loss of spines (Halpain et al., 1998). The NMDA receptor-mediated regulation of p250GAP may contribute to a neuroprotective mechanism by which the number of dendritic spines is reduced (Halpain et al., 1998). The idea is consistent with the result that expression of active RhoA dramatically reduces the spine number (Tashiro et al., 2000). Stimulation of cultured hippocampal neurons with 50  $\mu$ M NMDA for 5 min also results in disruption of AKAP– MAGUK complexes by remodeling the dendritic actin (Gomez et al., 2002). This triggers dephosphorylation of AMPA receptors, which subsequently induces homosynaptic longterm depression (Tavalin et al., 2002). Thus, NMDA receptor regulation of p250GAP may contribute to an induction of long-term depression as well by remodeling the dendritic actin. Further studies are needed to establish the mechanism by which NMDA receptors regulate p250GAP function as well as function of other regulators for Rho family proteins in the receptor complex, and thereby the localized actin remodeling.

Rho family GTPases in neural tissues regulate neuronal migration, axon growth, axon guidance, dendrite elaboration, and synapse formation (Jalink et al., 1994; Luo et al., 1996; Zipkin et al., 1997; Ruchhoeft et al., 1999; Bateman et al., 2000; Bito et al., 2000; Li et al., 2000; Luo, 2000). Because exogenous expression of p250GAP regulates neurite outgrowth in Neuro-2A cells (Figure 6), p250GAP may regulate dendrite outgrowth. Although, it is not clear whether the interaction between p250GAP and NMDA receptors is important in this regulation, it is worthy to note that NMDA receptors regulate growth of the dendritic arbor in *Xenopus* central neurons (Li et al., 2000). In immature neurons, p250GAP may also be involved in regulation of axon growth and guidance similar to Ephexin, a GEF for Rho GTPases that is involved in the Eph tyrosine kinase signaling (Shamah et al., 2001). Because p250GAP mRNA is highly expressed not only in adult brain but also in developing brain, p250GAP as well as p190 RhoGAP might modulate the activities of Rho family GTPases to direct several actindependent morphogenetic processes required for normal neural development (Brouns et al., 2000).

In summary, we suggest that p250GAP is an important link between NMDA receptors and Rho family GTPases, and thus the actin cytoskeleton. Further studies on p250GAP will unravel the importance of spine plasticity regulated by NMDA receptor activity.

During revision of this manuscript, others have reported cloning of Grit/p200RhoGAP/Rics (Nakamura *et al.*, 2002; Moon *et al.*, 2003; Okabe *et al.*, 2003) that is identical to p250GAP. Although Okabe *et al.* (2003) have demonstrated that Rics is associated with NMDA receptors and localized to the PSD, we would like to emphasize that our study is the first to characterize the functional involvement of p250GAP in NMDA signaling.

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