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# Collagen XIX Is Expressed by Interneurons and Contributes to the Formation of Hippocampal Synapses

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# Abstract

Extracellular matrix (ECM) molecules contribute to the formation and maintenance of synapses in the mammalian nervous system. We previously discovered a family of nonfibrillar collagens that organize synaptic differentiation at the neuromuscular junction (NMJ). Although many NMJorganizing cues contribute to central nervous system (CNS) synaptogenesis, whether similar roles for collagens exist at central synapses remained unclear. In the present study we discovered that coll9a1, the gene encoding nonfibrillar collagen XIX, is expressed by subsets of hippocampal neurons. Colocalization with the interneuron-specific enzyme glutamate decarboxylase 67 (Gad67), but not other cell-type-specific markers, suggests that hippocampal expression of col19a1 is restricted to interneurons. However, not all hippocampal interneurons express col19a1 mRNA; subsets of neuropeptide Y (NPY)-, somatostatin (Som)-, and calbindin (Calb)immunoreactive interneurons express coll9a1, but those containing parvalbumin (Parv) or calretinin (Calr) do not. To assess whether collagen XIX is required for the normal formation of hippocampal synapses, we examined synaptic morphology and composition in targeted mouse mutants lacking collagen XIX. We show here that subsets of synaptotagmin 2 (Syt2)-containing hippocampal nerve terminals appear malformed in the absence of collagen XIX. The presence of Syt2 in inhibitory hippocampal synapses, the altered distribution of Gad67 in collagen XIXdeficient subiculum, and abnormal levels of gephyrin in collagen XIX-deficient hippocampal extracts all suggest inhibitory synapses are affected by the loss of collagen XIX. Together, these data not only reveal that collagen XIX is expressed by central neurons, but show for the first time that a nonfibrillar collagen is necessary for the formation of hippocampal synapses.

# **INDEXING TERMS**

extracellular matrix; collagen; synaptogenesis; hippocampus; interneuron

Synapse formation is a multistep process orchestrated by developmentally regulated signals that are either passed between putative synaptic partners or present in the extracellular environment. Initial advances in identifying synaptic organizing signals came from studies of the accessible neuromuscular junction (NMJ), where extracellular factors embedded in the basal lamina separating motor nerve terminals from postsynaptic muscle membrane were sufficient to induce synaptogenesis (Sanes et al., 1978; Burden et al., 1979; for review, see

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Sanes and Lichtman, 1999; Fox and Umemori, 2006). Biochemical, molecular, and genetic studies have since identified roles for agrin, laminin a chains, and Wnts in the organization of the postsynaptic apparatus (Nitkin et al., 1987; Gautam et al., 1996; Sanes and Lichtman, 1999; Burgess et al., 1999; Lin et al., 2001, 2005; Misgeld et al., 2005; Kummer et al., 2006; Nishimune et al., 2008; Henriquez et al., 2008) and collagen IV, laminin  $\beta$ 2, and fibroblast growth factors (FGFs) in the formation of presynaptic terminals (Noakes et al., 1995; Nishimune et al., 2004; Fox et al., 2007). In contrast to the NMJ, narrow synaptic clefts and lack of basal laminae in the central nervous system (CNS) initially suggested that pre- and postsynaptic transmembrane molecules directed both the targeting and formation of central synapses. Indeed, several families of transmembrane adhesion molecules, including cadherins, protocadherins, NCAM, SynCAMs, dsCAMs, sidekicks, SALMs, nectins, neuroligins, neurexins, integrins, ephrins, and Eph receptors, are present at central synapses and have been implicated in synaptic targeting, differentiation, or maintenance (Yamagata et al., 2003; Scheiffele, 2003; Gerrow and El-Husseini, 2006; Fox and Umemori, 2006; Craig et al., 2006; Craig and Kang, 2007; Dalva et al., 2007; Sanes and Yamagata, 2009). More recently, however, it has been demonstrated that extracellular molecules, including growth factors, morphogens, proteolytically shed transmembrane molecules, and bulkier matrix molecules, also contribute to central synaptogenesis (e.g., O'Brien et al., 1999, 2002; Hall et al., 2000; Umemori et al., 2004; Christopherson et al., 2005; Bjartmar et al., 2006; Stevens et al., 2007; Umemori and Sanes, 2008). These findings raise the possibility that NMJorganizing molecules may also contribute to the formation of central synapses. Indeed, agrin, laminins, Wnts, and FGFs each contribute to central synaptogenesis (Libby et al., 1999; Hall et al., 2000; Bose et al., 2000; Umemori et al., 2004; Ksiazek et al., 2007; Egles et al., 2007; Davis et al., 2008). However, one family of NMJ organizing molecules, nonfibrillar collagens, has yet to be examined for its potential role in the formation of central synapses.

Nonfibrillar collagens have presumably been overlooked for CNS functions due to the widely held belief that the mammalian CNS lacks collagen, with the exception of that associated with vascular structures (Gallyas et al., 1970). Although early biochemical and histological studies demonstrated few collagen fibers in mammalian CNS tissue (e.g., Lowry et al., 1941), it is now clear that not all collagens are assembled into collagen fibers. In fact, while mammals express 45 collagen genes, fewer than 15 of these genes generate fibrillar collagen (Myllyharju and Kivirikko, 2004; Kadler et al., 2007; Fox, 2008). Despite not being assembled into fibers, CNS expression and function of nonfibrillar collagens still has received little attention (but see Sumiyoshi et al., 2001, Sund et al., 2001, Hashimoto et al., 2002, Claudepierre et al., 2005; Koch et al., 2006, Veit et al., 2006; Seppanen et al., 2007, Hubert et al., 2009). On the basis of collagen function at peripheral synapses, we examined the expression and function of *coll9a1*, the gene encoding nonfibril-forming collagen XIX (Yoshioka et al., 1992; Myers et al., 1993, 1994; Inoguchi et al., 1995) in mouse hippocampus. We focused on hippocampus because its circuitry, cell types, and synaptic morphologies have been well documented (Fig. 1A) (Danglot et al., 2006; Klausberger and Somogy, 2008).

Collagen XIX, although initially identified as a fibrilassociated collagen with interrupted triple helices (FACIT) by sequence analysis (Khaleduzzaman et al., 1997), does not appear to bind collagen fibers but rather accumulates in the extracellular matrix (ECM) of restricted tissues, including neural tissue (Myers et al., 1997; Sumiyoshi et al., 1997, 2001). Aggregates of collagen XIX have been proposed to modulate cell-matrix interactions and cell-cell communication (Myers et al., 2003). In esophageal muscle, collagen XIX is essential for both muscle physiology and differentiation (Sumiyoshi et al., 2004). Proper formation of a collagen XIX-rich basal lamina is required for nitric oxide (NO)-dependent relaxation of lower esophageal sphincter (LES) muscle, perhaps as a result of a disorganized

basal lamina at LES neuromuscular junctions (Sumiyoshi et al., 2004). More recently, the noncollagenous 1 (NC1) domain of collagen XIX was shown to exhibit bioactivities similar to collagens IV NC1 domains (Kalluri, 2003; Ramont et al., 2007). Since collagen IV NC1 domains act as presynaptic organizing molecules at the NMJ (Fox et al., 2007), we examined hippocampal nerve terminals in previously generated mutants lacking collagen XIX (Sumiyoshi et al., 2004). Although hippocampal organization appears grossly normal in these mutants, striking presynaptic defects were observed in the subiculum of the hippocampus, suggesting collagen XIX is necessary for the assembly of some hippocampal synapses.

# MATERIALS AND METHODS

# Animals

CD1 and C57BL/6 mice embryos were obtained from Charles River Laboratories (Wilmington, MA). The generation of collagen XIX null mice ( $col19a1^{-/-}$ ; previously referred to as N19) was previously described (Sumiyoshi et al., 2004). Mutant mice were backcrossed for > 10 generations on C57BL/6 mice. Genomic DNA was isolated from tail using the HotSHOT method (Truett et al., 2000) and genotyping was performed with the following primers: lacZ 5'-TTC ACT GGC CGT CGT TTT ACA ACGTCG TGA-3' and 5'-ATG TGA GCG AGT AAC AAC CCG TCG GAT TCT-3'; col19a1 (exon4) 5'-CTTCGC AAAACG CATGCCTCAGA-3' and 5'-TTG TTC GTT TGT TTG TTT TTA ATC AAT CAA-3'. The following cycling conditions were used on an Eppendorf Mastercycler EP: 95°C for 5 minutes, followed by 35 cycles of amplification (95°C for 30 seconds, 52°C for 30 seconds, 72°C for 45 seconds), and 10 minutes at 72°C. All analyses conformed to National Institutes of Health (NIH) guidelines and were carried out under protocols approved by the Virginia Commonwealth University (VCU) Institutional Animal Care and Use Committee.

#### Reagents

All chemicals and reagents were obtained from either Sigma (St. Louis, MO) or Fisher (Fairlawn, NJ), unless otherwise noted.

# Antibodies

Monoclonal and polyclonal antibodies used in these studies are listed and described in Table 1. Fluorescently conjugated secondary antibodies were obtained from Molecular Probes/ Invitrogen (Eugene, OR) and were applied at a 1:1,000 dilution. Horseradish peroxidase (HRP)-conjugated secondary antibodies were from Jackson ImmunoResearch Laboratories (West Grove, PA) and were used at 1:10,000 dilutions. Alkaline phosphatase- and HRPconjugated anti-DIG or anti-fluorescein antibodies were obtained from Roche (Mannheim, Germany) and were used at 1:1,000.

The following are characterizations of antibodies applied in the present studies.

**Actin**—The mouse anti-actin monoclonal antibody detects a 42-kDa band in Western blots of various vertebrate tissues, including mouse hippocampus and rat forebrain (shown here; Otey et al., 1987; Sano et al., 2006; Cowell et al., 2007).

**Calbindin**—The calbindin D-28k antibody recognizes a single band of ≈28 kDa on Western blots of mouse and rat brain extracts (see manufacturer's datasheet) and stained cells in the rodent hippocampus that were identical to previous reports (Sloviter, 1989; Danglot et al., 2006; Klausberger and Somogyi, 2008). Immunoreactivity of anti-calbindin in immunohistochemistry (IHC) was marginally enhanced following in situ hybridization (ISH) (Supporting Fig. 1; see also Fig. 3).

**Calretinin**—The calretinin antibody recognizes a single band of  $\approx 30$  kDa on Western blots with mouse hippocampal extracts (unpubl. obs., J.S. and M.A.F.) and stained cells in the mouse hippocampus and cortex that were identical to previous reports (Liu et al., 2003; Xu et al., 2004; Danglot et al., 2006; Klausberger and Somogyi, 2008). Immunoreactivity of anti-calretinin in IHC was marginally enhanced following ISH (Supporting Fig. 1).

**Gad65/67**—The Gad65/67 antibody detects a doublet of  $\approx$ 65 and 68 kDa in Western blots of rat brain extracts; immunoreactivity of the Gad65/67 antibody was abolished by preincubating with the immunizing peptide (manufacturer's datasheet). Previous IHC studies demonstrated that this antibody specifically labeled interneurons and inhibitory synapses in rat suprachiasmatic nuclei (Belenky et al., 2008).

**Gad67**—The Gad67 antibody detects a single band of ≈68 kDa in rat and mouse brain extracts and has no detectable cross-reactivity with Gad65 (manufacturer's datasheet; see also Varea et al., 2005). Previous IHC studies demonstrated that this antibody labels interneurons and inhibitory synapses in mouse cortex (Xu et al., 2006). Here, IHC with anti-Gad67 labeled similar, albeit fewer, interneurons and synaptic structures in hippocampus as anti-Gad65/67 (see Fig. 12).

**Gephyrin:** The gephyrin monoclonal antibody detects the 93-kDa isoform of gephyrin in mouse hippocampal and rat forebrain extracts (shown here; Henny and Jones, 2006). This antibody labels postsynaptic structures at inhibitory synapses in IHC of rat forebrains (Henny and Jones, 2006).

**Iba-1:** The Iba-1 antibody detects microglia and macrophages but not neural cells (see manufacturer's datasheet). In our hands this antibody labeled small cells in mouse hippocampus that resembled microglia, which matched previous descriptions (Imai et al., 1996).

**NeuN:** The NeuN antibody detects an uncharacterized nuclear protein present in most vertebrate neurons (Mullen et al., 1992). In our hands this antibody stains a pattern of cells in mouse hippocampus identical with previous reports (e.g., Mullen et al., 1992). In Western blots, the NeuN antibody detects two bands of 46 and 48 kDa (Mullen et al., 1992).

**Neuropeptide Y (NPY):** In IHC the NPY antibody labels subsets of cortical and hippocampal interneurons that were distributed as previously reported (Xu et al., 2004; Danglot et al., 2006; Klaus-berger and Somogyi, 2008). IHC with this antibody was blocked by preincubation with excess NPY, but not other related peptides such as peptide YY (manufacturer's datasheet). Importantly, this antibody worked poorly with our standard IHC protocol; however, immunolabeling was enhanced after ISH (Supporting Fig. 1).

**PSD-95:** The PSD-95 antibody detects a single 95-kDa protein in Western blots of mouse hippocampus (shown here; see also Kornau et al., 1995; Henny and Jones, 2006). This antibody labels postsynaptic densities in IHC of rat forebrains (Henny and Jones, 2006).

**Somatostatin (Som):** In IHC the Som antibody labels subsets of interneurons that were distributed as previously reported in mouse hippocampus, cortex, and retina (Oliva et al., 2000; Xu et al., 2006; Danglot et al., 2006; Klausberger and Somogyi, 2008; Acosta et al., 2008). Previous studies demonstrated that immunoreactivity was inhibited by

**Syt2:** The Syt2 antibody, called *znp1*, was identified in a screen for tissue-specific antibodies in zebrafish (Trevarrow et al., 1990) and was recently shown to detect mouse Syt2 by both Western blot and IHC (Fox and Sanes, 2007). In Western blots of mouse cerebellum, hippocampi, and synaptosome fractions this antibody detects a single band at 60 kDa (Fox and Sanes, 2007; see also Fig. 10). Protein immunoprecipitated with this antibody was identified as Syt2 by mass spectrometry and Western blots demonstrated that this antibody specifically detected recombinant Syt2 but not Syt1, a closely related family member (Fox and Sanes, 2007).

**Synapsin:** The synapsin antibody detects a single  $\approx$ 75-kDa protein in Western blots of mouse brain synaptosome fractions (Fox and Sanes, 2007) or mouse hippocampal extracts (shown here). In IHC, this antibody labels nerve terminals at the mouse NMJ and in mouse hippocampus (Fox et al., 2007; Armstrong et al., 2006).

VGlut1 and VGlut2: In Western blots, the VGlut1 antibody detects a single smeared band of 45–55 kDa and the VGlut2 antibody detects a single band at 60 kDa (shown here). In IHC these antibodies exhibit unique immunoreactivities in mouse hippocampus (manufacturer's data sheet); these patterns match previous descriptions of VGlut1 and VGlut2 distribution in mouse hippocampus (Herzog et al., 2006).

**Collagen XIX:** In addition to the antibodies used here, we tested commercial collagen XIX antibodies (from Abnova, Walnut, CA, and Santa Cruz Biotechnology, Santa Cruz, CA). Neither appeared specific to mouse collagen XIX protein in Western blots or IHC when compared with reactivity with collagen XIX-deficient tissue (unpubl. obs., J.S. and M.A.F.). For this reason, collagen XIX IHC was omitted from the current study.

#### IHC

Mouse brains were fixed in 4% paraformaldehyde (PFA) (in phosphate-buffered saline, PBS) for 12 hours at 4°C, then washed in PBS several times and incubated for at least 24 hours in 20% sucrose in PBS. Fixed tissue was frozen in Tissue Freezing Medium (Triangle Biomedical Sciences, Durham, NC), and 10–16-µm sections were cut on a Leica CM1850 cryostat. Sections were allowed to air dry for 15 minutes before being incubated with blocking buffer (2.5% normal goat serum, 2.5% bovine serum albumin, 0.1% Triton X-100 in PBS) for 30 minutes. Primary antibodies, diluted in blocking buffer, were incubated on tissue sections for 12 hours at 4°C. After washing in PBS, secondary antibodies, diluted in blocking buffer, were applied to the slides for 1 hour at room temperature. Tissue sections were washed thoroughly with PBS, coverslipped with VectaShield (Vector Laboratories, Burlingame, CA), and visualized on a Leica SP2 scanning confocal microscope or a Zeiss AxioImager A1 fluorescent microscope. When comparing mutant and control age-matched samples images were acquired by confocal microscopy using identical parameters (i.e., identical objective, zoom, laser intensity, gain, offset, scan speed, step size, and number of z-stacks) optimized for control tissues. Average fluorescent intensities were determined with Metamorph on maximum projection images without digital manipulation. For images shown here, gamma levels were adjusted in Adobe Photoshop CS3 (San Jose, CA). Identical gamma level adjustments were made for age-matched mutant and control images.

# ISH

Sense and antisense riboprobes were generated against full-length *coll9a1*, *syt 1*, and *syt2* IMAGE Clones (EMM1002-97504659 [col19a1]; MM1013-9199901 [syt1]; MMM1013-7512379 [syt2]; Open Biosystems, Huntsville, AL) or an 800-bp fragment of parv (corresponding to nucleotides 2–825) polymerase chain reaction (PCR)-cloned into pGEM Easy T vector (Promega, Madison, WI) with the following primers: 5'-TCT GCT CAT CCA AGT TGC AG-3' and 5'-TCC TGA AGG ACT CAA CCC C-3'. Riboprobes were synthesized using digoxigenin (DIG) or fluorescein-labeled UTP (Roche, Mannheim, Germany) and the MAXI-Script In Vitro Transcription Kit (Ambion, Austin, TX). Probes were hydrolyzed to  $\approx 500$  nt. Coronal brain sections were prepared and hybridized at 65°C as previously described (Yamagata et al., 2002). Bound riboprobes were either detected by alkaline phosphatase (AP)-conjugated anti-DIG antibodies and colorimetric staining with the AP substrate NBT/BCIP (Roche), or detected by horseradish peroxidase (POD)-conjugated anti-DIG or anti-fluorescein antibodies and fluorescent staining with Tyramide Signal Amplification (TSA) systems (PerkinElmer, Shelton, CT). For double fluorescent in situ hybridization (D-FISH), after the first TSA reaction sections were washed with TBS, incubated with 0.3% H<sub>2</sub>O<sub>2</sub> for 30 minutes, and reacted with the second POD-conjugated antibody. For fluorescent ISH coupled with immunohistochemistry (FISH-IHC) standard IHC was performed after completing the TSA amplification step described above. In some cases antibody-binding epitopes were destroyed during ISH, hampering IHC analysis. In such cases D-FISH was applied. However, most antibodies applied here were not hindered by ISH (see Supporting Fig. 1). Images were obtained on a Zeiss AxioImager A1 fluorescent microscope or a Leica SP2 scanning confocal microscope.

# Western blot analysis

Mouse brains were perfused with PBS and hippocampal or cerebellar tissues were dissected in ice-cold PBS. Tissue was lysed in modified loading buffer containing 50 mmol/L Tris-HCl, pH 6.8, 2% sodium dodecyl sulfate (SDS), 10% glycerol, and protease inhibitors (1 mmol/L PMSF). Samples were homogenized, boiled for 10 minutes, centrifuged at 12,000*g* for 10 minutes, and insoluble material was removed. Protein concentrations were determined by bicinchoninic acid (BCA) protein assay (Pierce, Rockford, IL). Equal amounts of protein were loaded and separated by SDS-PAGE and transferred to PVDF membrane as described previously (Fox and Sanes, 2007). After blocking in 5% nonfat milk in PBS (containing 0.05% Tween20), PVDF membranes were incubated with appropriate primary antibodies, followed by HRP-conjugated secondary antibodies. Immunoblotted proteins were detected with enhanced chemiluminescent detection system (ECL Plus, Amersham Pharmacia Biotech, Piscataway, NJ) as previously described (Fox et al., 2003). Densitometry was performed using NIH ImageJ (Bethesda, MD).

#### Cresyl violet stain

Mouse brains were fixed in 4% PFA (in PBS) for 12 hours at 4°C, washed in PBS several times, sectioned on an Oxford vibratome ( $\approx$ 70 µm), collected on slides, and air-dried overnight. Dried sections were subsequently hydrated in 95%, 70% ethanol, and distilled water, stained with filtered cresyl violet solution (5 mg/mL cresyl violet acetate, 0.34 M acetic acid, 60 mM sodium acetate) for 1–3 minutes, rinsed in water, and subsequently dehydrated with 70%, 95%, and 100% ethanol. Slides were immersed in HistoClear (National Diagnostics, Atlanta, GA) for 10 minutes, air-dried, and were mounted with Permount. Images were acquired on an Olympus BX51 microscope with an Olympus OLY-750 color CCD camera.

# **Reverse Transcription-Polymerase Chain Reaction (RT-PCR)**

RNA was isolated using the BioRad Total RNA Extraction from Fibrous and Fatty Tissue kit (BioRad, Hercules, CA). Concentrations of RNA samples were determined spectrophotometrically with a NanoDrop ND-1000 (Wilmington, DE). cDNAs were generated from 200 ng of RNA with the Superscript II Reverse Transcriptase First Strand cDNA Synthesis kit (Invitrogen, La Jolla, CA). For bench-top RT-PCR, the following coll9a1 primers were used: 5'-TTCTGT GGC AAC TGT CAA GC-3'; 5'-TTT CTC CCC GTG TAT TCC AG-3'. Gapdh primers were: 5'-AAC TTT GGC ATT GTG GAA GG-3' and 5'-ACA CAT TGG GGG TAG GAA CA-3'. PCR products were amplified on an Eppendorf Mastercycler EP with the following cycling conditions: 94°C for 2 minutes, followed by 30 cycles of amplification (95°C for 15 seconds, 55°C for 30 seconds, 68°C for 60 seconds), and 2 minutes at 68°C. Products were visualized by separation on 2% agarose gels with 0.0001% ethidium bromide and images acquired with a FOTO-Dyne system (Fisher, Pittsburgh, PA). For quantifying mRNA levels, real-time quantitative RT-PCR (qPCR) was performed on a Chromo 4 Four-Color Real-time system (BioRad) using iQ SYBRGreen Supermix (BioRad). Coll9a1 primers for qPCR were 5'-ATT GGA CAT AAG GGC GAC AA-3' and 5'-AGT CTC CTT TGG CTCCTG GT-3'. Gapdh primers for qPCR were 5'-CGTCCC GTA GAC AAA ATG GT-3' and 5'-TTG ATG GCA ACA ATC TCC AC-3'. qPCR primers were designed over introns. The following cycling conditions were used with 20 ng of RNA: 95°C for 15 minutes, followed by 40 cycles of amplification (94°C for 15 seconds, 60°C for 20 seconds, 72°C for 20 seconds, read plate) and a melting curve analysis. Relative quantities of RNA were determined using the DDCT method (Livak and Schmittgen, 2001).

## Immuno-electron microscopy (ImmunoEM)

Tissue was fixed in 4% PFA/ 1% glutaraldehyde in 0.125 M phosphate buffer (pH 7.4), sectioned on an Oxford vibratome (40–50 µm), and floating sections were stained with anti-Syt2 antibodies in IHC blocking buffer. Syt2 antibodies were detected with biotin-conjugated secondary antibodies (Vector Laboratories) followed by VectaStain ABC amplification (Vector) and 3,3'-diaminobenzidine (DAB) staining. ImmunoEM tissue was processed using standard procedures (Fox et al., 2004) in the Department of Anatomy and Neurobiology Microscopy Facility. Ultrathin sections were collected on 300 mesh Gilder thin bar grids (Electron Microscopy Sciences, Fort Washington, PA), stained with uranyl acetate and lead citrate, and imaged on a Jeol JEM-1230 transmission electron microscope equipped with a Gatan 4K × 4K CCD camera, interfaced with Digital micrograph software. Pseudo-coloring of EM micrographs performed in Adobe PhotoShop.

# RESULTS

# *Col19a1*, the gene encoding collagen XIX, is expressed by neurons in the mammalian hippocampus

To characterize the expression pattern of *col19a1* in the developing mouse brain, RT-PCR analysis was performed on RNA isolated from various regions of postnatal day 14 (P14) mouse brain. *Col19a1* mRNA was detected in hippocampus and cortex (Fig. 1B). To localize *col19a1* mRNA within the developing hippocampus, ISH was performed. At P14, hippocampal neurons, detected here with riboprobes directed against neuronally expressed *syt1* (which encodes the synaptic vesicle-associated protein synaptotagmin 1), are concentrated in stratum pyramidalis (of CA1-CA3 and subiculum) and in the granular layer of the dentate gyrus (DG) (Fig. 1C). These layers contain excitatory principle neurons (either pyradmidal neurons or granule cells) and sparsely distributed classes of interneurons. Other classes of *syt1*-expressing interneurons diffusely populate strata oriens, radiatum, and lacunosum-moleculare of CA1-3, the hilus of the DG, and the polymorphic and molecular

layers of the subiculum (Fig. 1C). In contrast to vast *syt1* expression, *col19a1* riboprobes labeled only a small population of hippocampal cells (Fig. 1D; sense controls shown in Fig. 1E). In the DG, *col19a1*-expressing cells were largely confined to the hilus (Fig. 1D). In CA regions, *col19a1* was most abundant in strata oriens, radiatum, and lacunosum-moleculare, although a few *col19a1*-expressing cells were also present in stratum pyramidalis (Fig. 1D'). In subiculum, *col19a1*-expressing cells more densely populated the stratum pyramidalis than in the flanking molecular and polymorphic layers (Fig. 1D, Fig. 2A). ISH also confirmed *col19a1* mRNA expression in cortex and demonstrated its absence in other regions of P14 mouse brain (Fig. 1D).

We next sought to determine the identity of hippocampal cells expressing *col19a1* mRNA. To accomplish this we combined localizing *col19a1* mRNA with mRNAs or proteins expressed by major subtypes of hippocampal cells, i.e., neurons, astrocytes, oligodendrocytes, microglia, and endothelial cells. Double fluorescent ISH (D-FISH) revealed widespread coexpression of *syt1* mRNA in *col19a1*-expressing cells (Fig. 2A,B). Thus, neurons express *col19a1*, which was confirmed by immunolabeling with the neuronal marker NeuN (Fig. 2C). The sparse distribution of *col19a1* mRNA (Fig. 1D, Fig. 2A) suggested interneurons may express *col19a1*. Indeed, *col19a1* mRNA was present in cells containing the interneuron-specific enzyme glutamate decarboxylase 67 (Gad67) (Fig. 2D).

While these data demonstrate interneuronal expression of *col19a1*, they do not rule out its expression by nonneuronal cells. Coupling fluorescent ISH with IHC (FISH-IHC) for GFAP (which labels astrocytes) and Iba-1 (which labels microglia) revealed no coexpression in *col19a1*-expressing cells (Fig. 2E,F). Thus, hippocampal *col19a1* mRNA expression appears restricted to interneurons.

# Developmental regulation of col19a1 in the hippocampus

Dynamic spatiotemporal expression patterns of several synaptic organizing molecules correlate with synaptogenesis (e.g., Lucas and Salinas, 1997; Hall et al., 2000; Umemori et al., 2004; Fox et al., 2007). Therefore, we examined the developmental regulation of hippocampal *col19a1* mRNA by qPCR. The highest levels of *col19a1* mRNA were present at birth (P0) and after the first postnatal week (P7; Fig. 3A). Significantly reduced *col19a1* mRNA levels were observed by P14, after which time no significant changes in expression were observed (Fig. 3A).

Developmental regulation of hippocampal coll9a1 was further assessed by FISH. As opposed to global quantities of *col19a1* mRNA measured by qPCR, FISH revealed relative numbers of *col19a1*-expressing neurons. Since hippocampal size and shape vary greatly based on rostral-caudal location, numbers of *col19a1*-expressing neurons were obtained only from sections containing both ventral and dorsal lateral geniculate nuclei (vLGN and dLGN), delineated by calbindin (Calb) immunostaining (Luth et al., 1993; for example, see Fig. 8A). Similar to qPCR results, significantly higher numbers of coll9a1-expressing neurons were present during the first postnatal week of development than in adults (Fig. 3B-E). Numbers of *col19a1*-expressing neurons in P14 hippocampi were also significantly higher than in adult tissue (Fig. 3B). In P14 hippocampi, *col19a1* riboprobes reactivity appeared reduced in subsets of cells, suggesting these cells had begun to downregulate coll9a1 (Fig. 3F,G). This likely explains the difference between levels of coll9a1 measured by qPCR and ISH at P14. Taken together, these results demonstrate that the highest levels of coll9a1 mRNA occur in the first 2 postnatal weeks coinciding with the peak of synaptogenesis (Vaughn, 1989). Interestingly, these spatiotemporal expression patterns were specific to hippocampus as levels of cortical col19a1 mRNA continue to increase with age (Sumiyoshi et al., 1997, 2001).

Importantly, developmental changes in the relative numbers of *col19a1*-expressing neurons were not similar in all regions of the hippocampus. In CA fields and the hilus of the DG, many *col19a1*-expressing neurons persisted into adulthood (Fig. 3C–E). However, in subiculum, which exhibited the highest density of *col19a1*-expressing neurons at P7 (see arrowheads in Fig. 2A), few *col19a1*-expressing neurons were present in adult tissue (Fig. 3H). In fact, in subiculum both the number of positive neurons and intensity of mRNA labeling were dramatically reduced by P14 (Fig. 3G). Based on both distribution and developmental regulation, these data suggest that multiple classes of interneurons express *col19a1* mRNA.

#### Distinct populations of hippocampal interneurons express col19a1

The rodent hippocampus is rich in neuronal diversity (reviewed in Klausberger and Somogyi, 2008; Danglot et al., 2006; McBain and Fisahn, 2001). Although hippocampal interneurons are classified based on multiple criteria (i.e., morphology, electrophysiology, or expression of neurochemicals), only one approach was compatible with our method to localize *col19a1* mRNA–immunolabeling for subclass-specific neurochemicals. Three such neurochemicals, NPY, Som, and Calb, were present in *col19a1*-positive neurons (Fig. 4A–D). Antibodies or riboprobes directed against other interneuron-specific neurochemicals, such as Calr or *parv* (the gene encoding parvalbumin) showed no coexpression with *col19a1* mRNA (Fig. 4E,F).

On the basis that *col19a1*-expressing neurons contain NPY, Som, or Calb, we asked whether these neurochemicals could distinguish the different populations of *col19a1*-expressing neurons described above. To this end, we examined coexpression of *col19a1* mRNA with NPY, Som, or Calb in each region of the hippocampus.

**NPY-immunoreactive interneurons**—A large majority of *col19a1*-expressing neurons in CA1, CA3, and the hilus contained NPY (Fig. 5A–C). In CA regions, NPY-*col19a1* coexpressing neurons were found in all strata (for example, see Fig. 5B). In subiculum, few (if any) NPY-immunoreactive cells contained *col19a1* mRNA (Fig. 5D).

**Som-immunoreactive interneurons**—Many Som-immunoreactive interneurons in CA1, CA3, and the hilus contained *col19a1* mRNA (Fig. 6A–D). However, two main differences were noted between NPY-*col19a1* and Som-*col19a1* cells. First, in CA1 and CA3 Som-*col19a1* coexpressing neurons were confined to stratum oriens (Fig. 6A–C). No Som-*col19a1* coexpressing neurons were observed in strata pyramidalis, radiatum, or lacunosum-moleculare of CA1 or CA3. Second, approximately half of the subicular *col19a1*-expressing neurons contained Som (Fig. 6E).

**Calb-immunoreactive interneurons**—Only a small subset of *col19a1*-expressing neurons contained Calb in CA1 and CA3 (Fig. 7A,B; see also Fig. 3C–E). These Calb-*col19a1*-expressing cells were randomly distributed throughout strata oriens, radiatum, and lacunosum-moleculare. Coexpression of *col19a1* mRNA and Calb was even less frequently observed in the hilus (Fig. 7C). In the developing subiculum, however, approximately half of the *col19a1*-expressing neurons contained Calb (Fig. 7D).

# Collagen XIX is required for normal nerve terminal formation in subiculum

Since nonfibrillar collagens direct peripheral nervous system (PNS) synaptogenesis in both vertebrates and invertebrates (Ackley et al., 2003; Fox et al., 2007; Fox, 2008), we next asked whether CNS-derived collagen XIX was necessary for the formation of hippocampal synapses in previously generated collagen XIX-deficient mouse mutants (Sumiyoshi et al., 2004).  $Col19a1^{-/-}$  mutants are smaller than littermate controls and most die by weaning,

both presumably due to defects in esophageal muscle physiology and morphology (Sumiyoshi et al., 2004). Here, cresyl violet staining revealed few differences between mutant and control brains besides a reduction in size in the absence of collagen XIX (Fig. 8). Size differences were not specific to hippocampus or cortex but were seen in all CNS regions (e.g., see dorsal lateral geniculate nuclei [dLGN] in Fig. 8). Besides being smaller, the morphological organization of mutant hippocampi appeared strikingly normal in the absence of collagen XIX (Fig. 8). Thus, collagen XIX was dispensable for the gross organization of the mammalian hippocampus.

To assess nerve terminal formation in the absence of collagen XIX, immunolabeling of synaptic vesicle-associated proteins–hallmark components of presynaptic terminals–was performed on mutant and control hippocampi. We focused on subiculum since the density of *coll9a1*-expressing neurons was highest in this region during synaptogenesis. While the expression and distribution of many synaptic vesicle-associated proteins was unchanged in mutant subiculum, the expression and distribution of synaptotagmin 2 (Syt2) was markedly altered in mutants (Fig. 9, Fig. 10).

Syt2 is a member of the large synaptotagmin family of vesicle-associated proteins previously shown to be present in synapses within stratum pyramidalis of CA1-3 (Wendland et al., 1991; Ullrich et al., 1994; Südhof, 2002; Fox and Sanes, 2007). After the first postnatal week of development Syt2 appeared largely concentrated in both stratum pyramidalis of CA2 and the adjacent portion of CA3 and in the pyramidal and polymorphic layers of subiculum (Fig. 9A; see Fig. 8C for subicular layers). Sparse Syt2-containing nerve terminals were also observed in strata oriens, radiatum and lacunosum-moleculare at this age (Fig. 9D). By the end of the third postnatal week, the distribution of Syt2-containing nerve terminals expanded to include stratum pyramidalis of all CA regions and appeared similar to its adult distribution (Wendland et al., 1991; Ullrich et al., 1994; Fox and Sanes, 2007). In collagen XIX-deficient mutants, a striking reduction in Syt2-immunostaining levels was observed in subiculum (Fig. 9E,F; see arrows). A less obvious, but equally significant, reduction in Syt2-immunoreactive nerve terminals was observed in strata oriens, radiatum, and lacunosum-moleculare of CA1-3 regions (Fig. 9H). Reduced levels of Syt2 were specific to subiculum and these sparsely distributed terminals; Syt2-immunoreactivity appeared similar to controls in mutant stratum pyramidalis of all CA regions (Fig. 9A,B; see arrowhead).

Reduced levels of hippocampal Syt2, but not other syn-aptic vesicle-associated proteins or presynaptic machinery, were confirmed and quantified by Western blot analysis (Fig. 10A,B). Quantities of Syt2 were significantly lower in mutant hippocampi in all ages examined; however, differences between mutant and control samples decreased with age. While this may suggest a compensatory mechanism assembles Syt2-positive nerve terminals in the absence of collagen XIX, it more likely reflects development of Syt2-containing terminals in CA1 and CA3 stratum py-ramidalis that do not require collagen XIX. Reduced levels of Syt2 were specific to mutant hippocampus as collagen XIX-deficient cerebella contained normal levels of Syt2 (Fig. 10A,B). Furthermore, the altered distribution and reduced levels of Syt2 in mutant hippocampi were not due to cell-autonomous defects in cells that normally express *col19a1* mRNA since *col19a1* and *syt2* were largely expressed by different subsets of hippocampal interneurons (Fig. 11).

To identify whether collagen XIX was necessary for excitatory or inhibitory synapses, we sought to determine the type of subicular synapses containing Syt2. IHC with antibodies directed against both isoforms of Gad (Gad65/67) demonstrated that most Syt2-containing nerve terminals in the mouse subiculum were inhibitory (Fig. 12A–C). A large percentage of these Gad/Syt2-containing nerve terminals resembled axo-somatic synapses (see white

arrowheads in Fig. 12A–C), although terminals not associated with cell somas also coexpressed Syt2 and Gad65/67 (see white arrows in Fig. 12A). Ultrastructural analysis of P10 wildtype subiculum confirmed the presence of Syt2 in at least axo-somatic synapses (Fig. 12D). While these analyses do not rule out Syt2 expression in excitatory terminals (see green arrows in Fig. 12A), they demonstrate that the vast majority of Syt2-containing subicular synapses are inhibitory.

To assess whether inhibitory synapses were malformed in the absence of collagen XIX we examined Gad67 distribution in mutant subiculum by IHC. In stratum pyramidalis of subiculum (where Syt2-immunoreactivity is concentrated in controls [Fig. 9a]) two notable differences in Gad67 distribution were observed in mutants. First, levels of Gad67 were higher in cell bodies and their processes in mutants than in controls (see arrows and arrowheads in Fig. 12F). Second, whereas a punctate synaptic distribution of Gad67 was apparent in controls, Gad67-immunoreactivity in mutants appeared diffuse (Fig. 12E,E',F,F'). Differences in Gad67 distribution were specific to stratum pyramidalis, as Gad67 distribution in the molecular layer of mutant subiculum resembled that of controls (Fig. 12E,E",F,F"). In addition to differences in Gad67 distribution, abnormal levels of gephyrin, a postsynaptic scaffolding molecule present only at inhibitory synapses (Cabot et al., 1995; Craig et al., 1996), were observed in mutant hippocampal extracts. Surprisingly, however, levels of gephyrin were significantly elevated in mutants (Fig. 12G,H). Levels of postsynaptic density 95 (PSD-95), a postsynaptic scaffolding component present at excitatory synapses (Hunt et al., 1996;El-Husseini et al., 2000), were indistinguishable between mutants and controls (Fig. 12G). Taken together, these data suggest collagen XIX is required for the organization of inhibitory subicular synapses.

# DISCUSSION

Many families of ECM molecules known to direct synapse formation at the NMJ also regulate CNS synaptogenesis. Agrin contributes to the organization and function of central synapses and dendritic spines, perhaps through interactions with transmembrane  $\alpha 3 \text{ Na}^+/\text{K}^+$  ATPase (Ferreira, 1999; Bose et al., 2000; Tournell et al., 2006; Hilgenberg et al., 2006; Reif et al., 2007; Ksiazek et al., 2007; Matsumoto-Miyai et al., 2009). Laminin heterotrimers containing  $\beta 2$  chains are present in central synaptic clefts and are necessary for synaptic organization in both retina and hippocampus (Libby et al., 1999; Egles et al., 2007). The results presented here suggest that a third family of NMJ-organizing matrix molecules, nonfibrillar collagens, are expressed by neurons and contribute to central synaptogenesis. Specifically, several classes of hippocampal interneurons express *col19a1*, which is necessary for the normal organization of subsets of Syt2-containing hippocampal nerve terminals. Thus, these studies not only advance our understanding of subicular synaptogenesis but they challenge the preexisting notion that collagens are absent from and do not contribute to the development of the mammalian brain.

# Subclasses of hippocampal interneurons express col19a1 mRNA

The complexity of interneuronal diversity is staggering. In CA1 alone, at least 21 subclasses of interneurons have been identified (Klausberger and Somogyi, 2008) based on the expression of distinct neurochemical markers (e.g., Calb, Calr, Som, NPY, Parv; Freund and Buzsaki, 1996; McBain and Fisahn, 2001; Danglot et al., 2006), action potential firing patterns (Lacaille et al., 1987; Kawaguchi and Hama, 1988), response to neuromodulators (Parra et al., 1998), and neuronal or synaptic morphology (Ramon y Cajal, 1911; Freund and Buzsaki, 1996; McBain and Fisahn, 2001; Danglot et al., 2006; Klausberger and Somogyi, 2008). Here we sought to identify the types of interneurons that express *col19a1* mRNA

based on coexpression of neurochemical markers. For a summary of these results, see Table 2.

We will focus our discussion here on classes of interneurons in CA regions, where interneuron diversity has been best characterized (Danglot et al., 2006; Klausberger and Somogyi, 2008). While we set out to identify classes of interneurons expressing *col19a1*, we were more successful in identifying classes of interneurons that do not generate col19a1. The sparsity of *col19a1* mRNA within stratum pyramidalis (Fig. 1D, Fig. 2A, Fig. 3C–E), and lack of expression in parvalbumin containing neurons (Fig. 4F), suggest basket and chandelier (or axo-axonic) cells do not express *col19a1* mRNA (Howard et al., 2005; Danglot et al., 2006; Klausberger and Somogyi, 2008). The absence of *col19a1* mRNA in Calr-immunoreactive interneurons (Fig. 4E) further ruled out *col19a1* expression in several classes of interneuron-specific interneurons (IS-1 and IS-3) (Gulyas et al., 1996; Freund and Gulvas, 1997). It remains unclear whether the third subclass of interneuronselective interneurons, which lack Calr but contain vaso-active intestinal peptide (VIP) (Acsády et al., 1996a,b; Freund and Gulyas, 1997) express coll9a1 mRNA. Lastly, our finding that col19a1-expressing cells in strata radiatum and lacunosum-moleculare do not contain Som (Fig. 6) revealed many stratum lacunosum-moleculare projecting interneurons, such as LM, R-LM, and P-LM cells, lack coll9a1 (Oliva et al., 2000; Danglot et al., 2006).

Identifying specific classes of interneurons that express collagen XIX proved more difficult due to the wide distribution of *col19a1* mRNA and only partial overlap with either NPY-, Som-, or Calb-immunoreactive cells (Figs. 3C–E, 4A–D, 5–7). In stratum oriens, however, it was evident that one well-characterized class of interneurons contained *col19a1* mRNA: stratum orienslacunosum-moleculare (O-LM) cells. O-LM cells, whose somas lie in stratum oriens and axons project to stratum lacunosum-moleculare, contain both NPY and Som (Ko<sup>-</sup>hler et al., 1987; Freund and Buzaki, 1996; Danglot et al., 2006). The high degree of overlap of *col19a1* mRNA with either Som- or NPY-immunoreactivity in stratum oriens (Fig. 5, Fig. 6) strongly suggests that O-LM cells generate collagen XIX.

Except for O-LM cells, definitive identification of *col19a1*-expressing cells remains unresolved. Outside of stratum oriens, NPY-immunoreactive *col19a1*-expressing neurons likely belong to neurogliaform, ivy cell, or bistratified subclasses of interneurons, based on both location and the absence of Parv, Calr, or Som (Markram et al., 2004; Price et al., 2005; Fuentealba et al., 2008). While Calb-immunoreactivity is associated with several widely distributed classes of interneurons, including bistratified cells, Schaffer collateral-associated cells, horizontal trilaminar cells, radial trilaminar cells, Calb-Calr coexpressing cells, and hippocampal-septal projecting cells (Sik et al., 1995; Cope et al., 2002; Markram et al., 2004; Danglot et al., 2006), the sparse, random distribution of Calb-*col19a1* coexpressing cells make it unclear what class of interneurons these belong to. It is noteworthy that a class of CA1 pyramidal neurons also express Calb (Rami et al., 1992; Molinari et al., 1996; Klausberger and Somogyi, 2008); however, the distribution and morphology of Calb*col19a1* coexpressing cells rule out the possibility that pyramidal neurons express *col19a1* mRNA (Fig. 3D,E).

It is also difficult from these analyses to accurately conclude what cell types express *col19a1* in other regions of the hippocampus. In subiculum, where *col19a1* expression is more concentrated and developmentally regulated (Fig. 2A, Fig. 3F–H), less is known about numbers or types of interneurons. Assuming similar classes of interneurons exist in subiculum (for example, see Knopp et al., 2008), our studies suggest that different subsets of interneurons express *col19a1* in subiculum than in CA regions. Not only do *col19a1*-expressing O-LM cells not exist in subiculum, but few, if any, NPY-containing interneurons express *col19a1* mRNA in this region (Fig. 5–Fig. 7). Furthermore, in subiculum a greater

ratio of Calb-containing interneurons express *col19a1* mRNA and the distribution of Som*col19a1* coex-pressing cells is far less restricted (Fig. 6, Fig. 7).

Despite spatial, temporal, and neurochemical diversity, *col19a1*-expressing cells may share one commonality-they may be derived from a single neurogenic region. Hippocampal interneurons are derived from two neurogenic regions during embryogenesis-the medial ganglionic eminence (MGE) and the caudal ganglionic eminence (CGE) (Pleasure et al., 2000; Nery et al., 2002). Fate mapping has shown Som-immunoreactive interneurons arise from the MGE (Wichterle et al., 2001). Mice lacking the Nkx2.1 homeobox gene, which exhibit malformed MGEs, fail to generate NPY-, Som-, and a large set of Calb-containing interneurons (Pleasure et al., 2000). Furthermore, in vitro cultures generated from these Nkx2.1 mutants generate Calr-immunoreactive interneurons but not Parv-, Som-, or NPY-containing interneurons (Xu et al., 2004). Comparing these data with our studies led us to speculate that *col19a1*-expressing interneurons may arise solely from MGE. Generation from the MGE alone, however, does not predetermine whether a neuron expresses *col19a1* since Parv-immunoreactive cells are also born from MGE progenitors.

# Collagen XIX is required for synapse formation in subiculum

Cell-type-specific expression and differential regulation suggest collagen XIX might have multiple functions in the mammalian hippocampus. However, collagen XIX appears largely dispensable for the gross organization of the mammalian hippocampus (Fig. 8). Distribution and expression of several cell-type-specific markers, axonal markers, and synaptic markers appear normal in the absence of collagen XIX (Fig. 9-Fig. 11). Furthermore, both the distribution and morphology of interneurons that normally express *col19a1*, such as Calbimmunoreactive subicular neurons, appear normal in the absence of collagen XIX (Fig. 9F'). Together, these analyses further confirm that much of hip-pocampal development proceeds normally in the absence of collagen XIX. However, the altered distribution of presynaptic Syt2 in mutants lacking collagen XIX (Fig. 9A,B-,D,E,F,H,I) suggests that collagen XIX is necessary for the normal organization of subsets of hippocampal nerve terminals. Interestingly, while these studies demonstrate an essential role of collagen XIX in synaptic organization, previous studies implicated this collagen in neuromuscular function in the PNS. Specifically, NO-dependent relaxation following contractions in lower esophageal sphincter muscle requires the presence of a collagen XIX-rich basal lamina. Although it remains unclear whether pre- and postsynaptic partners are malformed at esophageal sphincter synapses in collagen XIX-deficient mutants, it is likely that the absence of this collagen results in a disorganized syn-aptic basal lamina (Myers et al., 1997,2003;Sumiyoshi et al., 2004). Together with studies presented here, this suggests that collagen XIX contributes to synaptic organization and/or function at multiple anatomical locations.

The presence of Syt2 in inhibitory synapses throughout neocortex, hippocampus, brainstem, and cerebellum (Ullrich et al., 1994; Marquez et al., 1995; Pang et al., 2006a,b; Fox and Sanes, 2007) raised the possibility that collagen XIX is required for the formation of some inhibitory hippocampal nerve terminals. Indeed, IHC and ultrastructural analysis confirmed that Syt2 was present at inhibitory synapses (Fig. 12A–D). Altered distribution of Gad67 and abnormal levels of gephyrin in mutants (Fig. 12) suggest that inhibitory synapses require collagen XIX. Interestingly, mutant levels of gephyrin were increased in contrast to reduced levels of Syt2 (Fig. 10, Fig. 12G,H). Similar mismatched levels of pre- and postsynaptic components have been reported in other mutant mice exhibiting hippocampal synaptic defects (e.g., Rodena-Ruano et al., 2006). Several explanations for this mismatch are possible. Postsynaptic neurons might compensate for defective or reduced quantities of nerve terminals (and any transsynaptic organizing cues that they might generate) by increasing postsynaptic apparati size. Similar compensatory mechanisms have been well

documented for other types of intercellular signaling in the CNS (e.g., Rice et al., 1998). Alternatively, defects in inhibitory synapses in collagen XIX-deficient mutants may result in reduced inhibitory activity. As increased levels of synaptic activity speed the rate of postsynaptic density component turnover (Ehlers, 2003), decreased levels of inhibitory activity may slow gephyrin turnover in mutant hippocampi. Of course, it is also possible that increased levels of gephyrin are not directly linked to the altered distributions of Gad67 and Syt2 in collagen XIX-deficient mice.

# Mechanisms for collagen XIX in subicular synapse formation

*Col19a1* and *syt2* are both expressed by hippocampal interneurons. However, it is unlikely that defects in collagen XIX-deficient hippocampi arise cell-autonomously. Complementary expression patterns and the observation that Syt1 and Syt2 are present in distinct sets of central synapses suggest that mammalian neurons typically express either *syt1* or *syt2* (Ullrich et al., 1994; Marqueze et al., 1995; Berton et al., 1997; Pang et al., 2006a,b; Fox and Sanes, 2007; Mittelsteadt et al., 2009). Our data demonstrate that *col19a1* mRNA is present in *syt1*-expressing cells and is present in very few syt2-expressing cells (Fig. 2A,B). These results are supported by previous reports documenting spatial and temporal expression patterns of *syt2* in the rodent hippocampus that differ from those described here for *col19a1* (Berton et al., 1997; Mittelsteadt et al., 2009). As such, we postulate that synaptic defects in collagen XIX-deficient mutants likely arise largely through non-cell-autonomous mechanisms. At present the exact nature of these mechanisms remains unclear.

One possibility is that synaptic defects in collagen XIX mutants are secondary to alterations in other aspects of hippocampal development such as cell specification, migration, or differentiation. Our analysis, however, failed to identify any striking defects in number, position, or morphology of either excitatory or inhibitory neurons in mutant hippocampi (Fig. 8, Fig. 9A,B',E,F'). Moreover, the synaptic defects reported here do not reflect a general delay in development in the absence of collagen XIX since many aspects of hippocampal development proceeded normally in mutants: Calb-immunoreactive interneurons appear normally differentiated in collagen XIX mutants (Fig. 9A,B',E,F'); granular cell-derived mossy fibers targeted and innervated stratum lucidum of CA3 at similar times in mutants and controls (Fig. 9A,E); quantities of developmentally regulated synaptic machinery components, such as synapsin (Melloni et al., 1993;Melloni and Degennaro, 1994), PSD-95 (Chang et al., 2009), vesicular glutamate transporter 1 (VGlut1) and VGlut2 (Kaneko et al., 2002), appeared normal in mutant hippocampi (Fig. 10A, Fig. 12G); Syt2-containing presynaptic terminals in stratum pyramidalis of CA1-3 developed normally in the absence of collagen XIX (Fig. 9G).

Alternatively, collagen XIX might act indirectly at synapses by altering the expression or distribution of other synaptic organizers. Although few studies have examined cues that induce synapse formation in subiculum, several factors capable of directing synaptogenesis elsewhere in hippocampus have been identified. Neurons in CA subfields express an array of synaptic organizing factors, including SynCAMs (Fogel et al., 2007; Thomas et al., 2008), neuroligins (Song et al., 1999), neurexins (Ullrich et al., 1995), ephrins and Eph receptors (for review, see Martinez and Soriano, 2005), Wnts (Salinas and Zou, 2008; Davis et al., 2008), cadherins (Benson and Tanaka, 1998; Togashi et al., 2002; Bekirov et al., 2008), FGFs and FGF receptors (Kuzis et al., 1995; Li et al., 2002), agrin (O'Connor et al., 1994; Cohen et al., 1997; Lesuisse et al., 2000), and laminins (Egles et al., 2007). It remains unclear whether collagen XIX can bind or modulate the expression of any of these organizing molecules. Likely collagen XIX-interacting candidates are synaptogenic FGFs (FGF2, FGF7, FGF10, FGF22) (Li et al., 2002; Umemori et al., 2004; Fox et al., 2007), which could potentially complex with collagen XIX via their mutual ability to bind heparin

(Jang et al., 1997; Igarashi et al., 1998; Myers et al., 2003). However, synaptic defects reported to date in mutants lacking synaptogenic FGFs or their receptors do not resemble those reported here for collagen XIX (Umemori et al., 2004; Terauchi et al., 2008). In fact, synaptic defects reported in many of the previously characterized synaptic organizing molecules result in different phenotypes than those described here in the absence of collagen XIX (e.g., Missler et al., 2003; Henkemeyer et al., 2003; Egles et al., 2007; Ksiazek et al., 2007; Chubykin et al., 2007; Tabuchi et al., 2007; Xu and Henkemeyer, 2009).

A third possibility is that collagen XIX may act directly at synapses by binding and activating a transmembrane receptor. Collagenous sequences (hallmark features of both fibrillar and nonfibrillar collagens) are known to bind integrins, discoidin domain receptor tyrosine kinases (DDR1 and DDR2), and leukocyte-associated immunoglobulin-like receptor 1 (LAIR-1) (Vogel et al., 1997; Abdulhussein et al., 2004; Lebbink et al., 2006) several of which are present in the mammalian CNS (Pinkstaff et al., 1999; Bhatt et al., 2000). While little is known about the roles of DDRs and LAIR-1 in neural development (but see Bhatt et al., 2000), integrins contribute to axonal growth, dendritic development, synaptogenesis, synaptic plasticity, and synaptic function (e.g., DeFreitas et al., 1995; Chavis and Westbrook, 2001; Chun et al., 2001; Pasterkamp et al., 2003; Chan et al., 2003, <sup>2006</sup>, 2007; Huang et al., 2006; Shi and Ethell, 2006; Webb et al., 2007). In addition to activating collagenous receptors, noncollagenous (NC) domains of nonfibrillar collagens can act as signaling molecules after being proteolytically released (Ortega and Werb, 2002; Kalluri, 2003). In the PNS, cleaved collagen IV NC domains induce motor nerve terminal differentiation (Fox et al., 2007; Fox, 2008). Since collagen XIX NC domains share similar functions to those of collagen IV outside of the nervous system (Kalluri, 2003; Ramont et al., 2007), they may be capable of inducing presynaptic differentiation in hippocampal neurons. Receptors for NC domains also include integrins, albeit a different set of integrins than those capable of binding collagenous sequences. These include  $\alpha \beta \beta 1$ ,  $\alpha \beta \beta 1$ ,  $\alpha \gamma \beta 3$ , and αvβ5 integrins (Kalluri, 2003; Pedchenko et al., 2004; Borza et al., 2006), several of which are not only expressed by hippocampal neurons but are present at synaptic sites (Pinkstaff et al., 1999; Chan et al., 2003, 2007; Huang et al., 2006; Werb et al., 2007).

# Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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#### Figure 1.

*Col19a1* expression in the mammalian hippocampus. **A**: Schematic representation of the unidirectional excitatory circuit within the mouse hippocampus. Interneurons not depicted. Arrows indicate the direction of information flow. **B**: RT-PCR analysis demonstrated the presence of *col19a1* mRNA in hippocampus and cortex at P14. Glyceraldehyde 3-phosphate dehydrogenase (*gapdh*) was a loading control and a sample containing hippocampal RNA but no reverse transcriptase (nRT) was a negative control. **C,D**: Localization of *syt1* (C) and *col19a1* (D)mRNAs by in situ hybridization in P14 mouse hippocampus. C',D',E' show high magnification images of CA1 regions. C,C': Syt1 mRNA demonstrates the location of hippocampal neurons. D,D': *Col19a1* mRNA is sparsely distributed in hippocampus and

cortex. Note the absence of *col19a1* mRNA expression in other regions of the mouse brain, i.e., dLGN and VP. **E,E'** Sense controls for *col19a1* riboprobes. CA, Cornu Ammonis areas; DG, dentate gyrus; dLGN, dorsal lateral geniculate nucleus; EC, enthorinal cortex; h, hilus; slm, stratum lacunosum-moleculare; so, stratum oriens; sp, stratum pyramidalis; sr, stratum radiatum; Sub, subiculum; VP, ventral posterior thalamic nucleus. Scale bars = 400  $\mu$ m in E (applies to C–E); 100  $\mu$ m in E' (applies to C'–E').



#### Figure 2.

*Coll9a1* is expressed by neurons. A: D-FISH for *coll9a1* (green) and *syt1* (magenta) in P7 mouse hippocampus. Arrows indicate examples of *coll9a1* and *syt1* coexpression. Arrowheads highlight subiculum. B: High magnification of neurons coexpressing *syt1* and *coll9a1* mRNAs. Inset shows *coll9a1* sense control riboprobes combined with *syt1* riboprobes. C: Expression of *coll9a1* by neurons was verified with NeuN immunolabeling. D: FISH-IHC revealed *coll9a1* mRNA was present in Gad67-immunoreactive interneurons. E,F: Neither hippocampal astrocytes, labeled with GFAP antibodies (E), or microglia, labeled with Iba-1 antibodies (F), contained *coll9a1* mRNA. Label colors in black and white image panels correspond to the color of that image in the multicolored composite image. Scale bars = 200 µm in A,A',A"; 25 µm in C"-F".



#### Figure 3.

Developmental regulation of *col19a1* in hippocampus. A: Quantitative RT-PCR demonstrates highest levels of hippocampal *col19a1* mRNA at P0 and P7. Levels of *col19a1* were normalized to *gapdh*. n = 3 in triplicate. \*Differs from P14, P21 and adult samples at P < 0.001 by Holm-Sidak one-way analysis of variance (ANOVA). B: Relative numbers of *col19a1*-expressing cells, labeled by in situ hybridization, compared to adult levels. Similar regions of hippocampus were compared between ages. \*Differs from adult samples at P < 0.001 by Holm-Sidak one-way ANOVA. C–E: Examples of in situ hybridization for *col19a1* mRNA (green) at P3 (C), P7 (D), and adult (E). Note the higher density of *col19a1*-expressing cells at P3 and P7. Sections were costained with antibodies against Calb (magenta) to identify hippocampal regions. Arrowheads in C–E demonstrate coexpression of Calb and *col19a1* mRNA. F–H: In subiculum, ISH revealed *col19a1* expression peaked at P7 (F) and was dramatically decreased by P14(G) and in adult samples (H). This is

markedly different from other regions of the hippocampus, where expression continues into adulthood (E). Arrow in H indicates *col19a1*-expressing cell in adult subiculum. Scale bars = 200  $\mu$ m in E (applies to C–E); 100  $\mu$ m in H (applies to F–H).



# Figure 4.

Distinct subclasses of hippocampal interneurons express *col19a1* mRNA. **A–D**: FISH-IHC demonstrated subsets of NPY-(A), Calb-(C), and Som-(D) immunoreactive interneurons express *col19a1* mRNA. B shows *col19a1* sense control riboprobes combined with NPY IHC. **E**: FISH-IHC revealed Calr-immunoreactive neurons do not express *col19a1*. **F**: D-FISH demonstrated *col19a1* and *parv*, which encodes parvalbumin, are not coexpressed in hippocampus. Arrows indicate examples of coexpression of *col19a1*. Arrowheads indicate *col19a1*-expressing cells not labeled with the interneuron marker. Label colors in black and white image panels correspond to the color of that image in the multicolored composite image. Scale bar = 25  $\mu$ m.



#### Figure 5.

Regional coexpression of *col19a1* mRNA and NPY in the developing hippocampus. In situ hybridization for *col19a1* mRNA (green) and immunostaining for NPY (magenta) in P14 hippocampus. **A–C**: Most *col19a1*-expressing neurons in CA1 (A), CA3 (B), and the hilus of the DG (C) contain NPY. In CA1 and CA3 coexpression of *col19a1* and NPY was seen in all layers (see arrows in B). **D**: In subiculum, *col19a1*-expressing cells do not contain NPY. Inset in D shows *col19a1*-NPY coexpressing neuron in stratum oriens of CA1 adjacent to the same section of subiculum. Arrows highlight examples of *col19a1* and NPY coexpression. Arrowheads indicate *col19a1*-expressing cells that do not contain NPY. Asterisks indicate NPY-immunoreactive neurons that lack *col19a1* mRNA. "b" labels nonspecific immunoreactivity associated with blood vessels. CA, Cornu Ammonis areas; DG, dentate gyrus; h, hilus; so, stratum oriens; sp, stratum pyramidalis; sr, stratum radiatum; Sub, subiculum. Label colors in black and white image panels correspond to the color of that image in the multicolored composite image. Scale bar = 50 µm.



#### Figure 6.

Regional coexpression of *col19a1* mRNA and Som in the developing hippocampus. In situ hybridization for *col19a1* mRNA (green) and immunostaining for Som (magenta) in P14 hippocampus. A: *Col19a1*-expressing neurons in stratum oriens of CA1 (A) contain Som. **B,C**: *Col19a1*-expressing cells in strata pyramidalis, radiatum, and lacunosum-moleculare do not contain Som. **D,E**: Many *col19a1*-expressing cells in the hilus of the DG (D) and subiculum (E) contain Som. Arrows highlight examples of *col19a1* and Som coexpression. Arrowheads indicate *col19a1*-expressing cells that do not contain Som. Asterisks indicate Som-immunoreactive neurons that lack *col19a1* mRNA. CA, Cornu Ammonis areas; DG, dentate gyrus; h, hilus; so, stratum oriens; sp, stratum pyramidalis; sr, stratum radiatum; Sub, subiculum. Label colors in black and white image panels correspond to the color of that image in the multicolored composite image. Scale bar = 50 µm.



#### Figure 7.

Regional coexpression of *col19a1* mRNA and Calb in the developing hippocampus. ISH for *col19a1* mRNA (green) and immunostaining for Calb (magenta) in P7 hippocampus. A–C: Sparse coexpression of *col19a1* mRNA and Calb was observed in CA1 (A), CA3 (B), and the hilus of the DG (C). **D**: Many *col19a1*-expressing cells in subiculum contained Calb. Arrows highlight examples of *col19a1* and calbindin coexpression. Asterisks indicate Calb-immunoreactive neurons that lack *col19a1* mRNA. Arrowheads indicate *col19a1*-expressing cells that do not contain calbindin. CA, Cornu Ammonis areas; DG, dentate gyrus; h, hilus; mf, mossy fiber terminals; so, stratum oriens; sp, stratum pyramidalis; sr, stratum radiatum; Sub, subiculum. Label colors in black and white image panels correspond to the color of that image in the multicolored composite image. Scale bar = 50  $\mu$ m.



#### Figure 8.

Normal morphological development of the brain occurs in the absence of collagen XIX. Micrographs of cresyl violet stained hippocampi from P1 (**A**,**B**)andP21 (**C**,**D**) *col19a1<sup>-/-</sup>* mutants (-/-; **B**,**D**) and littermate controls (+/- A,**C**). Mutant hippocampi at both ages were slightly smaller than littermate controls; however, differences in size were not specific to the hippocampus; regions that normally lack *col19a1* mRNA were similarly smaller in mutant brains (see dLGN). C',**D**' show high magnification of CA1. C'',**D**'' show high magnification of stratum pyramidalis of subiculum. m, molecular layer; poly, polymorphic layer; so, stratum oriens; sp, stratum pyramidalis; sr, stratum radiatum; slm, stratum

lacunosum-moleculare; Sub, subiculum. Scale bars =  $400 \ \mu m$  in D (applies to A–D); 200  $\mu m$  in D" (applies to C',C",D',D").



#### Figure 9.

Collagen XIX is required for the normal formation of synaptic terminals in subiculum. **A–D**: IHC for Syt2 (green) in P10 control (+/-) hippocampi. At this age Syt2-positive nerve terminals were present in subiculum (see B and arrows in A), stratum pyramidalis of CA2 and CA3 (see C and arrowhead in A) and sparsely distributed terminals throughout the synaptic layers of all other CA regions (D) **E–H**: Drastically reduced levels of Syt2-immunoreactive nerve terminals were detected in *col19a1<sup>-/-</sup>* mutant (-/-) subiculum. Defects were specific to subiculum (see F and arrows in E) and the sparsely distributed terminals in stratum pyramidalis of CA2 and CA3 were present in normal numbers in mutant hippocampi (see G and arrowhead in E). B,F show high-magnification confocal image of Syt2-

immunoreactivity in control (B)and mutant (F) P10 subiculum. B',F'show corresponding Calb-immunoreactivity in control (B)and mutant (F) P10 subiculum in same regions shown in B,F. C,G show high-magnification confocal image of Syt2-immunoreactivity in control (C)and mutant (G) P10 CA2/CA3 regions. D,H show high-magnification confocal image of Syt2-immunoreactivity in control (D) and mutant (H) P10 CA1. A,E,B',F': Calb-immunoreactivity (magenta) label hippocampal interneurons (in A,E,B',F'), interneurons within vLGN (in A,E) and DG granular cells and mossy fibers (in A,E; asterisks indicate mossy fibers). Only sections containing vLGN, dLGN, and fimbria hippocampus (f) were analyzed. Mutant and control images acquired with identical settings. I: Quantification of average fluorescent intensities of Syt2-IHC in mutants and control swere compared in subiculum and CA2/CA3 regions. Dashed line represent control levels. Data shown are  $\pm$  SEM; n > 6. \*Differs from control, age-matched subiculum at P < 0.01 by Student's *t*-test. Scale bars = 400 µm in A (applies to A,E); 200 µm in B (applies to B–D,F–H); 100 µm in B' (applies to F').



#### Figure 10.

Decreased levels of Syt2 in collagen XIX-deficient hippocampi. A: Western blots demonstrate reduced Syt2 levels in P10, P14, P18, and P21 mutant (-/-) hippocampal extracts compared to littermate controls (+/-). No differences were observed for synap-sin (Syn), vesicular glutamate transporter 1 (VGlut1), or VGlut2. Nor were differences observed in Syt2 levels observed in mutant cerebella (Cblm), which normally lack *col19a1* mRNA. Levels of actin were used as loading controls. B: Quantification of hippocampal and cerebellar Syt2 protein levels detected by Western blot and normalized to actin. Dashed line represents control levels. Data shown are  $\pm$  SEM; n= 3. \*Differs from control age-matched sample at P < 0.05 by Student's *t*-test.

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## Figure 11.

Regional coexpression of *col19a1* and *syt2* mRNA in the developing hippocampus. In situ hybridization for *col19a1* mRNA (green) and *syt2* mRNA (magenta) in P14 hippocampus. **A,B**: Most *col19a1*-expressing neurons in CA1 (A) and CA3 (B)do not coexpress *syt2* mRNA (but see arrow in B). C: In the hilusof the DG, all *syt2*-expressiong neurons expressed *col19a1* mRNA (see arrow in C); however, many *col19a1*-expressing neurons lacked *syt2* mRNA (arrowheads). D: In subiculum, many cells expressed one of these genes (see asterisks and arrowhead). However, a small population of *col19a1*-expressing cells contained *syt2* mRNA, and vice versa (arrow in D). Arrows highlight examples of *col19a1* and *syt2*-expressing neurons that lack *col19a1* mRNA. CA, Cornu Ammonis areas; DG, dentate gyrus; h, hilus; so, stratum oriens; sp, stratum pyramidalis; sr, stratum radiatum; Sub, subiculum. Label colors in black and white image panels correspond to the color of that image in the multicolored composite image. Scale bar = 50  $\mu$ m.



#### Figure 12.

Collagen XIX is required for the formation of inhibitory synapses in the developing subiculum. A-C: IHC for Syt2 (green) and Gad65/67 (magenta) in wildtype P14 subiculum. Most Syt2-containing synapses contained Gad65/67, including both axo-somatic synapses (white arrowheads) and synapses not associated with cell bodies (white arrows). However, not all Gad65/67-immunoreactive synapses contained Syt2 (magenta arrows and arrowheads). A small population of Syt2-immunoreactive synapses lacked Gad65/67 (green arrows). In A, "B" and "C" denote regions enlarged in B and C, respectively. B,C: Highmagnification images demonstrating colocalization of Gad65/67 and Syt2 in axo-somatic synapses (white arrowheads). In B, inhibitory axo-somatic synapses are present on the soma of a Gad65/67-immunoreactive inhibitory interneuron. In A-C, arrowheads denote axosomatic synapses and arrows depict synapses not associated with cell somas. White arrows or arrowheads depict colocalization of Syt2 and Gad65/67, whereas those colored magenta or green highlight synapses containing only Gad65/67 or Syt2, respectively. D: Electron micrograph of a Syt2-positive axo-somatic inhibitory synapses in wildtype P10 subiculum. D' shows a pseudo-colored version of D: postsynaptic cell soma in magenta and DABlabeled Syt2-positive terminal in green. E,F: Gad67 immunolabeling in P10 col19a1<sup>-/-;</sup> mutant (-/-; F) and control (+/-; E) subiculum. In mutant stratum pyramidalis (sp), levels of Gad67 were increased in cell bodies and processes (see arrowheads and arrows, respectively) and decreased in synaptic structures compared with controls. In contrast to sp, reduced levels of Gad67 were not observed in the adjacent molecular layer (m) of mutant subiculum. Asterisks depict boundary between sp and m. E',F' show high-magnification confocal images of Gad67 labeling in control and mutant sp, respectively. E",F" show high-

magnification confocal images of Gad67 labeling in control and mutant *m*, respectively. **G**: Western blot analysis of gephyrin and PSD-95 in P10 and P14  $col19a1^{-/-}$  mutant (-/-) and control (+/-) hippocampal extracts. Levels of actin were used as loading controls. **H**: Levels of mutant gephyrin were quantified by densitometry, normalized to actin, and compared to normalized control levels. Dashed line represents control levels. Data shown are  $\pm$  SEM, *n* = 3. \*Differs from age-matched control at *P* < 0.05 by Student's *t*-test. Label colors in black and white image panels correspond to the color of that image in the multicolored composite image. Scale bars = 20 µm in A"; 20 µm in B" (applies to B,C); 800 nm in D; 60 µm in E (applies to F); 15 µm in E' (applies to E',E",F',F").

**TABLE 1** 

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Antibodies Used

Antigen	Isotype	Description of immunogen	Source/catalog number	Dilution for IHC	Dilution for WB
Actin	Mouse IgG1	Purified chicken gizzard actin	Chemicon #MAB1501		1:20,000
Calbindin	Rabbit polyclonal	Rat calbindin D28k	Swant, #CB-38a	1:1,000	
Calretinin	Rabbit polyclonal	Recombinant rat calretinin	Chemicon #AB5054	1:2,500	
Gephyrin	Mouse IgG1	Purified rat gephyrin	Synaptic Systems		1:1,000
Glial fibrillary acidic protein (GFAP)	Rabbit polyclonal	GFAP isolated from cow spinal cord	DAKO #Z0334	1:2,500	
Glutamate decarboxylase 67 (Gad 67)	Mouse IgG2a	Recombinant Gad67	Chemicon #MAB5406	1:1,000	
Glutamate decarboxylase 65 & 67 (Gad 65/67)	Rabbit polyclonal	Synthetic peptide containing a Cysteine residue and amino acids <i>5</i> 72–585 of rath Gad65	Chemicon #AB1511	1:500	
Ionizing calcium-binding adaptor 1 (Iba-1)	Rabbit polyclonal	Synthetic peptide corresponding to the first 29 amino acids of Iba-I	WAKO #016–20001	1:500	
Neuronal Nuclei (NeuN)	Mouse IgG1	Purified cell nuclei from mouse brain	Chemicon #MAB377	1:200	
Neuropeptide Y (NPY)	Rabbit polyclonal	Neuropeptide Y coupled to bovine thyroglobulin	ImmunoStar #22940	1:500	
Postsynaptic density protein 95 (PSD-95)	Mouse IgG2a	Purified recombinant rat PSD-95	Affinity BioReagents		1:3,000
Somatostatin	Rabbit polyclonal	Somatostatin conjugated to BSA	Chemicon #AB5494	1:250	
Synapsin	Mouse IgG1	Purified synapsin 1	Synaptic Systems, #106001	1:500	1:100
Synaptotagmin 2	Mouse IgG2a	1–5 day zebrafîsh embryo	Zebrafish International Resource Center	1:200	1:100
Vesicular glutamate transporter 1 (VGlut1)	Mouse IgG1	Recombinant fusion protein consisting of amino acids 493–560 of rat VGlut1	NeuroMab; Clone N28/9		1:400
Vesicular glutamate transporter 2 (VGhrt2)	Mouse IgG1	Recombinant fusion protein consisting of amino acids 501–582 of rat VGlut2	NeuroMab; Clone N29/29		1:400

# **TABLE 2**

Summary of Coexpression of Various Neurochemicals or Genes by col19a1-expressing Hippocampal Interneurons

egion	ΛPΥ	Som	Calb	Calr	parv	syt2
A1						
0	+++++++++++++++++++++++++++++++++++++++	+++++	+	Ι	Ι	  +
Ч	+++++++++++++++++++++++++++++++++++++++	T	+	I	I	- /+
ΓM	+++++++++++++++++++++++++++++++++++++++	Ι	+	Ι	Ι	  +
ц	+ +	I	+	I	I	- /+
43						
Q	+++++++++++++++++++++++++++++++++++++++	+++++++++++++++++++++++++++++++++++++++	+	Ι	Ι	  +
<u>d</u> ,	+ +	I	+	I	I	- /+
ΓM	+++++++++++++++++++++++++++++++++++++++	T	+	I	I	- /+
R	+ +	I	+	I	I	- /+
7						
jCL	I	I	Ι	Ι	Ι	Ι
Ŧ	+ +	+	-/+	I	I	+
biculu	в					
oly	I	+	I	I	I	-/+
d,	I	+ +	‡	I	I	+
I	I	I	+	I	I	I

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moleculare; SO, stratum oriens; Som, somatostatin; SP, stratum pyramidalis; SR, stratum radiatum; *xyl2*, gene encoding synaptotagmin 2; '--' no coexpression observed; '+/-' only occasional coexpression observed; '+-' large number of coexpressing cells observed. nolecular layer; NPY, neuropeptide Y; parv, gene encoding parvalbumin; Poly, polymorphic layer; SLM, stratum lacunosum