

Striatal-enriched Protein-tyrosine Phosphatase (STEP) Regulates Pyk2 Kinase Activity^{*S}

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Jian Xu^{†1}, Pradeep Kurup[‡], Jason A. Bartos^{§2}, Tommaso Patriarchi[§], Johannes W. Hell^{¶3}, and Paul J. Lombroso^{¶||**}

From the [†]Child Study Center and Departments of ^{||}Psychiatry and ^{**}Neurobiology, Yale University School of Medicine, New Haven, Connecticut 06520, [§]Department of Pharmacology, University of Iowa, Iowa City, Iowa 52242, and [¶]Department of Pharmacology, University of California, Davis, California 95615

Background: Proline-rich tyrosine kinase 2 (Pyk2) is implicated in synaptic plasticity; however, it remains unclear how Pyk2 is inactivated within neurons.

Results: Striatal-enriched protein-tyrosine phosphatase (STEP) directly binds to and dephosphorylates Pyk2 at Tyr⁴⁰².

Conclusion: STEP inactivates Pyk2 and its downstream signaling pathways.

Significance: These results identify an important regulatory mechanism for Pyk2 signaling that is critical for understanding the molecular mechanisms underlying synaptic plasticity.

Proline-rich tyrosine kinase 2 (Pyk2) is a member of the focal adhesion kinase family and is highly expressed in brain and hematopoietic cells. Pyk2 plays diverse functions in cells, including the regulation of cell adhesion, migration, and cytoskeletal reorganization. In the brain, it is involved in the induction of long term potentiation through regulation of *N*-methyl-D-aspartate receptor trafficking. This occurs through the phosphorylation and activation of Src family tyrosine kinase members, such as Fyn, that phosphorylate GluN2B at Tyr¹⁴⁷². Phosphorylation at this site leads to exocytosis of GluN1-GluN2B receptors to synaptic membranes. Pyk2 activity is modulated by phosphorylation at several critical tyrosine sites, including Tyr⁴⁰². In this study, we report that Pyk2 is a substrate of striatal-enriched protein-tyrosine phosphatase (STEP). STEP binds to and dephosphorylates Pyk2 at Tyr⁴⁰². STEP KO mice showed enhanced phosphorylation of Pyk2 at Tyr⁴⁰² and of the Pyk2 substrates paxillin and ASAP1. Functional studies indicated that STEP opposes Pyk2 activation after KCl depolarization of cortical slices and blocks Pyk2 translocation to postsynaptic densities, a key step required for Pyk2 activation and function. This is the first study to identify Pyk2 as a substrate for STEP.

Proline-rich tyrosine kinase 2 (Pyk2),⁴ also known as cell adhesion kinase β , is a member of the focal adhesion kinase

family and is highly expressed in the central nervous system (CNS) (1–3). Pyk2 is activated in response to increases in intracellular calcium levels (1, 4, 5), neuronal membrane depolarization (6, 7), hyperosmolarity (7), and activation of protein kinase C (1, 8, 9).

Upon stimulation, Pyk2 undergoes rapid autophosphorylation at Tyr⁴⁰², creating a docking site for the SH2 domain of Src family kinase members Src and Fyn. Pyk2 phosphorylates and activates Src and Fyn (10–12), either one of which then phosphorylates Pyk2 at Tyr^{579/580} within its activation loop (13, 14). Pyk2 activation results in postsynaptic translocation and association of Pyk2 with the SH3 domain of postsynaptic density (PSD)-95 (15), which is essential for Pyk2 activation and the induction of long term potentiation (LTP) (15). Src also phosphorylates Pyk2 at Tyr⁸⁸¹, leading to recruitment of the Grb2-SOS complex and subsequent activation of mitogen-activated protein kinase (MAPK) (1, 16). Thus, Pyk2 activates the Src family kinase and MAPK signaling pathways, both of which are required for the induction and maintenance of LTP (17, 18). Overexpression of a catalytically inactive mutant of Pyk2 (K457A) or disruption of Pyk2/PSD-95 interactions disrupts LTP, underscoring the importance of Pyk2 in regulating synaptic plasticity (15, 17).

Considerably more is known about the kinases that activate Pyk2 within the CNS compared with the tyrosine phosphatases that inactivate it. Several protein-tyrosine phosphatases (PTPs) have been reported to associate with Pyk2 outside of the CNS and regulate its activity (19–21). SHP1 dephosphorylates the autophosphorylation site Tyr⁴⁰² of Pyk2 and down-regulates integrin-mediated immune cell adhesion and inflammation (19). PTP-PEST also targets Tyr⁴⁰² as well as Tyr^{579/580} in the activation loop of Pyk2 and regulates cell motility (20, 22). However, a physiologically relevant PTP in the brain has not yet been reported.

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¹ To whom correspondence may be addressed: Child Study Center, Yale University School of Medicine, 230 South Frontage Rd., SHM I-269, New Haven, CT 06519. E-mail: jian.xu@yale.edu.

² Present address: Dept. of Internal Medicine, Stanford University, Palo Alto, CA 94305.

³ To whom correspondence may be addressed: Dept. of Pharmacology, School of Medicine, University of California at Davis, GBSF 3503, 451 East Health Sciences Dr., Davis, CA 95616. E-mail: jwhell@ucdavis.edu.

⁴ The abbreviations used are: Pyk2, proline-rich tyrosine kinase 2; LTP, long term potentiation; STEP, striatal-enriched protein-tyrosine phosphatase; PSD, postsynaptic density; PR, polyproline-rich; SH, Src homology; PTP, protein-tyrosine phosphatase; TAT, trans-activator of transcription; KIM, kinase-

interacting motif; aCSF, artificial cerebrospinal fluid; CsA, cyclosporin A; C/S, C300S; FP, fluorescence polarization; SOS, Son-of-sevenless; PEST, proline (P), glutamic acid (E), serine (S) and threonine (T); SYF cells, mouse embryo fibroblast cells deficient for Src, Yes and Fyn; SEM, standard error of the mean; ANOVA, analysis of variance.

TABLE 1

Primary and secondary antibodies used in this study

CaMKII, Ca²⁺/calmodulin-dependent protein kinase II.

Antibody	Format	Immunogen	Host	Dilution	Source
Anti-Tyr(P) ⁴⁰² Pyk2	Whole IgG, unconjugated	Human synthetic phosphopeptide	Rabbit	1:1,000	Invitrogen
Anti-Pyk2 N terminus	Whole IgG, unconjugated	N terminus of rat sequence	Rabbit	1:500	As described (15)
Anti-Pyk2 (H-102)	Whole IgG, unconjugated	N terminus of human Pyk2	Rabbit	1:1,000	Santa Cruz Biotechnology
Anti-STEP	IgG ₁ , unconjugated	Rat synthetic peptide	Mouse	1:1,000	As described (68)
Anti-Fyn	Whole IgG, unconjugated	Human synthetic peptide	Rabbit	1:600	Millipore
Anti-Tyr(P) ¹⁴⁷² NR2B	Whole IgG, unconjugated	Synthetic phosphopeptide	Rabbit	1:1,000	Phosphosolutions, Denver, CO
Anti-NR2B	Whole IgG, unconjugated	C terminus of mouse NR2B	Rabbit	1:1,000	Millipore
Anti-Tyr(P) ¹¹⁸ paxillin	Whole IgG, unconjugated	Human synthetic phosphopeptide	Rabbit	1:1,000	Cell Signaling Technology, Danvers, MA
Anti-paxillin	Whole IgG, unconjugated	Human synthetic peptide	Rabbit	1:1,000	Cell Signaling Technology
Anti-Tyr(P) ⁷⁸² ASAP1	Whole IgG, unconjugated	Mouse synthetic phosphopeptide	Rabbit	1:1,000	Rockland, Gilbertsville, PA
Anti-ASAP1	Whole IgG, unconjugated	Mouse synthetic peptide	Mouse	1:100	Rockland
Anti-Tyr(P) ²⁰⁴ ERK1/2	Whole IgG, unconjugated	Human synthetic phosphopeptide	Mouse	1:1,000	Santa Cruz Biotechnology
Anti-ERK2	Whole IgG, unconjugated	C terminus of rat sequence	Rabbit	1:5,000	Santa Cruz Biotechnology
Anti-PSD-95, clone K28/43	IgG2aκ, unconjugated	Fragment of human PSD-95 protein	Mouse	1:10,000	Millipore
Anti-β-actin	Whole IgG, unconjugated	Human synthetic peptide	Rabbit	1:1,000	Sigma-Aldrich
Anti-GAPDH, clone 6c5	IgG ₁ , unconjugated	Purified protein from rabbit muscle	Mouse	1:20,000	Millipore
Anti-tubulin	IgG ₁ , unconjugated	Purified chick brain tubulin	Mouse	1:500	Sigma-Aldrich
Anti-synaptophysin	Unpurified mouse IgG1, unconjugated	Rat retina synaptophysin	Mouse	1:2,000	Millipore
Anti-CaMKII	Whole IgG, unconjugated	Mouse synthetic peptide	Rabbit	1:2,000	Santa Cruz Biotechnology
Anti-histone H1	IgG _{2a} , unconjugated	Human synthetic peptide	Mouse	1:2,000	Santa Cruz Biotechnology
Anti-rabbit	Whole IgG peroxidase-conjugated	Rabbit Fc	Donkey	1:10,000	Amersham Biosciences
Anti-mouse	Whole IgG peroxidase-conjugated	Mouse Fc	Sheep	1:10,000	Amersham Biosciences
Anti-rabbit	Whole IgG Alexa Fluor 594-conjugated	Rabbit Fc	Goat	1:600	Molecular Probes
Anti-mouse	Whole IgG Alexa Fluor 488-conjugated	Mouse Fc	Goat	1:600	Molecular Probes

Here we focus on the brain-enriched striatal-enriched protein-tyrosine phosphatase (STEP) as a possible regulator of Pyk2 in neurons. Previous studies have established that STEP normally opposes the development of synaptic strengthening by dephosphorylating and inactivating ERK1/2 (23, 24) and Fyn (25). STEP also regulates glutamate receptor internalization. Dephosphorylation of the GluN2B subunit of the *N*-methyl-D-aspartate receptor (formerly NR2B) and the GluA2 subunit of the AMPA receptor (formerly GluR2) results in internalization of GluN1-GluN2B (26) and GluA1-GluA2 receptors, respectively (27). STEP is a critical regulator of synaptic function, and the identification of additional substrates will clarify its normal function. Here we identify Pyk2 as a novel substrate for STEP using biochemical, molecular, and immunocytochemical techniques in wild type (WT) and STEP knock-out (KO) mice.

EXPERIMENTAL PROCEDURES

Antibodies and Other Reagents—All antibodies used in this study are listed in Table 1. NMDA and ionomycin were purchased from Sigma-Aldrich, and M-PER mammalian lysis buffer was from Pierce.

Constructs and Purification of Fusion Proteins—PCR-amplified open reading frames of STEP₆₁ or STEP₄₆ were subcloned into pcDNA3-His/V5 (Invitrogen) or pGEX4T1 vector (GE Healthcare). Trans-activator of transcription (TAT)-STEP₄₆ was subcloned into the pTrcHis2-TOPO construct (Invitrogen) as described (27, 28). Point mutations were introduced using site-directed mutagenesis (kit from Stratagene, Santa Clara, CA), and all constructs were sequenced prior to use. Deletion constructs of STEP (polyproline-rich 1 and 2 (PR1 and PR2) and the kinase-interacting motif (KIM) domains) and pCMV-hFyn constructs were described previously (25). GST-tagged Pyk2 constructs (15) were PCR-amplified and subcloned into pcDNA3-His/V5 or pTrcHis2 construct (Invitrogen). See Fig. 1, which was made with the assistance of DOG software as described (29), for schematic domain structures of constructs used in this study.

Fusion constructs were expressed in *Escherichia coli* BL21(DE3) and purified on glutathione-Sepharose (GE Healthcare) or TALON metal affinity resin beads (Clontech) following the manufacturers' instructions. GST fusion proteins were eluted with 10 mM reduced glutathione in phosphate-buffered saline (PBS), pH 8. His-tagged proteins were eluted in PBS, pH 7.4, 150 mM imidazole. All proteins were concentrated using Amicon Ultra-4 filter units with 30- or 50-kDa cutoffs (Millipore, Billerica, MA). For some assays, STEP₄₆ fusion proteins, which lack the N-terminal 172 amino acids of STEP₆₁, were used, because of technical difficulty in purification of large amounts of the insoluble protein STEP₆₁.

Brain Slices and Treatments—The Yale University Institutional Animal Care and Use Committee approved all animal procedures used in the present study. Coronal corticostriatal slices (300 μm) were prepared from male WT or STEP KO mice (8–10 weeks on a C57B6 background as described (30)). Slices were sectioned in ice-cold oxygenated artificial cerebrospinal fluid (aCSF) (124 mM NaCl, 4 mM KCl, 26 mM NaHCO₃, 1.5 mM CaCl₂, 1.25 mM KH₂PO₄, 1.5 mM MgSO₄, 10 mM D-glucose). After recovery in aCSF for 60 min, slices were treated with 40 mM KCl for 2 min. Some slices were preincubated with 2 μM TAT-STEP₄₆ or TAT-STEP₄₆ C/S (27, 2) followed by KCl stimulation. Slices were placed on dry ice immediately after stimulations and homogenized.

Preparations of Brain Lysates and PSD Fractions—Slices were homogenized in TEVP buffer (10 mM Tris, pH 7.4, 5 mM NaF, 1 mM Na₃VO₄, 1 mM EDTA, 1 mM EGTA, protease inhibitor mixture (Roche Applied Science)), and P2 fractions were obtained as described previously (28). P2 fractions were extracted in detergent (0.5% Triton X-100)-containing buffers as described (31). The insoluble fractions (PSD) were lysed in radioimmune precipitation assay buffer with 1% SDS buffer followed by brief sonication.

Preparation of Synaptoneurosomal Fractions—Synaptoneurosomes from WT or STEP KO mice whole brains were

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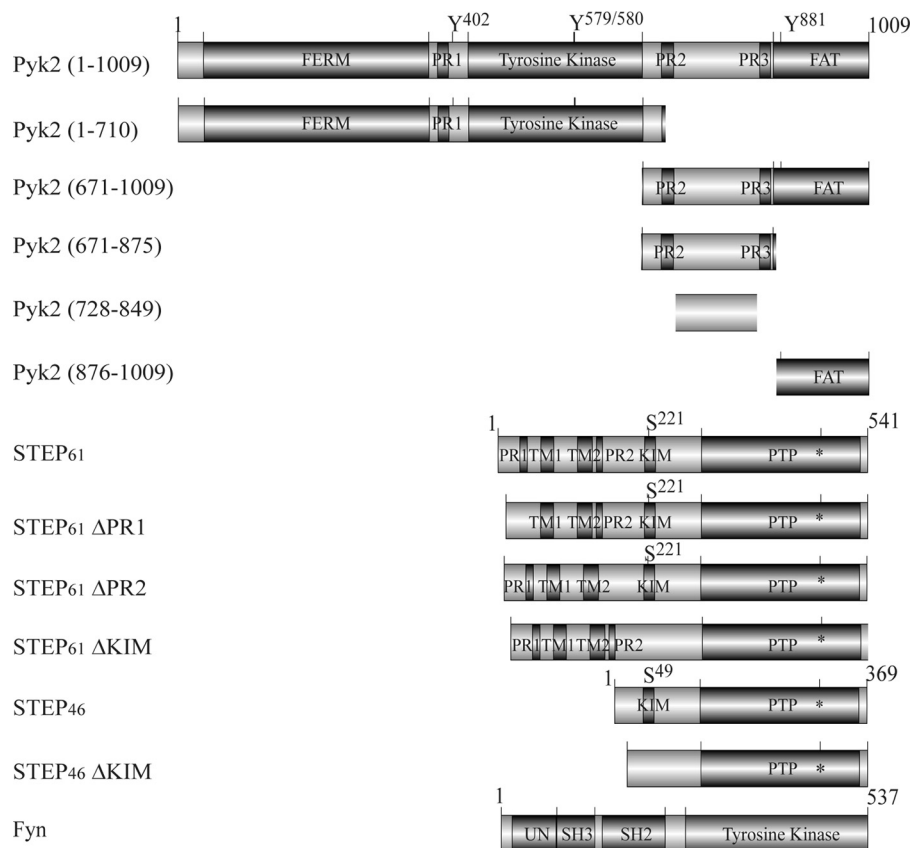


FIGURE 1. **Schematic domain structures used in this study.** FERM, band 4.1/ezrin/radixin/moesin homology domain; FAT, focal adhesion-targeting domain; TM1 and TM2, putative transmembrane domains; PTP, protein-tyrosine phosphatase domain; asterisk, cysteine residue in the catalytic core; UN, unique N-terminal domain. Regulatory phosphorylation sites are shown. Numbering refers to amino acid residues within the proteins.

obtained as described previously (27). Briefly, tissues were homogenized in homogenization buffer (20 mM HEPES/NaOH, pH 7.4, 124 mM NaCl, 1.06 mM KH₂PO₄, 26 mM NaHCO₃, 1.3 mM MgCl₂, 2.5 mM CaCl₂, 10 mM glucose, Complete protease inhibitor tablets (Roche Applied Science)). Homogenates were centrifuged at 2000 × *g* for 1 min. The supernatant was passed through two 100- μ m nylon mesh filters (Sefar America, Richfield, MN) followed by a 5- μ m nitrocellulose filter (Millipore) and centrifuged at 1000 × *g* at 4 °C for 10 min. Pellets were washed, resuspended in homogenization buffer, and dispensed into 100- μ l aliquots. All aliquots were preincubated at 37 °C for 10 min before stimulation with 40 mM KCl for various times as indicated. Some aliquots were pretreated with cyclosporin A (CsA; 100 nM) for 20 min before the addition of KCl. Thirty microliters of each aliquot were mixed with 6× SDS sample buffer and subjected to Western blotting.

Cell Culture and Transfection—HEK293 cells or SYF cells (a generous gift from A. M. Bennett, Yale University School of Medicine) were grown in DMEM supplemented with 10% heat-inactivated fetal bovine serum (FBS) and antibiotics. HEK293 or SYF cells were seeded at 1 × 10⁶ cells/35-mm dish 24 h before transfection. The next day, pcDNA3-STEP WT, mutants, or truncation constructs were co-transfected with pcDNA3-Pyk2 or pCMV-Fyn using Lipofectamine 2000 (Invitrogen) following the manufacturer's protocol. After 6 h of incubation at 37 °C, the medium was replaced, and cells were incubated for another 36–48 h. Cells were lysed in M-PER

mammalian extraction reagent (Pierce) and subjected to immunoprecipitation or Western blotting.

Immunoprecipitation and Pulldown Assays—Mouse brain homogenates or cell lysates were subjected to immunoprecipitation with anti-STEP or anti-Pyk2 antibodies in M-PER reagents overnight at 4 °C. The 2nd day, Protein A/G PLUS-Agarose beads (Santa Cruz Biotechnology) were added and incubated for another 4 h. Beads were collected by centrifugation and washed three times with lysis buffer. Immunoprecipitates were resuspended in SDS sample buffer after the final wash and analyzed by immunoblotting with anti-STEP, anti-Pyk2, or anti-Fyn antibody.

For pulldown assays, GST fusion proteins were adsorbed to glutathione-Sepharose beads for 2 h at 4 °C and then incubated with WT or STEP KO mouse brain homogenates (100 μ g) in radioimmune precipitation assay buffer overnight at 4 °C. In some experiments, the catalytically inactive GST-STEP₆₁ C472S protein was mixed with 1 μ g of His-Pyk2 and increasing amounts of His-Fyn. Beads were washed and subjected to SDS-PAGE followed by immunoblotting.

In Vitro Binding—GST-tagged Pyk2 constructs (either full-length Pyk2 (amino acids 1–1009) or with amino acid deletions to give amino acids 1–710, 671–1009, 671–875, 728–849, or 876–1009) or GST alone was immobilized on glutathione-Sepharose beads. After washes, His-tagged STEP₄₆ (500 nM) was added for 2 h at 4 °C. The samples were washed and subjected to SDS-PAGE. Prior to immunoblotting with anti-STEP antibody,

TABLE 2
Sequences of peptides used in fluorescence polarization and pulldown assay

Name	Sequence	Modification
STEP_PR2	HLLKAPPEPPAPLPEDRRQ	N terminus, FITC; C terminus, amide
STEP_KIM	TVKSMGLQERRGSNVSLTLDM	N terminus, FITC; C terminus, amide
Pyk2_671–694	RFTELVCSLSDIYQMERDIAIEQEQ	N terminus, FITC; C terminus, amide
Pyk2_689–712	IAIEQEERNARYRPPKILEPTAFQEQ	N terminus, FITC; C terminus, amide
Pyk2_707–723	PTAFQEPPPKPSRPKYK	N terminus, FITC; C terminus, amide
Pyk2_850–866	TEFTGPPQKPPRLGAQS	N terminus, FITC; C terminus, amide
TAT-Myc	YGRKKRRQRRREQLISEEDL	None

the membranes were stained with Ponceau S stain to visualize GST fusion proteins.

Fluorescence Polarization (FP) and Competitive Binding Assays—FP-based binding assays were performed in a Synergy 2 plate reader (BioTek, Winooski, VT) with Gen5 software using 96-well black polystyrene plates (Corning, Corning, NY). Fluorescein isothiocyanate (FITC)-labeled peptides were obtained from CHI Scientific (Maynard, MA). The sequences are shown in Table 2. Increasing concentrations of recombinant proteins (either GST-STEP₆₁, GST-STEP₄₆, or GST-Pyk2(671–875)) were incubated with FITC-labeled peptide at a final concentration of 1 μ M in FP buffer (50 mM HEPES, pH 7.4, 100 mM KCl, 1 mM MgCl₂, 0.05 mM EGTA, 5 mM nitrilotriacetic acid). Parallel and perpendicular intensities were determined with 485/20 λ excitation and 528/20 λ emission filters, and FP was calculated as described by Lim *et al.* (32) For each graph, signals were normalized by setting the lowest value as zero and the highest value as 100%.

Competitive binding by peptides was also examined in GST pulldown assays. GST-STEP₆₁ or GST-Pyk2(671–875) was bound to glutathione-Sepharose beads. Mouse brain lysates were preincubated with increasing concentrations of peptides for 2 h at 4 °C and then mixed with protein-Sepharose complexes overnight at 4 °C. Precipitates were washed extensively and resuspended in SDS sample buffer.

Dephosphorylation of Pyk2 by STEP in Vitro—Mouse brain lysates were incubated at 65 °C for 20 min to inactivate endogenous kinases and phosphatases. The same amount of lysates (100 μ g) was incubated with GST-STEP₄₆ (active) or GST-STEP₄₆ C/S (inactive) fusion proteins in dephosphorylation buffer (25 mM HEPES, pH 7.3, 5 mM EDTA, 5 mM DTT) for 30 min at 30 °C.

Dephosphorylation of Pyk2 by STEP was also carried out with Pyk2 immunoprecipitated from mouse brain lysates using anti-Pyk2 antibody and protein A/G-agarose. The precipitates were allowed to undergo autophosphorylation in the presence or absence of ATP and/or pervanadate. In some assays, active STEP (10 μ M) was added in the presence or absence of pervanadate (1 mM). Phosphorylation of Pyk2 at Tyr⁴⁰² was accessed with a phosphospecific antibody. The Tyr(P)⁴⁰² signal was normalized to total Pyk2 levels.

Immunoblotting—Samples were resolved by SDS-PAGE and transferred to nitrocellulose membranes (Bio-Rad) as described previously (28). Membranes were blocked in TBS-Tween 20 + 5% bovine serum albumin (BSA) and incubated with primary antibodies overnight at 4 °C. The next day membranes were washed and incubated in peroxidase-conjugated secondary antibodies (Amersham Biosciences) for 2 h at RT. Blots were developed using a chemiluminescent substrate kit (Pierce), and

immunoreactivity was captured by a G:BOX with the image program GeneSnap (Syngene, Cambridge, UK). All densitometric quantifications were performed using the Genetools program (Syngene).

Immunofluorescence—Primary hippocampal neurons were isolated from rat E18 embryos as described previously (28). Neurons were plated on poly-D-lysine-coated slides (2.5 \times 10⁴ cells/cm²; Thermo Scientific) in Neurobasal medium supplemented with 2% B27 (Invitrogen) and grown for 14–21 days. Cells were fixed in 4% paraformaldehyde with 4% sucrose and permeabilized with 0.2% Triton X-100 in PBS as described previously (28). After blocking with 10% normal goat serum and 1% BSA for 1 h, cells were stained with anti-Pyk2 and anti-STEP antibodies overnight at 4 °C. Goat anti-rabbit Alexa Fluor 594- or goat anti-mouse Alexa Fluor 488-conjugated secondary antibodies (Molecular Probes, Eugene, OR) were used to detect the primary antibodies. To exclude the possibility of nonspecific antibody staining, immunodepleted antibodies were also used as controls. Anti-STEP or anti-Pyk2 antibody was subjected to four sequential immunodepletion rounds with GST-STEP₆₁ or GST-Pyk2, which was preadsorbed to glutathione-Sepharose beads. Secondary antibodies alone were also included as controls. To visualize Pyk2 translocation to PSD fractions upon KCl stimulations, anti-Pyk2 and anti-PSD-95 antibodies were used to indicate colocalization. Microscopy was performed with a Zeiss Axiovert 2000 microscope with an apotome (Applied Scientific Instruments, Eugene, OR) using a 100 \times objective lens. A punctum was defined as a continuous group of pixels corresponding to 0.5–3.0 μ m. Colocalization analysis was performed on randomly selected images ($n = 17$) using NIH Image J software with the colocalization analysis plug-in at default settings (ratio, 50%; threshold for each channel, 50).

Statistical Analysis—All experiments were repeated at least three times. Data were expressed as means \pm S.E. For some experiments, statistical significance was determined by Student's *t* test, whereas in others, data were analyzed with one-way ANOVA with post hoc Tukey test. *p* values <0.05 were considered significant.

RESULTS

Inhibition of Tyrosine Phosphatases Leads to Activation of Pyk2—Our previous study showed that resin-bound anti-Pyk2 antibody facilitated Pyk2 dimerization and activation (15). We used this technique to activate Pyk2 in rat brain homogenates. We assessed autophosphorylation of Pyk2 in solution (Fig. 2A, *No Resin*) or bound to beads (Fig. 2A, *Resin Bound*) in the absence or presence of the general tyrosine phosphatase inhibitor pervanadate (1 mM). Similar to previous findings (15), Pyk2 antibody induced autophosphorylation of Pyk2 in lysate and on

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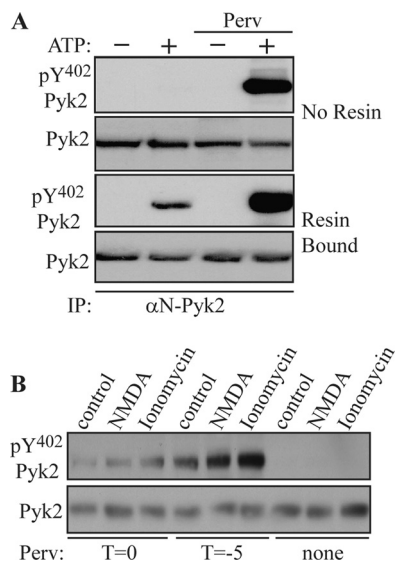


FIGURE 2. Phosphorylation of Pyk2 at Tyr⁴⁰² is increased in presence of protein-tyrosine phosphatase inhibitor. *A*, rat brain extracts were incubated with 1 μ g of α N-Pyk2 antibody in the absence of protein A-agarose. Mg-ATP was then added in the presence or absence of pervanadate (*Perv*) (1 mM) (*top, No Resin*). In another set of experiments, Pyk2 was first immunoprecipitated (*IP*) with α N-Pyk2 antibody and protein A-Sepharose and washed before the addition of Mg-ATP in the presence or absence of pervanadate (1 mM) (*Resin Bound*). After 1 h at 4 $^{\circ}$ C, EDTA (50 mM) was added to chelate the Mg²⁺ and halt further phosphorylation. Tyr(P)⁴⁰² Pyk2 levels were examined by immunoblotting with phosphospecific antibody. *B*, primary hippocampal cultures were treated with NMDA (50 μ M) or ionomycin (1 μ M) for 15 min. Pervanadate (1 mM) was added 5 min prior to (*T* = -5) or at the time of stimulation with the absence of pervanadate serving as a control.

resins presumably by promoting dimerization of Pyk2. No autophosphorylation of Pyk2 was detected in lysate when pervanadate was absent. However, immunoprecipitated Pyk2 underwent limited autophosphorylation at Tyr⁴⁰² in the absence of pervanadate. This phosphorylation could result from dissociation of a tyrosine phosphatase from a subpopulation of Pyk2 during washing procedures. Addition of pervanadate led to a significant increase in the tyrosine phosphorylation of Pyk2, suggesting that an unknown PTP antagonized the antibody-induced autophosphorylation of the subpopulation of Pyk2 that retained a PTP.

We used NMDA or ionomycin to activate Pyk2 in primary hippocampal neurons. Pretreatment of cultures with pervanadate for 5 min (*T* = -5) followed by stimulation with NMDA or ionomycin for 15 min led to a significant increase in the phosphorylation of Pyk2 at Tyr⁴⁰². In contrast, NMDA or ionomycin failed to induce Pyk2 phosphorylation in the absence of pervanadate, indicating that activation of Pyk2 was blocked by PTPs or that PTPs rapidly dephosphorylated Pyk2 at Tyr⁴⁰² (Fig. 2*B*). Taken together, these results suggest that activation of Pyk2 was counteracted by an unknown PTP in the brain.

STEP Binds to Pyk2—To evaluate whether STEP interacted with Pyk2, STEP was immunoprecipitated from mouse brain lysates. STEP KO lysates were used as a negative control. Pyk2 co-immunoprecipitated with STEP from WT mouse brains but not with mouse IgG control or from STEP KO mouse brains (Fig. 3*A, upper panel*). Fyn also co-immunoprecipitated with STEP, consistent with previous findings (25). We confirmed the

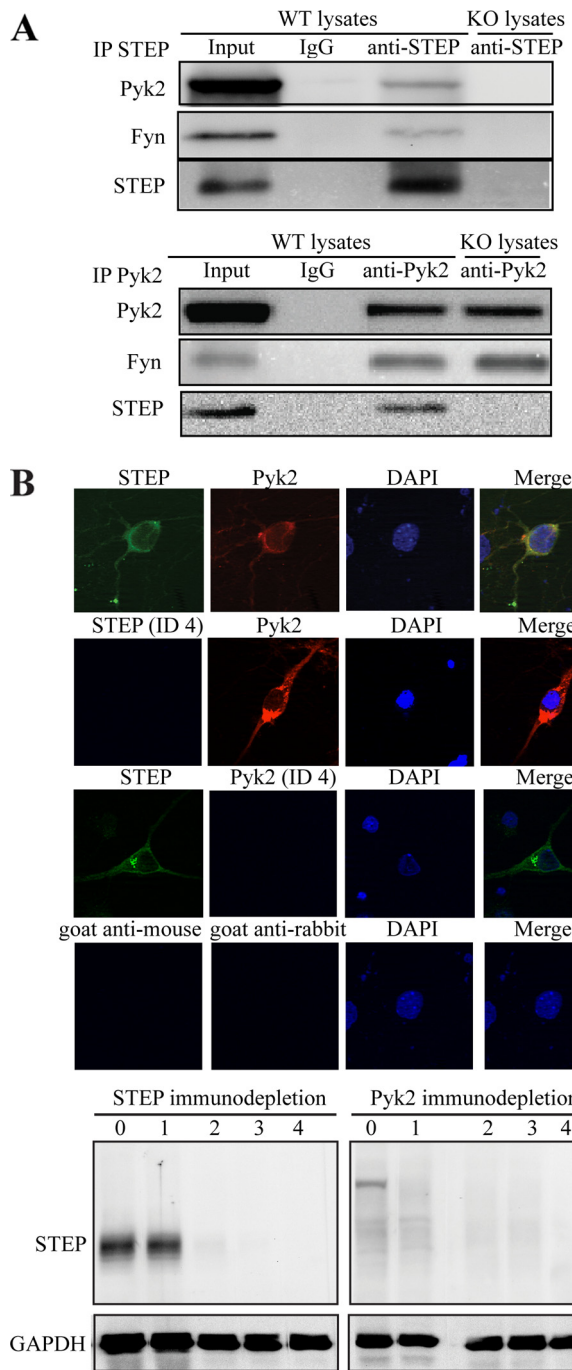


FIGURE 3. Pyk2 is associated with STEP *in vivo*. *A*, total brain homogenates from WT or STEP KO mice were immunoprecipitated (*IP*) with anti-STEP antibody (*upper panel*) or anti-Pyk2 antibody (*lower panel*). Immunoprecipitates were resolved by SDS-PAGE and immunoblotted with anti-Pyk2 or anti-Fyn antibody. Blots were reprobed with anti-STEP antibody. *B*, primary hippocampal neurons were labeled with anti-STEP (*green*) and anti-Pyk2 (*red*) antibodies, and nuclei were stained (*DAPI*; *blue*). Some cultures were stained with immunodepleted anti-STEP (*ID 4*) or anti-Pyk2 (*ID 4*) or secondary antibodies only. The specificity of immunodepleted antibodies was assessed using hippocampal neuronal lysates with each fraction. GAPDH was probed as the loading control.

interaction of STEP and Pyk2 by immunoprecipitating Pyk2 and probing with anti-STEP antibody (Fig. 3*A, lower panel*). We confirmed that Pyk2 interacts with Fyn (33). We also observed that Pyk2 associated with Fyn in the STEP KO lysates (Fig. 3*A*).

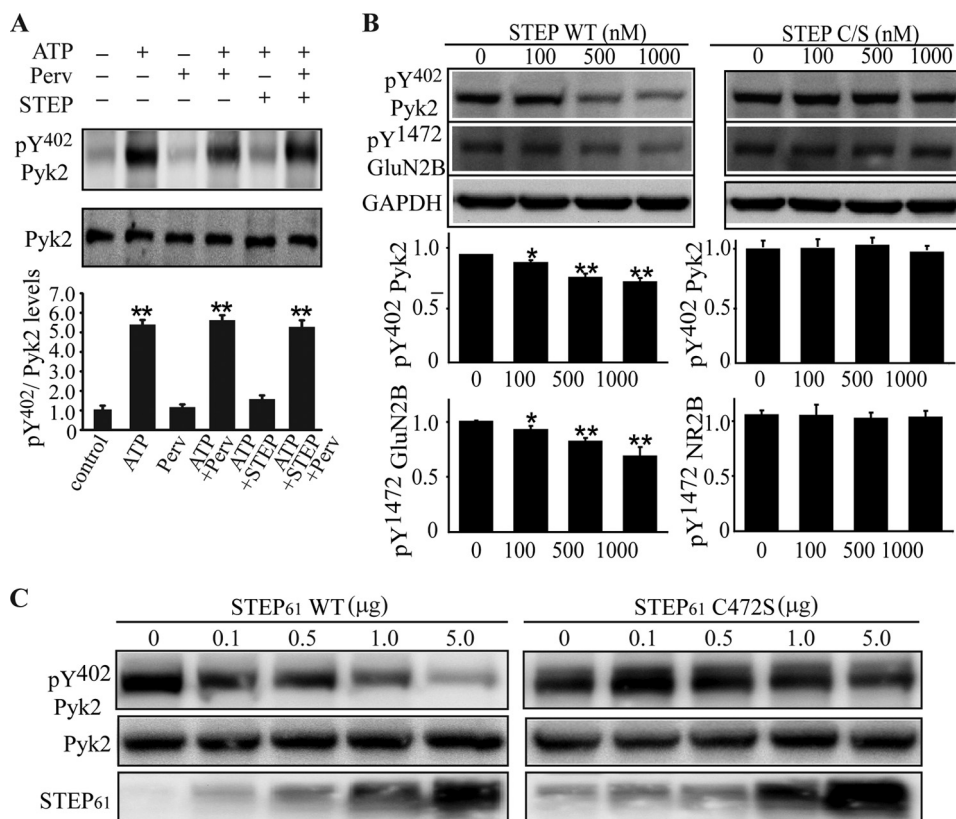


FIGURE 4. STEP dephosphorylates Pyk2 at Tyr⁴⁰². *A*, Pyk2 was immunoprecipitated from mouse brain lysates using anti-Pyk2 antibody and protein A/G-agarose in the presence of pervanadate (*Perv*) (1 mM). Mg-ATP, STEP (10 μM), and pervanadate (1 mM) were added as indicated. The Tyr(P)⁴⁰² signal was normalized to total Pyk2 levels. Error bars indicate the standard error of the mean (SEM) of at least three independent experiments (in this and subsequent panels). Asterisks indicate statistical significance as compared with control (**, $p < 0.01$; one-way ANOVA with post hoc Tukey test; $n = 4$). *B*, total brain lysates were heated at 65 °C for 20 min to inactivate endogenous kinases and phosphatases. Treated lysates (50 μg) were incubated with purified GST-STEP₄₆ WT (active) or GST-STEP₄₆ C/S (inactive) at the indicated concentrations and blotted with Tyr(P)⁴⁰² Pyk2 or Tyr(P)¹⁴⁷² NR2B. Quantitative analyses for each were normalized to GAPDH (*, $p < 0.05$; **, $p < 0.01$; one-way ANOVA with post hoc Tukey test; $n = 3$). *C*, full-length pcDNA3-Pyk2 (1 μg) construct was co-transfected with pcDNA3-STEP₆₁ WT (active) or pcDNA3-STEP₆₁ C472S (inactive) construct into HEK293 cells. Thirty-six hours post-transfection, cells were lysed in radioimmune precipitation assay buffer and blotted with antibodies as indicated in the figure.

To corroborate the association of Pyk2 and STEP, the cellular distribution of these proteins was determined by immunofluorescence microscopy in primary hippocampal neurons. Neurons were stained simultaneously with anti-Pyk2 (H102) and anti-STEP antibodies followed by Alexa Fluor-488-coupled anti-mouse and Alexa Fluor-594-coupled anti-rabbit secondary antibodies. Pyk2 and STEP colocalized throughout the soma as well as along neurites as indicated in the merged image (Fig. 3B). To establish that the staining was specific, immunodepleted anti-STEP and anti-Pyk2 or secondary antibodies alone were also examined (Fig. 3B). Collectively, the above results demonstrated that STEP, Pyk2, and Fyn associate with each other *in vivo*, although this does not indicate that they are all present in the same complexes, an issue addressed further below.

STEP Dephosphorylates Pyk2—Phosphorylation at Tyr⁴⁰² is essential for Pyk2 activation. To determine whether STEP dephosphorylates Pyk2 at Tyr⁴⁰², we performed *in vitro* autophosphorylation assays with immunoprecipitated Pyk2 from mouse brain lysates. Pyk2 was incubated with Mg-ATP in the presence or absence of pervanadate. Due to pervanadate inhibition of endogenous PTPs, including STEP, during lysis and immunoprecipitation procedures, no difference was seen in autophosphorylation of Pyk2 (Fig. 4A, lane 2 versus lane 4).

Addition of active STEP readily led to dephosphorylation of Pyk2 (Fig. 4A, lane 5), which was prevented by the presence of pervanadate (lane 6). These results indicated that autophosphorylation of Pyk2 at Tyr⁴⁰² was reversed by active STEP. Inhibition of STEP activity by pervanadate restored Pyk2 autophosphorylation. These results suggest that STEP is capable of dephosphorylating Pyk2 at Tyr⁴⁰² *in vitro*.

We confirmed STEP dephosphorylation of Pyk2 by mixing increasing amounts of active STEP (GST-STEP₄₆) or enzymatically inactive STEP (GST-STEP₄₆ C/S) with equal amounts of heat-inactivated brain lysates. Active STEP caused a significant reduction in Pyk2 phosphorylation, whereas inactive STEP did not (Fig. 4B, 1000 nM; $74.8 \pm 2.5\%$ of no STEP control; $p < 0.01$). Tyr(P)¹⁴⁷² GluN2B is a known substrate of STEP, and there was a significant decrease in Tyr(P)¹⁴⁷² GluN2B levels in the presence of active, but not inactive, STEP (Fig. 4B, 1000 nM; $68.8 \pm 4.6\%$ of no STEP control; $p < 0.01$). These results confirmed that Pyk2 is dephosphorylated at Tyr⁴⁰² by STEP.

To test whether STEP was able to dephosphorylate Pyk2 in intact cells, HEK293 cells were transfected with Pyk2 along with either active WT STEP₆₁ or a catalytically inactive STEP₆₁ C472S construct. Phosphorylation of Pyk2 at Tyr⁴⁰² was reduced when HEK293 cells were co-transfected with WT STEP₆₁ but not the inactive STEP₆₁ protein (Fig. 4C).

STEP₆₁ Regulates Pyk2 Signaling

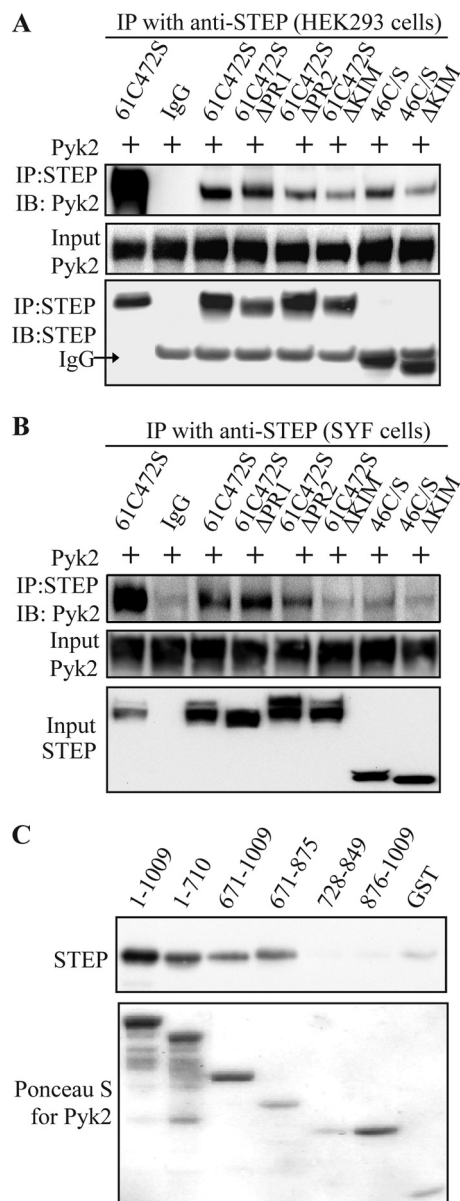


FIGURE 5. Interacting regions in STEP and Pyk2. *A*, HEK293 cells were transfected with full-length Pyk2 along with various STEP mutants (Fig. 1). STEP was immunoprecipitated, and Pyk2 levels were assessed with anti-Pyk2 antibody. *B*, SYF cells were co-transfected with the same STEP and Pyk2 constructs used in *A*. Association of Pyk2 with STEP was visualized by immunoprecipitation (IP) of STEP and probing for Pyk2. *C*, *in vitro* binding of STEP and Pyk2. GST-tagged Pyk2 fragments (Fig. 1) or GST alone was immobilized on glutathione-Sepharose. After washes, STEP (500 nM) was added for 2 h at 4 °C. Binding of STEP to various fragments was visualized with anti-STEP antibody (upper panel), and Pyk2 proteins were visualized by Ponceau S staining (lower panel). *IB*, immunoblotting.

STEP Interacts Directly with Pyk2—To map the binding regions involved in STEP/Pyk2 interaction, several STEP₆₁ deletion mutants were co-transfected with full-length Pyk2 into HEK293 cells. These proteins were immunoprecipitated with anti-STEP antibody, and Pyk2 levels were examined with anti-Pyk2 (H102) antibody (Fig. 5A). The full-length substrate-trapping mutant of STEP₆₁ (25) showed high affinity for Pyk2, whereas deletion of either the PR2 or KIM domain decreased the amount of Pyk2 pulled down. The substrate-trapping STEP₄₆ mutant that lacks the N-terminal region also interacted

but pulled down less Pyk2 (Fig. 5A). These results suggest that the PR2 and KIM domains are involved in the interaction of STEP with Pyk2. We confirmed the involvement of the KIM domain in STEP/Pyk2 interactions by GST pulldown assays (supplemental Fig. S1).

Previous studies have shown that Fyn interacts with Pyk2 (34) and STEP (25). We wanted to test whether the association of STEP and Pyk2 required Fyn to be present. STEP and Pyk2 constructs were transfected into SYF cells, which are deficient for Src, Yes, and Fyn (34, 35). STEP₆₁ was still able to pull down Pyk2, whereas deletion of PR2 or KIM domain impaired STEP/Pyk2 association (Fig. 5B). These results indicate that STEP is able to interact with Pyk2 in the absence of Fyn.

We next examined the domains within Pyk2 necessary for the association of Pyk2 with STEP. His-tagged STEP₄₆ C/S was incubated with different fragments of GST-tagged Pyk2 coupled to glutathione-Sepharose beads. Full-length Pyk2 (amino acids 1–1009) was effective in binding to STEP as was an ~200-amino acid sequence of Pyk2 (amino acids 671–875; Figs. 5C and 1). This region also binds PSD-95 (15) (see below).

To determine whether residues 671–875 of Pyk2 or the KIM and PR2 domains of STEP are required for binding, we utilized FP assays. Binding affinities of the FITC-conjugated peptides KIM and PR2 of STEP and residues 671–694, 689–712, 707–723, and 850–866 of Pyk2 were determined for GST-Pyk2(671–875) and for GST-STEP₆₁ and -STEP₄₆, respectively (Fig. 6A). Pyk2(671–694) but none of the other peptides bound STEP in a saturating and hence specific manner. It showed higher affinity for STEP₆₁ ($K_d = 2.63 \mu\text{M}$) than STEP₄₆ ($K_d = 11.83 \mu\text{M}$), suggesting involvement of the unique N terminus of STEP₆₁ in these interactions, which is consistent with our findings in Fig. 5 and supplemental Fig. S1. The PR2 domain of STEP₆₁ was also able to bind to Pyk2 directly (Fig. 6A) albeit with low affinity as often observed for peptides derived from proline-rich segments.

The KIM peptide showed poor solubility and strong adsorption to the polystyrene plates used in the FP assay, preventing its use in this assay. Therefore, we examined the effect of this and the other peptides in GST pulldown assays (Fig. 6B). The results confirmed that both PR2 and KIM domains of STEP and residues 671–694 of Pyk2 are involved in the STEP/Pyk2 interaction. In contrast, the STEP/ERK2 interaction was not affected by the PR2 domain, although it was inhibited by the KIM peptide in agreement with earlier work indicating that KIM mediates STEP binding to ERK (24, 36). As a control, Myc peptide did not have any impact on binding. Furthermore, the pulldown data confirm that Pyk2(671–694) interacts with STEP (Fig. 6C). The data further indicate that STEP and PSD-95 bind to different motifs within the Pyk2(671–875) region (15) with PSD-95 interacting with Pyk2(707–723) but not Pyk2(671–694).

Fyn and Pyk2 Compete for STEP Binding—Because the N terminus and the KIM domain of STEP are needed for binding to both Fyn and Pyk2, we next examined whether we could competitively disrupt the interaction of one by increasing the concentration of the other in transfection experiments. We co-transfected STEP₆₁ and full-length Pyk2 constructs with increasing amounts of Fyn. There was a decrease in the association of Pyk2 with STEP as Fyn levels were increased (Fig. 7A).

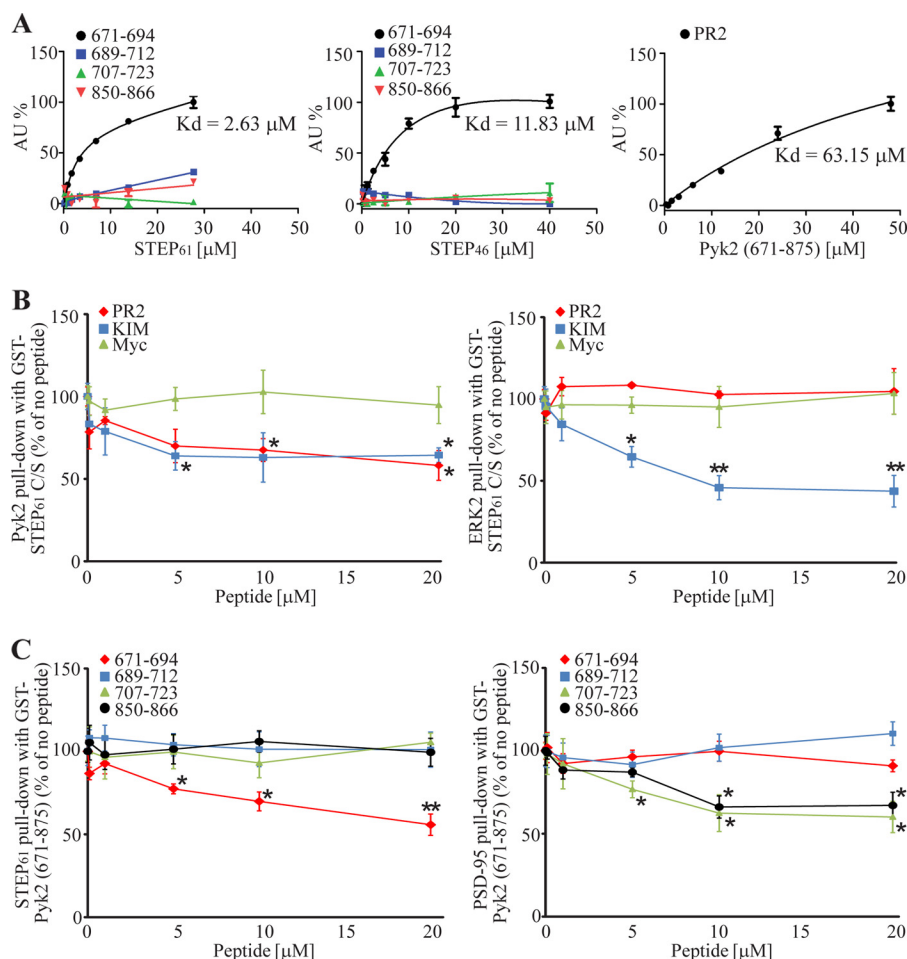


FIGURE 6. PR2 and KIM domains of STEP₆₁ and residues 671–694 of Pyk2 mediate STEP/Pyk2 interaction. *A*, FITC-conjugated Pyk2-derived peptides 671–694, 689–712, 707–723, and 850–866 were titrated with GST-STEP₆₁ (*left*) and -STEP₄₆ (*middle*), and STEP-derived PR2 peptide with GST-Pyk2(671–875) (*right*). Binding was monitored by FP. For each graph, the signals were normalized, setting as zero the lowest value and as 100% the highest value measured, and fitted to saturation curves. Calculated binding affinities of 671–694 for GST-STEP₆₁ and -STEP₄₆ and of PR2 for GST-Pyk2 671–875 are indicated. AU, absorbance units. *Error bars* indicate the SEM of at least three independent experiments (in this and subsequent panels). *B* and *C*, competition of PR2, KIM, and Myc (control) peptide with GST-STEP₆₁ for Pyk2 and ERK2 (*B*) and of the Pyk2-derived peptides with GST-Pyk2(671–875) for STEP₆₁ and PSD-95 (*C*) by increasing concentrations of peptides (as indicated) in pull-down assays with GST-STEP₆₁ (*B*) and GST-Pyk2(671–875) (*C*) using brain lysates as the source of native proteins. Pyk2 and ERK2 (*B*) and STEP₆₁ and PSD-95 (*C*) were determined by immunoblotting (*, $p < 0.05$; **, $p < 0.01$; one-way ANOVA with post hoc Tukey test; $n = 4$).

Similarly, there was a decrease in the association of Fyn with STEP as Pyk2 levels were increased (Fig. 7B). These results suggest that Pyk2 and Fyn compete for binding with STEP₆₁.

In vitro competitive binding was also assessed with purified proteins. GST-tagged STEP₆₁ C472S was incubated with His-tagged Pyk2 and increasing concentrations of His-tagged Fyn. Fyn competed in a concentration-dependent manner with Pyk2 for binding to STEP (Fig. 7C).

Increased Phosphorylation of Pyk2 in STEP KO Mice—Based on the findings that STEP binds to and dephosphorylates Pyk2 at Tyr⁴⁰², we predicted that STEP KO mice would have elevated Pyk2 phosphorylation. We first determined the basal levels of Tyr phosphorylation of Pyk2 in synaptosomal (P2) fractions from STEP KO *versus* WT mice. There was a significant increase of Tyr(P)⁴⁰² levels in STEP KO mice (Tyr(P)⁴⁰², 130.2 ± 7.5% of WT; $p < 0.01$), whereas total Pyk2 levels remained unchanged ($p > 0.05$) (Fig. 8A). We also looked at additional tyrosine phosphorylation sites of Pyk2 and showed increases of Tyr(P)⁸⁸¹ but not Tyr(P)⁵⁷⁹ or Tyr(P)⁵⁸⁰ levels in STEP KO mouse brains (supplemental Fig. S2), suggesting that

STEP might also directly dephosphorylate Tyr⁸⁸¹ or block the phosphorylation by kinases (such as Src and Fyn) at this site. Such blockage could be due to shifting Tyr⁴⁰² toward the dephosphorylated state, which then would lead to less binding of Src family kinases to Pyk2 and thereby less phosphorylation of the other sites on Pyk2.

To further confirm that dephosphorylation of Pyk2 by STEP had a functional consequence on Pyk2 signaling, we probed for the tyrosine phosphorylation levels of paxillin, a well known substrate for Pyk2 and focal adhesion kinase (11, 37), and ASAP1, a recently identified Pyk2 substrate that is not phosphorylated by focal adhesion kinase (38, 39). Phosphorylation of paxillin at Tyr¹¹⁸ and of ASAP1 at Tyr⁷⁸² was enhanced in STEP KO mouse brain lysates by 138.4 ± 5.1 and 149.5 ± 5.7% *versus* WT, respectively (Fig. 8B; $p < 0.01$).

Phosphorylation and activation of Pyk2 lead to its translocation to PSD fractions (15). We next examined whether translocation of Pyk2 was increased in STEP KO mice in which Pyk2 Tyr phosphorylation was increased. We measured phosphorylated and total Pyk2 levels in PSD fractions from WT and STEP

STEP₆₁ Regulates Pyk2 Signaling

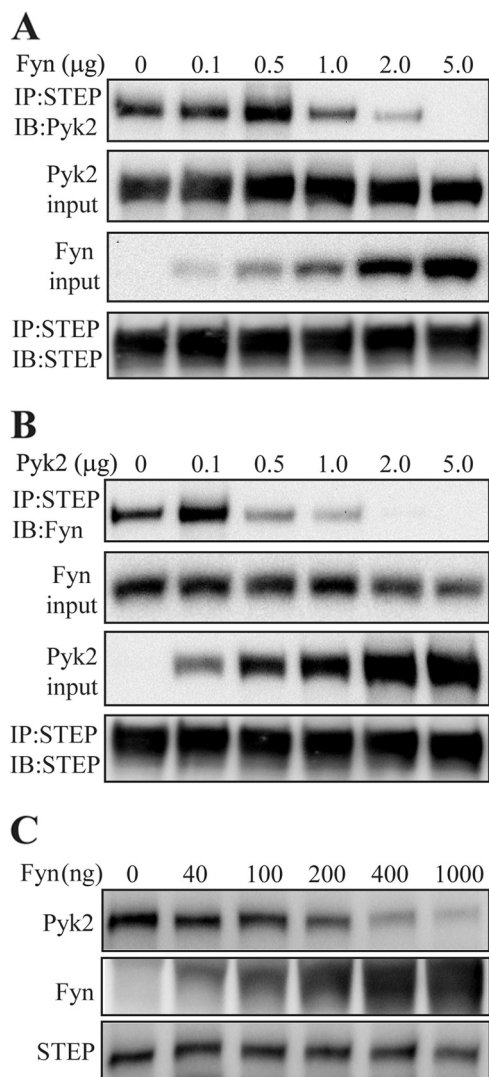


FIGURE 7. Fyn and Pyk2 compete for STEP binding. *A*, constant amounts (1 μg of cDNA) of full-length STEP and Pyk2 constructs were co-transfected with increasing amounts of Fyn construct into HEK293 cells. Thirty-six hours after transfection, cells were lysed before immunoprecipitation (IP) with anti-STEP antibody and immunoblotting (IB) with anti-Pyk2 antibody. Immunoblotting of lysates indicates increasing amounts of Fyn with increasing amounts of Fyn cDNA but unchanged amounts of Pyk2. Immunoblotting of STEP immunoprecipitates indicates unaltered amounts of STEP in all samples. *B*, constant amounts (1 μg of cDNA) of STEP and Fyn were co-transfected with increasing amounts of Pyk2. Co-immunoprecipitation of Fyn with STEP was measured by immunoblotting with anti-Fyn antibody. *C*, competitive binding was tested *in vitro* with all purified proteins. GST-tagged STEP was adsorbed to glutathione beads and incubated with a constant amount of Pyk2 (500 ng) and increasing amounts of Fyn as indicated.

KO mouse brains (Fig. 8C). Total Pyk2 levels were greater in the PSD from STEP KO mice ($146.4 \pm 9.4\%$ of WT; $p < 0.01$). No change in Tyr(P)⁴⁰² levels was seen when normalized to total Pyk2 levels. These data suggest that only Tyr⁴⁰²-phosphorylated Pyk2 associates with the PSD complex in a manner that is stable enough to endure purification of PSDs. However, catalytic activity of Pyk2 is not required for the translocation to postsynaptic sites in hippocampal cultures upon Ca²⁺ influx (15). Phospho-ERK1/2 levels were also increased in PSD from STEP KO mice ($153.1 \pm 4.0\%$ of WT; $p < 0.01$; Fig. 8C). There was no change in ERK2 or PSD-95 (Fig. 8C) levels in PSD frac-

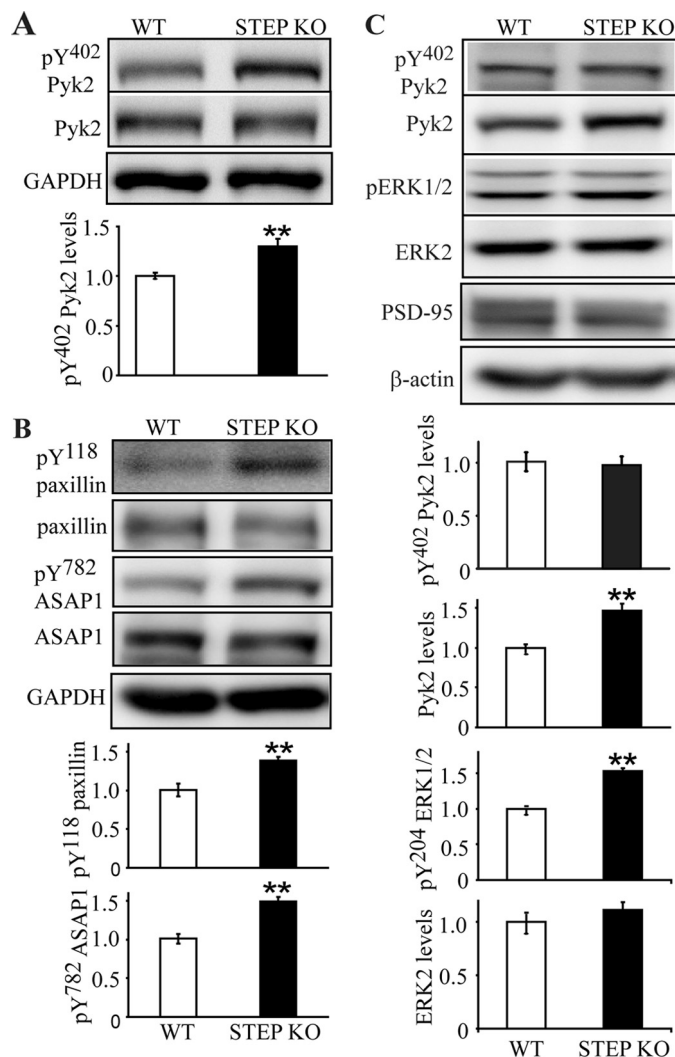


FIGURE 8. Basal phosphotyrosine levels of Pyk2 and Pyk2 substrates are elevated in STEP KO mouse brains. *A*, synaptosomal (P2) fractions from WT and STEP KO littermates were used to determine levels of tyrosine phosphorylation of Pyk2 at Tyr(P)⁴⁰² and total Pyk2 levels. Error bars indicate the SEM of at least three independent experiments (in this and subsequent panels). Quantitative analyses for each were normalized to GAPDH (*, $p < 0.05$; **, $p < 0.01$; Student's *t* test; $n = 4$). *B*, phosphorylation of paxillin (Tyr(P)¹¹⁸) and ASAP1 (Tyr(P)⁷⁸²) were determined in P2 fractions with phosphospecific antibodies. Quantitations were normalized to total protein levels, respectively, and then to GAPDH. *C*, PSD fractions from WT and STEP KO mice were purified. Tyrosine phosphorylation of Pyk2 and ERK1/2 was compared between WT and STEP KO mice (**, $p < 0.01$; Student's *t* test; $n = 4$).

tions. These data indicate that Pyk2 associates more stably with PSD fractions in STEP KO versus WT mice.

STEP Blocks KCl-induced Activation and Translocation of Pyk2 to PSD Fraction—Treatment of rat brain slices with KCl activates Pyk2 (40). We therefore examined the inhibition of Pyk2 by STEP in a KCl-treated brain slice model. We took advantage of efficient transduction of fusion proteins mediated by the human immunodeficiency virus, type 1 TAT domain, which is widely used to deliver exogenous proteins into various cell types (28, 41). Slices from WT or STEP KO mice were pretreated with WT TAT-STEP, inactive TAT-STEP C/S, or active STEP without TAT for 30 min followed by KCl stimulation and isolation of PSD fractions. KCl stimulation led to a significant increase in translocation of Pyk2 to the PSD fraction

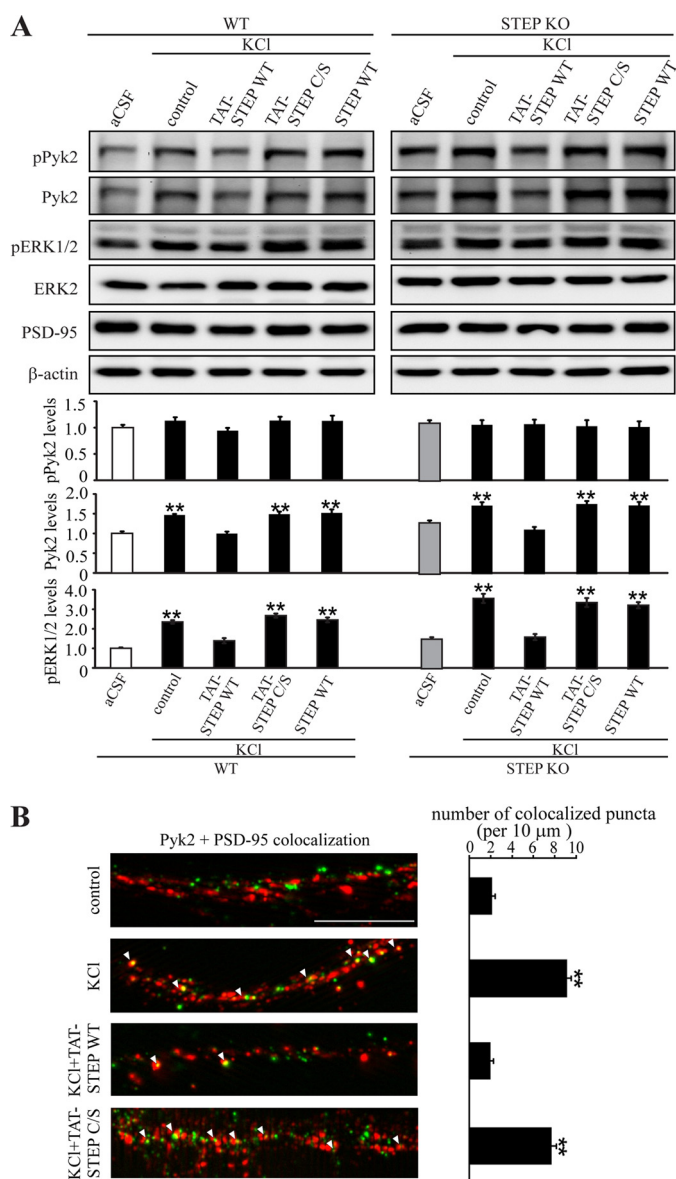


FIGURE 9. Active TAT-STEP protein blocks phosphorylation and translocation of Pyk2 to PSD upon KCl depolarization. *A*, WT or STEP KO mouse brain slices were pretreated with TAT-STEP WT (active), TAT-STEP C/S (inactive), or active STEP without TAT for 30 min; stimulated with 40 mM KCl for 2 min; and frozen on dry ice before isolation of PSD fractions. Phosphorylation levels were probed with phosphospecific antibodies (Tyr(P)⁴⁰² Pyk2 or Tyr(P)²⁰⁴ ERK1/2) and normalized to total Pyk2 and ERK1/2 levels, respectively, and then to β -actin as a loading control. Error bars indicate the SEM of at least three independent experiments (in this and subsequent panels). All values were compared with those in WT aCSF samples (**, $p < 0.01$; one-way ANOVA with post hoc Tukey test; $n = 4$). *B*, primary hippocampal neurons were pretreated with active TAT-STEP WT or inactive TAT-STEP C/S followed by KCl (40 mM; 2 min) stimulations. Colocalization of Pyk2 and PSD-95 was visualized using immunostaining with anti-Pyk2 (red) and anti-PSD-95 (green) antibodies. Arrowheads in the merged images indicate colocalized puncta. The number of Pyk2/PSD-95-colocalized puncta was counted per 10 μ m of dendrites; 17 neurons were used for quantification per treatment. All values were compared with control (**, $p < 0.01$; one-way ANOVA with post hoc Tukey test; $n = 17$). pERK1/2, phospho-ERK1/2, pPyk2, phospho-Pyk2.

(Fig. 9A) ($146.8 \pm 2.5\%$ of control; $p < 0.01$). Preincubation with TAT-STEP₄₆ WT antagonized the Pyk2 translocation to PSDs ($99.8 \pm 4.9\%$ of control; $p > 0.05$). The inactive TAT-STEP₄₆ C/S or active STEP without TAT did not antagonize the activation or translocation of Pyk2 ($148.7 \pm 6.6\%$ of control and

$152.1 \pm 8.8\%$ of control, respectively; $p < 0.01$). Phospho-Pyk2 levels remained constant in the PSD fractions when normalized to total Pyk2 levels regardless of treatments, suggesting that PSD-localized Pyk2 is mostly, if not all, phosphorylated at Tyr⁴⁰².

We repeated these experiments in STEP KO mice. aCSF-treated STEP KO slices showed higher levels of total Pyk2 ($128.8 \pm 6.1\%$ of WT aCSF; $p < 0.01$) in the PSD, indicating elevated basal levels in the STEP KO mice. KCl stimulation induced further increases in PSD-localized Pyk2 ($172.0 \pm 8.6\%$ versus $128.8 \pm 6.1\%$; $p < 0.01$). Translocation of Pyk2 was antagonized by the addition of active WT TAT-STEP protein ($111.9 \pm 6.6\%$ versus $172.0 \pm 8.6\%$; $p < 0.01$) but not by inactive TAT-STEP C/S protein or active STEP without the TAT tag (Fig. 9A).

ERK1/2 is a well established STEP substrate that is activated by KCl depolarization (40) and was examined as a positive control in these experiments. PSD fractions from STEP KO slices showed greater basal phosphorylation levels of ERK1/2 ($149.8 \pm 9.4\%$ of WT aCSF), confirming earlier findings (28, 30). KCl stimulations led to an increase of ERK1/2 phosphorylation in both WT and STEP KO slices (WT, $235.3 \pm 8.9\%$ of aCSF control; KO, $355.6 \pm 23.3\%$ of WT aCSF control) that was blocked by WT TAT-STEP but not inactive TAT-STEP C/S or active STEP without TAT.

Blockade of Pyk2 translocation to the PSD fractions by STEP was also visualized using immunostaining. Primary hippocampal neurons were pretreated with active TAT-STEP WT or inactive TAT-STEP C/S followed by KCl stimulations, and the number of Pyk2- and PSD-95-colocalized puncta/10 μ m of dendrites was counted. Consistent with previous findings (15), KCl stimulation led to increased colocalization of Pyk2 with PSD-95 (9.06 ± 0.46 puncta compared with 2.06 ± 0.39 puncta for control; $p < 0.01$). TAT-STEP WT blocked translocation of Pyk2 upon KCl stimulation (1.88 ± 0.37 puncta; $p > 0.05$), whereas inactive TAT-STEP C/S had no effect (7.65 ± 0.48 puncta; $p < 0.01$) (Fig. 9B).

Activation of STEP Results in Dephosphorylation of Pyk2 in Synaptoneurosomal Fractions—We examined whether Pyk2 phosphorylation would be stimulated by KCl depolarization in synaptoneurosomes and whether STEP modulated the dephosphorylation and inactivation of Pyk2 in these samples. Synaptoneurosomes were purified from WT or STEP KO mouse brain, and the purity of the preparation was examined by localization and expression of several marker proteins (27, 42). Synaptophysin (a presynaptic vesicular protein) and PSD-95 (a postsynaptic marker) were enriched in synaptoneurosomal fractions, whereas Ca²⁺/calmodulin-dependent protein kinase II (a pansynaptic protein) was detected in both synaptoneurosomal and cytosolic fractions. Histone H1 (a nuclear protein) was absent in synaptoneurosomal or cytosolic fractions, whereas tubulin (a non-synaptic protein) showed equal distribution in these compartments. We also confirmed the presence of Pyk2 and STEP₆₁ in synaptoneurosomes (Fig. 10A).

Synaptosomes were stimulated for different times with KCl. Phosphorylation of Pyk2 was rapid (1 min, $156.4 \pm 6.8\%$ of control; 2 min, $174.7 \pm 5.3\%$ of control) and started decreasing at 5 min (5 min, $147.6 \pm 5.6\%$ of control; 30 min, $103.6 \pm 3.0\%$

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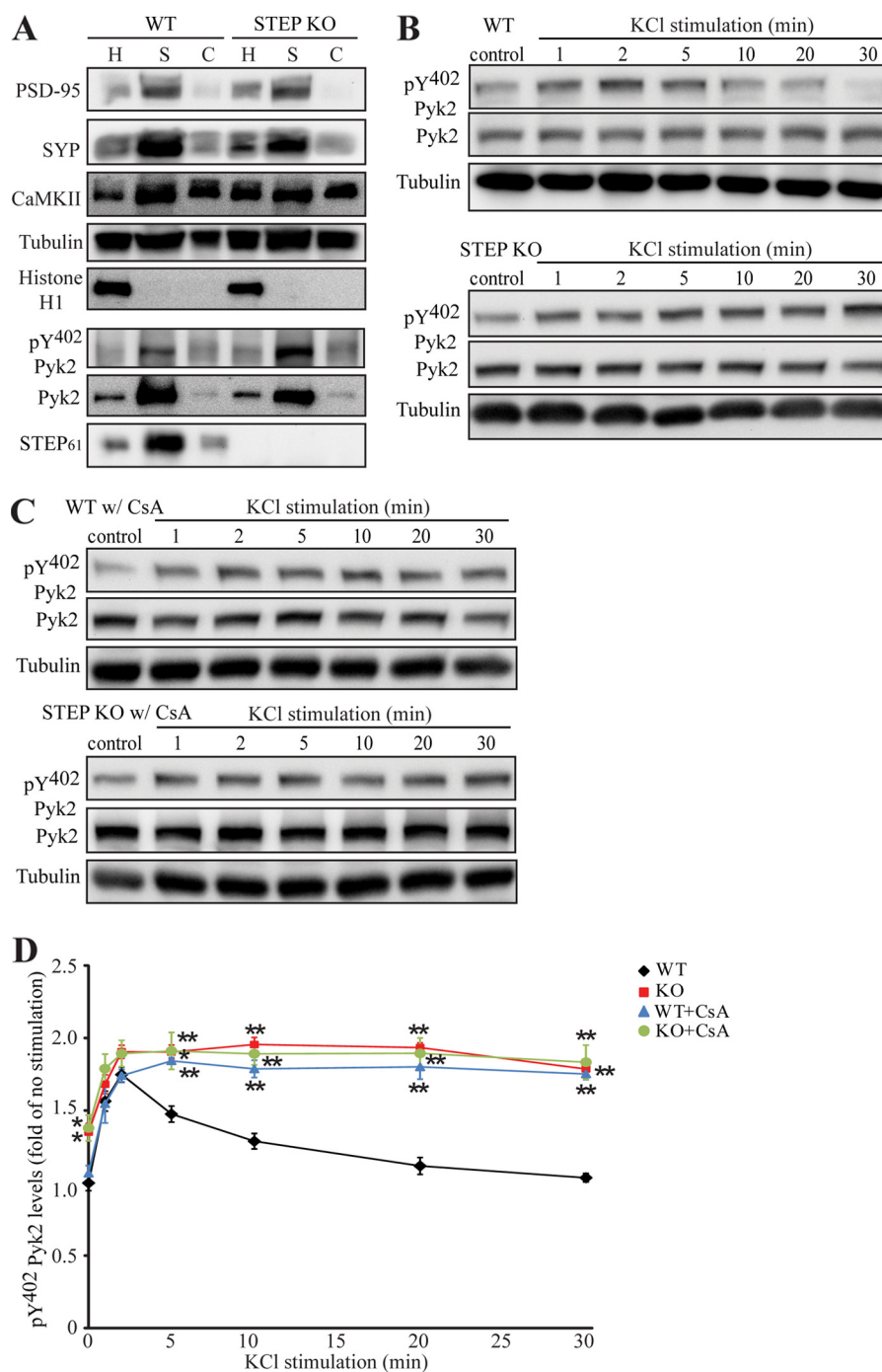


FIGURE 10. Activation of STEP leads to dephosphorylation of Pyk2 in synaptoneurosomes. *A*, expression of presynaptic and postsynaptic markers in synaptoneurosomes preparation. *SYP*, synaptophysin; *CaMKII*, Ca²⁺/calmodulin-dependent protein kinase II. *B*, synaptoneurosomes from WT (*upper panel*) or STEP KO (*lower panel*) mice were stimulated with 40 mM KCl for the indicated durations. Phosphorylation of Pyk2 was determined with Tyr(P)⁴⁰² Pyk2 antibody. *C*, CsA-pretreated synaptoneurosomes (100 nM; 10 min) from WT (*upper panel*) or STEP KO (*lower panel*) mouse brains were stimulated with 40 mM KCl as in *B*. *D*, quantitation of phospho-Pyk2 from *B* and *C*. Phosphorylation levels were first normalized to total protein and then to tubulin as a loading control. *Error bars* indicate the SEM of at least three independent experiments. All values were expressed as -fold changes compared with WT control levels (*, $p < 0.05$; **, $p < 0.01$; one-way ANOVA with post hoc Tukey test; $n = 4$).

of control) (Fig. 10, *B* and *D*), similar to earlier findings in hippocampal slices (39). Synaptoneurosomes from STEP KO mouse brains had higher levels of phospho-Pyk2 at base line ($135.0 \pm 6.0\%$ of WT control; $p < 0.01$). KCl depolarization further enhanced Pyk2 phosphorylation (1 min, $168.1 \pm 6.5\%$ of WT control), and dephosphorylation of Pyk2 was impaired in STEP KO synaptoneurosomes (2 min, $190.5 \pm 4.5\%$; 5 min, $190.3 \pm 4.8\%$; 30 min, $178.6 \pm 6.4\%$; $p > 0.05$; Fig. 10, *B* and *D*).

STEP activity is regulated by PKA phosphorylation, which decreases STEP activity, and by PP2B- and PP1-dependent dephosphorylation of Ser²²¹ within the KIM domain, which increases STEP activity (23, 43, 44). Preincubation with a PP2B inhibitor, CsA, prevented dephosphorylation of Pyk2 at 30 min in WT slices (5 min, $184.2 \pm 2.3\%$; 30 min, $175.2 \pm 4.0\%$; $p > 0.05$; Fig. 10, *C* and *D*). In addition, CsA-pretreated synaptoneurosomes from WT and STEP KO mice showed a pattern similar

to that of non-pretreated samples from the KO mice upon KCl stimulation except that CsA *per se* did not increase Pyk2 phosphorylation because PP2B would not be active under non-stimulated conditions (Fig. 10, C and D). Thus, CsA had no further effect in the absence of STEP. Taken together, these data indicate that STEP is required to dephosphorylate Pyk2 at Tyr⁴⁰² in the KCl depolarization paradigm. Similarly, we observed a prolonged activation of ERK1/2 in STEP KO synaptoneurosomes or CsA-pretreated samples (supplemental Fig. S3), indicating that STEP opposed ERK activation in the KCl depolarization paradigm.

DISCUSSION

Pyk2 is a member of the non-receptor tyrosine kinase family and is structurally related to focal adhesion kinase. Within the CNS, Pyk2 is implicated in the development of synaptic plasticity and LTP through its ability to increase the conductance of *N*-methyl-D-aspartate receptor (17, 18) and activate MAPK pathways (13). In addition, Pyk2 is involved in cytoskeletal reorganization (45, 46) as well as the modulation of cell death pathways due to glutamate excitotoxicity (47–49). How Pyk2 is inactivated within neurons is an important unanswered question in the field.

Activation of Pyk2 typically involves membrane depolarization and calcium influx and is initiated by autophosphorylation at Tyr⁴⁰² (1, 4–7), although additional kinases, including the Tyr receptor kinases EGF receptor and HER2/3, have also been implicated in this process (50, 51). Tyr⁴⁰² serves as a docking site for the binding of Src and Fyn through their SH2 domains (13, 53). Phosphorylation at additional Pyk2 sites (Tyr⁵⁷⁹, Tyr⁵⁸⁰, and Tyr⁸⁸¹) by Fyn or Src is required for the full activation of Pyk2 (13, 14). Recent mechanistic studies have demonstrated that Pyk2 interacts with PSD-95 and that translocation to PSDs is necessary for the full activation of Pyk2 and the induction of LTP (15, 17).

STEP is also present within the PSD as demonstrated by electron microscopy (31, 54) and biochemical analysis (28, 31). Unlike Pyk2, however, translocation of STEP to the PSD has not been reported. Thus, STEP might not control the initial translocation and activation of Pyk2 but rather may function to terminate Pyk2 signaling at the PSD. We also observed that the relative phosphorylation of Pyk2 increased in synaptoneurosome (Fig. 10D) but not PSD fractions (Figs. 8C and 9A). Based on our previous work (15), we speculate that Ca²⁺/calmodulin-dependent phosphorylation of Pyk2 at Tyr(P)⁴⁰² may stabilize Pyk2 binding to PSD-95. Other possible binding partners at the PSD for stable, Tyr⁴⁰² phosphorylation-dependent PSD association include Src, which binds to Tyr(P)⁴⁰² (13) and is anchored via NADH dehydrogenase subunit 2 to NMDA receptors (55). The importance of these experiments is that STEP reverses Pyk2 phosphorylation and thereby suppresses its binding to PSD, hence the increase in both total Pyk2 and phospho-Pyk2 in STEP KO mice (Fig. 8C) or the decrease by TAT-STEP in the KCl paradigm (Fig. 9A).

We identified the domains in STEP and in Pyk2 that mediate their association. The KIM motif is required for the binding of STEP to all substrates tested to date (24, 25, 28, 35). This finding was confirmed with Pyk2 as removal of this domain disrupted

the association of STEP with Pyk2. In addition, the unique N terminus of STEP₆₁ appeared to facilitate the binding of STEP to Pyk2 or Fyn. STEP₄₆, which lacks the N-terminal region, pulled down less Pyk2 or Fyn in GST pulldown assays (supplemental Fig. S1). There are two polyproline-rich domains within the N-terminal region (PR1 and PR2). In this study, we showed that the PR2 domain of STEP₆₁ is also involved in the interaction of STEP with Pyk2. In contrast, the PR1 domain is required for the binding of STEP with Fyn, and deletion of the PR2 domain enhanced the binding of STEP to Fyn (25). The presence of the PR2 domain may facilitate the association of Pyk2 and impair Fyn binding to STEP.

The C-terminal region of Pyk2 that lies between the kinase domain and focal adhesion-targeting domain and contains two proline-rich domains is sufficient for the binding of Pyk2 to STEP. These proline-rich domains are necessary for the interaction of Pyk2 with the SH3 domain of PSD-95 and play a critical role in the translocation and activation of Pyk2 during synaptic plasticity (15). The results of our pulldown assays with peptides indicate that STEP and PSD-95 bind to different motifs within the C-terminal region of Pyk2 (residues 671–875). The relative selectivity of peptide 671–694 may have further implications in modulating STEP/Pyk2 interaction in synaptic plasticity, although the usefulness of a cell-penetrating form of this peptide (such as a TAT fusion peptide) awaits further characterization.

An important observation in the present study was that STEP interacted with Pyk2 in the absence of Fyn, indicating that the binding of STEP to Pyk2 does not require the presence of Fyn. Similarly, Pyk2 and Fyn were co-immunoprecipitated from lysates obtained from STEP KO mice, indicating that they are able to associate in the absence of STEP. Competitive binding assays showed that increasing the amount of Fyn or Pyk2 resulted in displacement of Pyk2 or Fyn, respectively. Although these results suggest that Pyk2 and Fyn cannot simultaneously bind STEP directly and that distinct dyadic pools exist, our experiments do not rule out the possibility that these three molecules also form a tripartite complex perhaps via adaptor proteins.

The association of both Pyk2 and Fyn with STEP is of interest as it adds insight into the synergistic regulation of these enzymes. STEP dephosphorylates and inactivates both Pyk2 (this study) and Fyn (25), which are known to phosphorylate and activate each other. In this way, STEP inactivates two kinases involved in the regulation of synaptic plasticity. We also showed an elevated phosphorylation of Pyk2 at Tyr⁸⁸¹ in STEP KO samples (supplemental Fig. S2). Because Tyr⁸⁸¹ is involved in the activation of the MAPK pathway (1), these data suggest that STEP may regulate MAPK signaling via Pyk2. These findings are consistent with earlier studies that have shown that STEP normally opposes the development of synaptic plasticity (56, 57).

Another example of this type of coordinated modulation by STEP occurs in the internalization of *N*-methyl-D-aspartate receptor from synaptic membranes. Fyn phosphorylates Tyr¹⁴⁷² of the GluN2B subunit of the *N*-methyl-D-aspartate receptor, resulting in exocytosis of GluN1-GluN2B receptor complexes to synaptosomal surface membranes (58, 59).

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Tyr¹⁴⁷² of GluN2B is dephosphorylated by STEP, leading to internalization of GluN1-GluN2B receptors (26, 60). In addition, Fyn is dephosphorylated and inactivated by STEP. Thus, STEP dephosphorylates the Tyr residue on GluN2B targeted by Fyn and inactivates Fyn itself.

The regulation of STEP itself by dopamine signaling is relevant to this discussion. Dopamine D1 receptor stimulation leads to activation of PKA and phosphorylation of STEP at a regulatory serine residue within its KIM domain (42) so that STEP no longer interacts with its substrates. The Tyr phosphorylation and activity of STEP substrates are thereby increased in the case of Pyk2, Fyn, and ERK (23, 43), or the STEP substrates traffic to neuronal membranes in the case of GluN2B (60, 61). At the same time, PKA phosphorylates and activates DARPP-32, leading to the inhibition of PP1 (62–64). PP1 is the phosphatase that dephosphorylates STEP at the same regulatory serine residue within the KIM domain. In this case, a kinase (PKA) that phosphorylates and inactivates its substrate (STEP) is activated, while at the same time, the phosphatase (PP1) that normally activates STEP is inactivated.

STEP belongs to a subgroup of three highly homologous PTPs, which are the only proteins identified to date that contain a KIM domain. These PTPs include HePTP, which is enriched in hematopoietic cells (65), and STEP-like PTP (PTP-SL), which is enriched in cerebellum (66). STEP is not found in either of these tissues (67). As Pyk2 is present in both hematopoietic cells and the cerebellum, future studies are needed to test the prediction that the related PTPs regulate Pyk2 in these tissues.

In conclusion, the main finding of this study is that Pyk2 is a novel substrate of STEP. STEP directly binds to and dephosphorylates Pyk2 at Tyr⁴⁰², and Pyk2 and two of its downstream targets are up-regulated in STEP KO mouse brain. The importance of STEP in the regulation of Pyk2 was further confirmed in a model for synaptic plasticity (KCl depolarization). The present study extends earlier findings that suggest that STEP opposes the development of synaptic strengthening by regulating signaling pathways that play important roles in normal physiological functions within the CNS.

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