



Neuron-Type Specific Loss of CDKL5 Leads to Alterations in mTOR Signaling and Synaptic Markers

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Abstract

CDKL5 disorder is a devastating neurodevelopmental disorder associated with epilepsy, developmental retardation, autism, and related phenotypes. Mutations in the *CDKL5* gene, encoding CDKL5, have been identified in this disorder. CDKL5 is a protein with homology to the serine-threonine kinases and incompletely characterized function. We generated and validated a murine model bearing a floxed allele of *CDKL5* and polyclonal antibodies to CDKL5. CDKL5 is well expressed in the cortex, hippocampus, and striatum, localized to synaptosomes and nuclei and developmentally regulated in the hippocampus. Using Cre-mediated mechanisms, we deleted CDKL5 from excitatory CaMKII α -positive neurons or inhibitory GABAergic neurons. Our data indicate that loss of CDKL5 in excitatory neurons of the cortex or inhibitory neurons of the striatum differentially alters expression of some components of the mechanistic target of rapamycin (mTOR) signaling pathway. Further loss of CDKL5 in excitatory neurons of the cortex or inhibitory neurons of the striatum leads to alterations in levels of synaptic markers in a neuron-type specific manner. Taken together, these data support a model in which loss of CDKL5 alters mTOR signaling and synaptic compositions in a neuron-type specific manner and suggest that CDKL5 may have distinct functional roles related to cellular signaling in excitatory and inhibitory neurons. Thus, these studies provide new insights into the biology of CDKL5 and suggest that the molecular pathology in CDKL5 disorder may have distinct neuron-type specific origins and effects.

Keywords CDKL5 · mTOR · Synaptic · Signaling · CDKL5 disorder

Introduction

CDKL5 disorder is a devastating neurodevelopmental disorder associated with neurodevelopmental phenotypes, autism [1], intellectual disability, and epilepsy [2, 3]. *CDKL5* encodes CDKL5, a protein with homology to the serine-threonine kinases. Structurally, the protein has a kinase domain and putative nuclear localization and nuclear export signals. The functional roles of CDKL5 are incompletely characterized, but include roles in regulation of synaptic density, architecture

and stability [4–6], postsynaptic localization of NMDA receptors [7], surface expression of AMPA receptors [8], neuronal polarization [9], microtubule dynamics [10], RNA splicing [11], synaptic connectivity in the cortex [12], dendritic spine stability [13], and dendritic architecture [14]. Loss of CDKL5 in mouse models leads to phenotypes associated with CDKL5 disorder, including autistic phenotypes [15], memory impairment [16], increased seizure susceptibility [7], and sleep apnea [17]. Thus, CDKL5 is a critical regulator of neural circuit function and disruption of these functional roles in CDKL5 disorder likely contributes to neural circuit deficits and behavioral outcomes associated with the disorder.

Neurodevelopmental disorders with phenotypes similar to those observed in CDKL5 disorder vary in their origin and etiology and several genetic mouse models recapitulate core features of these disorders [18]. However, aberrations in mechanistic target of rapamycin (mTOR) signaling pathways [19–21] and synaptic density, function, and architecture are commonly observed in a variety of disorders associated with similar phenotypes [22, 23].

To begin to address the functional roles of CDKL5 in vivo, we generated and validated a mouse model bearing a floxed

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allele of *CDKL5*. We also generated a rabbit polyclonal antibody to *CDKL5* and validated this and two commercial antibodies on tissue from Cre-mediated recombination. We examined the brain region distribution of *CDKL5*. Our data indicate that *CDKL5* is well expressed in the cortex, hippocampus, and striatum, with little expression in the olfactory bulb and cerebellum. Further, *CDKL5* is localized in synaptosomes and nuclei and developmentally regulated in the hippocampus. By taking advantage of Cre-mediated recombination, we examined the effects of loss of *CDKL5* in excitatory neurons (CaMKII α -positive) or inhibitory (GAD65-positive) neurons on components of the mTOR signaling pathway and loss of *CDKL5* in excitatory (CaMKII α -positive) or inhibitory (GAD65-positive) neurons on excitatory synaptic markers. These data support a model in which loss of *CDKL5* alters mTOR signaling and synaptic compositions in a neuron-type specific manner and suggest that *CDKL5* may have distinct functional roles in excitatory and inhibitory neurons.

Methods

Experimental Procedures

CDKL5 Conditional Knockout Mouse The mouse *CDKL5* gene consists of 22 exons [24] of which the fourth exon was targeted for creating a conditional knockout allele. The targeting construct was commercially synthesized that contained a left and right homology arms of 7.3 and 6 kilobases respectively along with the upstream LoxP site in intron 3, and a Frt-Neo-Frt-LoxP cassette in intron 4. If a truncated protein is expressed from the upstream exons, it will produce only about 33 amino acid polypeptides, along with another 29 amino acids originating from frameshifted reading of the exon 6. Upon Cre-mediated deletion of the exon 4, the transcript will undergo nonsense-mediated decay due to frameshift in the protein coding sequence of the downstream exons. The targeting construct was linearized and electroporated into C57BL6/J-derived ES cells [25]; the positive clones were screened by long range PCRs and confirmed by southern blotting. The ES cell clones were injected into Albino C57BL6/J (<https://www.jax.org/strain/000058>) strain-derived blastocysts, to generate chimeras, at the mouse genome engineering core facility, UNMC. A genotyping PCR assay was developed for detecting the conditional knockout allele. The primer pairs were *CDKL5* Flox F TGCTCTTGAGTATGTTGATTGAC and *CDKL5* Flox R ACTTGAATCATAATACTGTATACCTTG. The expected amplicons sizes are 204 and 267 bp, for wild-type and conditional KO alleles respectively. The floxed mice were bred to Cre mice to generate neuron-specific conditional knockout allele for *CDKL5*. The loss of *CDKL5* protein expression, in the target tissue, was confirmed by Western blotting.

Animals

All animal experiments were approved by Institutional Animal Care and Use Committee of the University of Nebraska Medical Center. Mice were housed with 12/12-h dark/light cycle with free access to food and water. The heterozygous *CDKL5*^{fl} females were mated with homozygous CaMKII α -Cre (the Jackson Laboratory, Stock No. 005359) or Gad2-IRES-Cre (the Jackson Laboratory, Stock No. 019022) male. Three offspring from homozygous *CDKL5*^{fl} female and heterozygous Gad2-IRES-Cre male were also included and no significant difference were observed. Only male mice were included in this study.

Immunoblotting

Mice were anesthetized by isoflurane and brain tissues from the cortex and striatum were dissected out in cold 1 \times PBS on ice. Tissues were quick-frozen on dry ice and stored at -80°C . For tissue lysate preparation, cold lysis buffer, including 50 mM Tris pH 7.4, 107 mM NaCl, 1% Triton X-100, 0.1% SDS, 1:100 protease inhibitor (Sigma, P8340), 1:100 phosphatase inhibitor (Sigma, P0044), 5 mM EDTA, and 5 mM EGTA, was added to the samples before thawing, to minimize nonspecific cleavage by protease. Tissues were then homogenized by sonication (22–25% amplitude, 2-s sonication for 3–8 times according to the size of the tissue, with at least 60-s interval between each sonication) on ice and centrifuged 15,000 rpm for 5 min at 4°C . Supernatants were loaded on 7.5% or 10% hand-casted SDS-PAGE, with 15–50 μg of protein per well. The dilutions of antibodies for immunoblot are as follows: 1:100 NR2B (NeuroMab, clone N59/36, 73-101), 1:100 PSD-95 (NeuroMab, clone K28/43, 73-028), 1:1000 Arc (Santa Cruz Biotechnology C-7, sc-17839), 1:8000 VGLUT1 (Millipore, AB5905), 1:5000 N-cadherin (BD Bioscience, 610920), 1:2000 CaMKII α (Millipore, clone 6G9, 05-532), 1:1000 mTOR (Cell Signaling Technology, 2983), 1:1000 p-mTOR(S2448) (Cell Signaling Technology, 5536), 1:1000 p-mTOR(S2481) (Cell Signaling Technology, 2974), 1:1000 p-TSC2(S1387) (Cell Signaling Technology, 5584), 1:1000 p-p70S6K(T389) (Cell Signaling Technology, 9234), 1:1000 p70S6K (Cell Signaling Technology, 9202), 1:1000 TSC2 (Cell Signaling Technology, 4308), 1:1000 Rag C (Cell Signaling Technology, 5466), 1:1000 Rag B (Cell Signaling Technology, 8150), 1:1000 Rag A (Cell Signaling Technology, 4357), 1:1000 p-TSC2(S939) (Cell Signaling Technology, 3615), 1:10000 p62 (Abcam, ab109012), 1:200 β -tubulin (DHSB, E-7), 1:200 actin (DHSB, JLA20), 1:16000 HRP-conjugated anti-rabbit IgG (Jackson ImmunoResearch 711-035-152), 1:16000 HRP-conjugated anti-mouse IgG (Jackson ImmunoResearch 711-035-151), 1:6000 HRP-conjugated anti-guinea pig IgG (Invitrogen, 614620). The *CDKL5* antibody Rabbit 6680

was generated using a peptide spanning as indicated in Fig. 1 using a commercial vendor.

Quantitation of Westerns Blots were detected by SuperSignal West Dura Chemiluminescent Substrate (Thermo, 34075), imaged by FluorChem HD2 (Cell Biosciences), and quantified on AlphaView (ProteinSimple) or ImageJ. After background subtraction, band intensity was normalized to housekeeping protein (β -tubulin or actin accordingly). Individual values were then normalized to the geometric mean of the litter so that unpaired statistical tests can be performed. For every western blot band that was quantitated, we ensured that the

signal was not saturated using tools available with the AlphaView software.

Primary Neuron Culture from E18 Rats As previously described [26]

Nuclear Preparation Primary rat neurons were washed with $1\times$ PBS. Culture dishes were incubated on a shaker with $600\ \mu\text{L}$ per 100-mm dish of $1\times$ Buffer A (0.5 M HEPES, 2 M KCl, 0.5 M EDTA, water), 4% NP-40, and 1% protease and phosphatase inhibitors for 15 min at $4\ ^\circ\text{C}$ on ice. Cells were scraped using a disposable cell scraper. The homogenate was

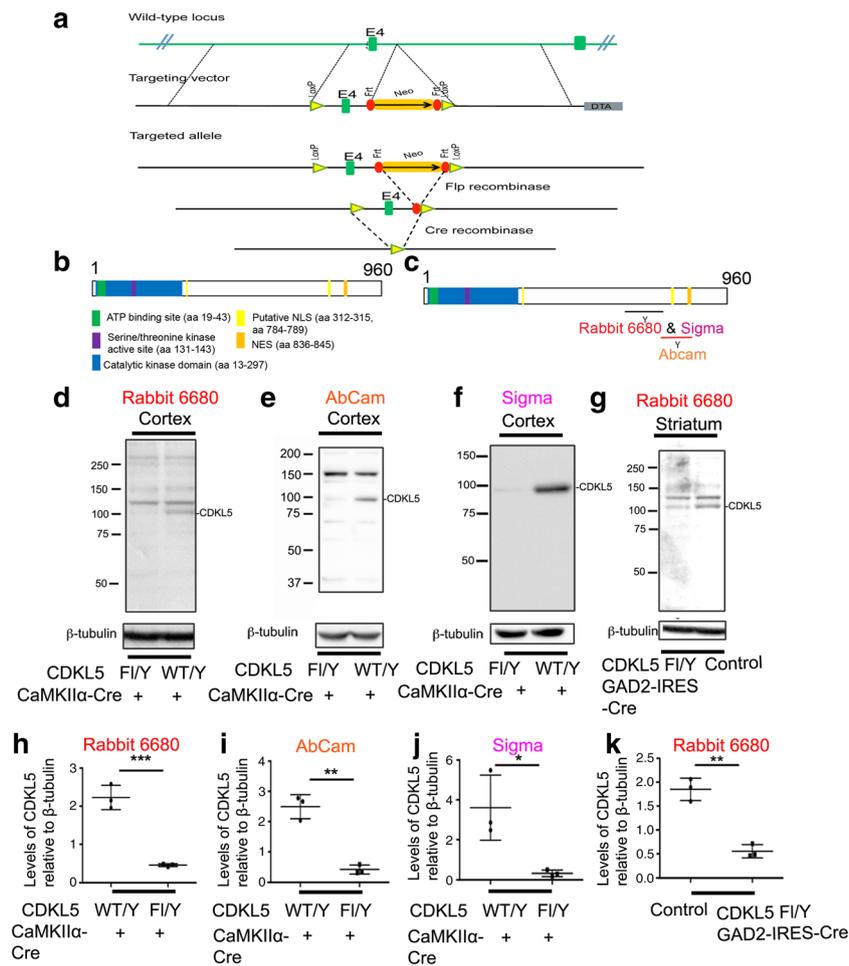


Fig. 1 Generation and validation of CDKL5 mouse model and CDKL5 antibodies. **a** Schematic of targeted locus and locus after Cre-mediated recombination. **b** Schematic of CDKL5 with different known domains indicated—sequence based on human CDKL5. **c** Schematic of CDKL5 with location of three antibody epitopes. The Sigma and Abcam are commercial antibodies and Rbt 6680 is a custom polyclonal peptide antibody. **d** Western blots of cortical lysates from CDKL5 F1/Y +/– CaMKII α -Cre with anti-CDKL5—Rbt6680. **e** Western blots of cortical lysates from CDKL5 F1/Y +/– CaMKII α -Cre with anti-CDKL5—Abcam. **f** Western blots of cortical lysates from CDKL5 F1/Y +/– CaMKII α -Cre with anti-CDKL5—Sigma. **g** Western blots of striatal

lysates from CDKL5 F1/Y +/– GAD2-IRES-Cre with anti CDKL5—Rbt 6680 (**d–g** data $N=3$ for each genotype). **h** Levels of CDKL5 relative to β -tubulin in cortical lysates from CDKL5 F1/Y +/– CaMKII α -Cre with anti CDKL5—Rbt 6680. **i** Levels of CDKL5 relative to β -tubulin in cortical lysates from CDKL5 F1/Y +/– CaMKII α -Cre with anti CDKL5—Abcam. **j** Levels of CDKL5 relative to β -tubulin in cortical lysates from CDKL5 F1/Y +/– CaMKII α -Cre with anti CDKL5—Sigma. **k** Levels of CDKL5 relative to β -tubulin in striatal lysates from CDKL5 F1/Y +/– GAD2-IRES-Cre with anti CDKL5—Rbt 6680 (**h–k** data presented \pm SEM, $*P<0.05$, $**P<0.005$, $***P<0.0005$, Student's t test assuming equal variances)

centrifuged at 15,000×g for 3 min at 4 °C. Tubes were placed on ice and the supernatant was collected as the cytosolic fraction. Three washes of 250 µL of 1× Buffer A (NP-40) were performed with centrifugation at 15,000×g for 3 min at 4 °C between washes. The pellet was resuspended in 1× Buffer B (0.5 M HEPES, 5 M NaCl, 0.5 M EDTA, 40% glycerol, water) and 1% protease and phosphatase inhibitors and vortexed for 10 s. The homogenate was placed on ice on a shaker in a cold room for 2 h. Tubes were centrifuged at 15,000×g for 5 min at 4 °C and the supernatant was collected as the nuclear soluble fraction. Three washes of 100 µL of 1× Buffer B were performed with centrifugation at 15,000×g for 3 min at 4 °C between washes. The final pellet was suspended in RIPA buffer and sonicated to produce lysates for Western blot analysis.

Synaptosome Preparation Dissected brain tissue (hippocampus ~20 mg; cortex ~40 mg from mouse P21 brain) was homogenized in 10 volumes of the Syn-PER Reagent (ThermoScientific No. 87785, both protein phosphatase inhibitors and protease inhibitors included) using a 2-mL Dounce tissue grinder with 13 up-and-down even strokes (all procedures on ice). The homogenate was centrifuged at 1200×g for 10 min to pellet synaptosomes. To further remove residual cell debris, the pellet was resuspended in Syn-PER Reagent and centrifuged again (1200×g, 10 min). For Western blot, the pellets, containing synaptosomes, were suspended in the RIPA buffer. When needed, to the supernatant (after the initial 1200×g centrifugation), 5× RIPA buffer was added and briefly sonicated to produce lysates for Western blot analysis (synptosome-minus fraction). To get cytosol fraction, the supernatant (after the initial 1200×g centrifugation) was centrifuged for 20 min at 15,000×g. When needed, the remaining pellet (enriched for big organelles and membrane) was resuspended in RIPA buffer for Western Blot analysis.

Statistics

All the statistical tests were performed on Prism 7 (GraphPad). Normality of every group was first tested by D'Agostino and Pearson normality test and statistical tests were performed accordingly. Groups with too few data points for the normality test were treated as normally distributed.

Results

Generation and Validation of Floxed CDKL5 Mice and CDKL5 Antibodies We generated a conditional murine allele (Fig. 1a) using standard techniques by generating a floxed allele of *CDKL5* flanking exon 4. Cre-mediated recombination is likely to generate a null allele (see the “Methods” section). We generated a rabbit polyclonal peptide antibody to the

C-terminal region of the mouse *CDKL5* (Fig. 1b), including amino acids 636–758 (Fig. 1c). In addition to this antibody, two commercial antibodies to *CDKL5* are also available (Sigma—aa 636–758 and Abcam—aa750–850). We generated mouse models in which *CDKL5* is deleted from the cortical excitatory neurons by crossing the *CDKL5* floxed allele into the *CaMKIIα-Cre* line or from GABAergic neurons by crossing the *CDKL5* floxed allele into the *Gad2-IRES-Cre* line. We examined the expression of *CDKL5* in the *CDKL5* F1/Y or *CDKL5* F1/Y-*CaMKIIα-Cre* cortex by Western blot analysis with all the three antibodies. The levels of *CDKL5* detected by all three antibodies, Rbt 6680 (Fig. 1d, h), Abcam (Fig. 1e, i), and Sigma (Fig. 1f, j), were significantly reduced in the *CDKL5* F1/Y Cre mice in comparison to control. Rbt 6680 also reacts with an additional higher molecular weight non-specific band. We similarly examined the expression of *CDKL5* in the striatum from the *CDKL5* F1/Y-*Gad2-IRES-Cre* mice. The striatum is predominantly composed of GABAergic neurons. Similar to the results observed with the *CDKL5* F1/Y-*CaMKIIα-cre* mice, the levels of *CDKL5* in the *CDKL5* F1/Y-*Gad2-IRES-Cre* striatum were significantly reduced (Fig. 1g, k). These results indicate that (1) Cre-mediated recombination of the floxed allele of *CDKL5* results in loss of *CDKL5* protein and (2) the three antibodies are specific to *CDKL5*.

Expression Pattern of CDKL5 We examined the expression of *CDKL5* in different regions of the mouse brain using Western blot analysis (Fig. 2a, b). *CDKL5* is predominantly expressed in the cortex, striatum, and hippocampus with little expression in the cerebellum and olfactory bulb. To examine the subcellular distribution of *CDKL5*, we examined the expression of *CDKL5* in synaptosomal preparations from the mouse cortex. *CDKL5* is well expressed in synaptosomal fractions as indicated by co-enrichment with PSD-95, an excitatory postsynaptic marker (Fig. 2c). This is consistent with literature. We also examined the subcellular distribution of *CDKL5* in the nucleus by Western blot analysis of cytosolic and nuclear fractions from cultured primary rat neurons. Nuclear fractions are enriched in histone H3. *CDKL5* is localized in nuclear fractions (Fig. 2d). Taken together, these results suggest that *CDKL5* is predominantly expressed in the cortex, hippocampus, and striatum and localized to synaptosomes and nuclei.

Developmental Expression of CDKL5 We examined the expression pattern of *CDKL5* in the hippocampus across development (Fig. 3a). *CDKL5* was well expressed at all stages during development and in the adult. Our data suggest that there may be trends towards expression peaks around P21–P28; however, these did not reach statistical significance (Fig. 3b). We compared the molecular weights of the mouse *CDKL5* from hippocampal tissue (p21) and rat *CDKL5* from

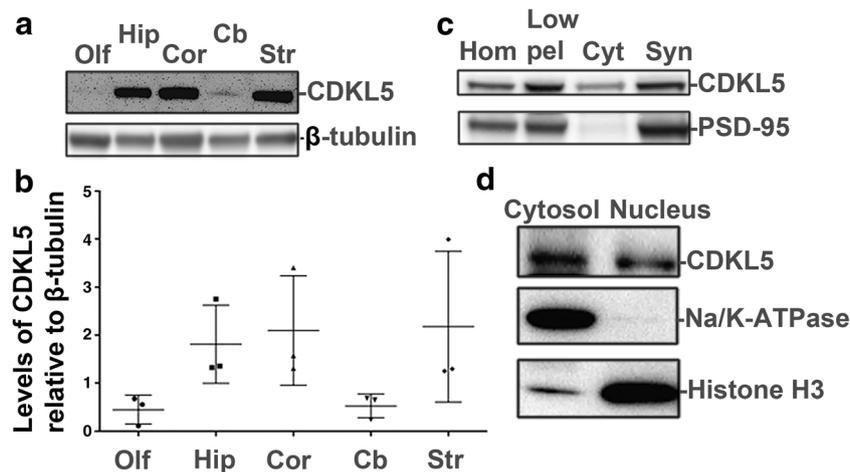


Fig. 2 Regional and temporal expression patterns for CDKL5. **a** Western blots for CDKL5 (Sigma) in different regions of the mouse brain as indicated (P28, male, $N=3$). **b** Levels of CDKL5 relative to β -tubulin in different regions of the mouse brain (P28, male, $N=3$) (data \pm SEM). **c**

Western blot for CDKL5 (Sigma) and PSD-95 (excitatory synaptic marker) in synaptosomal preparations from mouse cortex (adult, $N=3$). **d** Western blot for CDKL5 (Sigma), histone H3, and Na^+/K^+ -ATPase in cytosol and nuclear preparations from primary rat neurons

in vitro primary cultures by Western blot analysis with Rbt 6680 (Fig. 3c). Unlike the mouse lysates, Rbt 6680 only detects a single CDKL5 specific band in rat lysates. We also examined developmental expression of CDKL5 in the rat hippocampus (Fig. 3d, e). Similar to the mouse hippocampus, CDKL5 is well expressed at time points coincident with neural circuit formation and refinement. We further examined the

expression of CDKL5 in primary rat neurons at DIV 7, 14, and 21 (Fig. 3f, g). Similar to the in vivo data, we observe expression of CDKL5 in primary neurons at time points coincident with synapse formation and maturity. Taken together, these results indicate that the expression of CDKL5 is developmentally regulated in the hippocampus, both in vivo and in vitro.

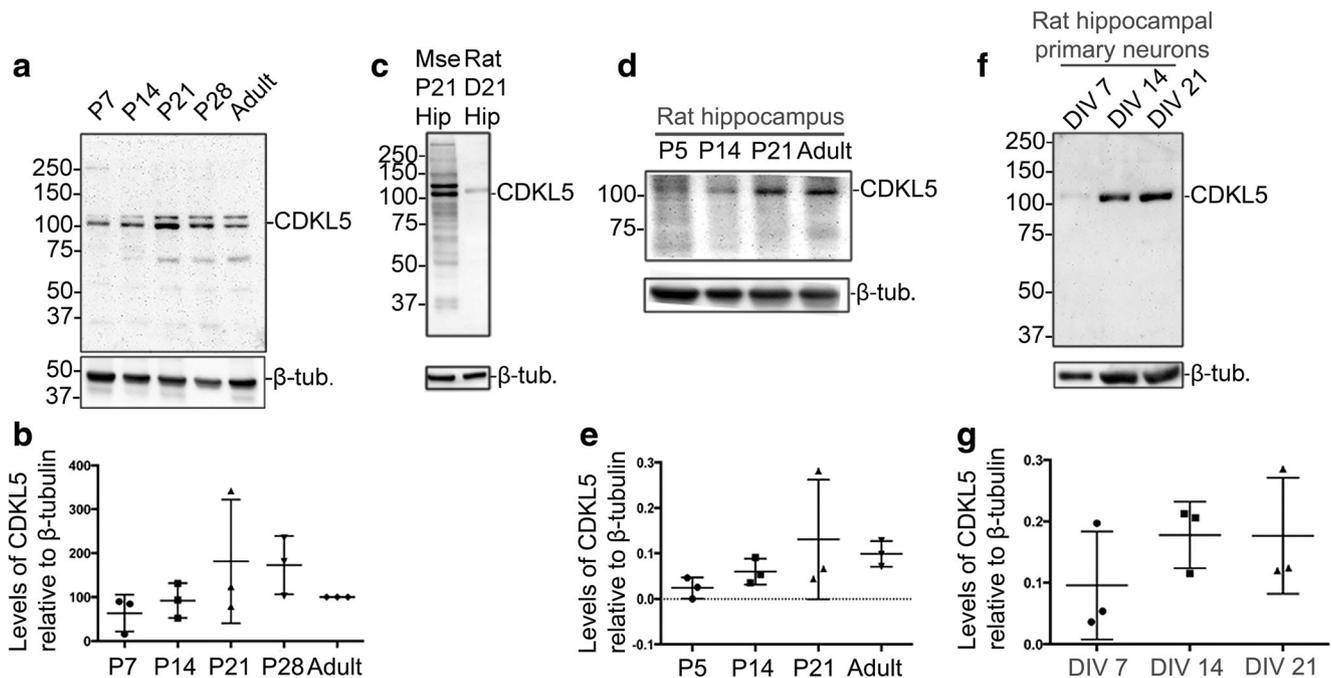


Fig. 3 Developmental expression of CDKL5 in rat and mouse hippocampus. **a** Western blot for CDKL5 in hippocampal lysates at indicated time points ($N=3$). **b** Levels of CDKL5 relative to β -tubulin at indicated time points in the mouse hippocampus. Levels were normalized to percentage of adult levels. **c** Western blot for CDKL5 (Rbt 6680) in P21 mouse hippocampal lysate and rat primary neuron

lysates. **d** Western blot for CDKL5 (Rbt 6680) in hippocampal lysates from P7 to adult rat tissue ($N=3$). **e** Levels of CDKL5 relative to β -tubulin at P7 to adult in the rat hippocampus. **f** Western blot for CDKL5 (Rbt 6680) in hippocampal lysates from primary rat neurons at DIV 7, 14, and 21 ($N=3$). **g** Levels of CDKL5 relative to β -tubulin in hippocampal lysates from primary rat neurons at DIV 7, 14, and 21

CDKL5. In addition, unlike the effects observed with loss of CDKL5 in excitatory neurons, we did not observe any strong trends for alterations in levels of PSD-95 with loss of CDKL5 in GABAergic neurons. In addition, the levels of Arc, an activity-regulated gene, and CaMKII α , a marker for excitatory glutamatergic neurons, were not significantly altered. Taken together, these data suggest that loss of CDKL5 in GABAergic neurons of the striatum does not significantly alter levels of excitatory synaptic markers.

Discussion

CDKL5 disorder is a disorder with neurodevelopmental phenotypes, including motor deficits, intellectual disability, autism, and epilepsy. In this study, we have made several significant observations relating to the biology of CDKL5, encoded by *CDKL5*, that are likely relevant to dissecting the molecular pathology of the disorder.

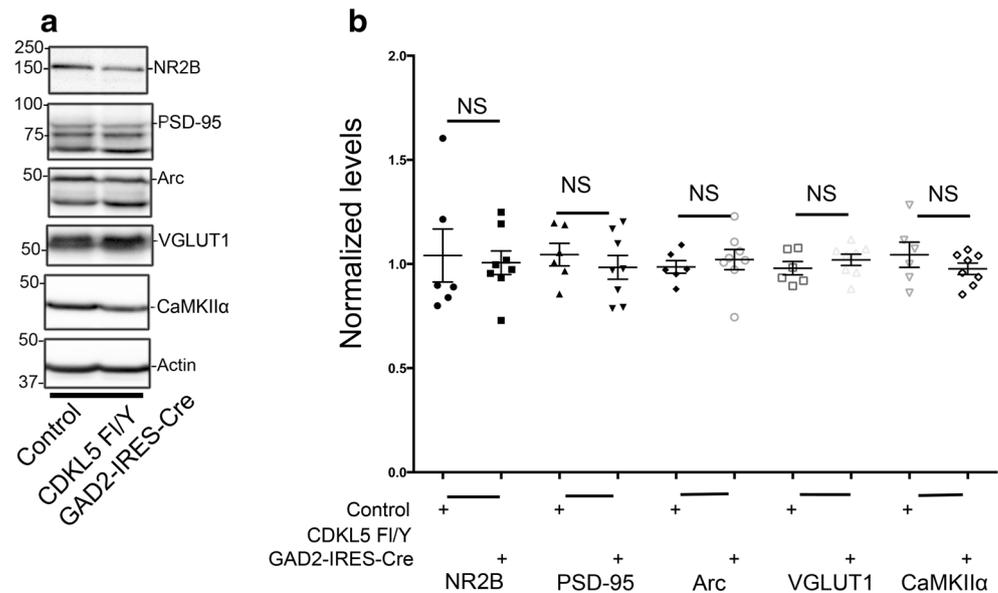
Our data indicate that CDKL5, encoded by *CDKL5*, is expressed predominantly in the cortex, hippocampus, and striatum with lower expression in the cerebellum and olfactory bulb. These regions are associated with higher order functions including thought, action, learning, memory, and voluntary movement. The expression pattern of CDKL5 in these regions and the phenotypes associated with CDKL5 disorder suggest that CDKL5 is a critical regulator of neural circuits predominantly in these brain regions. Previous studies indicate that loss of CDKL5 in the cerebellum [32] leads to impaired motor coordination and gait, accompanied by reduction of GAD67 in the molecular layer with no alterations in the levels of VGLUT1 and reduced levels of BDNF mRNA. These results suggest that while the expression levels of CDKL5 in the cerebellum are low, they are functionally significant and that

functional roles of CDKL5 in regions other than the hippocampus, cortex, and striatum may also be critical to the pathology of CDKL5 disorder. Further, the developmental expression of CDKL5 coincides with the periods of neural circuit formation and refinement, consistent with a role for CDKL5 in neural circuit assembly, function, and regulation.

Several mutations in *CDKL5*, including missense, point, frameshift, and splicing mutations, have been identified in CDKL5 disorder in humans. These mutations are predominantly localized in the kinase domain, suggesting that the ability of the protein to function kinase is critical. Our data demonstrating the localization of CDKL5 in synaptosomes and nuclei is consistent with data from other labs [4, 33–35]. Thus, it is likely that the predominant kinase substrates of CDKL5 are localized to synapses and nuclei. While some of these substrates, including MeCP2, Dnmt1, and amphiphysin1 [33, 36, 37], have been identified, many likely remain to be identified. It is likely that the dynamic phosphorylation of these substrates in different cellular compartments contributes to the functional roles of CDKL5 in neural circuit function.

The mTOR signaling pathway [38, 39] in neurons has key roles in a variety of signaling mechanisms associated with long-term potentiation, long-term depression, learning and memory, neuronal survival, differentiation, and morphogenesis [38]. We note that previous studies have demonstrated a reduction in the levels of pmTORS2448 in whole brain lysates of the complete null CDKL5 mouse model [15]. While our data show a slight trend towards reduction of pmTORS2448 in the CDKL5 F1/Y CaMKII α -Cre mouse cortex, these do not reach significance, suggesting that regional and neuronal or cell-type specific mTOR signaling mechanisms may be regulated by CDKL5.

Fig. 7 Synaptic composition is maintained with loss of CDKL5 in striatal inhibitory (GAD65-positive) neurons. **a** Western blots for synaptic markers as indicated in striatal lysates from CDKL5 F1/Y +/- Gad2-IRES-Cre tissue. **b** Levels of synaptic markers as indicated relative to actin as indicated in striatal lysates from CDKL5 F1/Y +/- Gad2-IRES-Cre tissue (data presented \pm SEM, * P < 0.05, ** P < 0.005, *** P < 0.0005, Student's t test with Welch correction; N = 6 for control and N = 8 for CDKL5 F1/Y +/- Gad2-IRES-Cre; age 4–25 weeks)



Our data indicate that loss of CDKL5 in glutamatergic neurons of the cortex leads to a significant reduction in levels of p70 ribosomal S6 protein kinase 1 (p70S6K1) and its phosphorylated form, p70S6K1T389. The ribosomal protein p70S6K1 [40] is a downstream target of the mTORC1 pathway. P70S6K1 can be phosphorylated at T389 by mTORC1. Phosphorylation of S6K1 by mTORc1 activates S6K1 and subsequently protein synthesis. One of the substrates of activated S6K1 is ribosomal protein S6, a component of the 40S ribosome. S6K1 functions have been implicated in a variety of mechanisms related to neuronal morphology, including axon regeneration [41], and dendrite morphology [42] and behaviors, including depressive behavior in the prefrontal cortex [43] and learning, memory, and synaptic plasticity [44]. Interestingly, published studies indicate that loss of CDKL5 in a mouse model leads to reduced S6 Ser240-244 phosphorylation [13], suggesting that deficits in mTOR-dependent translational regulation may be a key feature of CDKL5 disorder. How the loss of CDKL5 leads to an alteration in the levels of p70S6K1 remains to be identified; however, these observations are highly significant and suggest a mechanism by which CDKL5 may regulate translation via the mTOR pathway. Identifying such mechanisms and the translational products that are regulated by these mechanisms may have great significance for our understanding of the molecular pathology in CDKL5 disorder.

Our data also indicate that the loss of CDKL5 in inhibitory neurons, surprisingly, does not mirror the effects observed with loss of CDKL5 in excitatory neurons. Unlike, the alterations in glutamatergic neurons, loss of CDKL5 in GABAergic neurons of the striatum leads to a trend towards increase in the levels of p70S6K1 with a trend towards decrease of its T389 phosphorylated form, both of which were not significant. It is possible that heterogeneity of responses in subtypes of GABAergic neurons may contribute to these trends; however, these assessments require further experimental evidence. However, in stark contrast to the data from glutamatergic neurons, the levels of Rag C were significantly increased in GABAergic neurons with loss of CDKL5. The Rag family of proteins is GTPases [45]. They function as heterodimers of either Rag A or Rag B with either Rag C or Rag D and switch between engaging GTP and GDP to form part of a cellular mechanism that allows for nutrient sensing at the level of lysosomes and connect autophagy to mTORC1 signaling [46, 47]. Consequently, the precise control of this signaling pathway is essential for cells to respond to changing cellular energy demands. We note that the levels of Rag A and B are unaltered with loss of CDKL5 in inhibitory neurons, but the levels of Rag C are significantly increased. At the cellular level, this is likely to lead to an imbalance in the ability of the Rag proteins to couple nutrient sensing to autophagic mechanisms, leading to deficits in neuronal metabolism that could impact multiple aspects of neuronal function relevant to the

pathology of CDKL5 disorder, including synaptic physiology [48, 49]. The validation of this model requires in-depth assessments of nutrient sensing and neuronal responses in the absence of CDKL5 in inhibitory neurons and may lead to great insights into the molecular pathology in CDKL5 disorder.

Several studies indicate that CDKL5 is localized at excitatory synapses and loss of CDKL5 perturbs excitatory synaptic structure and function. Multiple mouse models for CDKL5 have been generated and recapitulate some aspects of the CDKL5 disorder. Complete CDKL5-null mice (exon 6 deletion [50]) exhibit behavioral features similar to autism and ADHD. Complete CDKL5-null mice (exon 2 deletion [7]) have increased susceptibility to NMDA-mediated seizures, enhanced anxiety, and altered depressive-like and social behaviors. Another complete null mouse model for CDKL5 [15] exhibits hyperactivity, motor impairments, decreased anxiety, and social behaviors reminiscent of autism. Interestingly, female heterozygous mice lacking one allele of *CDKL5* also display several behavioral phenotypes including autistic-like behaviors, motor deficits, and memory and breathing abnormalities [51]. These studies confirm that complete loss of CDKL5 in murine models leads to several behavioral features reminiscent of the human disorder.

CDKL5 is expressed in both glutamatergic and GABAergic neurons. Mice with selective loss of CDKL5 in glutamatergic neurons in the forebrain (using Nex-Cre [16]) exhibit a hindlimb clasp phenotype and have some deficits in hippocampal learning and memory. A similar hindlimb clasp phenotype is observed in mice in which CDKL5 is deleted from a mouse model bearing a floxed allele of *CDKL5* using the Emx-Cre line. Male mice that are null for CDKL5 in GABAergic neurons generated by crossing mice bearing a *CDKL5* floxed allele into the *Dlx5/6* Cre line demonstrate decreased locomotion [31]. Based on these data, it is likely that CDKL5 has differential functional roles in glutamatergic and GABAergic neurons.

Our results with loss of CDKL5 in excitatory neurons of the cortex are consistent with Western blot data from CDKL5 *Y*^{-/-} hippocampi demonstrating no alterations in total levels of NR2B and VGLUT1 in the CDKL5 *Y*^{-/-} mice in comparison to control [7]. However, we do observe an increase in the levels of PSD-95 with loss of CDKL5 in glutamatergic neurons. Our results are in contrast with data from [13] demonstrating a decrease in the levels of PSD-95 in the cortex of CDKL5 *Y*^{-/-} mice. While our data was obtained from entire cortical lysates, the data in [13] was obtained from the somatosensory cortex. Thus, it is possible that regional differences in the levels of excitatory synaptic markers exist within the cortex in the absence of CDKL5. Our data are also in contrast with data from [7] demonstrating no alterations in the levels of PSD-95 in hippocampal lysates from CDKL5 *Y*^{-/-} mice. Taken together, these data suggest that loss of CDKL5 may lead to regional differences in excitatory synaptic markers

within the brain and cortex. Further sophisticated electrophysiological and high-resolution microscopy studies are necessary to establish such differences.

Our results indicate that loss of CDKL5 in GABAergic neurons of the striatum does not significantly alter the levels of excitatory synaptic markers. However, similar to the data from excitatory neurons, these data do not rule out the possibility that synaptic levels of some of these markers are altered while total levels are not.

Previous studies indicate that mice with complete loss of CDKL5 have reduced levels of *c-fos*, a protein encoded by an activity-regulated immediate early gene, in both excitatory neurons and parvalbumin-positive inhibitory neurons [12]. Our data indicate that loss of CDKL5 in either excitatory or inhibitory neurons does not alter levels of *Arc*, an activity-regulated immediate early gene [52], suggesting that loss of CDKL5 may selectively alter expression of activity-regulated genes that may be relevant to the pathology of CDKL5 disorder.

We have identified neuron-type specific alterations with loss of CDKL5 in components of the mTOR signaling pathways and synaptic proteins (Fig. 8). Both of these pathways are critical for neural circuit formation and function. Taken together with published data, our results suggest that the differential functional roles of CDKL5 in excitatory and inhibitory neurons may be critical for its functional roles in neural circuit formation and function and disruptions in these

functional roles with loss or mutations in CDKL5 contribute to the pathology of CDKL5 disorder.

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Compliance with Ethical Standards

All animal experiments were approved by Institutional Animal Care and Use Committee of the University of Nebraska Medical Center.

Conflict of Interest The authors declare that they have no conflicts of interest.

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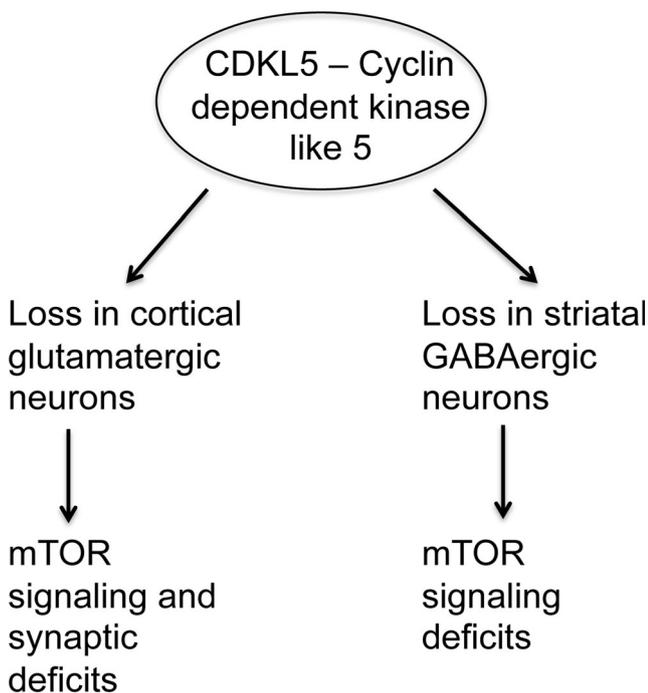


Fig. 8 Overall model. Loss of CDKL5 in glutamatergic or GABAergic neurons perturbs expression of components of mTOR pathway and synaptic markers in a neuron-type specific manner

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