Title Page

Title: Inhibitory parvalbumin basket cells are selectively impaired during hippocampal sharp wave ripples in a mouse model of familial Alzheimer's disease

Abbrev Title: PVBCs are impaired during SWRs in model of AD

Authors: Adam Caccavano[1*], P. Lorenzo Bozzelli[1], Patrick A. Forcelli[1,2], Daniel T.S. Pak[1,2], Jian-Young Wu[1,3], Katherine Conant[1,3], Stefano Vicini[1,2]

Affiliations: [1]Interdisciplinary Program in Neuroscience, Georgetown University Medical Center, Washington, DC, 20057, [2]Dept. of Pharmacology & Physiology, Georgetown University Medical Center, Washington, DC, 20057, [3]Dept. of Neuroscience, Georgetown University Medical Center, Washington, DC, 20057, *Corresponding Author

Corresponding author email address: ac1625@georgetown.edu

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1   Abstract

Memory disruption in mild cognitive impairment (MCI) and Alzheimer's disease (AD) is poorly

understood, particularly at early stages prior to neuronal or synaptic degeneration. In mouse models of

AD, there are observed disruptions to sharp wave ripples (SWRs), hippocampal population events with

a critical role in memory consolidation. However, the micro-circuitry underlying these disruptions are

under-explored. We tested the hypothesis that a selective reduction in parvalbumin-expressing (PV)

inhibitory interneuron activity underlies hyperactivity and SWR disruption. We employed the 5xFAD

model of familial Alzheimer's disease crossed with mouse lines that selectively label excitatory pyramidal

cells (PCs) and inhibitory PV cells. We observed a 33% increase in frequency, 58% increase in amplitude,

and 8% decrease in duration of SWRs in acute slices from 3-month 5xFAD mice versus littermate

controls. 5xFAD mice of the same age were impaired in a task of hippocampal-dependent memory.

Concurrent with SWR recordings, we performed calcium imaging, cell-attached, and whole-cell

recordings of PC and PV cells within the CA1 region. PCs in 5xFAD mice participated in enlarged

ensembles, with similar spiking activity, and increased synaptic E/I ratio, suggesting a disinhibitory

mechanism. In contrast, we observed a selective 46% spike rate reduction during SWRs in PV basket

cells (PVBCs), whereas PV bistratified and PV axo-axonic cells were unimpaired. Excitatory synaptic

drive to PVBCs was selectively reduced by 50%, resulting in decreased E/I ratio. Considering prior

studies of intrinsic PV cell dysfunction in AD, these findings suggest synaptic and network mechanisms

also play a prominent role.

Significance Statement

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We demonstrate that a specific sub-type of inhibitory neuron, PV-expressing basket cells, are

selectively impaired in a model of Alzheimer's disease during activity critical for the consolidation of

memory (i.e. SWRs). These results identify a cellular target for therapeutic intervention to restore aberrant

network activity in early amyloid pathology. While PV-expressing cells have previously been identified as

a potential therapeutic target, this study for the first time recognizes that other PV-expressing neuronal

sub-types, including bistratified and axo-axonic cells, are spared. It also represents the first attempt to

record synaptic and spiking activity during SWR events in early amyloid pathology, revealing that a

selective decrease in excitatory synaptic drive to PV basket cells likely underlies reduced function.

Introduction

Alzheimer's disease (AD) is the leading cause of dementia, and a growing public health crisis as worldwide life expectancy increases (Mattson, 2004). AD is characterized by learning and memory deficits, the pathological accumulation of amyloid beta (Aβ) plaques and neurofibrillary tangles, and synaptic and neuronal degeneration (Serrano-Pozo et al., 2011). The cause of memory disruption in the disease is poorly understood, particularly at early ages prior to widespread neurodegeneration. The hippocampus, a region particularly important for the encoding and consolidation of spatial memory, is one of the first regions impaired in AD (Braak and Braak, 1991). Hyperactivity within the hippocampus is observed in mouse models of AD (Palop et al., 2007; Busche et al., 2008, 2012; Palop and Mucke, 2010), as well as in clinical populations, where seizures are an increasingly recognized co-morbidity of AD (Hauser et al., 1986; Amatniek et al., 2006; Palop and Mucke, 2009). While it is well appreciated that Aβ impairs the synaptic function of excitatory pyramidal cells (PCs) in later disease progression (Kamenetz et al., 2003; Shankar et al., 2008; Pozueta et al., 2013), there is growing evidence of early deficits to inhibitory GABAergic cells (Li et al., 2016), potentially explaining this shift to hyperactivity through disinhibition. In particular, several functional impairments are observed in inhibitory parvalbumin-expressing (PV) fast-spiking interneurons (Verret et al., 2012; Mahar et al., 2016; Yang et al., 2016; Hijazi et al., 2019). However, there are at least three unique PV cell sub-types within the CA1 region of hippocampus with varying anatomical connections and function (Varga et al., 2014), and the separate impact of AD pathology on these sub-types is unknown.

PV cells play a critical role in hippocampal sharp wave ripples (Ellender et al., 2010; Schlingloff et al., 2014; Ognjanovski et al., 2017), spontaneous neuronal population events characterized by a low frequency sharp wave (1-30 Hz) and a high frequency ripple (120-250 Hz) (Buzsáki, 1986, 2015; Colgin, 2016). SWRs principally originate in the CA3 region and propagate to CA1 along the Schaffer collaterals, occurring in all mammalian species studied to date (Buzsáki et al., 2013). Even following decortication in brain slices, SWRs spontaneously arise in hippocampus (Buzsáki et al., 1983). SWRs have been extensively studied in large part due to their proposed role in memory consolidation (Wilson and McNaughton, 1994; Kudrimoti et al., 1999; O'Neill et al., 2008; Karlsson and Frank, 2009). Sequences of

place cells activated during spatial learning replay in temporally compressed neuronal ensembles within

SWRs during rest (Nádasdy et al., 1999; Lee and Wilson, 2002). Online interruption of SWRs through

both electrical (Girardeau et al., 2009; Ego-Stengel and Wilson, 2010) and optogenetic stimulation (Ven

et al., 2016; Roux et al., 2017) leads to learning and memory deficits, demonstrating their critical role in

memory consolidation. Notably, in several mouse models of AD, SWRs are disrupted (Gillespie et al.,

2016; Iaccarino et al., 2016; Nicole et al., 2016; Xiao et al., 2017; Hollnagel et al., 2019; Jones et al.,

2019; Jura et al., 2019). However, the micro-circuitry underlying these disruptions has yet to be explored

in detail. In this study we employed the 5xFAD mouse model of familial Alzheimer's disease crossed with

mouse lines that selectively fluoresce in excitatory pyramidal cells (PCs) and inhibitory PV cells. We

performed patch clamp recordings of PCs and three distinct PV cell sub-types to record the spiking

activity and synaptic input during SWR events. Our findings support the hypothesis that a preferential

reduction in synaptic input and activity of PV basket cells underlies downstream network alterations and

suggest that long-term alterations to PC-PVBC micro-circuitry contribute to dysfunction in early amyloid

pathology.

Materials and Methods

Experimental Animals

To record the activity of excitatory PCs and inhibitory PV cells in amyloid pathology, we employed a combined breeding strategy of transgenic and targeted knockin mice. Transgenic 5xFAD mice (RRID:MMRRC_034840-JAX) (Oakley et al., 2006) were back-crossed for over five generations to the C57BL/6J (RRID:IMSR_JAX:000664) background, which was common to all other strains used. To target the calcium activity of PCs under confocal microscopy, transgenic homozygous Thy1-GCaMP6f-GP5.5 (RRID:IMSR_JAX:024276) (Dana et al., 2014) were crossed with hemizygous 5xFAD mice to yield litters with both 5xFAD/+;Thy1-GCaMP6f/+ and Thy1-GCaMP6f/+ littermate controls. PV cells were identified by crossing double homozygous knockin PV^{Cre}/PV^{Cre};tdTom/tdTom (RRID:IMSR_JAX:008069, RRID:IMSR_JAX:007914) (Hippenmeyer et al., 2005; Madisen et al., 2010) with hemizygous 5xFAD mice to yield litters with both 5xFAD/+;PV^{Cre}/+;tdTom/+ and PV^{Cre}/+;tdTom/+ littermate controls. In a subset of experiments the reporter lines were crossed, yielding quadruple transgenic cohorts of 5xFAD/+;Thy1-GCaMP6f/+;PV^{Cre}/+;tdTom/+ and Thy1-GCaMP6f/+;PV^{Cre}/+;tdTom/+ littermate controls. Offspring were genotyped for 5xFAD genotype at age P7 by tail biopsy via automated genotyping services (Transnetyx, Cordoba, TN, USA). For all experiments, experimenters were blind to 5xFAD genotype until after data collection and analysis were fully complete. Mice were weaned at P21 and group housed in cages with 3-5 mice separated by sex. As a model of early amyloid pathology prior to neuronal or synaptic loss (Oakley et al., 2006), two experimental cohorts were chosen (each including both males and females) at 1 month (mo) and 3 mo of age (Table 1). Mice were kept on a standard 12 hr light/dark cycle, food and water were provided *ad libitum*, with all experimental procedures performed in accordance with the guidelines of the Georgetown University Animal Care and Use Committee.

Behavioral Testing

To test for hippocampal-dependent learning and memory deficits, mice were tested on the Barnes maze (Barnes, 1979), with some modifications. The Barnes maze was conducted on a white plastic apparatus (San Diego Instruments) 0.914 m in diameter, with overhead bright illumination (286 lx) serving as the aversive stimulus. The target hole was randomly selected, with four distal visual clues present for

visuospatial learning. The training phase consisted of four 180 s trials per day for 4 consecutive days.

The probe trial, in which the target hole was inaccessible, was conducted on the fifth consecutive day,

consisting of one 90 s trial. Mice were tracked using the ANY-maze tracking system, which was used for

distance and speed measurements. The primary measures of latency and number of entries to target

hole were hand-scored for increased reliability. Anxiety-like behavior was tested on the elevated plus

maze (Pellow et al., 1985). The mice could explore the maze for 5 min, in which time the number of

entries and fraction of time in the open arms were assessed by the ANY-maze tracking system. All tests

were conducted in the light cycle, at consistent times of the day for each mouse, in an enclosed behavior

room with 50 dB ambient sound and 23 lx ambient illumination. Males and females were run on the same

day, but in separate groups. Cohorts were not balanced by both sex and genotype, but as much as

possible testing order was prepared so that control and 5xFAD mice were alternated.

Acute Slice Preparation

Brain slices were prepared using NMDG and HEPES-buffered artificial cerebrospinal fluid (aCSF)

following a protective recovery protocol (Ting et al., 2014, 2018). Briefly, mice were anesthetized with

isoflurane, transcardially perfused, dissected, and sliced in iced (0º C) NMDG-aCSF containing in mM:

92 NMDG, 2.5 KCl, 1.25 NaH_2PO_4, 30 $NaHCO_3$, 20 HEPES, 25 Glucose, 10 Sucrose, 5 Ascorbic Acid,

2 Thiourea, 3 Sodium Pyruvate, 5 N-acetyl-L-cysteine, 10 $MgSO_4$, 0.5 $CaCl_2$, pH to 7.3-7.4 with HCl (300-

310 Osm). All common reagents were obtained from Thermo Fisher Scientific. The brains were sliced

horizontally at 500 µm thickness with a Vibratome 3000 to preserve hippocampal micro-circuitry and

spontaneous SWRs. 3-4 slices were typically obtained per brain, which were bisected so that 6-8

hemislices in total were studied per animal. Slices spanned the dorsal-ventral axis, though were primarily

medial, as only horizontal slices with intact DG, CA3, and CA1 were retained, ranging from bregma 2-4

mm. The slices were transferred together to heated (33º C) NMDG-aCSF, in which Na^+ was gradually

introduced along an increasing concentration gradient every 5 min before transferring to room

temperature HEPES-aCSF containing in mM: 92 NaCl, 2.5 KCl, 1.25 NaH_2PO_4, 30 $NaHCO_3$, 20 HEPES,

25 Glucose, 5 Ascorbic Acid, 2 Thiourea, 3 Sodium Pyruvate, 5 N-acetyl-L-cysteine, 2 $MgSO_4$, 2 $CaCl_2$,

pH to 7.3-7.4 with NaOH (300-310 Osm). Slices recovered for 4 hours in a custom-built 150 mL incubation

chambers with circulating oxygenated HEPES-aCSF.

Slice Electrophysiology

Slices were transferred to a Siskiyou PC-H perfusion chamber with a custom-built suspended Lycra

thread grid to allow perfusion below and above slice, modeled after (Hájos et al., 2009). Submerged

slices were anchored with Warner Instruments slice anchors so that they were sandwiched between two

grids, and perfused at a rate of 5 mL/min with heated (30º C) oxygenated aCSF containing in mM: 124

NaCl, 3.5 KCl, 1.2 NaH_2PO_4, 26 $NaHCO_3$, 10 Glucose, 1 $MgCl_2$, 2 $CaCl_2$, pH 7.3-7.4 (300-310 Osm).

Recordings were conducted with a Multiclamp 700B amplifier (Molecular Devices), digitized at 20

kHz and low-pass Bessel-filtered at 2 kHz with a personal computer running Clampex 11 and a DigiData

1440 (Molecular Devices). Two concurrent channels were captured: the local field potential (LFP) was

recorded with 0.5-1 MΩ borosilicate pipettes filled with aCSF, paired with 3-5 MΩ borosilicate pipettes for

cellular recordings. Cell-attached recordings were performed with aCSF + 5 µM Alexa Fluor® 488 nm

(Molecular Probes Cat# A-10440) or 594 nm (Molecular Probes Cat# A-10442) for pipette localization

under confocal microscopy. The selected concentration of Alexa dye was below reported alterations to

synaptic transmission (Maroteaux and Liu, 2016). Cell-attached recordings were followed with whole-cell

recordings of the same cell with a new pipette filled with a Cesium internal, containing in mM: 120

$CsMeSO_3$, 5 NaCl, 10 TEA•Cl, 10 HEPES, 1.1 EGTA, 4 QX314, 4 ATP•Na, 0.3 GTP•Na, pH to 7.2 with

CsOH (285 Osm). For pipette localization and *post hoc* morphological reconstruction, 5 µM Alexa (either

488 or 594 nm) and 0.5% wt/vl biocytin were added to the internal solution on the day of experiment.

The LFP electrode was placed in CA1 on the border of *stratum pyramidale* (*str. pyr.*) and *oriens*, a

location where both high amplitude sharp waves (SWs) and ripples are simultaneously detectable.

Recordings began 10 min after LFP electrode placement to allow slice to recover. If visually detectable

SWRs were not observed, the slice was logged as non-SWR producing (Table 1) and discarded. A

fluorescent cell was targeted for a loose (20-40 MΩ seal resistance) cell-attached recording of 3-5 min

duration. For Thy1-GCaMP6f slices, Ca^{2+} ensemble activity was recorded concurrently with a laser

scanning confocal microscope system (Thor Imaging Systems Division) equipped with 488/561/642 nm

lasers and green/red/far-red filters and dichroics mounted on an upright Eclipse FN1 microscope (Nikon

Instruments). One thousand 512 x 512 pixel frames were captured at a sample rate of 7.5 Hz. A 40x

water immersion objective was used, covering an imaging field of 350 x 350 μm, as a balance between

maximizing the imaging field while providing high enough magnification for patch clamp

electrophysiology.

Following the cell-attached recording, the same cell was targeted with a new Cesium internal

electrode. Upon reaching 1 GΩ seal resistance, the membrane was broken by a voltage pulse and quick

negative pressure. Access resistance was monitored periodically and recordings with a change >20%

were discarded. Putative excitatory post-synaptic currents (EPSCs) were measured in voltage-clamp at

a holding voltage of -70 mV, and putative inhibitory post-synaptic currents (IPSCs) in the same cell at 0

mV. Glutamatergic and GABAergic events were not pharmacologically isolated, as the primary goal was

to correlate synaptic activity with spontaneous SWRs, which would be affected by drug administration.

The reversal potentials of putative EPSCs and IPSCs matched closely with the expected glutamate and

GABA reversal potentials of 0 and -70 mV. This was determined by holding the cell from +20 to -100 mV

in 10 mV voltage steps and monitoring the current polarity inversion. Each voltage-clamp recording

ranged from 1-3 min. For PV cell recordings, the cell was then switched to current-clamp, with current

injection to offset the leak current and maintain a membrane potential of -70 mV. 35

hyperpolarizing/depolarizing steps of 5 pA increments were delivered to fill the cell with biocytin. A total

duration of at least 15 min of whole-cell configuration was maintained, after which an outside-out patch

was formed by slowly withdrawing the pipette.

Post Hoc Staining and Microscopy

Slices with biocytin-filled PV cells were returned to the HEPES-aCSF incubation chamber for the

remainder of the day, then fixed overnight in 4% PFA, 4% glucose in PBS at 4° C. Slices then received

four 15 min PBS washes, 2 hours of permeabilization with 0.5% Triton-X in PBS, 2 PBS rinses, 3 hours

in Fluorescein-Avidin (1:500; Vector Laboratories Cat# A-2001, RRID:AB_2336455) in PBS, and four

additional 15 min PBS washes. Free floating slices were imaged with a laser scanning confocal

microscope system (Thor Imaging Systems Division). Under 20x magnification, z-stacks were obtained

covering the span of visible cellular processes (40-80 µm in 1 µm steps), for both green (biocytin) and

red (PV^{Cre}-tdTom) channels. In a subset of 14 slices (5 Control, 9 5xFAD from n$_{mice}$ = 4 Control, 5 5xFAD),

an additional round of immuno-staining was performed for Ankyrin G, which labels the axon initial

segment of pyramidal cells. Antigen retrieval was performed on the 500 µm slices for 20 min in a steamer

with citrate buffer containing 10 mM Na$_3$C$_6$H$_5$O$_7$, 0.05% Tween20, and pH adjusted to 6.0 with HCl. Slices

were cooled to room temperature for 20 min in PBS, then blocked overnight with 10% NGS at 4° C. The

following day the slices were incubated with a primary monoclonal mouse antibody against Ankyrin G

(1:100; Thermo Fisher Scientific Cat# 33-8800, RRID:AB_2533145), 0.1% Tween20, 1% NGS in PBS.

After 48 hrs of primary incubation at 4° C, slices were given four 15 min PBS washes and incubated in

secondary containing Alexa Fluor® 647 conjugated goat anti-mouse IgG (1:500; Jackson

Immunoresearch Cat# 115-605-003, RRID:AB_2338902) and 1% NGS in PBS for 3 hrs at room

temperature. Slices were given four more 15 min PBS washes, rinsed in ddH$_2$0, and mounted on slides

between silicone isolators with Vectashield® antifade mounting medium with DAPI (Vector Laboratories

Cat# H-1200, RRID:AB_2336790).

Pre-processing of Electrophysiology Data and Event Detection

Pre-processing of files was conducted in Clampfit 11 (pClamp, Molecular Devices). Files for

calcium imaging experiments were trimmed around the confocal laser trigger signal for alignment of SWR

and calcium transients. Spikes were detected in cell-attached recordings with a 3 ms or 1.75 ms template

search for PCs or PV cells, respectively. A threshold of 6-8 was used (Clements and Bekkers, 1997) and

false negatives minimized (confirmed by manual inspection). False positives were removed by plotting

peak vs anti-peak amplitude to segregate noise from true spikes. Bursts were detected with the built-in

Burst Analysis, defined as three or more successive spikes, each within 60 or 40 ms (intra-burst interval)

for PCs or PV cells, respectively. Spike start, peak, and end times, burst start and end times, number of

events in burst, and intra-burst interval were exported from Clampfit for coincidence detection in

MATLAB.

Whole-cell recordings of post-synaptic current (PSC) signals were low-pass filtered below 1000 Hz

with a zero-phase Gaussian FIR filter. PSCs were detected with template searches. Multiple template

categories (3-4) of varying duration (ranging from 3-20 ms) were used to improve detection for

overlapping PSCs often seen around SWRs. Shorter duration templates used increasingly higher

thresholds, between 5-8, to minimize false negatives. Parameters were kept constant for each cell type.

PSC results including start, peak, and end times, amplitude, rise tau and decay tau were exported from

Clampfit and processed in Microsoft Excel to remove duplicate events with identical peak times. Limits

were set on rise and decay tau to remove false positives due to noise. Accepted EPSCs fell within a

range of 0.05-5 ms rise tau and 1-50 ms decay tau, while IPSCs fell within a range of 0.1-10 ms rise tau

and 3-100 ms decay tau.

Local Field Analysis and Sharp Wave Ripple Detection

All analysis for coincidence detection between the LFP and cellular events was conducted with

custom-built MATLAB functions. Raw traces were imported using the abfload protocol

(https://github.com/fcollman/abfload). All applied filters were finite impulse response (FIR) Gaussian filter

with constant and corrected phase delays. A wide band-pass (1-1000 Hz) was first applied to remove

both low frequency DC drift and high frequency instrument noise. The detection of SWR events was

based upon prior approaches (Siapas and Wilson, 1998; Csicsvari et al., 1999; Eschenko et al., 2008),

with refinements to minimize false positives and permit additional analyses. The LFP was filtered in both

the sharp wave (SW: 1-30 Hz) and ripple (120-220 Hz) ranges, and the root mean square (RMS) was

computed every 5 ms in a 10 ms sliding window. The threshold for peak detection was set to 4 standard

deviation (SD) above the baseline (lower 0.95 quantile) RMS mean. Event start and end times were set

at 2 SD crossings. SWR events were defined as the intersection of concurrent SW and ripple events.

The duration of SWR events was determined from the union of concurrent SW and ripple events. The

peak of the SWR event was defined as the peak of the SW-RMS signal, and the amplitude as the

difference between the peak and baseline values of the SW signal. The power of the SW and ripple were

determined by the bandpower MATLAB function of the relevant filtered signal, which computes an

approximation of the integral of the power spectral density between the start and end times of the SWR

event. Additional filters were applied in the slow gamma (20-50 Hz) and fast/pathological ripple (250-500

Hz) ranges, and the power computed on a SWR-event basis, as the power of these SWR-nested

oscillations has been implicated in memory performance (Carr et al., 2012) and epileptogenesis (Foffani

et al., 2007), respectively.

To visualize the spectral components of the LFP as a function of time, spectral analysis was

performed for the duration of the recording as well as per SWR event via a Short-Time Fourier Transform

(STFT) between 1-500 Hz. To better observe deviations from baseline power, the Z-score for each 1 Hz

frequency band was calculated. A Fast-Fourier Transform (FFT) was also computed for a 200 ms window

centered around each SWR peak and averaged across all events as an additional visualization of spectral

power. The determination of the phase of slow gamma and ripple oscillations during SWRs was based

on the analysis of (Varga et al., 2012). Within a 200 ms window centered around the SWR peak, the

extrema of the filtered signal of interest were identified, and a piece-wise linear function fit with values

from 0º to 180º between a maximum and minimum, 180º to 360º between a minimum and maximum, and

then resetting to 0º. The number of cycles within the duration of the SWR event was recorded, from which

the peak frequency was calculated as $n_{cycle}/SWR_{duration}$.

Pre-processing of Ca²⁺ Imaging Data

Raw time series were converted to the change in fluorescence normalized to baseline (*ΔF/F*) with

custom-built ImageJ (FIJI) macros, in which batches of raw TIF images were imported with the Bio-

Formats plugin (Open Microscopy Environment) and saved as TIF stacks. The TIF stacks were corrected

for photo-bleaching via two iterations of the built-in Correct-Bleach plugin. Photo-bleaching was modeled

as a sum of two exponentials, a fast 5 s decay and a slower decay over the duration of the recording

(133 s). To assist in region-of-interest (ROI) placement, a semi-automated algorithm was applied to

highlight regions of highest fluorescence change. For each TIF stack, the squared coefficient of variation

(SCV) image was calculated, defined as the variance divided by the average squared for each pixel, or

equivalently:

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$$Img_{SCV} = \frac{1}{n}\sum_{i=1}^{n}\left(\frac{Img_i - \overline{Img}}{\overline{Img}}\right)^2$$

Circular ROIs were manually drawn over all identified cells in the SCV image and confirmed with

the time series to encompass active cells. Notably, in this way only cells with variable fluorescence were

identified, and static highly fluorescent Ca^{2+}-loaded cells were excluded. The *ΔF/F* for each cell was

calculated by first subtracting the background fluorescence F_b, defined as the lowest intensity pixel across

the entire time series. F_0 for each ROI was defined as the average of the ten images with the lowest

intensity. The *ΔF/F* was thus calculated as:

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$$\Delta F_i / F_0 = \frac{F_i - F_0}{F_0 - F_b}$$

These values were exported from ImageJ, along with a separately calculated timing file for each

image, computed from a threshold search in Clampfit of the confocal laser trigger channel.

Calcium Transient Detection and SWR Coincidence Analysis

Automatic detection of calcium transients was performed by first correcting for slow changes in

fluorescence, either from remaining photo-bleaching or gradual drift of the imaging plane. A smoothed

moving average, calculated with robust locally-weighted regression (Cleveland, 1979) with a window 25%

of the file duration (33 s), was subtracted from each *ΔF/F* trace. The baseline-corrected *ΔF/F* traces were

interpolated from the raw sampling rate of 7.5 Hz to 2 kHz, and the LFP downsampled from 20 kHz to 2

kHz for coincidence detection. Automatic threshold detection for each cell was set at 4 SD above

baseline, with the start and end times for each event set at 2 SD. The baseline of each cell was

determined by an iterative algorithm of gaussian fitting to the histogram of all data points, which for most

cells was a skewed one-tailed distribution with a large baseline peak at zero and a long positive tail

representing transient events. For uncommon cells without a skewed distribution (kurtosis < 0), a single

gaussian fit was applied to the entire histogram, providing an estimate of the baseline mean and SD.

However, for most cells, two iterations were employed, with the first a double-gaussian fit to the entire

histogram. The higher amplitude gaussian SD was then used to constrain the upper limit on a second

iteration single-gaussian refinement fit of only the baseline. Special logic was necessary in rare situations.

For excessively skewed distributions (high *ΔF/F*, kurtosis > 5) the double-gaussian fit was constrained to

the lower 0.95 quantile of data. For extremely active cells, because of the slow decay kinetics of GCaMP,

the signal peak rivaled or exceeded the baseline peak in amplitude. For these cells, the more negative

rather than the higher amplitude peak was used as an estimate of the baseline. In the situation where

two peaks were not clearly differentiated (peak separation < 0.1 *ΔF/F*), the gaussian means and SDs

were averaged together to arrive at an estimate for constraining the second iteration.

Once the baseline mean, SD, and thresholds were determined for each cell, events were detected

on a cell-by-cell basis, and characteristics calculated including start, peak, and end times, IEI, duration,

amplitude, and frequency. The interpolated calcium traces were trimmed and aligned with the down-

sampled LFP trace. Each calcium transient was classified as SWR-coincident if there was any overlap

between the start and end of the calcium transient and the start and end of the SWR, otherwise it was

classified as spontaneous. Cellular participation during SWRs was assessed by constructing a simplified

event matrix with SWRs in one dimension, and cells in the other, with a zero or one if the cell reached

threshold during the SWR. For fields with five or more active cells, the ensemble diversity was assessed

by calculating the pairwise Jaccard Similarity index between SWR events, ranging from a value of zero

if two SWR events had no cells in common, to a value of one if all cellular participants were identical,

modeled after the analysis of (Miyawaki et al., 2014). The cell-cell pairwise index was also calculated,

ranging from zero if two cells never participated in the same SWR events, to one if they participated in

precisely the same SWRs. The cumulative distribution functions were determined for each recording as

well as for all recordings grouped together by considering all off-diagonal values in one half of the

symmetric similarity matrices.

Spike and SWR Coincidence Analysis

Each spike/burst was classified as SWR-coincident if there was any overlap between the start and

end of the spike/burst and the start and end of the SWR, otherwise it was classified as spontaneous. To

examine spike rate in more detail around SWR events, the peri-SWR spike probability was calculated by

sorting all spikes that occurred within a 200 ms window centered around each SWR peak into 2 ms bins

and normalizing to all SWR events. Spike-phase coupling was determined by identifying the previously

calculated gamma and ripple phases at the spike peak time. Spike phase times were only considered for

further analysis if trough-peak amplitude exceeded 4 SD of the gamma or ripple signal.

Post-Synaptic Current and SWR Coincidence Analysis

Each EPSC/IPSC was classified as SWR-coincident (swrEPSC/swrIPSC) if there was any overlap between the start and end of the event and a 100 ms window centered around each SWR peak, otherwise it was classified as spontaneous (sEPSC/sIPSCs). The more conservative window to classify spontaneous events (compared to the calcium and spike analysis) better captured the buildup of EPSCs/IPSCs preceding SWRs (Schlingloff et al., 2014). As events overlap and complicate detection during SWRs, for quantification the current was integrated in a 100 ms window centered at the SWR peak to determine the total charge (swrEPSQ/swrIPSQ). For a view of the temporal progression of synaptic input during SWRs, the charge was also calculated by integrating a sliding 100 ms window every 2 ms in a 200 ms window centered around the SWR peak. PSC-LFP phase coupling during SWR events was quantified by band-pass filtering the whole-cell channel in the low gamma (20-50 Hz) and ripple (120-220 Hz) ranges, and cross-correlating the gamma and ripple signals between the whole-cell and LFP channels.

Experimental Design and Statistical Analyses

Most experiments in this study have been presented in a case-control experimental design, in which data from 5xFAD mice are compared to littermate controls. With behavioral learning on the Barnes Maze we have employed a longitudinal repeated measures (RM) design. In analyzing the impact of factors on LFP activity in a large sample of *ex vivo* slices, we have taken a factorial design. All data were tested for normality and lognormality via Shapiro-Wilks tests. If all groups were normally distributed, they were analyzed with parametric tests (unpaired t-test, n-way ANOVA, n-way RM ANOVA) and have been displayed on bar plots with error bars representing the mean ± SEM. If any group was not normally distributed, the data have been presented on box-whisker or violin plots, with lines indicating median and quartiles, and full error bars representing range. If all groups were lognormally distributed, the data were log transformed, the results of which were analyzed with parametric tests, with the log-means compared. For clarity, the original non-transformed data have been displayed in plots. If any group was neither normal nor lognormal, non-parametric statistical tests of rank were employed. Circular data (phase angles) were analyzed with a similar approach. Data were tested for non-uniformity via a Rayleigh test

to determine if they could be sampled from a von Mises (circular normal) distribution. If the Rayleigh test

reached significance for all groups, means were compared with the Watson-Williams test, otherwise a

circular median test was performed.

The particular statistical tests used are listed primarily in the figure legends, with some details in

the main text. Any values cited in the text are mean ± SEM. All *post hoc* multiple comparisons used the

Šidák correction. Within each plot all individual data points are presented. No data were excluded based

on their values, but only for experimental reasons (e.g. no SWRs present, excessive slice movement,

unstable patch clamp recording). The *n* is indicated in the text and figure legends, and differs between

experiment, either n_{mice}, n_{slice}, or n_{cell}. Raw p-values are displayed in plots; if less than a significance level

of 0.05 they are bold. Data originating from male or female mice are presented as closed or open circles

respectively. Sex differences were examined for some endpoints, but in general the experiments were

insufficiently powered to determine sex differences. A power analysis of the principal experiments was

performed based on preliminary data, guiding the number of animals/cells chosen.

Graphpad Prism 8 was used for all 1 and 2-sample statistical tests. Microsoft Excel and MATLAB

2019 were used for some simple calculations of mean, SD, SEM, ratio, and error propagation. n-way

ANOVAs were performed in the Statistics and Machine Learning Toolbox of MATLAB 2019. Non-

parametric factorial data were aligned and ranked with ARTool (Wobbrock et al., 2011), before running

ANOVAs. Circular statistics were run in the Circular Statistics Toolbox for MATLAB (Berens, 2009).

Code Accessibility

All code is open-source and available in public repositories, including current versions in active

development (Github) as well as archival copies used for this manuscript (Zenodo). MATLAB functions

are available at https://github.com/acaccavano/SWR-Analysis (archival copy: DOI: 10.5281/zenodo.

3625236). ImageJ (FIJI) macros are available at https://github.com/acaccavano/deltaFoF (archival copy:

DOI: 10.5281/zenodo.3625130).

Results

Three month 5xFAD mice have a minor spatial memory impairment

The 5xFAD model of familial Alzheimer's disease is an aggressive though useful model of amyloid pathology, as it exhibits heavy amyloid accumulation in hippocampus and associated cortices, and is accompanied with memory impairment (Oakley et al., 2006). 5xFAD mice are unimpaired in performance on the T-maze at 2 months (mo) but become impaired by 4-5 mo when amyloid burden is greater (Oakley et al., 2006). Interestingly, at 3 mo there is no evidence for neuronal or synaptic degeneration, while several synaptic markers begin to decline at 4 mo and are significantly reduced from controls by 9 mo. Here, we examined the performance of two cohorts of 5xFAD mice and littermate controls on the Barnes Maze: a 1 mo cohort with minimal reported amyloid accumulation (Oakley et al., 2006), and a 3 mo cohort (Table 1). Both cohorts learned the task, as seen by decreased latency to find escape hole over progressive days of training (Fig. 1A-B). There were no differences observed in training between genotype for either the 1 mo cohort (Fig. 1A) or the 3 mo cohort (Fig. 1B). On the probe day, 1 mo 5xFAD had similar latencies to controls (Fig. 1C), while 3 mo 5xFAD mice had a significantly longer latency to find the escape hole from 18.4 ± 7.6 s to 37.4 ± 9.8 s (Fig. 1D,E). The number of entries to the area of the escape hole, another commonly reported endpoint, was not significantly different for either cohort (1 mo: $t_{(18)}$ = 0.735, p = 0.472; 3 mo: $t_{(25)}$ = 0.691, p = 0.496; unpaired t-tests). 5xFAD mice displayed no obvious motor impairments, as the total distance traveled did not differ between genotype at either age (1 mo: 3.98 ± 0.91 m (Control = CT), 3.77 ± 0.49 m (5xFAD), $t_{(18)}$ = 0.203, p = 0.842; 3 mo: 3.98 ± 0.49 m (CT), 3.40 ± 0.49 m (5xFAD), $t_{(25)}$ = 0.816, p = 0.422; unpaired t-tests), neither did the mean speed (1 mo: 4.4 ± 1.0 cm/s (CT), 4.2 ± 0.5 cm/s (5xFAD), $t_{(18)}$ = 0.186, p = 0.856; 3 mo: 4.4 ± 0.6 cm/s (CT), 3.8 ± 0.5 cm/s (5xFAD), $t_{(25)}$ = 0.819, p = 0.420; unpaired t-tests).

To test if this observed memory impairment could be attributed to altered anxiety-like behavior, the cohorts were also tested on the Elevated Plus Maze. Neither age cohort showed a significant difference in fraction of time spent in open arms (1 mo: 15.4 ± 2.2% (CT), 15.1 ± 0.9% (5xFAD), $t_{(18)}$ = 0.129, p = 0.900; 3 mo: 10.7 ± 1.0 (CT), 9.3 ± 1.5 (5xFAD), $t_{(25)}$ = 0.848, p = 0.404; unpaired t-tests), nor in number of open arm entries (1 mo: 7.9 ± 0.6 (CT), 7.4 ± 0.6 (5xFAD), $t_{(18)}$ = 0.570, p = 0.576; 3 mo: 9.2 ± 0.7

(CT), 7.5 ± 0.6 (5xFAD), $t_{(25)}$ = 1.863, p = 0.074; unpaired t-tests). Therefore, we concluded that 3 mo

5xFAD mice on our genetic background had a mild spatial memory impairment. As memory impairment

has been widely reported in 5xFAD mice at later ages (Oakley et al., 2006; Ohno, 2009; Tohda et al.,

2012), no further memory tasks were performed.

Sharp wave ripples are increased in 3 month 5xFAD mice

As spatial memory relies heavily on the activity of the hippocampus, and sharp wave ripples

(SWRs) are critical for the consolidation of new memories (Buzsáki, 1986; Wilson and McNaughton,

1994), we next recorded spontaneous SWRs in hippocampal slices from control and 5xFAD mice (Fig.

2A-B). SWRs were recorded in multiple slices for each animal and averaged in both a 1 mo cohort (n_{mice}

= 10 CT, 10 5xFAD), and a 3 mo cohort (n_{mice} = 27 CT, 29 5xFAD, Table 1). In the 1 mo cohort, the SWR

event frequency did not differ (Fig. 2C), nor were there changes for any other LFP endpoints (data not

shown). However, in the 3 mo cohort, SWR event frequency was increased in 5xFAD mice versus

controls from 0.94 ± 0.07 Hz to 1.25 ± 0.08 Hz (Fig. 2C). We next verified if there was an altered

percentage of slices exhibiting SWRs in 5xFAD mice (Table 1), as this could underlie observed

differences in event frequency. While a 2-way ANOVA revealed a significant effect of 5xFAD genotype

($F_{(1,72)}$ = 6.51, p = 0.0129) and age ($F_{(1,72)}$ = 5.21, p = 0.0254) on percentage of slices with SWRs, the

only significant difference observed when corrected for multiple comparisons was between control slices

at 1 mo and 3 mo (p = 0.0059, Šidák correction), while 3 mo slices did not differ between genotype (p =

0.882, Šidák correction). Therefore, the observed differences in 3 mo mice are not likely due to altered

viability of the slices.

In addition to an increased event frequency, SWR amplitude was increased by 58 ± 17% in 3 mo

5xFAD mice and surprisingly were 3.7 ± 1.2 ms shorter in duration (Fig. 2D). This decrease in duration

was likely attributable to both increased peak ripple frequency and decreased number of complete ripple

cycles (Fig. 2E), and is of interest as longer duration SWRs have been demonstrated to improve memory

(Fernández-Ruiz et al., 2019). Spectral features of SWRs also differed between genotype (Fig. 2F-J).

Low-gamma (20-50 Hz) nested within SWRs, speculated to play a role in coordinating CA3 and CA1

memory replay (Carr et al., 2012), was increased in 5xFAD mice (Fig. 2H). While the ripple peak

frequency was shifted (Fig. 2E,G), the total power within the frequency range 120-220 Hz was unchanged

(Fig. 2I). The power of fast or pathological ripples (250-500 Hz) did not differ between 5xFAD and control

slices (Fig. 2J), suggesting the increased activity in 5xFAD slices was distinct from epileptiform activity

(Foffani et al., 2007).

Spontaneous SWRs recordings were repeated in three separate 3 mo sub-cohorts with different

reporter mouse lines for subsequent patch-clamp and Ca^{2+} imaging experiments (Table 1). SWR

frequency increased in 5xFAD mice in both larger cohorts: PV^{Cre}/+;tdTom/+ mice (135 ± 18%, n_{mice} = 13

CT, 11 5xFAD) and Thy1-GCaMP6f mice (156 ± 21%, n_{mice} = 10 CT, 11 5xFAD). In the third smaller

Thy1-GCaMP6f;PV^{Cre}/+;tdTom/+ cohort, this increase was not observed (93 ± 18%, n_{mice} = 4 CT, 7

5xFAD). A 2-way ANOVA for 5xFAD genotype and reporter line revealed only a significant effect of

5xFAD genotype ($F_{(1,50)}$ = 5.407, p = 0.024) and not reporter line ($F_{(2,50)}$ = 1.500, p = 0.233) nor interaction

term ($F_{(2,50)}$ = 2.064, p = 0.138), therefore the data for the three sub-cohorts were combined into the

results presented in (Fig. 2). To test if sex, brain hemisphere, and dorsal-ventral slice position had an

effect, an additional 4-way ANOVA of all slices was performed. A small effect of 5xFAD genotype was

found (n_{slice} = 101 CT, 88 5xFAD; $F_{(1,178)}$ = 10.42, p = 0.0015), and a small effect of dorsal-ventral position

($F_{(1,178)}$ = 10.46, p = 0.0015), with ventral slices (bregma 3-4 mm) 126 ± 12% the frequency of more dorsal

slices (bregma 2-3 mm) for both control and 5xFAD slices. Correcting for multiple comparisons, within

each genotype the difference between dorsal and ventral slices was not significant (D vs V: p = 0.078

(CT), p = 0.235 (5xFAD), Šidák correction). No significant effects were observed for sex ($F_{(1,178)}$ = 0.728,

p = 0.395), brain hemisphere ($F_{(1,178)}$ = 0.873, p = 0.351), nor any interaction terms.

Altered ensembles of pyramidal cells are recruited in 5xFAD slices

The replay of pyramidal cell (PC) ensembles during SWRs is critical for the consolidation of spatial

memory (Wilson and McNaughton, 1994; Skaggs and McNaughton, 1996; Lee and Wilson, 2002; O'Neill

et al., 2008). Given the observed alterations to SWRs in 3 mo 5xFAD mice, we next sought to determine

if ensembles of PCs were also altered. The ensemble activity of PCs was recorded under confocal

microscopy in slices from 5xFAD/+;Thy1-GCaMP6f mice and Thy1-GCaMP6f littermate controls. Active

cells were detected with a semi-automated algorithm and both spontaneous and SWR-coincident Ca^{2+}

transient events were detected (Fig. 3A-B). Within 5xFAD slices, the number of active cells detected per

imaging field was increased from 17.0 ± 2.6 to 24.0 ± 1.6 cells in n_{slice} = 25 CT, 23 5xFAD (Fig. 3C).

Likewise, a greater number of cells were active during SWR events in 5xFAD slices (CT: 3.6 ± 0.6,

5xFAD: 4.9 ± 0.8 cells) (Fig. 3D). This increased cellular participation during SWRs may explain the

increased SWR amplitude in 5xFAD slices (Fig. 2D). While the total number of active as well as SWR-

coincident cells was increased, the fraction of SWR-coincident cells was unchanged between genotype

(20.0 ± 1.7% (CT) vs 18.9 ± 2.0% (5xFAD), $t_{(46)}$ = 0.755, p = 0.454, unpaired t-test). We next asked if

characteristics of the Ca^{2+} events differed between genotype, as an indirect measure PC firing activity.

Averaging across cells from each slice, no differences were found in the frequency, amplitude, nor

duration of Ca^{2+} transient events (Fig. 3E). This suggests that on an individual cell level, PCs exhibit

similar activity in 5xFAD mice as compared to controls, with differences only becoming apparent on the

ensemble level. Finally, we sought to determine if the cellular composition of PC ensembles was altered.

The pairwise similarity of cellular participation between SWR events showed a reduced degree of

similarity in PC ensembles during SWRs in 5xFAD, as compared to control slices (Fig. 3F-G), indicating

an increased repertoire of ensembles. Cell-cell similarity was also decreased in 5xFAD slices (Fig. 3H),

suggesting aberrant cell participation may be disrupting ensembles.

Pyramidal cell spiking is relatively unchanged in 5xFAD mice

To test more directly if pyramidal cell activity was altered, GCaMP6f+ PCs (n_{cell} = 41 CT, 55 5xFAD)

were targeted for loose cell-attached recordings (Fig. 4A). The majority of cells (n_{cell} = 41 CT, 46 5xFAD)

came from 5xFAD;Thy1-GCaMP6f and Thy1-GCaMP6f littermate controls. A small number (n_{cell} = 9

5xFAD) came from 5xFAD;Thy1-GCaMP6f;PV^{Cre}/+;tdTom/+ mice, which labeled both excitatory PCs in

green and inhibitory PV cells in red. Spikes and bursts (three or more spikes each within 60 ms) were

delineated as spontaneous or SWR-coincident (Fig. 4B). Consistent with prior studies (Mizuseki and

Buzsáki, 2013), the distribution of spike rates was lognormal, however there were no genotype

differences during either spontaneous or SWR periods (Fig. 4C). In both control and 5xFAD mice the PC

spike rate increased during SWRs, by 217 ± 56% in controls and 187 ± 48% in 5xFAD mice. To examine

spike rate in more detail around SWR events, the peri-SWR spike probability was averaged across all

cells within each genotype, showing similar spiking probabilities between genotype (Fig. 4D). The rate of

spike bursts did not differ between genotype, although the intraburst interval was decreased from 13.5 ±

1.1 ms to 11.3 ± 0.6 ms (Fig. 4E), indicating that although PCs had the same number of spikes, in 5xFAD

mice they did spike faster within bursts. The percentage of cells with bursts did not differ between

genotype (97.6% CT, 96.1% 5xFAD; $\chi^2_{(1)}$ = 0.158, p = 0.691; Chi-Squared Test). We also examined if

the fractional participation of PCs in SWRs differed, quantified as the fraction of spikes that occurred

during SWRs, and the fraction of SWRs that had one or more spikes. Neither endpoint differed between

genotype (Fig. 4F).

Finally, we examined the phase-locking of spikes in both the slow gamma and ripple ranges (Fig.

4G). Phase-locking of PCs to the trough of ripples has been widely reported *in vivo* (Ylinen et al., 1995;

Csicsvari et al., 1999; Le Van Quyen et al., 2008). However, phase-locking of PCs to SWR-nested slow

gamma has not been widely investigated. We also examined this endpoint considering the robust

increase we observed in slow gamma power in 5xFAD mice (Fig. 2H). In the gamma range there was a

significant phase-locking of spikes in control mice preceding the trough at 135° (108°-161° 95%), while

the mean phase of 158° (99°-217° 95%) for 5xFAD mice did not reach significance (Fig. 4H). In the ripple

range, cells were not significantly phase-locked for either genotype. However, in control mice, the mean

phase at the trough of 186° more closely matches prior findings than for 5xFAD mice, with a mean phase

of 239° following the trough (Fig. 4I). These results may indicate that spike-phase coupling is impaired in

5xFAD mice, though the lack of significant ripple phase-locking for either genotype suggests there may

be limitations to this analysis in our slice preparation, as this finding differs from the robust ripple phase-

locking observed *in vivo* (Ylinen et al., 1995; Csicsvari et al., 1999; Le Van Quyen et al., 2008). One

difference between our study and prior *in vivo* recordings is that the spikes and LFP were recorded from

different electrodes, while *in vivo* LFP and spikes are typically recorded from the same set of channels.

As ripples are highly localized events, the distance between electrodes may confound spatial phase

locking. Taken together with the Ca^{2+} imaging data, these results indicate relatively minimal alterations

to the spiking activity of PCs in 5xFAD slices. However, the large variability in spiking rate may mask

small differences in activity.

Pyramidal cells receive increased synaptic E/I ratio

Following the cell-attached recording of spiking activity, the electrode was replaced with one

containing a Cesium-based internal solution and the same cell targeted for a whole-cell voltage-clamp

recording to detect excitatory and inhibitory post-synaptic currents (EPSCs and IPSCs) at -70 mV and 0

mV (Fig. 5), respectively. Events were sorted as spontaneous (sEPSCs/sIPSCs) or SWR-coincident

(swrEPSCs/swrIPSCs). sEPSC frequency and amplitude were unchanged across genotype (Fig. 5D),

but there was a 96.8 ± 23.4% increase in total excitatory charge during SWRs (swrEPSQ) in 5xFAD mice

(Fig. 5F). Considering we observed that SWRs in 5xFAD mice were larger in amplitude and recruited

more PCs, this was not an altogether surprising result. This increase indicates that the enlarged SWRs

were accompanied with increased excitatory synaptic activity, likely originating from the CA3 region. The

lack of any increase in spontaneous excitatory activity may also be consistent with our cell-attached

results showing that at least locally in CA1, PCs fired similarly across genotype. We also tested coupling

between synaptic currents and oscillations in the LFP by filtering both channels in the slow gamma and

ripple ranges (Fig. 5E) and correlating between channels. Both gamma and ripple LFP oscillations were

more strongly anti-correlated to synaptic activity in 5xFAD mice (Fig. 5G), which is expected if both

channels are of higher amplitude. Together these results suggest that excitatory synaptic input is

increased during SWRs in 5xFAD mice, consistent with expectations from the LFP and Ca^{2+} imaging

experiments.

In contrast, the frequency and normalized charge of sIPSCs were decreased in 5xFAD mice, while

the amplitude was unchanged (Fig. 5H). Unlike excitatory charge, the total inhibitory charge during SWRs

(swrIPSQ) did not significantly differ between genotype (Fig. 5J). In both genotypes, inhibitory currents

were positively correlated with both slow gamma and ripple, however unlike excitatory currents, there

was no genotype difference (Fig. 5K). Given the observed increase in SWR activity in 5xFAD mice, this

result suggests that inhibition is not scaling proportionally to the increased excitation, thus shifting the

synaptic E/I balance. We directly assessed this for both spontaneous and SWR-driven currents. During

both spontaneous and SWR periods, the synaptic E/I charge ratio was significantly increased (Fig. 5L-

M), though for different reasons. Outside of SWRs, the E/I ratio of spontaneous synaptic activity was

increased due to a decrease in inhibition, whereas during SWRs, it was driven principally by an increase

in excitation. To examine the temporal progression of synaptic input during SWRs, we calculated the

swrEPSQ and swrIPSQ in a sliding 100 ms window across the SWR peak, from which a time course of

the synaptic E/I ratio could be determined (Fig. 5N). There was an early peak in the synaptic E/I ratio for

5xFAD mice that was not present in controls (Fig. 5O), which can be attributed to a build-up in excitation

with a delayed increase in inhibition.

PV basket cells have selectively reduced spiking

While there are numerous inhibitory cell sub-types in the CA1 region that could underlie a shift in

E/I synaptic input to PCs (Pelkey et al., 2017), we focused on parvalbumin-expressing (PV) interneurons,

as they are the most highly active during SWR events (Somogyi et al., 2014). We performed LFP + cell-

attached recordings in 5xFAD/+;PV^{Cre}/+;tdTom/+ and PV^{Cre}/+;tdTom/+ littermate control mice for n_{cell} =

54 CT, 37 5xFAD (Fig. 6A). A smaller number of cells (n_{cell} = 19 CT, 19 5xFAD) were recorded from

5xFAD;Thy1-GCaMP6f;PV^{Cre}/+;tdTom/+ and Thy1-GCaMP6f;PV^{Cre}/+;tdTom/+ littermate controls. One

complication with the PV cell population is that there are at least three distinct sub-types within CA1 *str.*

pyr., which vary in function and axonal target: basket cells (PVBCs), which target perisomatic regions of

PCs, bistratified cells (PVBSCs), which target both apical and basal dendrites of PCs, and axo-axonic

cells (PVAACs), which selectively target the axon initial segment (AIS) (Fig. 6B). To distinguish these,

we morphologically reconstructed the cells *post hoc* after filling with biocytin in whole-cell configuration

(Fig. 6C) and sorted them by axonal target. While PVBSCs were easily distinguished from both PVBCs

and PVAACs (Fig. 6C.2), PVBCs (Fig. 6C.1) and PVAACs (Fig. 6C.3) can look quite similar, as their

axonal targets overlap and not all PVAACs exhibit the characteristic "chandelier" phenotype. To address

this, we also examined the spike rate. Both PVBCs and PVBSCs are known to strongly increase their

spike rate during SWRs (Lapray et al., 2012; Katona et al., 2014), while for PVAACs spike rate does not

increase (Viney et al., 2013). Thus, cells that had ambiguous PVBC/PVAAC morphology and no spike

rate increase during SWRs were sorted as PVAACs. In a subset of 14 slices (5 CT, 9 5xFAD from n_{mice}

= 4 CT, 5 5xFAD), we additionally stained for Ankyrin G, which labels the AIS, and confirmed

colocalization with two expected PVAACs (Fig. 6C.4). The proportion of cells sorted in this way matched

reasonably well with prior published findings of 60% PVBC, 25% PVBSC, 15% PVAAC in CA1 *str. pyr.*

(Baude et al., 2007) and did not significantly differ between genotype (Fig. 6D).

Based on these delineations, we observed that PVBCs had a selective and robust reduction in

spike rate during SWR periods, from 62.9 ± 10.6 Hz to 34.0 ± 6.2 Hz, whereas the PVBC spike rate did

not significantly differ during spontaneous periods (Fig. 7A.1). Spikes rates during both spontaneous and

SWR periods did not differ between genotype in PVBSCs (Fig. 7B.1) or PVAACs (Fig. 7C.1). As expected

from sorting the cell sub-types, spike rates increased during SWRS for both PVBCs (CT: 5.6 ± 1.2 fold,

5xFAD: 5.9 ± 2.4 fold, Fig. 7A.1) and PVBSCs (CT: 4.4 ± 1.2 fold, 5xFAD: 6.8 ± 5.0 fold, Fig. 7B.1), while

PVAACs only saw minor and non-significant increases (CT: 1.0 ± 0.4 fold, 5xFAD: 2.4 ± 0.8 fold, Fig.

7C.1). The peri-SWR spike probability revealed that in 5xFAD mice, PVBCs spikes fell in a significantly

narrower window (Fig. 7A.2), with a reduced full-width half-maximum value from 44 ± 19 ms to 18 ± 5

ms. Intriguingly, this narrower window of spiking in 5xFAD mice was accompanied by shorter duration

SWRs (Fig. 2D), suggesting the activity of these cells is critical for normal ripple progression. In contrast,

PVBSCs appeared to increase their firing after the SWR peak (Fig. 7B.2) in 5xFAD mice, perhaps playing

a compensatory role. PVAACs appeared to have decreased probability of spiking in 5xFAD mice,

particularly before the SWR peak (Fig. 7C.2). However, unlike PVBCs, neither PVBSCs nor PVAACs

showed significant genotype differences when corrected for multiple comparisons (Fig. 7A-C.2).

Considering the rate of bursts, defined as three or more spikes each within 40 ms, there was a

tendency for a reduction for PVBCs (Fig. 7A.3) and no change for PVBSCs (Fig. 7B.3) or PVAACs (Fig.

7C.3). No differences were observed in the proportion of cells that exhibited bursts for PVBCs (100% CT,

93.8% 5xFAD; $\chi^2_{(1)} = 0.842$, p = 0.359; χ^2 Test), PVBSCs (80.0% CT, 90.0% 5xFAD; $\chi^2_{(1)} = 0.288$, p =

0.591), or PVAACs (50.0% CT, 83.3% 5xFAD; $\chi^2_{(1)} = 1.500$, p = 0.221). In PVBCs, the fraction of SWRs

that coincided with a PV burst was significantly reduced from 65.4 ± 8.5% to 32.9 ± 8.5% (Fig. 7A.4),

while there was no genotype difference for PVBSCs (Fig. 7B.4) or PVAACs (Fig. 7C.4).

We also examined the spike phase-locking of these three PV cell types, as these have been

carefully studied *in vivo* for theta (8-12 Hz, during mobility) and ripple oscillations (Varga et al., 2014).

The precise temporal ordering of PV cell sub-types during network oscillations has been proposed to play

a critical role in the spatiotemporal control of PCs. During ripples, PVBCs have been observed to fire just

after the trough of the ripple, followed by PVBSCs and then PVAACs. Less studied is the phase-locking

of PV cells during SWR-nested slow gamma oscillations, which we examined as we observed alterations

in this endpoint for the PC population (Fig. 4H). We found significant gamma phase-locking of PVBCs for

5xFAD mice at 273° (247°-298° 95%), but not for control mice (Fig. 7A.6). PVBSCs were similarly gamma

phase-locked for 5xFAD mice at 292° (249°-336° 95%), but not for control mice (Fig. 7B.6). In contrast,

in PVAACs we observed phase-locking in control mice at 246° (224°-368° 95%), but not for 5xFAD mice

(Fig. 7C.6). While the precise significance of gamma phase-locking has yet to be demonstrated, these

genotype differences point to a temporal disordering of PV cell inhibition.

Within the ripple range, in PVBCs, there was a significant phase-locking in control mice at 228°

(198°-259° 95%), and in 5xFAD mice at 208° (186°-231° 95%), with no significant genotype difference

(Fig. 7A.7). These values are in line with prior *in vivo* studies, where 0° in our study was defined as the

peak of the ripple cycle and 180° as the trough. PVBSCs did not exhibit significant phase-locking in the

ripple range, although the average angles are line with *in vivo* studies (CT: 241°, 5xFAD: 225°) (Fig.

7B.7). PVAACs exhibited ripple phase preference for control mice at 257° (219°-296° 95%), in line with

in vivo studies. However, in 5xFAD mice, PVAACs spiked earlier, at 204° (164°-245° 95%) (Fig. 7C.7).

Although we observed no significant change in PVAAC spike rate, this disruption in temporal ordering

may still have downstream network consequences.

PV basket cells have selective decrease in excitatory synaptic drive and decreased E/I ratio

Following cell-attached recording of spiking activity, the electrode was replaced with a Cesium

internal and the same PV cell was targeted for a whole-cell voltage-clamp recording (Fig. 8A). EPSCs

were recorded at -70 mV (Fig. 8B-D.1). Surprisingly, none of the three PV cell subtypes had any change

in spontaneous excitatory activity between genotype (Fig. 8B-D.2). However, PVBCs from 5xFAD mice

saw a 50.1 ± 10.7% reduction in excitatory charge during SWR events (Fig. 8B.3), whereas there was no

change for PVBSCs (Fig. 8C.3) or PVAACs (Fig. 8D.3). In a subset of cells, we also recorded IPSCs at

0 mV (Fig. 8E.1 for PVBCs, insufficient number of PVBSCs and PVAACs for analysis). Inhibitory input to

PVBCs was unchanged for both spontaneous (Fig. 8E.2) and SWR periods (Fig. 8E.3). This selective

decrease in excitation to PVBCs during SWRs, in contrast to the observation in PCs (Fig. 5F), resulted

in a significant decrease in the synaptic E/I ratio during SWRs, though not during spontaneous periods

(Fig. 8F-H). Since we recorded the cell-attached spiking activity from the same PVBCs, we were next

interested if reduced SWR spike rate (Fig. 7A.1) was correlated with altered synaptic E/I ratio during

SWRs. We observed a moderate positive correlation for control PVBCs, but no correlation between spike

rate and E/I ratio for 5xFAD PVBCs (Fig. 8I), suggesting that not only is excitatory synaptic input during

SWRs reduced, potentially through altered PC-PVBC connectivity, but there are also deficits in PVBC

input-output function, consistent with prior studies of intrinsic PV cell dysfunction (Verret et al., 2012).

Discussion

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Here we identified a preferential impairment in PVBC function in a model of AD, while PVBSCs,

PVAACs, and excitatory PCs were relatively spared. By investigating the synaptic input and spike output

of these cell types, we present a careful description of hippocampal micro-circuitry alterations in early

amyloid pathology during activity critical for memory consolidation (i.e. SWRs). PVBCs displayed a

reduced synaptic E/I ratio during SWRs (Fig. 8G), driven by a reduction in excitatory synaptic input (Fig.

8F). PVBCs spiked less during SWRs (Fig. 7A.1), thus providing reduced inhibitory control to excitatory

PCs. In contrast, PCs displayed an increased synaptic E/I ratio (Fig. 5O), with similar spiking activity

between genotype (Fig. 4C). As the strong inhibition PVBCs provide is critical for the selection of PC

ensembles (Klausberger and Somogyi, 2008; Ellender et al., 2010), this selective reduction may explain

the enlarged PC ensembles (Fig. 3D), aberrant cellular participation (Fig. 3G), and more frequent and

larger amplitude SWRs in 5xFAD mice (Fig. 2C). Intriguingly, the increase in SWRs appears detrimental,

despite their role in memory consolidation, as we also observed spatial memory deficits (Fig. 1D).

Considering the surprising role SWRs play in down-regulating synapses and reducing memory-irrelevant

activity (Norimoto et al., 2018), these aberrant SWRs may be interfering with memory-relevant

reactivations. Several mechanisms likely contribute to the increase in SWRs. The reduction of sIPSCs

that PCs receive between SWRs (Fig. 5H) may permit the buildup of excitation necessary for SWR

initiation. The decreased duration of SWRs (Fig. 2D) may more quickly reset the system for subsequent

events. A more complete description would also require investigation of CA3 and CA2 micro-circuitry.

Hyperactivity and inhibitory disruption in Alzheimer's disease

Our findings are consistent with growing evidence linking hyperactivity and Aβ aggregation (Zott et

al., 2018). Hippocampal hyperactivity is seen in mouse models of early amyloid pathology as increased

seizure risk (Palop et al., 2007) and enlarged ensemble activity (Busche et al., 2012). Our results extend

these findings to the study of SWRs. In addition, several studies have demonstrated that a preferential

disruption to inhibitory cells underlies hyperactivity (Verret et al., 2012; Hazra et al., 2013; Mahar et al.,

2016; Hijazi et al., 2019). In the clinical population, seizures are more prevalent and associated with

earlier onset of cognitive decline in amnestic MCI patients (Vossel et al., 2013). Additionally, task-related

engagement of the hippocampus, as tested via event-related fMRI, indicates hippocampal hyper-activation in MCI patients relative to aged controls, while more progressed AD patients experience hypo-activation (Dickerson et al., 2005; Pariente et al., 2005). These studies suggest our observed phenotype may better model MCI rather than fully progressed AD.

Pyramidal cell diversity

While this study focuses on inhibitory cell diversity, there is growing appreciation for PC diversity in the hippocampus, and a delineation between calbindin-positive (CB+) superficial and CB- deep cells (Valero et al., 2015; Soltesz and Losonczy, 2018). As PVBCs receive more innervation from superficial PCs, and provide more inhibition to deep PCs (Lee et al., 2014), we expect a PVBC spike rate reduction would asymmetrically affect the PC population. Our Thy1-GCaMP6f mice sparsely labeled both superficial and deep PCs, and in more ventral hippocampus we observed CB+ expression in a bilayer as previously observed (Baimbridge and Miller, 1982; Slomianka et al., 2011), complicating segregation based purely on location. A combinatorial approach of Calb^{Cre}-tdTom and pan-glutamatergic GCaMP6f expression would be a promising avenue to distinguish ensemble activity of these two PC subtypes.

Sharp wave ripple alterations in aging and disease

In normal aging, SWR event and ripple frequency decrease (Wiegand et al., 2016; Cowen et al., 2018), contrasting with the phenotype we observed in young adult mice. While it is accepted that AD is distinct from accelerated aging (Toepper, 2017), similar decreases in SWRs have been observed in aged AD models. In an apoE-ε4 knockin model of sporadic AD, SWR event frequency and gamma power are reduced in 12-18 mo mice (Gillespie et al., 2016; Jones et al., 2019). Similarly, in 9-12 mo TgF344-AD rats, SWR event frequency, power, and gamma power are reduced (Stoiljkovic et al., 2018). In younger adults the findings are somewhat mixed. In a small cohort of 3 mo 5xFAD mice, SWR event frequency and gamma power are reduced (Iaccarino et al., 2016). In 2-4 mo rTg4510 mice, SWR event frequency is unchanged while amplitude and ripple power are reduced (Ciupek et al., 2015). Another study has suggested a failure of PC-PV circuits in amyloid pathology is due to regulation of the GluA4 AMPA receptor, resulting in more frequent SWRs with reduced ripple frequency in 3-4 mo APP$_{swe}$/PS1ΔE9 mice (Xiao et al., 2017). Aside from effects on SWR event frequency, propagation of SWRs is also disrupted;

3 mo APP-PS1 mice show impaired propagation from CA3 to CA1 correlated with increased

immunoreactivity for PV (Hollnagel et al., 2019).

One notable difference between our study and many prior ones is the acute slice versus *in vivo*

preparation. Slice electrophysiology permits a careful study of the synaptic inputs to different neuronal

sub-types during SWRs, an infeasible task *in vivo*. The choice of AD model also surely has implications.

While the 5xFAD model has several advantages for this study, its primary disadvantage is APP

overexpression, common to all first-generation transgenic models. Some have noted electrophysiological

alterations are more related to APP overexpression than Aβ aggregation (Born et al., 2014). We

attempted to address this by examining a 1 mo cohort (preceding Aβ aggregation), in which APP

overexpression would still presumably have an effect, a cohort in which we observed no alterations (Fig.

1A,C,2C). There are fewer studies of second-generation APP knockin models which address the problem

of APP overexpression, yet have less pronounced disease phenotypes (Sasaguri et al., 2017). In one

relevant study, sIPSC amplitude from putative PV cells is decreased in parietal cortex PCs from 18-20

mo App^{NL-F} mice, although synaptic E/I balance is unchanged, perhaps through homeostatic mechanisms

(Chen et al., 2018). It will be critical to study hippocampal network alterations in novel AD mouse models

with greater validity as they become increasingly available.

Potential mechanisms for PVBC deficit

Several mechanisms may underlie PVBC dysfunction in amyloid pathology. Intrinsic factors

including downregulation of the voltage-gated Na$_{v1.1}$ channel can explain decreased PV cell excitability

and cortical network hyperactivity (Verret et al., 2012). It remains to be shown if different PV sub-types

are differentially affected, but according to the Allen Brain Institute Cell Types Database, all identified

murine PV clusters express the Scn1a gene encoding Na$_{v1.1}$ (Lein et al., 2007). Another potential

mechanism is loss of peri-neuronal nets (PNNs), part of the extracellular matrix surrounding soma and

proximal dendrites that preferentially ensheathe PV cells (Kwok et al., 2011; Sorg et al., 2016). The

function of PNN is incompletely understood, but both enhances PV cell excitability and activity (Slaker et

al., 2015; Balmer, 2016). In a prior study, we observed degradation of PNN increases SWR event

frequency by ~50% (Sun et al., 2017), a similar magnitude effect as the current study. Additionally, the

selective reduction of excitatory input to PV cells (Fig. 8B.3) is consistent with the decrease in miniature EPSCs in PV cells in a brevican knockout, a major component of PNN (Favuzzi et al., 2017). Moreover, PNN staining is reduced in 3 mo Tg2576 mice (Cattaud et al., 2018). PNNs are more selectively located around PVBCs (>90%) than PVBSCs (25-50%) or PVAACs (<10%) (Yamada and Jinno, 2015), potentially explaining the specificity we observe. However, our experiments would also be consistent with upstream deficits in excitatory input to PV cells. This reduction is unlikely to occur locally, as we observed similar spiking yet enlarged ensembles in the CA1 PC population. In 4 mo Tg2576 mice, there is a preferential degeneration of direct entorhinal input to CA1 PV cells; optogenetic restoration of this input rescues synaptic and spatial learning deficits (Yang et al., 2016). The overall cause of disruption to PV cells is likely from several contributing factors, and further studies are required to identify the most salient impairment, and thus the most promising avenue for intervention.

Implications of PVBC specific deficit

Here, we identified a preferential impairment in PVBC function, concurrent with altered network activity. The selectivity of synaptic alterations in PVBCs suggest they may be a promising target for intervention to restore hippocampal network activity in early amyloid pathology. Given the rapid evolution of tools to manipulate activity in a cell-type specific manner, this finding is of particular importance considering optogenetic (Iaccarino et al., 2016) and chemogenetic (Hijazi et al., 2019) approaches to ameliorate memory decline in AD. A limitation of these strategies is that the PV^{Cre} driver will also target PVBSCs and PVAACs, potentially leading to unintended off-target consequences in temporal sequencing. Novel combinatorial approaches utilizing both Cre and Flp (He et al., 2016) provide a promising avenue to selectively manipulate distinct neuronal sub-types. In conclusion, this study investigated the synaptic input and spiking output of distinct cell-types over the course of SWR events, providing insight into synaptic deficits in early amyloid pathology, and informing future attempts to manipulate the hippocampal micro-circuit.

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Legends

Table 1: *Mouse cohorts used in study*. *Top*, Electrophysiology/imaging cohorts were distinct from behavioral cohorts. For both experiments, mice were studied at an age of 1 and 3 months (mo). *Bottom*, The 3 mo electrophysiology/imaging cohort consisted of three sub-cohorts with different reporter genes.

Figure 1: *Three month (mo) 5xFAD mice have a minor spatial memory impairment*. 1 mo (n_{mice} = 10

Control (CT), 10 5xFAD) and 3 mo (n_{mice} = 15 CT, 12 5xFAD) cohorts were trained on the Barnes Maze,

consisting of four days of training, each with four 180 s trials (***A,B***) and a final 90 s probe trial on the fifth

day (***C,D***). ***A,*** 1 mo control and 5xFAD mice learned the task, as seen through a decreased latency to

find the target escape hole and a significant effect of training day ($F_{(3,54)}$ = 23.89, p = 5.7 × 10^{-10}; 2-way

RM ANOVA, align-rank transformed). Each data point represents the day average of four trials of the

latency to enter the target. No genotype difference was observed ($F_{(1,18)}$ = 0.096, p = 0.760), nor was

there a significant interaction of genotype × training day ($F_{(3,54)}$ = 0.496, p = 0.687). ***B,*** 3 mo control and

5xFAD mice similarly learned the task ($F_{(3,75)}$ = 31.56, p = 2.7 × 10^{-13}; 2-way RM ANOVA, align-rank

transformed), with no significant effect of genotype ($F_{(1,25)}$ = 1.086, p = 0.307), nor interaction of genotype

× training day ($F_{(3,75)}$ = 0.983, p = 0.405). ***C,*** Latency to reach covered target hole on the 5th day probe for

1 mo cohort. No genotype difference was observed ($t_{(18)}$ = 0.212, p = 0.835; unpaired t-test, log

transformed). ***D,*** The latency on the final probe day for 3 mo mice was significantly increased ($t_{(25)}$ =

2.566, p = 0.0167; unpaired t-test, log transformed). ***E***, Representative heat map for 3 mo animals on the

final probe trial. Warmer colors represent longer duration. Control mice spent more time at the target and

surrounding region than 5xFAD mice. For all plots, individual data points represent an animal. Closed

circles represent males, open circles females. Box-whisker plots represent non-normal data as Median

and IQRs. p-values indicated above brackets.

Figure 2: ***Sharp wave ripples are increased in 3 month 5xFAD mice***. ***A***, SWRs were recorded in acute

horizontal slices with the LFP electrode located in CA1. ***B***, Example traces of 3 mo control (*left*) and

5xFAD (*right*) slices. *1st trace*, LFP filtered between 1-1000 Hz, raster below indicates detected SWR

events as overlap of sharp wave (SW) and ripple events. *2nd trace*, SW, filtered between 1-30 Hz, raster

below indicates detected SW events. *3rd trace*, low gamma, filtered between 20-50 Hz. *4th trace*, ripple,

filtered between 120-220 Hz, raster below indicates detected ripple events. *Bottom*, z-scored time-

frequency spectrogram from 1-250 Hz. ***C***, SWR event frequency for 5xFAD and littermate controls for

both 1 mo and 3 mo cohorts. *Left*, No difference was observed in the 1 mo cohort (n_{mice} = 10 CT, 10

5xFAD; $t_{(18)}$ = 0.946, p = 0.357; unpaired t-test). *Right*, there was a significant increase in SWR event

frequency in 3 mo 5xFAD mice (n_{mice} = 27 CT, 29 5xFAD; $t_{(54)}$ = 2.887, p = 0.006; unpaired t-test). ***D***, In

3 mo 5xFAD mice, SWR event amplitude was increased ($t_{(48.9)}$ = 3.592, p = 0.0008; Welch's t-test) and

of shorter duration ($t_{(54)}$ = 3.175, p = 0.0025; unpaired t-test). ***E***, In 3 mo 5xFAD mice the peak ripple

frequency was increased ($t_{(54)}$ = 3.422, p = 0.0012; unpaired t-test), and the number of ripple cycles

reduced ($t_{(54)}$ = 3.480, p = 0.0163; unpaired t-test). ***F***, Example SWR events for traces displayed in ***B***,

with average z-scored time-frequency spectrogram of all events below. ***G***, Average Fast-Fourier

Transform (FFT) of 200 ms window around all SWR events from characteristic subset of n_{slice} = 7 CT, 7

5xFAD from n_{mice} = 4 CT, 5 5xFAD. Shaded region represents SEM. ***H***, In 3 mo 5xFAD mice, low gamma

(20-50 Hz) power was increased (U = 193, p = 0.0009, Mann-Whiney), while ***I***, ripple power (120-220 Hz)

and ***J***, fast ripple (250-500 Hz) were unchanged (U = 358, p = 0.591; U = 379, p = 0.845; Mann-Whitney).

Note that in ***H***, one value was identified as an outlier by the ROUT method but was retained in analysis,

as the data point appeared valid, and even with removal did not alter the observed increase (U = 193, p

= 0.0015; Mann-Whitney). For all plots, individual data points represent the average of all slices recorded

from an animal (n_{slice}/animal in Table 1). Closed circles represent males, open circles females. Bar plots

indicate normal data with Mean ± SEM. Box-whisker plots represent non-normal data with Median and

IQRs. p-values indicated above brackets.

Figure 3: *Altered ensembles of pyramidal cells are recruited in 5xFAD slices*. *A*, *Top*, Confocal imaging of PC ensembles were recorded concurrently with SWRs. *Middle*, Example frame of time series. *Bottom,* Semi-automated algorithm to identify active cells, from which ROIs were drawn to extract ΔF/F. Scale bars = 50 µm. *B*, Example LFP and ΔF/F for identified cells in slices from 3 mo control (*left*) and 5xFAD (*right)* mice*. Top trace,* LFP trace with identified SWR events in raster below. Green SWR events signify there was at least one cell with a concurrent Ca^{2+} transient, gray indicates there were no cells active. *Middle green traces*, individual ΔF/F for each cell. *Bottom raster*, identified Ca^{2+} events above threshold. Dark colored event (blue or black) indicate concurrence with SWR, light gray indicates spontaneous event. *C*, The total number of active cells was increased in 5xFAD slices (n_{slice} = 25 CT, 23 5xFAD; $t_{(31.2)}$ = 3.091, p = 0.0042; Welch's t-test, log transformed), as well as *D*, the number of cells active during SWRs ($t_{(40.1)}$ = 2.063, p = 0.046; Welch's t-test, log-transformed). *E*, Ca^{2+} transient events averaged across cells for each slice, showed no differences between genotype, with no significant difference observed in frequency ($t_{(46)}$ = 0.616, p = 0.541; unpaired t-test), amplitude ($t_{(46)}$ = 0.176, p = 0.861; unpaired t-test), or duration ($t_{(46)}$ = 1.021, p = 0.312; unpaired t-test, log transformed). *F*, *Top*, Event matrix displaying for one example recording, the SWR events on the x-axis, and cells on the y-axis. *Bottom left*, pairwise Jaccard similarity between SWR events (columns in event matrix). Similarity matrix is symmetric and the diagonal = 1 by definition—these have not been plotted for clarity. *Bottom right*, pairwise Jaccard similarity between cells (rows in event matrix). *G*, Cumulative distribution function for all pairwise correlations from all slices between SWRs. SWR-SWR correlations revealed that ensembles were less correlated in 5xFAD slices ($n_{SWR-SWR}$ = 152880 CT, 396292 5xFAD; D = 0.179, p < 10^{-15}; Kolmogorov-Smirnov). Note that curves do not start at origin, as a substantial proportion of SWR-SWR pairs have no cells in common (22.7% CT, 40.6% 5xFAD). *H*, Cell-cell correlations were also reduced for 5xFAD slices ($n_{cell-cell}$ = 5560 CT, 7170 5xFAD; D = 0.133, p < 10^{-15}; Kolmogorov-Smirnov). Individual data points represent a slice. Closed circles represent slices from males, open circles females. Bar plots indicate normal data with Mean ± SEM. Box-whisker plots represent non-normal data with Median and IQRs. p-values indicated above brackets.

Figure 4: *Pyramidal cell spiking is relatively unchanged in 5xFAD mice. A*, Diagram of a loose cell-

attached recording of spikes from a GCaMP+ PC paired with LFP recording of SWRs. *B*, Example traces

from 3 mo control (*left*) and 5xFAD (*right*) slice. *Top trace*, LFP with SWR events in raster below. Gray

shaded events indicate spontaneous SWR. Green shading indicates SWR coincident with at least one

spike. Dark green shading indicates SWR coincident with burst, defined as 3 or more spikes each within

60 ms. *Bottom trace*, Cell-attached recording from PC. Detected spikes and bursts indicated in raster

below. Dark shading indicates they are coincident with SWR event, light gray shading indicates

spontaneous events. *C*, Spike rate during spontaneous and SWR periods. No effect of genotype was

observed (n_{cell} = 41 CT, 55 5xFAD; $F_{(1,94)}$ = 0.542, p = 0.464; 2-way RM ANOVA, align-rank transformed—

zero-values preclude log-transform). No differences were observed during spontaneous (p = 0.982;

Mann-Whitney *post hoc*, Šidák correction) or SWR periods (p = 0.547; Mann-Whitney *post hoc*, Šidák

correction). PC spike rate significantly increased during SWRs, with a significant effect of

spontaneous/SWR time period ($F_{(1,94)}$ = 27.17, p = 1.1 × 10^{-6}; 2-way RM ANOVA), both in control (p =

0.0079; Wilcoxon *post hoc*, Šidák correction) and 5xFAD mice (p = 0.00001, Wilcoxon *post hoc*, Šidák

correction). There was no significant interaction of genotype × period ($F_{(1,94)}$ = 1.393, p = 0.241). *D*, Peri-

SWR spike probability. Dark lines indicate average of all cells within a genotype, shaded regions indicate

SEM. There was no effect of genotype ($F_{(1,9500)}$ = 0.722, p = 0.396; 2-way ANOVA), nor interaction of

genotype × bin ($F_{(99,9500)}$ = 0.869, p = 0.819; 2-way ANOVA). *E*, The burst rate did not differ between

genotype (U = 998, p = 0.276; Mann-Whitney), while the intra-burst interval was decreased (U = 793, p

= 0.028; Mann-Whitney). *F*, *left*, The fraction of spikes that occurred during SWRs was unchanged (U =

999, p = 0.3438; Mann-Whitney), as well as *right*, the fraction of SWRs that had one or more spikes (U =

1019, p = 0.4244; Mann-Whitney). *G*, Example of SWR (*top trace*), with filtered slow gamma (20-50 Hz)

and ripple (120-220 Hz) signals (*middle traces*). The phase of oscillations was set at 0° at peaks and

180° at troughs. *Bottom trace*, cell-attached recording, with spike times marked by vertical dashed lines.

H, Polar phase plots of phase-locking of spikes to SWR-nested slow gamma. The angles of individual

data points represent the average phase of all spikes for a cell. Length from origin (0-1) indicates the

degree of phase-locking. A length of 1 signifies perfect phase-locking (every spike at same phase); a

length of 0 indicates random or no phase-locking. Spikes were phase-locked in the gamma range in CT

mice (Z = 8.28, p = 0.0001; Raleigh's test), though not for 5xFAD mice (Z = 2.60, p = 0.074; Raleigh's

test). The median phase angles differed between genotype (P = 6.82, p = 0.009; Circular median test). *I*,

No phase-locking was observed in the ripple range for either genotype (CT: Z = 1.23, p = 0.296; 5xFAD:

Z = 1.42, p = 0.244; Raleigh's test), nor did the median phase angle differ (P = 1.05, p = 0.306; Circular

median test). Individual data points represent a cell. Closed circles represent cells from males, open

circles females. Violin plots represent non-normal data as Median and IQRs. p-values indicated above

brackets.

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Figure 5: *Pyramidal cells receive increased synaptic E/I ratio*. **A**, Example traces of LFP + whole-cell recording voltage-clamped at -70 mV. Excitatory post-synaptic potentials (EPSCs) were sorted as spontaneous (sEPSCs) or SWR-coincident (swrEPSCs). **B**, Example traces of LFP + whole-cell recording voltage-clamped at 0 mV to detect sIPSCs and swrIPSCs. **C**, Diagram of LFP + whole-cell PC recording in 5xFAD/+;Thy1-GCaMP6f and Thy1-GCaMP6f littermate controls. **D**, The frequency, amplitude, and normalized charge (integrated current per unit time) of sEPSCs did not differ between genotype (n_{cell} = 19 CT, 14 5xFAD; Frequency: $t_{(31)}$ = 0.706, p = 0.486; Amplitude: $t_{(31)}$ = 1.286, p = 0.208; Charge: $t_{(31)}$ = 0.961, p = 0.343; unpaired t-tests). **E**, Example of swrEPSCs. Both LFP and intracellular traces were filtered in the gamma (20-50 Hz) and ripple (120-220 Hz) ranges to cross-correlate. **F**, The total excitatory charge during SWRs (swrEPSQ) was increased in 5xFAD mice ($t_{(31)}$ = 2.849, p = 0.0077; unpaired t-test). **G**, Cross-correlation of gamma (*left*) and ripple (*right*) between LFP and swrEPSCs. For both genotypes, the gamma and ripple band of swrEPSCs were significantly anti-correlated with the LFP (Gamma CT: $t_{(18)}$ = 7.393, p = 7.4×10^{-7}; Gamma 5xFAD: $t_{(13)}$ = 7.225, p = 6.7×10^{-6}; Ripple CT: $t_{(18)}$ = 5.249, p = 5.4×10^{-5}; Ripple 5xFAD: $t_{(13)}$ = 5.504, p = 0.0001; 1-sample t-tests). In addition, the strength of anti-correlation was increased in 5xFAD mice for both gamma ($t_{(31)}$ = 2.363, p = 0.025; unpaired t-test) and ripple ($t_{(31)}$ = 2.064, p = 0.047, unpaired t-test). **H-K** same as **D-G** for IPSCs. **H**, In 5xFAD mice, sIPSC frequency was decreased (n_{cell} = 21 CT, 16 5xFAD; $t_{(35)}$ = 2.276, p = 0.0291; unpaired t-test), the amplitude was unchanged ($t_{(35)}$ = 1.514, p = 0.139, unpaired t-test), and the normalized charge decreased ($t_{(35)}$ = 2.515, p = 0.0166; unpaired t-test). **I**, Example of swrIPSCs. **J**, Inhibitory charge during SWRs (swrIPSQ) did not differ between genotype ($t_{(35)}$ = 1.328, p = 0.1928, unpaired t-test). **K**, The cross-correlations of LFP and swrIPSCs in the gamma and ripple bands were significantly correlated for both genotypes (Gamma CT: $t_{(20)}$ = 9.221, p = 1.2×10^{-8}; Gamma 5xFAD: $t_{(15)}$ = 13.36, p = 9.8×10^{-10}; Ripple CT: $t_{(20)}$ = 6.823, p = 1.2×10^{-6}; Ripple 5xFAD: $t_{(15)}$ = 6.777, p = 6.2×10^{-6}; 1-sample t-tests). Unlike for swrEPSCs, the strength of correlation was no different between genotype (Gamma: $t_{(35)}$ = 1.125, p = 0.268; Ripple: $t_{(35)}$ = 1.938, p = 0.0607; unpaired t-tests). **L**, Spontaneous synaptic E/I ratio of normalized charge for each cell (sEPSQ/sIPSQ). Spontaneous E/I ratio was significantly increased, driven by a decrease in inhibition (n_{cell} = 17 CT, 14 5xFAD; $t_{(29)}$ = 2.972, p = 0.0059; unpaired t-test). **M**, Synaptic E/I

ratio for 100 ms window centered around SWR peak (swrEPSQ/swrIPSQ). As with spontaneous charge,

the SWR E/I ratio was significantly increased ($t_{(29)}$ = 2.086, p = 0.0459; unpaired t-test), however it was

driven by an increase in excitation rather than a decrease in inhibition. *N*, For both EPSCs and IPSCs

during SWRs, the charge for each cell (EPSQ and IPSQ) was calculated in 2 ms bins by integrating the

current in a 100 ms window centered around that bin. The dark lines represent the average charge across

all cells, while the shaded region represents the SEM. *F* and *J* thus represent these curves at the y-

intercept. For excitatory charge, there was a significant effect of genotype ($F_{(1,3100)}$ = 488.4, p < 10^{-15}; 2-

way ANOVA), as well as an interaction of genotype × bin ($F_{(99,3100)}$ = 2.820, p < 10^{-15}). Asterisks indicate

regions that survived Šidák's multiple comparisons * < 0.05, ** < 0.01. There was also a significant effect

of genotype for inhibitory charge ($F_{(1,3500)}$ = 126.8, p < 10^{-15}; 2-way ANOVA), however no bins survived

multiple comparisons. *O*, the ratio of curves in *N* yields the synaptic E/I ratio during SWRs. There was a

significant effect of genotype ($F_{(1,3100)}$ = 146.4, p < 10^{-15}; 2-way ANOVA). *** < 0.001 indicates region that

survived multiple comparisons. *M* represents these curves at the y-intercept. For all plots, individual data

points represent a cell. Closed circles represent cells from males, open circles females. Bar plots

represent normal data with Mean ± SEM. p-values indicated above brackets.

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Figure 6: *PV cells in CA1 delineate into basket (PVBCs), bistratified (PVBSCs), and axo-axonic*

(PVAACs) cells. A, Diagram of LFP + PV cell recording in 3 mo 5xFAD/+; PV^{Cre}/+;tdTom/+ and

PV^{Cre}/+;tdTom/+ littermate controls. *B*, Diagram of PV cell subtypes and their axonal targets in CA1 *str.*

pyr. Examples of *C.1*, PVBCs, *C.2*, PVBSCs, and *C.3*, PVAACs. Green fluorescence indicates avidin-

fluorescein bound to the biocyin in the filled PV cell. Red fluorescence indicates PV^{Cre}/+;tdTom/+

expression. Dashed grey lines approximately distinguish layers of hippocampus, *str. l.m. = stratum*

lacunosum-moleculare, *str. rad. = stratum radiatum*, *str. pyr. = stratum pyramidale, str. or. = stratum*

oriens. Notice that *str. pyr.* is dimly red due to the expression of other non-filled PVBCs targeting

perisomatic regions of PCs. Scale bars = 100 µm. *Bottom traces*, Examples of LFP and cell-attached

recording of spikes, which was used to aid in distinguishing PVBCs and PVAACs. PVAACs are unique

in that they reduce their firing during SWRs. *C.4*, Ankyrin G immunostaining showing co-localization of

synaptic boutons with AIS of PCs for identified PVAAC. Scale bar = 10 µm. *D*, Proportions of sorted cells

in each genotype. There was no significant difference in proportions between genotype ($\chi^2_{(2)}$ = 1.09, p =

0.580; χ^2 Test), nor was there a significant deviation from expected proportions of 60% PVBC, 25%

PVBSC, and 15% PVAAC ($\chi^2_{(2)}$ = 0.754, p = 0.686; χ^2 Test).

Figure 7: *PV basket cells have selectively reduced spiking*. Spiking data for **A**, PVBCs, **B**, PVBSCs,

and **B**, PVAACs. **A.1**, Spike rate of PVBCs during spontaneous and SWR periods, with an effect of

genotype (n_{cell} = 13 CT, 16 5xFAD; $F_{(1,27)}$ = 10.42, p = 0.0033; 2-way RM ANOVA, align-rank transformed),

no difference in spontaneous spike rate, but a decreased SWR spike rate in 5xFAD mice (Spont: p =

0.209, SWR: p = 0.044; Mann-Whitney *post hoc*, Šidák correction). PVBC spike rate increased during

SWR periods, with an effect of period ($F_{(1,27)}$ = 179.4, p = 1.9×10^{-13}), and increases in both control and

5xFAD mice (CT: p = 0.00049, 5xFAD: p = 0.00012; Wilcoxon *post hoc*, Šidák correction). Additionally,

there was an interaction of genotype × period ($F_{(1,27)}$ = 16.76, p = 0.00034), indicating that PVBC

modulation of spiking during SWRs differed between genotype. **A.2**, PVBC peri-SWR spike probability,

with an effect of genotype ($F_{(1,2700)}$ = 267.3, p < 10^{-15}; 2-way ANOVA), and interaction of genotype × bin

($F_{(99,2700)}$ = 1.446, p = 0.0030). Asterisks indicate regions surviving Šidák's multiple comparisons

correction. * < 0.05, ** < 0.01, *** < 0.001. **A.3**, PVBC burst rate had tendency for decrease (U = 60, p =

0.056, Mann-Whitney). **A.4**, *left*, The fraction of SWRs with one or more PVBC spike did not differ (U =

72, p = 0.170, Mann-Whitney), but *right,* the fraction of SWRs with a PVBC burst was reduced (U = 53,

p = 0.025, Mann-Whitney). **A.5**, Example of LFP and PVBC cell-attached traces for CT (*left*) and 5xFAD

(*right*). Spike and SWR events are color-coded as in Fig. 4B. **A.6**, PVBC spikes were phase-locked in

the gamma range in 5xFAD mice (Z = 7.944, p = 0.00012; Raleigh's test), though not for controls (Z =

2.477, p = 0.082; Raleigh's test), and with no difference in median phase angle (P = 0.144, p = 0.705;

Circular median test). **A.7**, PVBCs were phase-locked in the ripple range for both genotypes (CT: Z =

6.006, p = 0.0014; 5xFAD: Z = 9.35, p = 1.7×10^{-5}; Raleigh's tests), with no difference in mean phase

angle ($F_{(1,27)}$ = 1.335, p = 0.258; Watson-Williams). **B.1**, Spike rates for PVBSCs during spontaneous and

SWR periods, with no effect of genotype (n_{cell} = 5 CT, 10 5xFAD; $F_{(1,13)}$ = 1.345, p = 0.267; 2-way RM

ANOVA, align-rank transformed), and no genotype differences for either period (Spont: p = 0.980, SWR:

p = 0.763; Mann-Whitney *post hoc*, Šidák correction). PVBSCs increased their spike rate during SWRs,

with an effect of period ($F_{(1,13)}$ = 30.6, p = 9.7×10^{-5}), and increases in 5xFAD but not control mice (CT: p

= 0.121, 5xFAD: p = 0.019; Wilcoxon *post hoc*, Šidák correction). There was no interaction of genotype

× period ($F_{(1,13)}$ = 2.563, p = 0.133). **B.2**, PVBSC peri-SWR spike probability, with an effect of genotype

$(F_{(1,1300)} = 33.9$, $p = 7.3 \times 10^{-9}$; 2-way ANOVA), no interaction of genotype × bin $(F_{(1,1300)} = 33.9$, $p = 7.3 \times$

10^{-9}), and no bins surviving multiple comparisons. **B.3**, Burst rate for PVBSCs was unchanged (U = 22.5,

p = 0.793, Mann-Whitney). **B.4**, In PVBSCs the fraction of SWRs with at least one spike and with a burst

were both unchanged (U = 21, p = 0.655; U = 16.5, p = 0.323; Mann-Whitney). **B.5**, Example LFP and

PVBSC cell-attached traces for control (*left*) and 5xFAD (*right*). **B.6**, PVBSC spikes were phase-locked

in the gamma range in 5xFAD mice (Z = 3.543, p = 0.024; Raleigh's test), though not for controls (Z =

1.566, p = 0.216; Raleigh's test), and with no difference in median phase angle (P = 0.311, p = 0.577;

Circular median test). **B.7**, PVBSCs were not phase-locked in the ripple range (CT: Z = 1.631, p = 0.202;

5xFAD: Z = 1.334, p = 0.270; Raleigh's tests). **C.1**, Spike rates for PVAACs during spontaneous and

SWR periods, with no effect of genotype (n_{cell} = 6 CT, 6 5xFAD; $F_{(1,10)}$ = 3.832, p = 0.079; 2-way RM

ANOVA, align-rank transformed), and no genotype differences for either period (Spont: p = 0.909, SWR:

p = 0.178; Mann-Whitney *post hoc*, Šidák correction). While PVAACs did see an effect of period ($F_{(1,10)}$ =

16.67, p = 0.0022), neither in control nor 5xFAD mice was the increase significant (CT: p = 0.527, 5xFAD:

p = 0.062; Wilcoxon *post hoc*, Šidák correction), nor was there an interaction of genotype × period ($F_{(1,10)}$

= 3.208, p = 0.104). **C.2**, PVAAC peri-SWR spike probability, with an effect of genotype ($F_{(1,1000)}$ = 30.15,

$p = 5.1 \times 10^{-8}$; 2-way ANOVA), no interaction of genotype × bin ($F_{(99,1000)}$ = 0.339, p > 0.999), and no bins

surviving multiple comparisons. **C.3**, Burst rate for PVAACs was unchanged (U = 24, p > 0.999, Mann-

Whitney). **C.4**, In PVAACs, the fraction of SWRs with at least one spike and with a burst were both

unchanged (U = 6, p = 0.065; U = 10.5, p = 0.182; Mann-Whitney). **C.5**, Example LFP and PVAAC cell-

attached traces for CT (*left*) and 5xFAD (*right*). **C.6**, PVAAC spikes were phase-locked in the gamma

range in CT mice (Z = 4.427, p = 0.005; Raleigh's test), though not for 5xFAD mice (Z = 0.913, p = 0.421;

Raleigh's test), and with a tendency for a difference in median phase angle (P = 3.600, p = 0.058; Circular

median test). **C.7**, PVAACs were phase-locked in the ripple range for both genotype (CT: Z = 3.749, p =

0.0015; 5xFAD: Z = 3.542, p = 0.0020; Raleigh's tests), with a difference in mean phase angle ($F_{(1,9)}$ =

5.677, p = 0.044; Watson-Williams). For all plots, individual data points represent a cell. Closed circles

represent cells from males, open circles females. Box-whisker plots represent non-normal data with

Median and IQRs. p-values indicated above brackets.

Figure 8: *PV basket cells have selective decrease in excitatory synaptic input and decreased E/I ratio*. **A**, Diagram of LFP + whole-cell PV cell recording in 3 mo 5xFAD/+; PV[Cre]/+;tdTom/+ and PV[Cre]/+;tdTom/+ littermate controls. **B-D**, Example recordings of excitatory synaptic input during spontaneous and SWR periods in **B.1**, PVBCs, **C.1**, PCBSCs, and **C.1**, PVAACs, voltage-clamped at -70 mV. **E.1**, Inhibitory synaptic currents voltage-clamped at 0 mV in a subset of PVBCs. **B.2**, sEPSCs were unchanged in PVBCs (n_{cell} = 12 CT, 16 5xFAD; Frequency: $t_{(26)}$ = 1.298, p = 0.2056; Amplitude: $t_{(26)}$ = 0.5448, p = 0.5906; unpaired t-tests). **B.3**, In PVBCs, the excitatory charge in a 100 ms window centered around the SWR peak (swrEPSQ) was significantly reduced ($t_{(26)}$ = 3.196, p = 0.0036, unpaired t-test). **C.2-3**, In PVBSCs, sEPSCs and swrEPSQ were unchanged (n_{cell} = 4 CT, 6 5xFAD; Frequency: $t_{(8)}$ = 0.9898, p = 0.3513; Amplitude: $t_{(8)}$ = 0.0576, p = 0.9555; swrEPSQ: $t_{(8)}$ = 0.9968, p = 0.3480; unpaired t-tests). **D.2-3**, In PVAACs, sEPSCs and swrEPSQ were unchanged (n_{cell} = 5 CT, 6 5xFAD; Frequency: $t_{(9)}$ = 0.1289, p = 0.9003; Amplitude: $t_{(9)}$ = 2.112, p = 0.0639; swrEPSQ: $t_{(9)}$ = 1.625, p = 0.1385; unpaired t-tests). **E.2-3**, In PVBCs at 0 mV, sIPSCs are swrIPSQ were unchanged (n_{cell} = 8 CT, 8 5xFAD; Frequency: $t_{(14)}$ = 0.4477, p = 0.6612; Amplitude: $t_{(14)}$ = 3390, p = 0.7396; swrIPSQ: $t_{(14)}$ = 0.00832, p = 0.9935; unpaired t-tests). **F**, The running charge (EPSQ and IPSQ) in a 100 ms window for PVBCs. Dark lines represent the average charge across all cells, shaded region represents the SEM, y-axis represents SWR peak. For EPSQ, there was a significant effect of genotype ($F_{(1,2500)}$ = 664.2, p < 10^{-15}; 2-way ANOVA), as well as an interaction of genotype × bin ($F_{(99,2500)}$ = 2.211, p = 1.9 × 10^{-10}). Asterisks indicate regions that survived Šidák's multiple comparisons * < 0.05, ** < 0.01, *** < 0.01. There was no effect of genotype for IPSQ ($F_{(1,1400)}$ = 2.123, p = 0.1453, 2-way ANOVA). **G**, the ratio of curves in **F** gives the synaptic E/I ratio during SWRs, with a significant effect of genotype ($F_{(1,1300)}$ = 338.7, p < 10^{-15}, 2-way ANOVA). ** < 0.01 indicates region that survived multiple comparisons. **H**, There was no change in spontaneous E/I ratio (ratio of normalized charge (integrated current / unit time)) for PVBCs ($t_{(14)}$ = 0.929, p = 0.368, unpaired t-test). However, the SWR E/I ratio was significantly decreased ($t_{(14)}$ = 2.701, p = 0.017, unpaired t-test). **I**, Linear regression of spike rate during SWRs vs the E/I ratio. For PVBCs from CT mice, there was a non-zero slope, indicating a positive correlation (n_{cell} = 8, R^2 = 0.6245, $F_{(1,6)}$ = 9.977, p = 0.020, Linear Regression), however there was no correlation for cells from 5xFAD mice (n_{cell} = 8, R^2

1226 $= 0.0092$, $F_{(1,6)} = 0.0555$, $p = 0.822$). For all plots, individual data points represent a cell. Closed circles

1227   represent cells from males, open circles females. Bar plots represent normal data with Mean ± SEM. p-

1228   values indicated above brackets.

	Electrophysiology + Imaging (Fig. 2-8)				Behavior (Fig. 1)			
	Control 1mo	*5xFAD 1mo*	**Control 3mo**	**5xFAD 3mo**	*Control 1mo*	*5xFAD 1mo*	*Control 3mo*	*5xFAD 3mo*
n_{mice}	10 (6f)	10 (4f)	27 (17f)	29 (12f)	10 (2f)	10 (6f)	15 (7f)	12 (8f)
Age (postnatal days)	40.2 ± 4.4 (34-46)	40.4 ± 4.6 (34-46)	95.8 ± 6.0 (83-105)	94.5 ± 5.8 (85-105)	42.0 ± 5.2 (36-47)	43.8 ± 4.2 (36-47)	91.8 ± 5.2 (87-99)	92.5 ± 5.4 (87-99)
n_{slice} *(range 2 - 8)*	5.6 ± 0.8	4.0 ± 1.8	3.9 ± 1.3	3.2 ± 1.4				
% slices with SWRs	93.8 ± 8.1%	70.8 ± 22.0%	72.4 ± 19.8%	66.3 ± 26.1%				

	Thy1-GCaMP6f (Fig. 3-5)		PV^{Cre}/+;tdTom/+ (Fig. 6-8)		Thy1-GCaMP6f;PV^{Cre}/+;tdTom/+ (Fig. 4-8)	
	Control	*5xFAD*	*Control*	*5xFAD*	*Control*	*5xFAD*
n_{mice}	10 (5f)	11 (5f)	13 (8f)	11 (5f)	4 (4f)	7 (2f)
Age (postnatal days)	95.0 ± 7.4 (83-105)	93.4 ± 3.2 (85-102)	96.8 ± 5.7 (88-104)	97.4 ± 6.0 (88-105)	94.3 ± 2.9 (90-97)	91.6 ± 2.1 (90-95)
n_{slice} *(range 2 - 8)*	3.9 ± 1.1	2.8 ± 1.3	3.8 ± 1.5	4.9 ± 2.1	4.5 ± 1.3	3.6 ± 1.8
% slices with SWRs	75.5 ± 20.2%	67.9 ± 26.2%	67.4 ± 20.5%	68.2 ± 25.3%	80.8 ± 16.4%	60.7 ± 30.5%
$n_{cell-attached}$	41 (PC)	46 (PC)	54 (PV)	37 (PV)	19 (PV)	9 (PC); 19 (PV)
$n_{whole-cell}$	19 (PC)	13 (PC)	11 (PV)	16 (PV)	10 (PV)	1 (PC); 13 (PV)

A

str. oriens LFP CA1 str. pyr. str. radiatum

B

PV BSC — PC — PV BC — PV AAC

C.1 PV^Cre-tdTom Biocytin

LFP | 50µV |100ms
PVBC (cell-attached) | |50pA

C.2 str. l.m. str. rad. str. pyr. str. or.

LFP | 50µV |100ms
PVBSC | 50pA

C.3

LFP | 50µV |100ms
PVAAC | 50pA

C.4 Biocytin Ankyrin G

D

Control
PVAAC n = 6
PVBSC n = 5
PVBC n = 15

5xFAD
PVAAC n = 6
PVBSC n = 10
PVBC n = 16