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Neurobiology:
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Prion Protein Interacts with BACE1 Protein and Differentially Regulates Its Activity toward Wild Type and Swedish Mutant Amyloid Precursor Protein

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In Alzheimer disease amyloid-β (Aβ) peptides derived from the amyloid precursor protein (APP) accumulate in the brain. Cleavage of APP by the β-secretase BACE1 is the rate-limiting step in the production of Aβ. We have reported previously that the cellular prion protein (PrP C) inhibited the action of BACE1 toward human wild type APP (APPWT) in cellular models and that the levels of endogenous murine Aβ were significantly increased in PrP C-null mouse brain. Here we investigated the molecular and cellular mechanisms underlying this observation. PrP C interacted directly with the prodomain of the immature Golgi-localized form of BACE1. This interaction decreased BACE1 at the cell surface and in endosomes where it preferentially cleaves APPWT but increased it in the Golgi where it preferentially cleaves APP with the Swedish mutation (APP Swel). In transgenic mice expressing human APP with the Swedish and Indiana familial mutations (APP Swel, Ind), PrP C deletion had no influence on APP proteolytic processing, Aβ plaque deposition, or levels of soluble Aβ or Aβ oligomers. In cells, although PrP C inhibited the action of BACE1 on APPWT, it did not inhibit BACE1 activity toward APP Swel. The differential subcellular location of the BACE1 cleavage of APP Swel relative to APPWT provides an explanation for the failure of PrP C deletion to affect Aβ accumulation in APP Swel, Ind mice. Thus, although PrP C exerts no control on cleavage of APP Swel by BACE1, it has a profound influence on the cleavage of APPWT, suggesting that PrP C may be a key protective player against sporadic Alzheimer disease.

A small minority (<1%) of Alzheimer disease (AD) cases are inheritable and are caused by mutations in the genes encoding the amyloid precursor protein (APP), presenilin-1 (PS1), and PS2 (1). Specific examples include the Swedish familial AD double point mutation K670N/M671L in APP (2) and the Indiana familial AD point mutation V717F in APP (3). However, the underlying causes remain elusive for the majority of late onset sporadic AD cases. AD is characterized by the deposition in the brain of amyloid plaques composed primarily of the 40–42-amino acid amyloid-β (Aβ) peptide (4), which is derived from APP through sequential proteolytic cleavage by the β-secretase (β-site APP-cleaving enzyme-1 (BACE1)) and the PS1- or PS2-containing γ-secretase complex (5). Cleavage of APP at the Met671–Asp672 peptide bond by BACE1 is the first and rate-limiting step in the production of Aβ (6).

The activity of BACE1 is increased in the brain in sporadic AD and correlates with increased Aβ load (7, 8), suggesting a deregulation of normal homeostatic control mechanisms in the disease. The activity of BACE1 is regulated by a number of proteins (9), including the cellular prion protein (PrP C) (10). PrP C inhibited the action of BACE1 toward human APPWT in cellular models, and the level of endogenous murine Aβ was significantly increased in the brain of PrP C-null mice (10). Following this, we proposed that a normal function of PrP C may be to protect against AD (11). Consistent with this hypothesis is the observation that the level of PrP C is decreased in the hippocampus of sporadic, but not familial, AD subjects, indicating that the reduced level of PrP C is a primary mechanism of disease and is not a secondary consequence of AD-associated changes (12).

BACE1 is synthesized in the endoplasmic reticulum (ER) as an immature but catalytically active zymogen of approximately 60 kDa with an N-terminal prodomain (amino acids 22–45). Subsequent removal of the prodomain by furin-like convertases in the trans-Golgi network (TGN) along with other post-translational modifications transforms BACE1 into the mature protein of approximately 70 kDa (13–16). The mature BACE1 traffic from the TGN to the plasma membrane before being...

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reinternalized into the endosomal pathway along with APP. It is within these acidic endosomal compartments that BACE1 primarily acts on wild type APP (APP<sub>WT</sub>) (14, 17–19). In contrast to APP<sub>WT</sub>, the β-secretase cleavage of APP with the Swedish mutation (APP<sub>Swe</sub>) occurs primarily within the secretory pathway (20, 21).

In this study, we have extended our work on the role of PrP<sup>C</sup> in regulating BACE1 activity by determining the molecular and cellular mechanisms involved. We demonstrate that BACE1 coimmunoprecipitates with PrP<sup>C</sup> from murine and human brain and by surface plasmon resonance that PrP<sup>C</sup> interacts directly with the prodomain of BACE1. Site-directed mutagenesis revealed that Pr<sup>C</sup> in the prodomain of BACE1 is critical for this interaction. Furthermore, by immunofluorescence microscopy and fluorescence-activated cell sorting (FACS), we show that this interaction with the prodomain-containing form of BACE1 retains the secretae in the cell surface and endosomes. As our previous data indicated that PrP<sup>C</sup> functions upstream of Aβ production, we also examined the effect of PrP<sup>C</sup> deletion on Aβ production and deposition in a transgenic mouse model expressing human APP with the Swedish and Indiana familial mutations (APP<sub>Swe,Ind</sub>). Although deletion of PrP<sup>C</sup> had no effect on amyloid deposition in these transgenic mice, in a cellular model, we demonstrate that PrP<sup>C</sup> did not inhibit the activity of BACE1 toward APP<sub>Swe</sub> but did inhibit the activity of BACE1 toward APP<sub>WT</sub>. As APP<sub>Swe</sub> is preferentially cleaved by BACE1 in the TGN rather than in endosomes as for APP<sub>WT</sub>, this substrate-specific differential subcellular site of action of BACE1 provides a molecular explanation for the lack of effect of PrP<sup>C</sup> on Aβ production and deposition in the APP<sub>Swe,Ind</sub> transgenic mice.

**EXPERIMENTAL PROCEDURES**

Coimmunoprecipitation—Frozen human brain tissue was obtained from the Medical Research Council London Neurodegenerative Diseases Brain Bank (Institute of Psychiatry, King’s College London). All materials were obtained with informed consent and approval of the relevant local ethics committees. All subsequent experiments were performed with the approval of the Leeds (Central) Research Ethics Committee. Human hippocampal brain tissue from a non-demented individual (male; age, 57; cause of death, left ventricular failure; post-mortem delay, 45 h) and 129/Ola wild type mice (22) (age, 5 weeks) were homogenized in 9 volumes of phosphate-buffered saline (PBS; without Ca<sup>2+</sup> and Mg<sup>2+</sup>), 0.5% (w/v) Nonidet P-40, 0.5% (w/v) sodium deoxycholate, pH 7.4 in the presence of Complete protease inhibitor mixture (Roche Applied Science) using an electric homogenizer. Samples were centrifuged at 14,000 × g for 10 min, and the protein content of the supernatant was quantified using bicinchoninic acid. Residual material was washed away, and the plate was incubated with PBS containing 0.1% (v/v) Tween 20 and 5% (w/v) dried milk powder. Antibody incubations were performed in PBS-Tween 20 containing 2% (v/v) BSA. The following antibodies were used: 3F4 and 6D11 (both Eurogentec Ltd., Southampton, UK) and SAF32 (Cayman Chemical, Ann Arbor, MI) recognize PrP<sup>C</sup>, 22C11 (Millipore Ltd., Livingston, UK) recognizes APP, and AC-15 recognizes actin (Sigma). 1A9 raised against a neoepitope formed on wild type sAPPβ following β cleavage of APP and the antibody recognizing the neoepitope on Swedish sAPPβ were kindly provided by Dr. I. Hussain (GlaxoSmithKline, Harlow, UK). EE-17 (Sigma-Aldrich) recognizes residues 46–61 of BACE1. BACE-Cat1 raised against the BACE1 catalytic domain was kindly provided by Dr. R. Vassar (23). Antibody against the prodomain of BACE1 (residues 26–45) was from Merck Chemicals Ltd., and antibody against BACE2 was from Abcam (Cambridge, UK). Antibodies against the Aβ-degrading enzymes neprilysin (R&D Systems, Inc.) and insulin-degrading enzyme (Abcam) and antibodies against the synaptic markers synaptophysin (Synaptic Systems GmbH), PSD95 (Synaptic Systems GmbH), and drebrin (MBL International Corp., Woburn, MA) were from the sources indicated. Antibody against the γ-secretase complex components nicastrin was from Abcam, and antibody against presenilin-1 N-terminal fragment was from Covance (Cambridge, UK). Horseradish peroxidase (HRP)-conjugated secondary antibodies were used at 1:4000 in the same buffer. Bound antibody was detected using the enhanced chemiluminescence detection method (Amersham Biosciences). Blots were stripped using 100 mM glycine, pH 2.5 for 30 min, blocked by incubation for 1 h with PBS containing 0.1% (v/v) Tween 20 and 5% (w/v) dried milk powder, and reprobed using the anti-actin antibody as described above. Anti-Fc-HRP was diluted in PBS-Tween 20.

**BACE1 ELISA**—96-well plates (BD Biosciences) were coated overnight with murine recombinant PrP (rPrP) (Allprion AG, Schlieren, Switzerland) (20 pmol/well; 5 μg/ml). The plates were washed with washing buffer (Dulbecco’s phosphate-buffered saline (DPBS) containing 0.05% (v/v) Tween 20 and 0.02% (w/v) sodium azide) before being blocked for 2 h in 3% (w/v) BSA diluted in DPBS containing 0.02% (w/v) sodium azide. The plates were then incubated with various concentrations (0–20 pmol) of recombinant BACE1-Fc (a kind gift from Dr. R. Matico, GlaxoSmithKline, Collegeville, PA) or recombinant Thy1-Fc (Alexis Biochemicals, Lausen, Switzerland) for 2 h. Residual material was washed away, and the plate was incubated with anti-Fc-HRP (1:5000) for 2 h. Bound protein was detected using 3,3′,5,5′-tetramethylbenzidine reagent (Kirkegaard & Perry Laboratories, Inc., Gaithersburg, MD) and allowed to develop for 30 min prior to the addition of 1 M H<sub>3</sub>P<sub>4</sub> to stop.
the reaction. The absorbance was then measured at 450 nm on an Anthon plate reader.

**Surface Plasmon Resonance**—All reagents and systems used in this technique were obtained from Amersham Biosciences. Surface plasmon resonance was performed on Biacore 3000 system. A carboxymethylated chip (CM5) was primed with running buffer (DPBS, 0.005% Tween 20) and normalized using BIA-normalizing solution (70% (w/v) glycerol). rBACE1 obtained from pepsin digestion of the rBACE1-Fc (provided by Dr. R. Matico, GlaxoSmithKline, Collegeville, PA) were diluted in running buffer to a range of concentrations at a rate of 5 μg/min for 7 min to a level of 1500 resonance units (RU) by amine coupling. Recombinant rBACE1-Fc and ΔPD-rBACE1 obtained from pepsin digestion of the rBACE1-Fc (provided by Dr. R. Matico, GlaxoSmithKline, Collegeville, PA) were diluted in running buffer to a range of concentrations (0–10,000 nM) and passed over the sensor chip surface at a flow rate of 40 μl/min. Each cycle consisted of a 300-s analyte injection (association phase) followed by a 300-s dissociation phase. Regeneration was not necessary, but a 300-s stabilization period was applied. The data were analyzed using Biacore evaluation software (BIAevaluation 3.2RC1). Base lines were adjusted to zero for all curves and double referenced by subtracting a sensorgram of buffer injected over the rPrP surface from the experimental sensorgrams to give the curves representing specific binding. Curves were modeled assuming a simple 1:1 interaction to generate kinetic data. The χ² value was below 5 RU², indicating a good fit to the binding model.

**Fluorometric BACE1 Activity Assay**—Membrane fractions (10 μg) were diluted in 100 mM sodium acetate, pH 4.5, 40 mM NaCl, 10% (v/v) glycerol, 0.2% CHAPS, 1 mM EDTA, protease inhibitor mixture (P8340, Sigma-Aldrich). The samples were incubated in the presence or absence of β-secretase inhibitor IV (Merck Chemicals Ltd.) for 30 min at 37 °C before addition of the quenched fluorescence peptide based on the APP₅₉₃ sequence (FAM-ISEVNLDAEFR-TAMRA where FAM is carboxyfluorescein and TAMRA is carboxytetramethylrhodamine; GlaxoSmithKline, Stevenage, UK) (5 μM) in 100 mM sodium acetate, pH 4.5, 0.06% Triton X-100. The fluorescence was then measured on a Synergy HT Bio-Tek fluorometer using KC4 software with excitation and emission wavelengths set to 485 and 585 nm, respectively.

**Surface plasmon resonance (SPR) assay**—IFN-γ treated lymphocytes were incubated in the presence or absence of BACE1 or BACE1 ΔPD and the fluorescence was measured using a Synergy HT Bio-Tek fluorometer.

**Fluorometric BACE1 Activity Assay**—Membrane fractions (10 μg) were diluted in 100 mM sodium acetate, pH 4.5, 40 mM NaCl, 10% (v/v) glycerol, 0.2% CHAPS, 1 mM EDTA, protease inhibitor mixture (P8340, Sigma-Aldrich). The samples were incubated in the presence or absence of β-secretase inhibitor IV (Merck Chemicals Ltd.) for 30 min at 37 °C before addition of the quenched fluorescence peptide based on the APP₅₉₃ sequence (FAM-ISEVNLDAEFR-TAMRA where FAM is carboxyfluorescein and TAMRA is carboxytetramethylrhodamine; GlaxoSmithKline, Stevenage, UK) (5 μM) in 100 mM sodium acetate, pH 4.5, 0.06% Triton X-100. The fluorescence was then measured on a Synergy HT Bio-Tek fluorometer using KC4 software with excitation and emission wavelengths set to 485 and 585 nm, respectively.

**Site-directed Mutagenesis and Stable Transfection**—BACE1 mutants were generated from the template cDNA encoding human BACE1 in pIREShyg using the QuikChange II XL site-directed mutagenesis kit (Stratagene, Cambridge, UK) with the following primers (Eurogentec Ltd.) (mutant bases are indicated in bold): For L28Q/L30Q mutant, the sense primer was 5′-GGATGGACACAGCAGCGG-3′, and the antisense primer was 5′-CCGCTGCGTCCGCGATGCCG-3′, and the anti-sense primer was 5′-CCGCTGCGATGCCGCTCGC-3′. For P29G mutant, the sense primer was 5′-GGATGGACACAGCAGCGG-3′, and the antisense primer was 5′-CCGCTGCGATGCCGCTCGC-3′. For APP₅₉₃, the sense primer was 5′-GGACACAGCAGCGG-3′, and the antisense primer was 5′-GGATGGACACAGCAGCGG-3′. The resultant constructs were verified by DNA sequencing. cDNA encoding the human BACE1 mutants, BACE2, and APP₅₉₃ in the expression vector pIREShyg were introduced by electroporation into human embryonic kidney (HEK) cells expressing murine PrPC (containing the 3F4 epitope tag at amino acids 108–111) (24) in the expression vector pIRENeo or into cells expressing pIRENeo expression vector only as a control. Cells were selected using 150 μg/ml hygromycin B. SH-SY5Y cells were stably transfected with cDNA encoding BACE1 and PrPC as described previously (10).

**Cell Culture**—Human neuroblastoma (SH-SY5Y) and HEK cells were cultured in Dulbecco’s modified Eagle’s medium containing 4.5 g/liter glucose with 2 mM l-glutamine supplemented with 50 units/ml penicillin and 0.1 mg/ml streptomycin (Lonza) and 10% (v/v) fetal bovine serum (FBS) (Sigma-Aldrich). Cells were maintained in a humid atmosphere at 37 °C containing 5% (v/v) CO₂ in air. All cell lines were grown to 100% confluence and washed twice in DPBS (without Ca²⁺ and Mg²⁺) prior to a 24-h incubation in Opti-MEM and GlutaMAX (Invitrogen). Medium was harvested and stored at –20 °C for use in the αβ ELISA or concentrated to 200 μl in a Vivaspin 20 ml concentrator (10,000 molecular weight cutoff membrane) centrifuged at 1900 × g for ~1 h in a bench top centrifuge maintained at 4 °C. For analysis of cell-associated proteins, cells were washed in DPBS, scraped, and pelleted at 1400 × g for 3 min. Cells were lysed in 50 mM Tris/HCl, 150 mM NaCl, 0.5% (w/v) sodium deoxycholate, 1% (v/v) Nonidet-P40, pH 8.0. For the preparation of membranes, cells were resuspended in 3 ml of 50 mM HEPES, pH 7.5 and sonicated at an amplitude of 7 μm for 30 s using a Sonoprep150. The cell suspension was then centrifuged at 2500 × g for 10 min at 4 °C to pellet cell membranes and nuclei. The supernatant was then centrifuged in a Beckman Coulter Optima at 100,000 × g for 1 h at 4 °C. Membranes were resuspended in 50 mM Tris/HCl, pH 7.5, 2 mM EDTA, 150 mM NaCl, 1% (w/v) CHAPSO. siRNA Transfection—siRNAs corresponding to the human PRNP gene were synthesized by Thermo Scientific Dharmacon (Sussex, UK) as ON-TARGET plus SMARTpool. The sequences of the siRNAs are as follows: UCACCGAGACCGACGUUAA, GAUCGAGCAUGGCUCUCU, AGAUGUGAAUCACCCAGAU, and GACGGUACUAUGUGAGAA. HEK293 cells were seeded at 60–70% confluence in a T80 flask 24 h before transfection. siRNA (1 μM of the stock solution) was mixed with the corresponding half-volume of Dharmafect 1 reagent in Opti-MEM (Invitrogen) for 20 min and applied to the cells in a final volume made up to 5 ml with DMEM supplemented with 10% FBS. After incubation for 48 h at 37 °C, cells were washed with PBS, and medium was conditioned for 24 h.

**Immunofluorescence Microscopy**—Cells grown on coverslips were fixed with 4% (v/v) paraformaldehyde for 10 min and then permeabilized in DPBS containing 0.1% (v/v) Triton X-100 or fixed and permeabilized in ice-cold 50% (v/v) methanol, 50% (v/v) acetone for 10 min. Coverslips were incubated in DPBS containing 5% (v/v) fish skin gelatin (Sigma-Aldrich) for 3–4 h at room temperature before being incubated overnight at 4 °C with the following primary antibodies: EE-17 against BACE1, 3F4 against PrPC, a mouse monoclonal antibody against early endosomal antigen-1 (EAA1; BD Biosciences Pharmingen), a sheep polyclonal antibody against the trans-Golgi network protein-46 (TGN-46; a kind gift from Dr. V. Ponnambalam, University of Leeds, Leeds, UK), and a chicken polyclonal antibody
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against calreticulin (Abcam). Finally, coverslips were incubated with the appropriate fluorescent probe-conjugated secondary antibodies (Jackson ImmunoResearch Laboratories Inc. and Invitrogen) for 1 h and mounted on slides using Fluoromount-G mounting medium (SouthernBiotech). Individual cells were visualized using a DeltaVision Optical Restoration Microscopy System (Applied Precision Inc.). Data were collected from 20.0.1-μm-thick optical sections, and three-dimensional data sets were deconvolved using the SoftWoRx program (Applied Precision Inc.). Where indicated, the presented images represent individual Z-slices. Colocalization of BACE1 with intracellular markers was performed using ImageJ.

FACS—SH-SY5Y cell suspensions were diluted to 5 × 10<sup>6</sup> cells/ml with DPBS containing 2.5 mM EDTA, pH 8 (DPBS/EDTA buffer) and blocked for 20 min in 2% (v/v) fish skin gelatin diluted in DPBS/EDTA buffer. A 1 in 50 dilution of EE-17 was added to half the samples and incubated for 1 h. Following this, cell suspensions were washed twice and centrifuged at 10,000 × g for 5 min before being resuspended in 2% (v/v) fish skin gelatin diluted in DPBS/EDTA buffer containing fluorescently conjugated secondary antibody (1:200) for 1 h. The cells were then washed as described above and resuspended in DPBS/EDTA buffer. Cells were sorted using a Partec PASII (Partec UK Ltd., Kent, UK), and data were analyzed using WinMDI software version 2.9, or cells were sorted using a BD-LSRFortessa (BD Biosciences), and data were analyzed using BD FACSDiva software.

Transgenic Animals—Transgenic APP<sub>Swe,Ind</sub> mice overexpressing human APP with the Swedish (K670N/M671L) and Indiana (V717F) familial AD mutations (line J20) (25) were obtained from The Jackson Laboratory (Line B6.Cg-Tg(PDGFB-APPSwInd)20Lms/2J, stock number 006293) and The J. David Gladstone Institutes (San Francisco, CA) and crossed with inbred PrP knock-out mice (129Ola PrP<sup>−/−</sup>) (22). All the transgenic mice used in this study were genotyped. DNA was prepared from ear punch tissue using a DNeasy kit (Qiagen). PCR was performed using the protocol specific for these mice from The Jackson Laboratory. Brain hemispheres were either frozen at −80 °C for biochemical analysis or fixed in 10% formal saline for histopathological analysis. Animal care was in accordance with institutional guidelines.

Fixed brain tissue was processed, and tissue sections were prepared as described (26). Paraffin sections (6 μm) were immunostained with a series of antibodies. The following antibodies were used: 4G8 (1:100) monoclonal antibody raised against Aβ(17–24) (Abcam), A11 (1:1000) anti-prefibrillar oligomer polyclonal antibody (AB9234, Millipore, Watford, UK), OC (1:5000) anti-fibrillar oligomer polyclonal antibody (a gift from Professor C. Glabe, Department of Neurology, University of California at Irvine School of Medicine, Irvine, CA), drebrin (10 μg/ml) monoclonal antibody to detect dendritic spines (D029-3, MBL International Corp.), synaptophyisin (Envision kit K4001) polyclonal antibody to presynaptic vesicle protein (N1566, Dako, Cambridgeshire, UK), anti-glia fibrillary acidic protein (1:400) polyclonal antibody (Z0334, Dako), and Iba1 (1:1000) polyclonal antibody, a microglial marker (01-1974, Wako Chemicals USA, Inc.). Amyloid plaques were visualized with 1% thioflavrin S (Sigma).

Brain hemispheres were homogenized using a two-step extraction protocol (27). Briefly, initial homogenization (120 mg/ml wet weight) was carried out using an electric homogenizer in 2% (w/v) SDS containing protease mixture inhibitor (Roche Diagnostics GmbH) followed by centrifugation at 100,000 × g for 1 h at 4 °C. The resultant supernatant was collected and analyzed using the Aβ ELISA and SDS-PAGE followed by immunoblotting. The pellet was extracted in 70% (v/v) formic acid in distilled H<sub>2</sub>O followed by centrifugation at 100,000 × g for 1 h at 4 °C. The supernatant was collected and analyzed using the Aβ ELISA.

Aβ ELISA—Sandwich ELISAs for the detection of human Aβ(1–40) and Aβ(1–42) were performed as described previously (28). Briefly, 96-well microtiter plates were coated overnight at 4 °C with primary antibodies against Aβ(1–40) (33.1.1) and Aβ(1–42) (2.1.3.35.86) (kind gifts from C. & L. Eckman, Mayo Clinic, Jacksonville, FL). Following blocking and incubation with conditioned medium, SDS-extracted brain homogenate, or formic acid-extracted brain homogenate, bound Aβ peptides were detected with HRP-conjugated detection antibody (for Aβ(1–40), 13.1.1-HRP (C. & L. Eckman); for Aβ(1–42), 4G8-HRP (Covance)).

Statistical Analysis—Densitometric analysis was performed using the advanced image data analyzer (AIDA) program (Raytest Scientific Ltd.). The non-parametric two-tailed Mann-Whitney U test was used to compare two independent samples when sample numbers were less than n = 6. For sample numbers of n ≥ 6, the Kolmogorov-Smirnov test was used to test that the data in each group were normally distributed. Following this, Levene’s test was used to ensure that the data sets were of equal variance. In samples where the data met the criteria of a normal distribution and equal variance, the parametric independent t test was used to calculate significance. p ≤ 0.05 was considered significant (*, p < 0.05; ***, p < 0.005). Error bars, ±S.E. The data were analyzed using the Statistical Package for Social Sciences (SPSS 12.0.1) program (Chicago, IL).

RESULTS

PrP<sub>C</sub> directly interacts with the prodomain of BACE1. Previously, we reported that BACE1 coimmunoprecipitated with PrP<sub>C</sub> in SH-SY5Y cells (10), although it remained to be established whether this was due to a direct protein-protein interaction. Initially, we extended this observation by examining whether the two endogenous proteins interacted in the brain. BACE1 coimmunoprecipitated with PrP<sub>C</sub> in both murine and human brain (Fig. 1A), providing further evidence that the interaction between the two proteins is physiologically. Then, to investigate whether this was a direct protein-protein interaction, we utilized an ELISA system using recombinant proteins. Recombinant human BACE1 with an Fc tag at the C terminus (rBACE1-Fc; Fig. 1, B and C) bound specifically to immobilized rPrP (Fig. 1D). In contrast to rBACE1-Fc, a control Fc-tagged form of human Thy1 (rThy1-Fc) did not interact with the immobilized rPrP to the same extent (7.4-fold less bound at the highest concentration tested) (Fig. 1D), indicating that the PrP-BACE1 interaction was specific. Next, we utilized surface plasmon resonance to interrogate further the interaction between
**PrPC Interacts with BACE1 to Regulate APP Metabolism**

PrPC and BACE1. rBACE1-Fc bound to the immobilized rPrP in a dose-dependent manner with a $K_d$ of 3.19 μM (Fig. 1E).

The coimmunoprecipitation studies indicated that PrPC was interacting with the lower molecular weight immature form of BACE1 (Fig. 1A) (10). The rBACE1-Fc used in the above studies contains the prodomain as evidenced by its reactivity to an antibody raised against residues 26–45 in the prodomain (Fig. 1, B and C). Therefore, to determine whether PrPC was indeed interacting with the prodomain of BACE1, we utilized a form of BACE1 lacking the prodomain (ΔPD-rBACE1) that migrated on SDS-PAGE as a single band at ~62 kDa and was no longer recognized by the prodomain antibody (Fig. 1C). N-terminal sequencing confirmed that ΔPD-rBACE1 indeed lacked the prodomain, beginning at residue 46.

ΔPD-rBACE1 displayed a specific activity toward a quenched fluorescent peptide substrate similar to that of the original prodomain containing rBACE1-Fc (11.73 and 12.4 units/min/μg of protein, respectively), consistent with reports that the prodomain does not inhibit the catalytic activity of the enzyme (15, 16). Using surface plasmon resonance, ΔPD-rBACE1 was observed not to bind to the immobilized rPrP (Fig. 1F). Together, these data indicate that the N-terminal prodomain of BACE1 (residues 22–45) is required for the direct interaction between BACE1 and PrPC.

**Pro29 in Prodomain of BACE1 Is Critical for Interaction with PrPC**

To gain further insight into the direct interaction between BACE1 and PrPC, we investigated whether PrPC would inhibit the action of the homolog of BACE1, BACE2. BACE2 shares 45% sequence identity with BACE1 and also cleaves APP albeit at the Phe19-Phe20 bond in the Aβ sequence (29, 30).

Upon coexpression in HEK293 cells, PrPC significantly inhibited the action of BACE2 on APPWT (Fig. 2, A and B). As PrPC inhibits both BACE1 and BACE2, we identified a conserved sequence (LPLR) in the prodomains of both proteins (Fig. 2C) that we interrogated in BACE1 by site-directed mutagenesis. L28Q/L30Q and P29G mutants were coexpressed in HEK293 cells with PrPC. The P29G mutant was expressed at a level similar to that of the wild type BACE1 with the majority being complex glycosylated and appearing as the 75-kDa mature form (Fig. 2D), whereas the L28Q/L30Q mutant was predominantly (~90%) expressed as the 65-kDa immature ER form (Fig. 2D). The P29G mutant had an activity toward the quenched fluorescent peptide substrate similar to that of wild type BACE1 (Fig. 2E). As the L28Q/L30Q mutant did not appear to traffic through the secretory pathway correctly being present mainly as the immature ER form (Fig. 2F), it did not efficiently fold into a fully catalytically active form (Fig. 2E), it was not studied further. The prodomain containing a complex glycosylated immature form of BACE1 (~75 kDa) was increased in the presence of PrPC in the wild type BACE1-expressing cells but not in the P29G-expressing cells (Fig. 2, F and G). In the wild type

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**FIGURE 1. PrP directly interacts with prodomain of BACE1.** A, brain homogenates from 129/Ola wild type mice and a non-demented individual were immunoprecipitated in the presence (IP) or absence (Control) of 6H4, and the immunoprecipitates were subjected to SDS-PAGE and immunoblotting alongside total brain homogenate (Input) with antibody SAF32 for murine and 3F4 for human PrPC and antibody EE-17 for BACE1. B, schematic of the prodomain-containing (rBACE1-Fc) and prodomain-lacking (ΔPD-rBACE1) BACE1 showing the epitopes recognized by antibody EE-17 and the prodomain antibody (pro-BACE1). C, rBACE1-Fc (lane 1) and ΔPD-rBACE1 (lane 2) immunoblotted with EE-17, prodomain antibody (pro-BACE1), or anti-Fc-HRP.

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**D, rPrP was immobilized and incubated with rBACE1-Fc or rThy1-Fc before detection with anti-Fc-HRP (n = 3). E, rPrP was immobilized onto the surface of a CM5 sensor chip, and rBACE1-Fc was passed over the surface. The response from the reference was subtracted, and the base lines were adjusted to zero to give response over time binding curves. F, rBACE1-Fc (2500 nM) and ΔPD-rBACE1 (2500 nM) were passed over the rPrP-immobilized sensor chip. Error bars, ± S.E.
BACE1-expressing cells, coexpression of PrP<sup>C</sup> significantly reduced the amount of sAPP<sub>/H9252</sub> in the conditioned medium derived from the endogenous human APP<sub>WT</sub>, whereas PrP<sup>C</sup> failed to inhibit the amount of sAPP<sub>/H9252</sub> secreted from the P29G-expressing cells (Fig. 2, H and I). These data indicate that PrP<sup>C</sup> is interacting with the prodomain of BACE1 and that Pro<sup>29</sup> is critical for this interaction. Furthermore, these observations suggest that this interaction with PrP<sup>C</sup> prevents the removal of the prodomain, thus influencing the proportion of BACE1 that is cleaved to generate the mature form.

PrP<sup>C</sup> Alters Subcellular Localization of BACE1—Next, we investigated whether this interaction between PrP<sup>C</sup> and the prodomain of BACE1 altered the subcellular location of BACE1 by assessing whether the colocalization of BACE1 with various subcellular markers was altered by PrP<sup>C</sup>. In SH-SYS5 cells, immunofluorescence microscopy revealed that PrP<sup>C</sup> caused a significant reduction (28.9 ± 4.7%, p = 0.025) in the colocalization of BACE1 with the early endosomal marker EEA1 (Fig. 3, A and B) and as assessed by FACS reduced the amount of BACE1 at the cell surface by 28.2 ± 9.1% (p = 0.015) (Fig. 3, C and D).
As both the cell surface and endosomal localization of BACE1 was reduced in the presence of PrP<sup>C</sup>, we investigated whether PrP<sup>C</sup> was retaining BACE1 within the secretory pathway. Immunofluorescence microscopy revealed that PrP<sup>C</sup> significantly increased (29.4 ± 7.6%, p = 0.028) the colocalization of BACE1 with the TGN-specific protein TGN-46 (Fig. 3, E and F).
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but did not alter the amount of BACE1 colocalized with the ER marker calreticulin (Fig. 3, G and H). Together, these results indicate that the interaction of PrP C with the prodomain of BACE1 slows its trafficking following its exit from the ER, increasing its localization in the TGN and thereby reducing the amount at the cell surface and in endosomes.

To confirm that the above results were not caused by forced interactions due to overexpression of the proteins, we used FACS analysis to determine the surface level of endogenous BACE1 in HEK293 cells following siRNA knockdown of endogenous PrP C (Fig. 4A). Knockdown of endogenous PrP C (Fig. 4B) resulted in a 151% increase in the amount of endogenous BACE1 at the cell surface (Fig. 4, C and D). Together with the coimmunoprecipitation experiments of endogenous proteins in brain (Fig. 1A), these results indicate that the interaction between BACE1 and PrP C is of physiological relevance and has a physiological effect.

**Deletion of PrP C Does Not Affect APP Processing or Aβ Deposition in Mouse Model**—We extended our analysis of PrP C function in AD by examining the effect of PrP C deletion on Aβ production and deposition in a transgenic mouse model expressing human APP. PrP C-null 129/Ola mice (22) were crossed with mice expressing human APP with APP Swe,Ind (25). Immunoblot analysis confirmed the lack of PrP C in the APP Swe,Ind/PrP C−/− mice (Fig. 5, A and B); however, PrP C deletion had no effect on the level of sAPPβ (Fig. 5, A and B). Histopathological analysis indicated that there was no apparent difference in thioflavin S fluorescence (Fig. 5C) or in total Aβ plaque load (Fig. 5D) in the hippocampus between the APP Swe,Ind/PrP C−/− mice and the APP Swe,Ind/PrP C+/+ mice. As oligomeric forms of Aβ more closely correlate with cognitive dysfunction than Aβ plaque load (31), we investigated whether depletion of PrP C affected the level of prefibrillar Aβ oligomers using the A11 antibody (32) and fibrillar Aβ oligomers using the OC antibody (33). However, no apparent differences in the level of prefibrillar Aβ oligomers detected with the A11 antibody (Fig. 5E) or in fibrillar Aβ oligomers detected with the OC antibody (Fig. 5F) were observed between the APP Swe,Ind/PrP C−/− and the APP Swe,Ind/PrP C+/+ mice. Further analysis revealed that there was no difference in the amount of soluble (SDS-extracted) Aβ(1–40) and Aβ(1–42) (Fig. 5G) in the APP Swe,Ind/PrP C−/− mice compared with the APP Swe,Ind/PrP C+/+ mice at either 20 or 40 weeks of age. There were small but significant increases in the amount of insoluble (formic acid-extracted) Aβ(1–40) at 40 weeks (Fig. 5H) and in the amount of insoluble Aβ(1–42) at both 20 and 40 weeks (Fig. 5H) in the APP Swe,Ind/PrP C−/− mice compared with the APP Swe,Ind/PrP C+/+ mice. Furthermore, deletion of PrP C had no apparent effect on the synaptic immunoreactivity of synaptophysin or drebrin or on microglial or astrocyte activation in the hippocampus (supplemental Fig. S1, A–D). In addition, immunoblot analysis revealed that there was no significant difference in the levels of the synaptic proteins synaptophysin, PSD95, and drebrin in the APP Swe,Ind/PrP C−/− mice compared with the APP Swe,Ind/PrP C+/+ mice (supplemental Fig. S1, E and F). Also, there was no difference in the level of the γ-secretase complex components presenilin-1 and nicastrin in the APP Swe,Ind/PrP C−/− mice compared with the APP Swe,Ind/PrP C+/+ mice (supplemental Fig. S1, E and F). Finally, we investigated whether the lack of effect of PrP C deletion on Aβ deposition was due to an increase in Aβ degradation by examining the levels of the Aβ-degrading enzymes neprilysin and insulin-degrading enzyme. However, no significant difference in the levels of these two enzymes was observed between the APP Swe,Ind/PrP C−/− and the APP Swe,Ind/PrP C+/+ mice (supplemental Fig. S1, E and F), indicating that the lack of effect of PrP C deletion on Aβ deposition was unlikely due to an increase in Aβ degradation. Taken together, these extensive biochemical and histopathological analyses indicate that deletion of PrP C does not modulate the deposition of Aβ in this APP Swe,Ind transgenic mouse model.

**FIGURE 4.** siRNA knockdown of endogenous PrP C increases cell surface localization of BACE1. A, siRNA knockdown of endogenous PrP C in HEK293 cells. Lysates were subjected to SDS-PAGE and immunoblotting to detect endogenous APP, PrP C, and actin. B, endogenous BACE1 cell surface fluorescence in the presence and after knockdown of endogenous PrP C as determined by FACS analysis. C, quantitation from FACS analysis of BACE1 surface fluorescence following siRNA knockdown of PrP C (n = 9). *, p < 0.05; error bars, ± S.E.
Our previous observations showed that PrPC inhibited the activity of BACE1 toward human APPWT in cellular models and toward murine APPWT in PrP-null mice (10). To reconcile these observations with the lack of effect of deletion of PrPC on Aβ/H9252 production and deposition in the APPSwe,Ind transgenic mice, we considered whether this was due to the Swedish double-point mutation K670N/M671L N-terminal to the BACE1 cleavage site. To investigate this, the effect of PrPC on Aβ/H9252 production was examined in HEK293 cells stably expressing either APPWT (Fig. 6A) or APPSwe (Fig. 6B). PrPC dramatically reduced the secretion of Aβ(1–40) and Aβ(1–42) from the...
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![Figure 6. PrP<sup>C</sup> does not inhibit production of Aβ from cells expressing APP<sub>Swe</sub> from the cells expressing APP<sub>WT</sub> (Fig. 6C), consistent with our previous data in other cell lines (10). However, there was no inhibitory effect of PrP<sup>C</sup> on the secretion of the Aβ peptides from the cells expressing APP<sub>Swe</sub> (Fig. 6D). To confirm this result, we performed the converse experiment using siRNA to knock down the endogenous PrP<sup>C</sup> in the HEK293 cells expressing either APP<sub>WT</sub> (Fig. 6E) or APP<sub>Swe</sub> (Fig. 6F). Knockdown of PrP<sup>C</sup> resulted in an increase in sAPPβ in the cells expressing APP<sub>WT</sub> (Fig. 6G) but had no effect in the cells expressing APP<sub>Swe</sub> (Fig. 6H). These data clearly show that PrP<sup>C</sup> differentially affects the activity of BACE1 toward APP<sub>WT</sub> and APP<sub>Swe</sub>.

**DISCUSSION**

We have reported previously that PrP<sup>C</sup> inhibits the BACE1 cleavage of APP<sub>WT</sub> and that deletion of PrP<sup>C</sup> in both cell and animal model systems resulted in an increase in endogenous Aβ levels (10). From this, we proposed that a normal function of PrP<sup>C</sup> may be to regulate the production of the neurotoxic Aβ and therefore to protect against AD (11). In the present study, we have extended these observations by determining the molecular and cellular mechanisms involved in the regulation of BACE1 by PrP<sup>C</sup>. Here, we show that PrP<sup>C</sup> interacts directly with the prion domain of the immature, Golgi-localized form of BACE1 and that PrP<sup>C</sup> in the prion domain is critical for this interaction.

Prion domain cleavage, which occurs in the TGN by furin-like convertases, is required for the generation of mature BACE1 (13–16). The mature BACE1 is present at the cell surface from where it is internalized into endosomes where it preferentially cleaves APP<sub>WT</sub> (6). Our data show that PrP<sup>C</sup> interacts with the prion domain of BACE1 and that Pro<sup>29</sup> in the prion domain appears to be critical for this protein-protein interaction. This interaction of PrP<sup>C</sup> with the immature prion domain-containing form of BACE1 results in an increased proportion of the secretase in the TGN with a subsequent reduction in the amount at the cell surface and in endosomes. We propose that this retention of BACE1 in the secretory pathway provides a mechanism to explain the inhibitory effect of PrP<sup>C</sup> on the amyloidogenic processing of APP<sub>WT</sub>, which is cleaved by BACE1 in endosomes (14, 17–19). Although there is only an approximately 30% reduction in BACE1 localization to the endosomes, this is enough to nearly abolish the generation of Aβ. It is unlikely that the total cellular pool of BACE1 is intended for localization to the appropriate subcellular compartments for processing of APP<sub>WT</sub> as BACE1 is required for the processing of several other substrates (34).

The mechanism of action of PrP<sup>C</sup> on BACE1 processing of APP is reminiscent of that of the sorting protein-related receptor, which also inhibits the proteolytic processing of APP and production of Aβ (35). Like PrP<sup>C</sup>, sorting protein-related receptor coimmunoprecipitated only with the smaller prion domain-containing immature form of BACE1, suggesting an interaction in the Golgi (36). However, unlike sorting protein-related receptor, which also interacts with APP, impairing its transport through the Golgi and blocking access of APP to BACE1 (35, 36), PrP<sup>C</sup> does not interact with APP (10).

We also sought to confirm a role for PrP<sup>C</sup> upstream of Aβ production by examining the effect of deletion of PrP<sup>C</sup> in a transgenic mouse model expressing mutant human APP. For this purpose, we chose the widely used J20 transgenic mouse model, which expresses human APP with the Swedish and Indiana mutations under the control of the platelet-derived growth factor (PDGF) promoter (25). Surprisingly, despite extensive biochemical and histopathological analysis, we could find no evidence for an affect of PrP<sup>C</sup> deletion on APP proteolytic processing, Aβ plaque deposition, or levels of soluble Aβ or Aβ...
oligomers. Consistent with our observations in the APP<sub>Swe,Ind</sub> (J20) transgenic mice, it has also been reported recently that deletion of PrP<sup>C</sup> failed to alter BACE1 processing of APP, Aβ levels, and Aβ deposition in the APP<sub>Swe/PS1<sub>ΔE9</sub></sub> (37) and the APP<sub>Swe/PS1<sub>116<sup>66</sup>Δ</sub></sub> (38) transgenic models and previously that overexpression of PrP<sup>C</sup> in APP<sub>Swe,Ind</sub> transgenic mice resulted in only a minor increase in Aβ plaque formation but no significant change in Aβ(1–40) or Aβ(1–42) (39). However, considering that APP<sub>WT</sub> is primarily cleaved by BACE1 in endosomes (17–19), whereas the cleavage of APP<sub>Swe</sub> occurs primarily within the TGN (20, 21), our current data indicating that PrP<sup>C</sup> interacts directly with the prodomain of BACE1, retaining APP<sub>WT</sub> PM, plasma membrane.

FIGURE 7. Schematic diagram showing differential effect of PrP<sup>C</sup> on cleavage of APP<sub>WT</sub> and APP<sub>Swe</sub> by BACE1. PrP<sup>C</sup> interacts with the prodomain of BACE1 in its immature form in the TGN, slowing its maturation and trafficking to the cell surface and subsequent internalization into endosomes. In the TGN, BACE1 preferentially cleaves APP<sub>Swe</sub> in the endosomes, it preferentially cleaves APP<sub>WT</sub>. PM, plasma membrane.

REFERENCES
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