Unnatural Amino Acid-Substituted (Hydroxyethyl)urea Peptidomimetics Inhibit γ-Secretase and Promote the Neuronal Differentiation of Neuroblastoma Cells

Yung-Feng Liao, Bo-Jeng Wang, Wen-Ming Hsu, Hsinyu Lee, Chia-Yin Liao, Shin-Ying Wu, Hui-Ting Cheng, and Ming-Kuan Hu

ABSTRACT

γ-Secretase, exhibiting characteristics of aspartyl protease, mediates the intramembranous proteolysis of β-amyloid precursor protein (APP) and Notch, and it is considered to be a prime pharmacological target in the development of therapeutics for Alzheimer’s disease (AD). To identify compounds that block γ-secretase-mediated proteolysis, we used a highly sensitive cell-based reporter gene assay for γ-secretase in which Gal4/VP16-tagged C99-APP was expressed as the immediate substrate of γ-secretase, and Gal4/VP16-tagged APP intracellular domain released by the γ-secretase cleavage then activated the expression of the Gal4-driven luciferase reporter gene. Using this reporter assay, we demonstrated that the newly synthesized (hydroxyethyl)urea peptidomimetics, which contain unnatural amino acid moieties at positions P1’ and/or P3’, can effectively inhibit γ-secretase activity and significantly reduce Aβ production. The γ-secretase-dependent S3 cleavage of Notch was also consistently blocked by these (hydroxyethyl)ureas as evidenced by the decreased generation of the Notch intracellular domain, a prerequisite for the activation of Notch signaling. The inhibition of Notch signaling by active Jia compounds efficiently promotes the neuronal differentiation of neuroblastoma cells, intervening in tumorigenesis and the malignancy of neuroblastomas. Our results suggest that (hydroxyethyl)urea peptidomimetics containing unnatural amino acid substitutions could represent a novel class of γ-secretase inhibitors with enhanced stability, providing the basis for the further development of effective therapeutics for AD and neuroblastomas.

γ-Secretase catalyzes the final proteolytic step in the generation of Aβ (the principal constituent of senile plaques in the AD brain), and it has thus been regarded as a prime therapeutic target for AD. Mounting evidence from pharmacological studies, mutagenesis, affinity labeling, and biochemical isolation strongly suggests that γ-secretase is an aspartyl protease and that the active site of γ-secretase is located at the interface of the presenilin (PS) heterodimer (Wolfe and Haass, 2001). The heterodimeric PS consisting of an ~30-kDa N-terminal fragment (NTF) and a ~20-kDa C-terminal fragment (CTF) is thought to be the active form of γ-secretase in which γ-secretase cleavage then activates the expression of the Gal4-driven luciferase reporter gene. Using this reporter assay, we demonstrated that the newly synthesized (hydroxyethyl)urea peptidomimetics, which contain unnatural amino acid moieties at positions P1’ and/or P3’, can effectively inhibit γ-secretase activity and significantly reduce Aβ production. The γ-secretase-dependent S3 cleavage of Notch was also consistently blocked by these (hydroxyethyl)ureas as evidenced by the decreased generation of the Notch intracellular domain, a prerequisite for the activation of Notch signaling. The inhibition of Notch signaling by active Jia compounds efficiently promotes the neuronal differentiation of neuroblastoma cells, intervening in tumorigenesis and the malignancy of neuroblastomas. Our results suggest that (hydroxyethyl)urea peptidomimetics containing unnatural amino acid substitutions could represent a novel class of γ-secretase inhibitors with enhanced stability, providing the basis for the further development of effective therapeutics for AD and neuroblastomas.

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ABBREVIATIONS: AD, Alzheimer’s disease; PS, presenilin; NTF, N-terminal fragment; CTF, C-terminal fragment; NICD, Notch intracellular domain; HIV, human immunodeficiency virus; ELISA, enzyme-linked immunosorbent assay; HEK, human embryonic kidney; DMEM, Dulbecco’s modified Eagle’s medium; FBS, fetal bovine serum; DMEM, modified Eagle’s medium; FBS, fetal bovine serum; DMSO, dimethyl sulfoxide; APP, amyloid precursor protein; C99, 99-residue C-terminal fragment of amyloid precursor protein; PBS, phosphate-buffered saline; PLB, passive lysis buffer; DAPT, N-[N-(3,5-difluorophenacyl-l-alanyl)]-S-phenylglycine t-butyl ester; GV, Gal4/VP16 DNA binding domain; GAP-43, growth-associated protein 43; PAGE, polyacrylamide gel electrophoresis; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; PBST, phosphate-buffer saline/Tween 20; Aβ, β-amyloid; HRP, horseradish peroxidase; CHAPS, 3-[[(3-cholamidopropyl)dimethyl-ammonio]-2-hydroxy-1-propanesulfonate; siRNA, small interfering RNA; RNAi, RNA interference; ESI, electrospray ionization; MS, mass spectrometry, MS/MS, tandem mass spectrometry; LC, liquid chromatography; OD, optical density; Chy, cyclohexylmethyl; RA, retinoic acid; L-685–458, (2R,3R*,4R*,5S*)N-(5-[[1,1-dimethylethoxy]carbonyl]amino)-4-hydroxy-1-oxo-6-phenyl-2-(phenylmethyl)tetrahydro-2-yl-leucyl-L-phenylalaninamide.
transition state of aspartyl protease catalysis have been derived from sequences around the γ-cleavage site of APP and are shown to block γ-secretase activity, indicating that γ-secretase is an aspartyl protease (Wolfe et al., 1999a). Two highly conserved aspartate residues residing within the sixth and seventh transmembrane domains of presenilins are required for γ-secretase activity (Wolfe et al., 1999b), suggesting that the active site of this novel aspartyl protease might be located at the heterodimeric interface. A number of compounds designed to interact with the protease active site have been shown to bind directly to both PS subunits (Esler et al., 2000; Li et al., 2000b). Together, these findings strongly support the notion that PS heterodimers constitute the active site of γ-secretase.

Biochemical and genetic analyses further reveal that PSs are part of a multimeric γ-secretase complex whose constituents include a heterodimeric PS, a mature glycosylated nicastrin (NCT), Aph-1, and Pen-2 (Iwatsubo, 2004). Compelling evidence has shown that the full spectrum of γ-secretase activity can be reconstituted by the coexpression of human PS, nicastrin, Aph-1, and Pen-2 in yeast (Edbauer et al., 2003), providing definitive proof for the minimal required constituents of a functional γ-secretase.

The γ-secretase not only mediates the proteolysis of APP but also is critical for the processing of Notch receptor. The Notch signaling pathway is essential for cell fate decisions during development (Mumm and Kopan, 2000). This pathway is initiated by the binding of the Delta-Serrate-Lag2 ligand family, followed by the shedding of extracellular domain (S2 cleavage) mediated by the ADAM family members. The resultant C-terminal membrane-tethered fragment of Notch, termed Notch extracellular membrane truncation (NEXT), is then cleaved within the transmembrane domain (S3 cleavage) by γ-secretase to release the Notch intracellular domain (NICD). Once released from membrane, NICD bounds to mammalian CBF1/RBPj, Drosophila melanogaster Suppressor of hairless, and Caenorhabditis elegans Lag-1 DNA-binding proteins and converts them from transcription repressors to activators, resulting in the expression of Notch downstream target genes. The inhibition of γ-secretase would likewise block NICD production and reduce Notch signaling (Wolfe et al., 1999b, 2002).

(Hydroxyethyl)urea peptidomimetics have recently been identified as a new class of transition state analog inhibitors that mimic the transition state of aspartyl protease catalysis and block γ-secretase much more efficiently than any of the difluoro ketones or difluoro alcohols (Wolfe et al., 2002). Highly potent and selective inhibitors containing hydroxyl ethyl isostere have also been developed and used to block such aspartyl proteases as renin and HIV protease (Greenlee, 1990; Huff, 1991). Five HIV protease inhibitors currently available as approved treatments for AIDS all contain the hydroxyethyl isostere (Flexner, 1998), and the core structure of (hydroxyethyl)ureas is known to have apparent low toxicity, a prerequisite for clinical applications. (Hydroxyethyl)urea peptidomimetics have been developed for the affinity isolation and characterization of γ-secretase, and for probing the active site of this protease (Esler et al., 2004). These compounds can be generated through systematic replacements in five positions (P2, P1, P2', P3', and P4') with small, medium, and large hydrophobic l-amino acids (Wolfe et al., 2002). Furthermore, (hydroxyethyl)urea peptidomimetics systematically altered at positions P2-P3' either with hydrophobic L- or D-amino acids are shown to effectively block γ-secretase activity (Bakshi and Wolfe, 2004; Esler et al., 2004). These studies not only substantiate the loose sequence specificity of γ-secretase but also raise the possibility that γ-secretase could be targeted by transition state analog inhibitors encompassing unnatural amino acids that can confer peptidomimetics extraordinary biological stability along with enhanced biological activity and proteolytic resistance. Herein, we report the development of (hydroxyethyl)urea peptidomimetics containing unnatural amino acid substitutions that can effectively block γ-secretase activity for lowering Aβ production and attenuating Notch signaling so as to promote the neuronal differentiation of neuroblastoma cells. Our studies provide the proof-of-concept for the use of unnatural amino acids as building blocks in the generation of biologically stable γ-secretase inhibitors for AD treatments and the promotion of neuronal differentiation.

Materials and Methods

Reagents. The BCA protein assay reagent kit and SuperSignal West Pico and SuperSignal West Dura reagents were purchased from Pierce Chemical (Rockford, IL). The rabbit anti-Notch(Val1744) antibody was from Cell Signaling Technology Inc. (Danvers, MA). Horseradish peroxidase-conjugated anti-rabbit IgG was from Santa Cruz Biotechnology, Inc. (Santa Cruz, CA). Horseradish peroxidase-conjugated anti-mouse IgG and ECL Western Blotting detection reagents were from GE Healthcare (Little Chalfont, Buckinghamshire, UK). The FuGENE6 transfection reagent, Expand long template polymerase chain reaction system, and polymerase chain reaction nucleotide mix were from Roche Applied Science (Indianapolis, IN). Dual luciferase assay reagents, Steady-Glo luciferase assay reagents, and the pRL-TK vector were from Promega (Madison, WI). Human Aβ40 and Aβ42 colorimetric ELISA kits were from BioSource International (Camarillo, CA). All other reagents were of at least reagent grade and were obtained from standard suppliers.

Synthesis of (Hydroxyethyl)ureas. The (hydroxyethyl)urea peptidomimetics containing unnatural amino acid moieties were synthesized using methods described previously with some modifications (Getman et al., 1993) (Scheme 1). In brief, a commercially available Boc-protected amino acid derivative 1, which fits the desired structural feature of the P1 residue, was reduced to an α-amino acid derivative 2 via the Weinreb amide and then transferred to the corresponding epoxide 4 through alkene 3. The epoxide was ring-opened by treatment with benzylamine or cyclohexylmethylamine under heated reflux to give the amino alcohols 5 and 6. These intermediates were condensed with isocyanates 9a and 9b (in turn obtained from α-amino methyl esters and phosgene) at room temperature to provide the (hydroxyethyl)urea P1-P2 isoesters 10a, 10b, and 11a. C-Terminal incorporation of P3' residues was accomplished by hydrolysis of the methyl ester with LiOH and subsequent coupling of P3' residues 14a-g with the HATU coupling reagent in DMF to yield the desired (hydroxyethyl)urea isoesters (see Table 1 as Jia compounds). In this synthesis scheme, the epoxide was treated with a variety of alkylamines that came up with P1-P1' isoesters in which the P1' site was modified with nitrogen at the backbone and an unnatural cyclohexyl side chain that is not seen in essential amino acids. Moreover, the selected amines and unnatural amino acid derivatives 14a-g were incorporated to the P1-P2' fragments to yield entire P1-P3' (hydroxyethyl)ureas. Through this synthesis scheme, a collection of (hydroxyethyl)urea peptidomimetics that contained unnatural amino acid moieties mainly distributed either at the P1' and/or P3' positions was generated. The characterization and the purity of each compound were confirmed by 1H NMR spectro-
copy, high-resolution mass spectroscopy, and high-pressure liquid chromatography.

**Cell Culture and Cell Lines.** Human embryonic kidney (HEK)293 cells were maintained in Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% fetal bovine serum (FBS) and 0.1 mg/ml penicillin and streptomycin. T-REx293 cells were purchased from Invitrogen and cultured in DMEM supplemented with 10% FBS and 5 μg/ml blasticidin. The generation of stably transfected cell lines, T16, T20, N7, and -30 has been described previously (Kimberly et al., 2003; Liao et al., 2004; Bakshi et al., 2005). Cells of the SH-SY5Y human neuroblastoma cell line were grown in DMEM/Ham's F-12 supplemented with 10% FBS. Cells were incubated in a humidified incubator at 37°C in 5% CO₂.

**Cell-Based γ-Secretase Assays.** The generation of these stable cell lines has been reported previously (Liao et al., 2004). To examine the inhibitory effects of the compounds specifically on γ-secretase, T16 or T20 cells were trypsinized and washed with serum-free DMEM before plating onto 12-well microplates in 1 ml/well DMEM supplemented with 10% FBS at 5 × 10⁵ cells/well. After incubation at 37°C overnight, cells were treated with 10 μM concentrations of individual (hydroxyethyl)urea peptidomimetics in culture medium containing 1% DMSO and 1 μg/ml tetracycline, the inducer of APP695-Gal₄/VP16 and the 99-residue C-terminal fragment of APP-Gal₄/VP16 (C99-GV) expressions, and they were incubated at 37°C for 24 h or various intervals as specified. For the dose-response studies, various concentrations of (hydroxyethyl)urea peptidomimetics were included in the medium as specified. Cells incubated with the culture medium containing 1 μg/ml tetracycline and 1% DMSO were used to define the basal level of γ-secretase activity, whereas cells treated with DMSO-containing medium without tetracycline were used to estimate the nonspecific background emission of the luciferase signal. To terminate the reactions, cells were harvested with PBS containing 20 mM EDTA and lysed in 100 μl of 1× passive lysis buffer (PLB; Promega). Cell debris was removed by centrifugation at 13,200 g for 5 min, and luciferase activity in clarified lysates was determined using 20 μl of lysates and 20 μl of Steady-Glo luciferase assay reagent in a 96-well LumiNunc microplate (Nalge Nunc, International, Rochester, NY). After incubation at room temperature for 5 min, emitted luminescence in individual microwells was determined by an MLX Microplate luminometer (Dynex Technologies, Chantilly, VA) and subsequently normalized by the protein content of the lysates. The protein content of clarified lysates was determined using the BCA protein assay kit (Pierce Chemical) following the manufacturer's instructions. The normalized luciferase signal emitted by T20 cells in regular culture medium without tetracycline was referred as 1-fold of activation. Known γ-secretase inhibitors, such as compound E and DAPT (Seiffert et al., 2000; Dovey et al., 2001), were included as positive controls of γ-secretase inhibition.

To examine compound inhibition of γ-secretase-dependent S3 cleavage of Notch, we generated a HEK293-derived stable line (N7) that was constitutively expressing NΔE (Liao et al., 2004). The NΔE

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**Scheme 1.** Reagents and conditions: i, EDC, HOBt, HNMe(OMe)HCl, then LAH. ii, MePPh₃Br, 35% KH, HMDS. iii, m-CPBA. iv, isopropanol. v, room temperature, overnight. vi, LiOH. vii, HATU, DIEA.
was a Notch mutant protein lacking its extracellular domain but retaining its membrane-spanning region. The recombinant NAÆ was thus expressed as a membrane-tethered protein that can be cleaved directly by γ-secretase independently of its ligand activation and that served as an alternative substrate for the measurement of γ-secretase activity (Kopan et al., 1996). N7 cells were plated onto 12-well microplates in 1 ml/well DMEM supplemented with 10% FBS at 5 × 10⁵ cells/well. After incubation at 37°C overnight, cells were treated with compounds at 10 μM as described above and incubated at 37°C for 24 h. Treated cells were harvested using PBS containing 20 mM EDTA and dissolved in 50 μl of 1 × PLB, followed by centrifugation at 13,200 × g for 5 min to remove cell debris. The protein concentrations of clarified supernatants were determined using a BCA protein assay reagent kit, and cell extracts containing equivalent amounts of proteins were resolved by SDS-PAGE and analyzed by Western blotting using an anti-Notch (Val1744) polyclonal antibody as described below.

**Cell Viability Assay.** T20 cells (5 × 10⁵) were seeded onto the wells of 96-well microplates in culture medium containing respective compounds at 10 μM and incubated at 37°C for 24 h. Viable cells were determined using the CellTiter 96 AQueous non-radioactive cell proliferation assay (Promega) as specified by the manufacturer’s instructions. In brief, after the addition of the combined 3-(4,5-dimethylthiazol-2-yl)-5-(3-carboxymethoxyphe- ny)l-2-(4-sulfophenyl)-2H-tetrazolium, inner salt/phenazine methosulfate solution (20 μl/well), microplates were incubated for 3 h at 37°C. The conversion of 3-(4,5-dimethylthiazol-2-yl)-5-(3-carboxyphenox- y)methyl-2-(4-sulfophenyl)-2H-tetrazolium, inner salt into formazan in viable cells was quantitated by the absorbance at 490 nm using a Synergy HT ELISA plate reader (Bio-Tek Instruments, Winooski, VT). The number of living cells in culture was directly proportional to the absorbance at 490 nm. Viable cells in culture medium containing vehicle alone (1% DMSO, control) were referred to as 100% viability. The background absorbance shown at 0 cells/well was subtracted from these data.

**TABLE 1**

Structures of (hydroxyethyl)urea isosteres and their IC₅₀ values for the inhibition of γ-secretase.

<table>
<thead>
<tr>
<th>Compound</th>
<th>P₁⁺</th>
<th>AA₄ (HN-CH(P₂/C)-CO⁻)</th>
<th>HN-P₁⁺</th>
<th>IC₅₀</th>
</tr>
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<tr>
<td></td>
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<td></td>
<td></td>
<td>Lucifer</td>
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<td></td>
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<td></td>
<td></td>
<td>μM</td>
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<tr>
<td>Jia040</td>
<td>Phenyl</td>
<td>Ala</td>
<td>(1R,2S)-Al</td>
<td>N.D.</td>
</tr>
<tr>
<td>Jia046</td>
<td>Phenyl</td>
<td>Leu</td>
<td>(1R)-Phg-OMe</td>
<td>0.946</td>
</tr>
<tr>
<td>Jia047</td>
<td>Phenyl</td>
<td>Leu</td>
<td>(1R,2R,3S,5S)-IPCA</td>
<td>5.459</td>
</tr>
<tr>
<td>Jia097⁺</td>
<td>Phenyl</td>
<td>Leu</td>
<td>(1R)-Val-OMe</td>
<td>N.D.</td>
</tr>
<tr>
<td>Jia101</td>
<td>Phenyl</td>
<td>Leu</td>
<td>(1R)-Phg-OMe</td>
<td>3.159</td>
</tr>
<tr>
<td>Jia104</td>
<td>Phenyl</td>
<td>Leu</td>
<td>(S)-(+)-1-PEA</td>
<td>4.513</td>
</tr>
<tr>
<td>Jia105</td>
<td>Phenyl</td>
<td>Leu</td>
<td>(R)-(+)-1-PEA</td>
<td>3.149</td>
</tr>
<tr>
<td>Jia138</td>
<td>Cyclohexyl</td>
<td>Leu</td>
<td>(1R)-Phg-OMe</td>
<td>0.172</td>
</tr>
<tr>
<td>Jia142</td>
<td>Cyclohexyl</td>
<td>Leu</td>
<td>(R)-(+)-1-PEA</td>
<td>0.999</td>
</tr>
<tr>
<td>Jia143</td>
<td>Cyclohexyl</td>
<td>Leu</td>
<td>(1R)-Val-OMe</td>
<td>4.863</td>
</tr>
<tr>
<td>DAPT⁺</td>
<td></td>
<td></td>
<td></td>
<td>0.478</td>
</tr>
<tr>
<td>Compound E³</td>
<td></td>
<td></td>
<td></td>
<td>0.013</td>
</tr>
</tbody>
</table>

N.D., not determined; AI, 1-amino-2-indanol; IPCA, isopinocampheylamine; Phg-OMe, phenylglycine methyl ester; 1-PEA, 1-phenylethylamine

⁺ Jia097 was the known inhibitor III-31-C.

β-Amyloid ELISA. To determine the inhibitory effects of compounds on Aβ production, T20 or γ-30 cells (5 × 10⁵ cells/well) were seeded onto 12-well tissue culture plates and treated with various amounts of compounds in serum-free DMEM with (for T20) or without (for γ-30) 1 μg/ml tetracycline, followed by incubation at 37°C for 24 h. Conditioned media were harvested, clarified by centrifugation, supplemented with the Complete protease inhibitor cocktail, and stored at −80°C until ready for the assay. Levels of secreted Aβ40 and Aβ42 in conditioned media were determined using quantitative human Aβ40 and Aβ42 sandwich ELISA kits (BioSource International) as described in the manufacturer’s instructions. Contents of Aβ40 and Aβ42 in the conditioned media of T20 and γ-30 cells treated with regular culture medium alone were defined as the blank for the quantitation of Aβ production.

**Compound-Induced Neuronal Differentiation of Neuroblastoma Cells.** SH-SY5Y human neuroblastoma cells were seeded onto six-well microplates (5 × 10⁵ cells/well) and incubated at 37°C overnight. Adherent SH-SY5Y cells were then treated with 10 μM respective Jia compounds or vehicle alone (0.1% DMSO) in DMEM/Ham’s F-12 medium containing 10% FBS, followed by incubation at 37°C for 24 h or various intervals as specified. Compound-treated SH-SY5Y cells were harvested and lysed by PLB (Promega) containing the Complete protease inhibitor cocktail. Clarified lysates containing equivalent amounts of proteins were resolved by SDS-PAGE. The expression levels of calreticulin and GAP-43, two markers for neuronal differentiation of neuroblastoma cells (Grynfeld et al., 2000; Hsu et al., 2005), were visualized by Western blotting using specific antibodies. The level of GAPDH was also determined as a protein load control.

To quantify neurite outgrowth of neuroblastoma cells induced by γ-secretase inhibitors, 50 or more SH-SY5Y cells whose dendritic trees were relatively isolated and did not have discontinuities in their dendritic trees were chosen for quantification of neurite length. Image for Windows was the morphometric program used to measure the neurite length.
SDS-Polyacrylamide Gel Electrophoresis and Western Blot Analysis. Cleared cell extracts containing equivalent amounts of proteins were mixed with equal volumes of 2× SDS sample buffer (125 mM Tris-HCl, pH 6.8, 4% SDS, 20% glycerol, and 5% β-mercaptoethanol) and boiled at 100°C for 5 min. Denatured proteins were resolved in Tris-glycine polyacrylamide gels (10 or 12%). Separated proteins were transferred electrothermally to polyvinylidene difluoride membranes (Immobilon-P; Millipore Corporation, Billerica, MA). Membranes were then treated with blocking buffer (5% nonfat dry milk and 0.1% Tween 20 in PBS (PBST)) at room temperature for 1 h, followed by a brief rinse with PBST. Blocked membranes were probed with appropriate dilutions of primary antibody in PBST at room temperature for 1 h. The unbound primary antibody was removed by extensive washes with PBST. After extensive washes with PBST, antibody-reacted proteins were visualized by chemiluminescence using SuperSignal West Dura and Pico reagents (Pierce Chemical). The antibodies used and their dilutions were as follows: anti-Notch1 (Val1744), 1:1000; HRP-conjugated anti-mouse IgG (GE Healthcare), 1:10,000; and HRP-conjugated anti-rabbit IgG (Santa Cruz Biotechnology, Inc.), 1:1000.

Preparation and Detergent Solubilization of Microsome Membrane. Freshly harvested γ-30 cells that overexpressed all four γ-secretase components (Kimberly et al., 2003) were resuspended and homogenized in a HEPES buffer (50 mM HEPES, 5 mM MgCl2, 5 mM CaCl2, and 150 mM NaCl). After removal of cell debris and nuclei, the supernatant solution was centrifuged at 100,000 g for 1 h. The microsome-enriched pellets were solubilized in a CHAPSO-containing buffer (50 mM HEPES, 5 mM MgCl2, 5 mM CaCl2, and 1% CHAPSO) at 4°C for 60 min. The ensuing supernatant solution was then desalted isocratically on an LC-Packings PepMap C18 2 μM-Precolumn Cartridge (5 μm, 300 μm i.d. × 5 mm; Dionex, Sunnyvale, CA) for 2 min with 0.1% formic acid delivered by the auxiliary pump at 30 μl/min after which the peptides were eluted off from the precolumn and separated on an analytical C18 capillary column (15 cm × 75 μm i.d., packed with 5 μm, Zorbax 300 SB C18 particles; Micro-Tech Scientific, Vista, CA) connected inline to the mass spectrometer, at 300 nL/min using a 40-min fast gradient of 5 to 85% acetonitrile in 0.1% formic acid. Online nano-ESI-MS survey scan was fully automated and synchronized with the nano-LC runs under the full software control of MassLynx 4.0. Before online analysis, the nano-LC sprayer and Z-spray source parameters were tuned and optimized with glufibrinopeptide B.

Preparation of Jia138-Conjugated Affinity Resins and Affinity Chromatography of γ-Secretase. The Jia138-conjugated affinity resins were prepared by a previously described protocol (Esler et al., 2002). In brief, the methyl esters of Jia138 were hydrolyzed by using LiOH in aqueous dioxane. The carboxylic acids were coupled in DMSO using 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide (3 equivalents) to the primary amine of a six-atom hydrophilic linker present on the agarose resin Affi-Gel 102 (Bio-Rad Laboratories, Hercules, CA). The conjugation mixtures were incubated at room temperature overnight with continuous gentle inversion, followed by extensive washes with DMSO. The affinity resins were subsequently maintained in aqueous buffer.

The solubilized γ-secretase was incubated with Jia138-conjugated resins for 2 h at room temperature with gentle rocking, and the resin was washed twice with a CHAPSO-containing buffer (50 mM HEPES, pH 7.0, 150 mM NaCl, and 1% CHAPSO). The bound proteins were then released by SDS-PAGE sample buffer and analyzed by SDS-PAGE and Western blotting as specified above.

Transfection of Small Interfering RNAs Targeting Notch1. The chemically synthesized siRNA duplex oligoribonucleotides against human Notch1 (siNotch1, accession no. NM_017617) and a nonspecific scrambled siRNA were purchased from Ambion (Austin, TX). The target sequences for siNotch1 were 5′-CGA CGC AUG CAU CAG CAA C-3′ (sense strand) and 5′-GUU GCU GCA UGC GUC G-3′ (antisense strand). siRNA oligoribonucleotides (50 or 100 pmol) were then transiently transfected into SH-SY5Y or N7 cells using the Lipofectamine 2000 transfection reagent (Invitrogen) according to the manufacturer’s instructions. After transfection with siRNAs in DMEM supplemented with 10% FBS at 37°C for 6 h, transfected cells were incubated with fresh culture medium at 37°C for an additional 24 h or as specified. Transfected cells were harvested by PBS containing 20 mM EDTA, and clarified lysates were prepared by using 1× PLB containing Complete protease inhibitor cocktail. Protein content of cell lysates was determined with a BCA protein assay reagent kit. A nonspecific oligoribonucleotide that is not homologous to any known genes was used as a negative control to rule out nonspecific cellular events caused by the introduction of the siRNAs into cells. The levels of calreticulin and NICD in transfected cells were examined by Western blotting using anti-Notch1 Val1744) as described above. The efficiency of the Notch1-targeting RNAi knockdown was determined by visualizing the endogenous full-length Notch1 (300 kDa) and NICD (110 kDa) in SH-SY5Y and N7 cells, whereas the production of exogenous NLe-derived NICD (50 kDa) in N7 cells was not affected by RNAi.

Mass Spectrometry Analysis. Purified peptidomimetics DAPT and Jia142 were dissolved in 50% acetonitrile and 0.1% formic acid to a final concentration of 1 mM and incubated at various temperatures for 2 days. Treated compounds were subjected to one-dimen- sional LC-nano-ESI-MS/MS analysis performed on an integrated nano-LC-MS/MS system (Micromass, a division of Waters, Bedford, MA) of a three-pumping Micromass Waters CapLC system with an autosampler, a slow select module configured for precolumn plus analytical capillary column, and a Micromass Q-ToF Ultima API mass spectrometer fitted with nano-LC sprayer, operated under MassLynx 4.0 control. Injected samples were first trapped and desalted isotropically on an LC-Packings PepMap C18 μM-Precolumn Cartridge (5 μm, 300 μm i.d. × 5 mm; Dionex, Sunnyvale, CA) for 2 min with 0.1% formic acid delivered by the auxiliary pump at 30 μl/min after which the peptides were eluted off from the precolumn and separated on an analytical C18 capillary column (15 cm × 75 μm i.d., packed with 5 μm, Zorbax 300 SB C18 particles; Micro-Tech Scientific, Vista, CA) connected inline to the mass spectrometer, at 300 nL/min using a 40-min fast gradient of 5 to 85% acetonitrile in 0.1% formic acid. Online nano-ESI-MS survey scan was fully automated and synchronized with the nano-LC runs under the full software control of MassLynx 4.0. Before online analysis, the nano-LC sprayer and Z-spray source parameters were tuned and optimized with glufibrinopeptide B.

Results

Synthesis of (Hydroxyethyl)urea Peptidomimetics Containing Unnatural Amino Acids. The incorporation of transition-state mimicking moieties into the substrate-based substructure has recently been used to develop aspartyl protease inhibitors (e.g., HIV protease inhibitors; Huff, 1991). This approach using substrate-based modifications has also been successfully applied to the generation of potent and selective γ-secretase inhibitors and is efficient for probing the active site of this aspartyl protease. Previous studies showed that the hydroxyethylene peptidomimetic L-685,458 and the (hydroxyethyl)urea III-31-C can both inhibit APβ production with IC50 values of approximately 10 nM in the cell-free assays and 200 nM in cell-based systems (Shearman et al., 2000; Kornilova et al., 2003). It is intriguing that the P1-P1’ residues of both inhibitors consisted of Phe-Phe isosteres, whereas APP substrate-based hydroxyethylene analogs with Ala-Thr and Val-Ile isosteres showed no inhibitory effects on the γ-secretase-mediated formation of Ap42 (Nadin et al., 2003). These results suggest that inhibitors such as L-685,458 and III-31-C were functioning as direct transition state analogs of the APP γ-secretase active site. We thus sought to determine whether (hydroxyethyl)urea isosteres with modifications especially at positions P1-P1’ could allow us to delineate the structure-activity relationships of these (hydroxyethyl)ureas to the binding pocket of the γ-secretase active site.

To incorporate unnatural amino acids into newly synthetized (hydroxyethyl)urea peptidomimetics, we introduced a cyclohexyl residue into the P1’ position. The treatment of...
epoxide 4 with a variety of alkylamines altered the P1-P1′ isosteres in which the P1′ site was modified with nitrogen at the backbone and unnatural side chains that are not seen in essential amino acids (Scheme 1). Alternatively, the selected amines and unnatural phenylglycine analogs were included in the P3′ position of certain (hydroxyethyl)ureas. Therefore, two series of (hydroxyethyl)urea peptidomimetics were generated. One series of (hydroxyethyl)urea isosteres, including Jia040, Jia046, Jia047, Jia097, and Jia101, carried a phenyl group at their P1′ site, whereas the other series, including Jia138 and Jia143, carried a cyclohexyl group. Subsequently, more lipophilic analogs were prepared by the introduction of decarboxylated phenylglycine residues [e.g., (+)- and (−)-1-phenylethylamines] into the P3′ position (Jia 104, Jia105, and Jia142) to optimize the relative activities and probe the stereochemical diversity of the binding sites. The effects of these synthesized compounds after purification on the inhibition of γ-secretase activity were examined using the specific cell-based γ-secretase assays as described.

**Inhibition of γ-Secretase-Mediated Cleavage of APP by (Hydroxyethyl)urea Peptidomimetics Containing Unnatural Amino Acid Moieties.** To determine the effects of (hydroxyethyl)urea peptidomimetics containing unnatural amino acid moieties on the inhibition of γ-secretase-mediated cleavage of APP, two highly efficient and quantitative cell-based assays, one assay specifically measuring the β/γ-cleavages of APP (AP-GL-T16) as a whole and the other assay the γ-cleavage of C99 (C99-GL-T20) alone, were used. The generation and validation of both cell-based assays were described previously (Liao et al., 2004; Bakshi et al., 2005). The effects of a series of (hydroxyethyl)urea peptidomimetics containing unnatural amino acid moieties (Jia compounds) are shown in Fig. 1. These Jia compounds were structurally related to two well characterized nontransient state analog inhibitors of γ-secretase, compound E and DAPT (Seiffert et al., 2000; Doyev et al., 2001). Initial screening of these Jia compounds showed that compounds Jia046, Jia047, Jia101, Jia104, and Jia105 at 10 μM exhibited potent inhibition of both APP proteolysis and γ-secretase, comparable with the levels displayed by compound E and DAPT (Fig. 1, A and B). The comparable potency of these effective Jia compounds to those of compound E and DAPT suggested that these Jia compounds could directly target γ-secretase. Most of these Jia compounds, with only the exception of Jia105, presented no significant cellular toxicity (Fig. 1C). All five effective Jia compounds, with only the exception of Jia105, presented comparable potency of these effective Jia compounds to those of compound E and DAPT suggested that these Jia compounds could directly target γ-secretase. Most of these Jia compounds, with only the exception of Jia105, presented no significant cellular toxicity (Fig. 1C). All five effective Jia compounds, with only the exception of Jia105, presented comparable potency of these effective Jia compounds.
It is noteworthy that four active Jia compounds (Jia047, Jia101, Jia104, and Jia105) at lower concentrations (1 μM) induced an approximate 3-fold rise in the level of Aβ42 production (Fig. 4), but they inhibited Aβ42 generation at 10 μM, whereas there was no significant elevation in Aβ40 production by any of the active Jia compounds at the concentrations examined (Fig. 2). Similar effects of active Jia compounds were shown when either T20 cells overexpressing C99 or γ-30 cells stably transfected with APPsw, PS1, Aph-1, and Pen-2 were treated with these compounds. The elevation of Aβ42 at subinhibitory concentrations was previously reported for a set of difluoro ketone peptidomimetic γ-secretase inhibitors (Wolfe et al., 1999a). How these active Jia compounds can differentially affect γ-secretase-dependent production of Aβ40 and Aβ42 remains to be defined.

γ-Secretase-Mediated S3 Cleavage of Notch Is Blocked by Effective Jia Compounds. We next examined whether these γ-secretase-inhibiting Jia compounds also affect the γ-secretase-mediated S3 cleavage of Notch. To do so, a stable cell line (N7) constitutively expressing NACε that acted as the direct substrate of γ-secretase-catalyzed proteolysis independent of ligand activation was treated with various amounts of respective Jia compounds. The efficiency of the N7 stable cell line as an alternative cell-based assay was described previously (Liao et al., 2004). By using Western blotting analyses with the anti-Notch(Val1744) antibody, these effective Jia compounds (Jia046, Jia047, Jia101, Jia104, Jia105, Jia138, Jia142, and Jia143) were shown to significantly block γ-secretase-mediated S3 cleavage of NACε in N7 cells, resulting in complete ablation of NICD production (Fig. 5A). We found that these effective Jia compounds consistently exhibited dose-dependent inhibition of γ-secretase-catalyzed S3 cleavage of NACε (Fig. 5B). Our findings demonstrated that the efficacies of these active Jia compounds as shown by their IC50 values for blocking the γ-secretase-mediated S3 cleavage of NACε were comparable with those for the γ-cleavage of APP (Table 1). The present data suggested that these novel (hydroxyethyl)urea isosteres containing unnatural amino acid moieties can target γ-secretase independent of substrate selection.

In Vitro Stability of (Hydroxyethyl)urea Peptidomimetics Is Dramatically Enhanced by the Replacement of Phenylethylamine at P3′ Site. To examine whether the unnatural amino acid substitution in Jia compounds can prolong the half-life of these peptidomimetics in culture con-

**Fig. 2.** Dose response of Jia compounds on the inhibition of γ-secretase activity and Aβ production. T20 cells (5 × 10⁴ cells/well) in 96-well microplates were treated with various concentrations of respective Jia compounds in DMEM containing 10% FBS and 1 μg/ml tetracycline for 24 h at 37°C. Clarified cell lysates and conditioned media were subjected to the luciferase reporter gene assay for γ-secretase (A) and the quantitation of secreted Aβ40 (B), respectively. Basal levels of γ-secretase activity and Aβ40 production in the presence of vehicle alone (1% DMSO; Control) were determined. Treatments of DAPT were included for the comparison of inhibitory potency. Data are shown as the mean ± S.D. of triplicate measurements from a representative experiment.

**Fig. 3.** Inhibition of γ-secretase by (hydroxyethyl)urea peptidomimetics containing a cyclohexylmethyl moiety at the P1′ site. A, T20 cells (5 × 10⁴ cells/well) in 96-well microplates were treated with 10 μM respective Jia compounds (Jia138, Jia142, or Jia143) in DMEM containing 10% FBS and 1 μg/ml tetracycline for 24 h at 37°C. B, T20 cells were treated with various amounts of Jia138, Jia142, and Jia143 for 24 h at 37°C to determine the dose-dependent effects on the inhibition of γ-secretase. γ-Secretase activities in compound-treated cells were determined by the Steady-Glo luciferase reporter gene assay as specified by the manufacturer. C, secreted Aβ40 in the conditioned media of compound-treated cells was quantitated by an Aβ40 sandwich ELISA kit. Basal levels of γ-secretase activity and Aβ40 production in the presence of vehicle alone (1% DMSO; Control) were also determined. Treatments of DAPT were included for the comparison of inhibitory potency. Data are shown as the mean ± S.D. of triplicate measurements from a representative experiment.
dition, Jia compounds (Jia046, Jia097, Jia138, and Jia142) were added into culture media of T20 cells whose \( \gamma \)-secretase activity was then monitored daily for a span of 8 days. Whereas Jia046 and Jia138 exhibited an approximate half-life of 6 to 8 days that is comparable with the stability of DAPT and compound E, the potency of Jia142 can be fully sustained for at least 8 days (Fig. 6A). Using UV-spectrometry, we found that both Jia142 and DAPT have a characteristic absorbance peak at 244 nm (Fig. 6B). We reasoned that the peak absorbance at 244 nm (OD\(_{244}\)) could be a biophysical property of both compounds and that alteration in OD\(_{244}\) of these peptidomimetics could be indicative of their conformational integrity and chemical stability. Our data demonstrated that the incubations at room temperature for 4 and 24 h both result in a 25% reduction in the OD\(_{244}\) of Jia142, whereas the OD\(_{244}\) of DAPT significantly decreases 50 and 70% after incubations at room temperature for 4 and 24 h, respectively (Fig. 6C). Using mass spectrometry (MS) analyses, we further confirmed that Jia142 (637.4 Da) is thermally more stable than DAPT (433.2 Da). The MS spectra of untreated Jia142 (Jia142-Control) exhibited a corresponding peak intensity of \(2.2 \times 10^5\) at 637.4 m/z that was diminished to \(2.0 \times 10^5\) (Jia142–37°C) or \(7.7 \times 10^4\) (Jia142–50°C) after incubation at 37°C or 50°C for 2 days, whereas those of untreated DAPT (DAPT-Control) displayed a corresponding peak intensity of \(6 \times 10^4\) at 433.2 m/z that is reduced to \(4 \times 10^4\) (DAPT-37°C) or 5000 (DAPT-50°C) after incubation at 37°C or 50°C for 2 days (Fig. 6D). Our data revealed that the abundance of intact Jia142 after incubation at 37 or 50°C for 2 days is reduced to 86 or 33%, whereas only 66 or 8% of DAPT are retained after respective treatments (Fig. 6D, bottom). Together, our findings clearly demonstrated that the substitution of a cyclohexyl moiety at P1 site and a phenylethylamine at P3 site could dramatically enhance the in vitro stability of (hydroxyethyl)urea peptidomimetics.

The Affinity Precipitation of \( \gamma \)-Secretase by Jia138.
To establish the mode of action of active Jia compounds in the inhibition of \( \gamma \)-secretase, we examined whether Jia138 can directly target to \( \gamma \)-secretase. Jia138 was covalently linked to the free primary amine of a six-atom hydrophilic spacer on an agarose affinity resin (Affi-Gel 102; Bio-Rad). Immobilized Jia138 was then used to precipitate PS1 and nicastrin from a CHAPSO-solubilized microsome preparation of \( \gamma \)-30 cells. Solubilized \( \gamma \)-secretase complexes were incubated with the Jia138-conjugated affinity resin in batch format for 2 h at room temperature. Protein-bound resins were washed with a CHAPSO-containing buffer, and affinity-precipitated pro-

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Fig. 4. Effects of active (hydroxyethyl)urea peptidomimetics on A\( \beta \)42 production. Conditioned media of T20 (A) or \( \gamma \)-30 (B) cells that were treated with active Jia compounds for 24 h at 37°C were harvested, and secreted A\( \beta \)42 was determined by an A\( \beta \)42 sandwich ELISA kit. Basal levels of A\( \beta \)42 production in the presence of vehicle alone (1% DMSO; Cont.) were also determined. Treatments of DAPT were performed to show the complete inhibition of A\( \beta \)42 production in these cells. Data are shown as the mean \( \pm \) S.D. of triplicate measurements from a representative experiment.

Fig. 5. Inhibition of \( \gamma \)-secretase-mediated S3 cleavage of Notch by the novel (hydroxyethyl)urea peptidomimetics of Jia compounds. Screening of Jia compounds (A) and dose-dependent response of Jia compounds (B) for the inhibition of \( \gamma \)-secretase-mediated S3 cleavage of Notch. HEK293 cells stably transfected with N\( \gamma \)(7) in 12-well microplates (5 \( \times \) 10\(^5\) cells/well) were treated with 10 \( \mu \)M (A) or various concentrations (B) of individual compounds in DMEM containing 10% FBS for 24 h at 37°C. Clarified lysates of treated cells containing equivalent amounts of proteins were resolved by SDS-PAGE and analyzed by Western blotting using anti-Notch(Val1744). Vehicle alone (1% DMSO) was included as control. Treatment with DAPT was included for comparison.
proteins were analyzed by SDS-PAGE and Western blotting. We found that PS1 and nicastrin can be effectively retained on the Jia138-immobilized matrix, but not on an unconjugated control matrix (Fig. 7A). Proteins isolated by unconjugated or Jia138-conjugated resin visualized by silver staining consistently revealed that only Jia138-conjugated resin can pull down γ-secretase components (Fig. 7B). Using various amounts of solubilized proteins, we further demonstrated that γ-secretase can bind to Jia138 resin in a dose-dependent manner (Fig. 7C). These results clearly suggested that Jia138, and probably other active Jia compounds as well, can exert a specific inhibitor-active site interaction that is required for the binding of PS1 and nicastrin. Our findings also confirmed that the formation of heterodimeric PS1 (PS1-NTF and PS1-CTF) is prerequisite for the constitution of functional γ-secretase.

γ-Secretase-Blocking (Hydroxyethyl)urea Peptidomimetics Promote Neuronal Differentiation of Neuroblastoma Cells. We next sought to determine whether these γ-secretase-inhibitory Jia compounds can promote neuronal differentiation of neuroblastomas through the blocking of Notch activation that is required for maintaining neuroblastoma cells in an undifferentiated state. Recent evidence has suggested that the inhibition of Notch signaling leads to maturation of neuroblastomas, whereas constitutively active Notch signaling can impede the induction of differentiation and neurite formation of neuroblastoma cells (Pahlman et al., 2004). We thus reasoned that these effective Jia compounds can block γ-secretase-dependent Notch signaling and promote neuronal differentiation of neuroblastoma cells. The possible enhancement of neuroblastoma differentiation through the inhibition of γ-secretase was first explored by treating a human neuroblastoma cell line (SH-SY5Y) with various γ-secretase inhibitors. We found that, in 24 h, all seven active Jia compounds examined (Jia046, Jia097, Jia104, Jia105, Jia138, Jia142, and Jia143) could significantly induce the expression of GAP-43 and calreticulin, two differentiation markers of neuroblastoma cells, in SH-SY5Y cells, although to varying degrees (Fig. 8). GAP-43 is the most abundant neuron-specific protein in the growth cones.
and has been shown to be critical for neuronal differentiation (Mani et al., 2001; Singh et al., 2003). Calreticulin is essential for neurite formation during neuronal differentiation, and its expression is tightly associated with reduced malignancy of neuroblastoma (Hsu et al., 2005). The compound-induced neurite outgrowth of SH-SY5Y cells was readily observed after 72 h of treatment (data not shown) and became prominent after 5 days (Fig. 9A). Quantitative analyses showed that the average neuritic length of compound-treated SH-SY5Y cells is significantly increased, ranging from 100 to 200% increase (Fig. 9B). To validate the direct link of γ-secretase-mediated cleavage of Notch to the phenotypic changes of neuroblastoma cells, we used an RNAi approach to define whether specific down-regulation of endogenous Notch signaling is sufficient to drive increased expression of neuronal differentiation markers in neuroblastoma cells. The expression of calreticulin in SH-SY5Y cells that were partially depleted of Notch1 by RNAi was consistently significantly increased, but it was unchanged or slightly reduced in those that were transfected with a Notch1-targeting siRNA in conjunction with the expression of a constitutively active NΔE (Fig. 10A). This Notch1-specific siRNA targeted the exon 7 of endogenous human Notch1 gene that encodes part of its extracellular domain and efficiently down-regulated the expression of endogenous Notch1 and its intracellular domain, evidenced by the decreased levels of endogenous full-length Notch1 and NICD (Fig. 10B, top and top middle). The expression of the exogenous NΔE that encoded only the transmembrane and intracellular domains of mouse Notch1 (Kopan et al., 1996) was not affected by the transfection of...
Notch1 siRNA (Fig. 10B, bottom middle). Thus, even the endogenous Notch signaling was significantly down-regulated by this Notch1-siRNA, the expression of exogenous N[\text{A}]E can still render continuous activation of Notch signaling in transfected SH-SY5Y cells. These results demonstrated that Jia compound-induced neuronal differentiation of neuroblastoma cells was intimately associated with the inhibition of Notch signaling and that the expression of an exogenous N[\text{A}]E can rescue the phenotype of undifferentiated neuroblastoma cells. These data provided direct evidence strongly suggesting that the attenuation of Notch signaling by \( \gamma \)-secretase inhibitors could effectively initiate the neuronal differentiation of neuroblastoma cells. Together, our findings not only identified a novel class of (hydroxyethyl)urea isosteres that contain unnatural amino acid moieties and exhibit potent inhibition of \( \gamma \)-secretase activity but also provided the direct evidence that the inhibition of Notch signaling by \( \gamma \)-secretase inhibitors is sufficient to induce the differentiation of neuroblastomas.

**Discussion**

\( \beta \)-amyloid, the principal constituent of senile plaques in the AD brain, is derived by sequential proteolyses mediated by \( \beta \)- and \( \gamma \)-secretases. Thus, these proteases have been regarded as the prime targets for the development of therapeutics against AD. The present study provides evidence that (hydroxyethyl)urea isosteres containing unnatural amino acid moieties retain their potency toward the inhibition of \( \gamma \)-secretase. This inhibition is verified by using cell lines that over-express APP695, C99, or N[\text{A}]E as substrates of \( \gamma \)-secretase-mediated proteolysis. Although the active Jia compounds might not possess as strong a potency as DAPT and compound E do in terms of IC\(_{50}\) values, they exhibit comparable levels of potency at submicromolar concentrations to other reported active (hydroxyethyl)urea peptidomimetics in cell-based systems (Bakshi and Wolfe, 2004; Esler et al., 2004). Furthermore, the active (hydroxyethyl)urea peptidomimetics reported here can efficiently promote the neuronal differentiation of neuroblastoma cells, probably through the inhibition of Notch signaling. These findings substantiate the notion that the incorporation of unnatural amino acid moieties, such as phenylethylamine (e.g., Jia142), could stabilize synthetic (hydroxyethyl)urea peptidomimetics without compromising their biological effects and their mode of action. Our results also suggest that the integration of unnatural peptidomimetics can be a valid methodology for further drug development.

Active Jia compounds are selected for their abilities to inhibit \( \gamma \)-secretase-mediated processing of APP695-GV or C99-GV. We have shown that most of the (hydroxyethyl)ureas with a leucyl residue at the P2 position (Jia046, Jia047, Jia101, Jia104, and Jia105) display excellent potencies for the inhibition of \( \gamma \)-secretase-dependent processing of APP695 and C99, as demonstrated by the reduction in \( \gamma \)-secretase

![Fig. 9. Neuronal phenotypic changes of neuroblastoma cells induced by active (hydroxyethyl)urea peptidomimetics. A, human neuroblastoma SH-SY5Y cells that were treated with vehicle alone (0.1% DMSO), 1 \( \mu \)M RA, 10 \( \mu \)M DAPT, or 10 \( \mu \)M concentrations of respective Jia compounds were incubated at 37°C for 5 days. SH-SY5Y cells treated with active Jia compounds exhibited significant neurite outgrowth, exemplifying the neuronal differentiation similar to RA-induced phenotypic changes. Phase-contrast images were taken by Sony DSC-W5 digital camera and processed with Adobe Photoshop software (Adobe Systems, Mountain View, CA). Scale bar, 20 \( \mu \)m. B, neuritic length of DMSO- and compound-treated SH-SY5Y cells \((n > 50\) for each treatment) were measured and analyzed by NIH Image as described under Materials and Methods. Results are expressed as the average (\pm S.D.) neurite length and analyzed by Student\’s \( t \) test. *, \( p < 0.001 \).](molpharm.aspetjournals.org)
activity down to the basal level. These results are in agreement with previous reports, in which the S2’ active site pocket apparently accommodates moderate isobutyl substituents (Esler et al., 2004). In addition, alterations in the P3’ position reveal that Jia compounds substituted with an unnatural phenylglycine residue exhibit better potencies than the compounds containing a valine residue (Jia097). Consistent with previous studies (Esler et al., 2004), our results suggest that the S3’ pocket presents relatively loose specificity and can accommodate great variation in stereochemistry as shown by the similar potencies between Jia104 and Jia105 or between Jia046 and Jia101. Furthermore, removal of the carboxyl residue at position P3’ (such as Jia046 changed to Jia104 or Jia 101 changed to Jia105) does not abrogate the inhibitory potency. Therefore, the reduction in the molecular weight and improvement in the lipophilic properties of theses (hydroxyethyl)urea peptidomimetics could be optimized without compromising their pharmaceutical profiles.

The modification of dipeptide isosteres at the P1-P1’ position has also been shown to be critical to $\gamma$-secretase inhibition (Nadin et al., 2003). To test this idea, the P1’ residues (Phe) of Jia 097, Jia046, and Jia105 are thus replaced with an isosteric cyclohexylmethyl (Chy) moiety to generate Jia138, Jia142, and Jia143. We show that the Chy-substituted Jia138 exhibits significantly improved efficacy of inhibiting $\gamma$-secretase, whereas Jia143 and Jia142 maintained their inhibitory potencies. It is noteworthy that the Chy-substituted Jia138 presents dramatic improvement on the inhibition of $\gamma$-secretase-mediated production of APP (IC$_{50}$ values of 0.704 for Jia138 versus 0.794 for DAPT), whereas its efficacy of inhibiting S3 cleavage of Notch fares less well than DAPT does (with an IC$_{50}$ of 0.235 versus 0.039). Both Jia138 and its Phe-containing analog Jia046 consistently exhibit better potency toward the processing of APP (IC$_{50}$ values of 0.704 $\mu$M for Jia046 and 0.074 $\mu$M for Jia138 in $\beta$-secretase production) than that of Notch (IC$_{50}$ values of 3.965 $\mu$M for Jia046 and 0.235 $\mu$M for Jia138 in NICD production). Moreover, all of these active Jia compounds have better potency toward the inhibition of Aβ production than that of NICD production, whereas DAPT and compound E have better potency in blocking $\beta$-secretase production. It is thus likely that the incorporation of selective unnatural amino acids at the P1’ and P3’ sites of (hydroxyethyl)urea peptidomimetics could have greater impact in the $\gamma$-secretase-mediated processing of APP than that of Notch. The possibility exists that we can technically drive the transition state analog inhibitors, based on the structural features of Jia138, to preferentially block the Aβ production without tampering with the physiological function of Notch signaling and other $\gamma$-secretase substrates. Together, the combination of a Chy moiety at the P1’ site and a phenylglycine analog at the P3’ position might offer the structural scaffold for the subsequent development of $\gamma$-secretase inhibitors that selectively block only the pathogenic APP processing.

Our findings also demonstrate that the inhibitory potency of the Chy-containing Jia142, a C-terminal decarboxylated analog of Jia046, can be fully sustained for at least 8 days under cell culture conditions, suggesting that the stability of (hydroxyethyl)urea peptidomimetics could be dramatically improved by the substitution of distinctive unnatural amino acid moiety. Furthermore, these unnatural amino acid-substituted (hydroxyethyl)urea peptidomimetics, as exemplified...
by Jia138, can inhibit γ-secretase and bind directly to heterodimeric PSs, resembling the characteristics of previously reported (hydroxyethyl)urea peptidomimetics and hydroxyethylene transition state analogs (Li et al., 2000a,b; Esler et al., 2002). The present data are thus in accordance with the conception that γ-secretase can tolerate unnatural d-amino acids as well as natural L-amino acids in transition state analog inhibitors (Bakshi and Wolfe, 2004; Esler et al., 2004), and they reveal that these unnatural amino acid-substituting (hydroxyethyl)urea peptidomimetics, like other transition state analog inhibitors, could specifically target to the active site of γ-secretase. Our findings also substantiate the model that the formation of heterodimeric PS1 (PS1-NTF and PS1-CTF) is prerequisite for the functional γ-secretase.

These effective Jia compounds significantly blocked the production of Aβ40, but they dramatically augmented the production Aβ42 at a subinhibitory concentration (1 μM). This effect has previously been observed for various γ-secretase inhibitors (Citron et al., 1996; Wolfe et al., 1999a). The mechanism underlying the increased production of Aβ42 by some active Jia compounds at lower concentrations remains unclear. Accumulating evidence has suggested that Aβ42 production mostly occurs in intracellular compartments, including endoplasmic reticulum and Golgi (Cook et al., 1997; Hartmann et al., 1997; Wild-Bode et al., 1997). Given that Jia047, Jia104, and Jia105 all cause dramatic increases in the levels of Aβ42 without affecting the levels of Aβ40 at a 1 μM concentration, our findings are in agreement with the notion that selective inhibition of Aβ40 formation can result in more efficient production of Aβ42 from the accumulated C99 substrate in these intracellular localizations (Wolfe et al., 1999a). Further development of (hydroxyethyl)urea isosteres using the structural scaffold identified in the present study might allow us to selectively target the Aβ42-generating γ-secretase that is localized intracellularly without perturbing Aβ40 production.

The γ-secretase-dependent S3 cleavage of Notch is a prerequisite for its downstream signaling that is essential for a variety of cell fate determination events during development and in adults (Mumm and Kopan, 2000). In addition, the protransfoming role of Notch signaling has recently been recognized and well defined in a variety of cancers (Weng and Aster, 2004). The constitutive activation of Notch signaling in neuroblastomas has been shown to block induced differentiation and neurite formation (Grynfeld et al., 2000; Levy et al., 2002), suggesting the oncogenic effect of Notch in neuroblastomas. It is thus plausible that the inhibition of Notch signaling by specific γ-secretase inhibitors might interrupt its oncogenic effect and promote the differentiation of neuroblastoma cells, resulting in a decrease in their malignancy. We demonstrated by biochemical and morphological analyses that all active Jia compounds can block Notch signaling by reducing the generation of NICD and induce the neuronal differentiation of neuroblastoma cells. These data are in accordance with the idea that neurite outgrowth is markedly altered upon the inhibition of γ-secretase (Figueroa et al., 2002) and that activation of Notch signaling results in shrinkage of neuritic processes of cultured neuroblastoma cells (Ishikura et al., 2005). Our findings thus not only validate the efficacy of unnatural amino acid-containing (hydroxyethyl)urea peptidomimetics in biological systems but also demonstrate the beneficial effects of active Jia compounds on the maturation and differentiation of neuroblastoma cells.

Taken together, we demonstrate the identification of a novel class of γ-secretase inhibitors that contain unnatural amino acid moieties as a scaffold structure using various cell-based γ-secretase assays. These active (hydroxyethyl)urea peptidomimetics effectively reduce Aβ production and Notch signaling, and they present beneficial effects on neuroblastomas beyond their capacity for blocking the Aβ-centered pathogenesis of AD. The present evidence further suggests that the substitution of a peptidic moiety with selective unnatural amino acids will not compromise the potency for the inhibition of γ-secretase and could pave the way for the development of synthetic peptidomimetics of γ-secretase inhibitors with great stability in biological systems. The novel structural features of (hydroxyethyl)urea peptidomimetics are thus useful molecular tools for further characterization of this protease, and they could have great implications for the development of anti-AD drugs and therapeutics for neuroblastomas.

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Address correspondence to: Dr. Yung-Feng Liao, Institute of Cellular and Organismic Biology, Rm 238, Academia Sinica, 128 Academia Rd. Sec. 2, Taipei 115, Taiwan. E-mail: yiliao@sinica.edu.tw