The brain-specific double-stranded RNA-binding protein Staufen2 is required for dendritic spine morphogenesis

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Introduction

Local translation of certain mRNAs at synapses in response to activation critically contributes to asymmetric cell polarity and synaptic plasticity (Kiebler and DesGroseillers, 2000; Steward and Schuman, 2001; St Johnston, 2005). The double-stranded RNA-binding protein Staufen has been implicated both in dendritic RNA transport and translational regulation (Tang et al., 2004; Kim et al., 2005). In Drosophila, Staufen (Stau) is required for both bicoid and oskar mRNA localization in the oocyte (St Johnston, 2005) and for the localization of prospero mRNA in embryonic neuroblasts (Li et al., 1997; Broadus et al., 1998). In Xenopus, two Staufen isoforms (XStau1 and XStau2) are present in the oocytes and move to the vegetal cytoplasm, where both VegT and Veg1 mRNAs become localized (Allison et al., 2004; Yoon and Mowry, 2004). In mammals, Stau1 and 2 proteins are implicated in the microtubule-dependent transport of RNAs to dendrites of polarized neurons (Kiebler et al., 1999; Tang et al., 2001). Both Stau proteins are present in ribonucleoprotein particles (RNPs) in the cell body and dendrites (Kiebler et al., 1999; Duchaine et al., 2002; Kanai et al., 2004; Thomas et al., 2005). Due to alternative splicing, four Stau2 isoforms are expressed in rat brain with molecular weights ranging from 52 to 62 kD (Duchaine et al., 2002; Monshausen et al., 2004). A first indication that Staufen proteins may actually contact their cargo RNAs already inside the nucleus came from recent work demonstrating that two isoforms of Stau2, Stau262 and Stau259, are imported into the nucleus and then become exported via exportin-5 (Brownawell and Macara, 2002; Macchi et al., 2004; Kiebler et al., 2005) and exportin-1 (CRM1; Miki and Yoneda, 2004), respectively. The function of the brain-specific Stau2 in the central nervous system is, however, still elusive. Therefore, we investigated the function of Stau2 by RNA interference (RNAi) in polarized hippocampal neurons.

Results

To determine at which stage of neuronal development Stau2 is expressed, we performed semi-quantitative RT-PCR on RNA extracted from cultured hippocampal neurons at different days in vitro (DIV) (see Fig. S1 A, available at http://www.jcb.org/cgi/content/full/jcb.200509035/DC1). Stau2 mRNA could be

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Abbreviations used in this paper: DIV, days in vitro; FMRP, Fragile X mental retardation protein; mEPSC, miniature excitatory postsynaptic current; RNAi, RNA interference; shRNA, short hairpin RNA; siRNA, small interfering RNA; TLS, translocated in liposarcoma.

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detected at all stages examined, indicating that Stau2 is expressed throughout neuronal development. We then performed loss-of-function analyses using RNAi in polarized hippocampal neurons to investigate the function of Stau2. Two 19mer oligonucleotides directed against different regions of the Stau2 cDNA were cloned into the pSUPER vector (Brummelkamp et al., 2002). Their expression yields short hairpin RNAs (shRNAs) that are subsequently converted into small interfering RNAs (siRNAs). Cotransfection of HeLa cells with either of the two plasmids, si2-1 (unpublished data) or si2-2 (Fig. S1 B), together with Staun2-EYFP significantly down-regulated Staun2-EYFP expression as assessed by fluorescence microscopy. In contrast, neither of these plasmids affected the level of the paralogous protein, Staun1-EYFP (Fig. S1 B). Furthermore, a control Staun2 siRNA with 5 bp substitutions (mismatch siRNA) did not affect the level of Staun2-EYFP expression (unpublished data).

We then determined the level and the specificity of Staun2 down-regulation in neurons by Western blot analyses. Primary hippocampal neurons were transfected by nucleoporation (Hamm et al., 2002) before plating with plasmids yielding shRNAs against Staun2 (si2-2) and an unrelated protein, CDC10 (siCDC10, negative control). As additional controls, neurons were either mock treated (citrine) or transfected with pSUPER vector expressing the mismatch sequence of si2-2 (mis) (Fig. 1 A). Neurons were allowed to develop for 3 d and processed for Western blot analysis. Only siRNAs directed against Staun2 significantly down-regulated the expression of three Staun2 isoforms (62, 59, and 52 kD), whereas all other control plasmids did not (Fig. 1 A). The same results were obtained by using short interfering oligos (Dharmacon) (Fig. S1 C). Importantly, we did not observe any compensatory change in Staun1 expression levels upon Staun2 down-regulation (Fig. 1 A, bottom). To verify down-regulation of Staun2 in mature cells, 15 DIV neurons were cotransfected with plasmids encoding cyan fluorescent protein (ECPF) and si2-2 RNA, and immunostaining was performed for Staun2 3 d after transfection. Both Staun2 shRNAs, si2-2 and si2-1, reduced or completely abolished Staun2 expression in neurons (Fig. 1 B, and unpublished data). Staun2 signal in dendrites was strongly reduced in Staun2 down-regulated neurons compared with untransfected cells (Fig. 1 B, enlarged insets). Neither mismatch shRNA against Staun2 (Fig. 1 B) nor shRNA against red fluorescent protein (RFP) (unpublished data) affected Staun2 expression. Moreover, the expression level of Staun1 remained unchanged (Fig. 1 B, middle), suggesting that this RNAi approach targeting Staun2 was specific.

**Stau2 down-regulation in mature neurons decreases the number of dendritic spines**

We first assessed the subcellular localization of Staun2 in dendrites of mature hippocampal neurons (Fig. 2) and asked whether Staun2 is present near synapses. Immunostaining using affinity-purified anti-Stau2 antibodies and mAbs specific for the postsynaptic marker protein PSD95 revealed that discrete Staun2 particles were distributed along the dendritic shaft beneath PSD95-positive puncta. The distribution of such Staun2 RNPs was not homogenous, but in close proximity to dendritic spines (Fig. 2). This was a first indication that Staun2 might actually play a role in synapse formation or maintenance of dendritic spines.

This prompted us to analyze whether down-regulation of Staun2 expression by RNAi in 15 DIV neurons alters dendritic spine morphology. Neurons expressing EYFP showed normal mushroom-like dendritic spines (Fig. 3 A, EYFP, see arrowheads). In contrast, expression of both si2-1 and si2-2 shRNAs resulted in an altered phenotype: the number of protrusions was significantly reduced, whereas extended filopodia appeared (Fig. 3 A, see arrows and inset). Both structures can be discriminated based on their morphology because dendritic protrusions and filopodia share some structural and biological properties similar to synapses.
spines are usually less than 2 μm, filopodia in contrast are usually longer (Hering and Sheng, 2001).

Although RNAi is thought to display a high degree of specificity and to act on selective targets, it may activate the Jak–Stat pathway, yielding retrograde dendritic retraction and inhibiting synapse formation in neurons (Kim et al., 2002; Sledz et al., 2003). We, therefore, devised control experiments to determine whether the observed phenotype was specific for Stau2. First, expression of an unrelated shRNA directed against RFP did not affect the morphology of dendritic spines (Fig. 3 A, siRFP). Second, a Stau2 shRNA that contains mismatches does not alter the morphology of dendritic spines (unpublished data and Fig. 3 B). Third, we expressed a truncated form of Stau2 (dn2) missing its COOH terminus, which has been shown to accumulate in the cell body, thereby acting as a dominant-negative protein (Tang et al., 2001). Interestingly, this frequently caused a change in morphology of dendritic spines displaying an extended neck (Fig. 3 A, see asterisk). Overexpression of dn2, therefore, yields an intermediate phenotype compared with wild-type and si-2–treated neurons (see Fig. 3 B). It is important to note that overexpression of full-length Stau2 does not yield the same phenotype (see also Fig. 6). Collectively, these controls demonstrate that our RNAi approach against Stau2 is indeed specific.

To quantify the observed effects, the length of protrusions was measured and the percentage of protrusions longer than 2 μm was determined. We observed a 10-fold increase in the percentage of extended protrusions in Stau2 down-regulated neurons, compared with siRFP or EYFP-transfected neurons (Fig. S1 D). Fig. 3 B shows a cumulative frequency plot of the measured protrusion lengths underlining the increase in long protrusions upon Stau2 down-regulation or overexpression of dn2. In total, Stau2 down-regulation causes a 49.4% loss of protrusions compared with mismatch shRNA (Fig. 3 B, inset). Collectively, down-regulation of Stau2 critically alters the morphology of protrusions from dendritic spines toward extended filopodia as well as their total number.

### Stau2 down-regulation in mature neurons decreases the number of synapses

A criterion for mature excitatory synapses is the presence of postsynaptic densities (PSDs) that cluster neurotransmitter receptors, in close contact with presynaptic nerve terminals.
We first determined whether Stau2 down-regulation affected the number of endogenous PSD95. Hippocampal neurons were stained with an anti-PSD95 antibody upon expression of either mismatched (control) or si2-2 vectors were immunostained for the postsynaptic marker PSD95. A reduction of 68% was observed in Stau2 down-regulated neurons compared with mismatch. In total, 25 and 29 dendrites were analyzed for si-2 and mismatch treated neurons, respectively, and a total of 690 and 2,226 PSD95 puncta were counted. As expected, we observed a significant reduction of 26% (***, P < 0.0001) in synapsinI puncta was observed in Stau2 down-regulated neurons compared with mismatch. In total, 36 and 39 dendrites of 6 neurons were analyzed for si-2 and mismatch treated neurons, respectively, and a total of 273 and 464 synapsinI puncta were counted. (C) Most GFP-PSD95 clusters adjoin synapsinI. 15 DIV neurons were transfected with GFP-PSD95, fixed and immunostained for synapsinI 3 d later. Insets show enlargements of a dendritic segment where most postsynaptic dendritic spines (green) receive presynaptic input (red). Arrowheads indicate adjacent GFP-PSD95 and synapsinI puncta. Bars, 10 μm.

We next asked the question of whether the presynaptic input was also affected by the Stau2 shRNA approach. Neurons were stained with a polyclonal anti-synapsinI antibody upon expression of either mismatch (control) or si2-2 pSUPERIOR plasmid, and synapsinI-positive puncta adjacent to dendrites of transfected cells were counted and compared with untransfected cells (Fig. 4 B). As expected, we observed a significant reduction of 48% ± 14.8% (***, P < 0.0001). Overexpression of ds2 had a similar effect (39% ± 0.8% reduction; ***, P < 0.0001). For 15 DIV neurons, 95 cells were analyzed and 9,203 dendritic spines were counted; for 8 DIV neurons, 53 cells were analyzed and 4,683 dendritic spines were counted. The graph represents a representative example of three independent experiments. Error bars represent the SD; n.s., statistically not significant. (B) SynapsinI immunostaining in GFP-PSD95 transfected neurons lacking Stau2. A significant reduction in GFP-PSD95 clusters was observed in Stau2 down-regulated neurons (see Fig. 4 A and quantification therein). The majority of the remaining GFP-PSD95–positive dendritic spines still receive presynaptic input as shown in the enlarged dendritic segment and in the higher magnifications below. Arrowheads indicate adjacent GFP-PSD95 and synapsinI puncta. Bar, 10 μm.
fected with the pSUPERIOR vector expressing both Stau2 shRNA and

treated neurons with anti-synapsinI antibodies. Interestingly,

have a presynaptic input, by immunostaining Stau2 shRNA-

ing dendritic spines in the Stau2 down-regulated neurons still

by 48% (Fig. 5 A, graph). We then asked whether the remain-

In total, the GFP-PSD95 clusters in dendritic spines de creased

was signifi  cantly reduced in Stau2 down-regulated cells (Fig. 5 A).

The number of dendritic spines in Stau2 down-regulated neu-

reduction in synapsinI puncta (26%). These results indicate that

the described si-Stau2 RNA approach not only drastically re-

duces the number of dendritic spines, but also coincides with a

reduction in presynaptic inputs. This was a first hint for a possi-

ble functional defi ciency of these neurons.

To establish a more convenient and faster assay to evalu-

ate the observed effects, we cotransfected hippocampal neurons

with plasmids coding for Stau2 shRNA and GFP-PSD95 together with the EYFP-Stau262 (R62) and EYFP-Stau259

(R59) cleavage-resistant isoforms. The total number of neurons (in paren-

theses) and PSD95 puncta counted are listed in the graph. **, P < 0.005;

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The observed phenotype can be rescued by

overexpression of RNAi cleavage-resistant

Stau2 isoforms

We cotransfected neurons with Stau228 plasmids that express

the following two RNAi-cleavage-resistant Stau2 protein

isoforms: EYFP-Stau262 and EYFP-Stau259. To limit the num-

ber of cotransfected plasmids, PSD95 cDNA was cloned in frame with EGF that is already present in the pSUPERIOR

vector. This allows for down-regulating Stau2 and expressing

GFP-PSD95 using the same construct (see Materials and meth-

ods for details). The expression of either Stau262 or Stau259 res-

cues the observed phenotype to a signifi cant extent. The number

of GFP-PSD95 puncta in rescued cells was thereby comparable
to cells that had been transfected with the mismatch Stau2 plas-

mid (Fig. 6), or that had been mock transfected (see Fig. 5 A).

Interestingly, the 62-kD isoform was signifi cantly more effec-
tive than the 59-kD isoform in relieving the phenotype. It is

important to note that the mere overexpression of exogenous

full-length Stau2 does not cause a loss in dendritic spines as

observed when overexpressing the dominant-negative dn2. Collec-
tively, the rescue of the observed phenotype is another

strong indication that our RNAi approach is Stau2 specifi c.

Stau2 down-regulation alters the dendritic

actin cytoskeleton

Because the actin cytoskeleton plays an important role in den-
dritic spine homeostasis (Fischer et al., 1998; Matus, 2005), we

used Alexa546-coupled phalloidin to assess the actin cytoskeleton

in Stau2 down-regulated neurons. Fig. 7 shows two phalloidin-
stained neurons (red), an untransfected cell (UT), and a Stau2

shRNA-treated (T) cell. Untransfected neurons had a regular

subcortical F-actin staining pattern preferentially in dendritic

spines (Fig. 7, inset 2, arrowheads). In contrast, F-actin organi-
sation in the dendrite itself was severely affected in neurons

lacking Stau2. These cells displayed clusters of actin in the

the majority of GFP-PSD95-positive puncta in Stau2 down-

regulated cells are still in close contact with presynaptic termi-
nals (Fig. 5 B). To further rule out the possibility of unspecifi 
cshRNA effects, we coexpressed dn2 (see Fig. 3 A) together with

GFP-PSD95 in mature neurons. Dn2 reduced the amount of

GFP-PSD95-positive puncta to a similar extent than Stau2

shRNA. Collectively, this suggests that Stau2 is necessary for

the maintenance of dendritic spines.

Because dendritic spines in cultured hippocampal neurons

are observed to form as early as 10 DIV (Papa et al., 1995; Yuste

and Bonhoeffer, 2001), RNAi was performed on 8 DIV neurons
to investigate whether Stau2 is also necessary for dendritic spine

formation (Fig. 5 A, 8+3 DIV). Neurons coexpressing GFP-

PSD95 and either siStau2 or mismatch Stau2 were analyzed 3 d

after transfection and the GFP-PSD95 puncta were counted.

The number of dendritic spines in Stau2 down-regulated neu-

rons was significantly reduced compared with either mismatch

or mock-transfected neurons (Fig. 5 A, graph; unpublished

data). These data, together with the previous analysis in mature

neurons, suggest an important role for Stau2 in both morpho-
genesis and maintenance of dendritic spines.
dendrite and had extended filopodia (Fig. 7, inset 1, arrows). It is interesting to note that axons (YFP-labeled in blue) of Stau2 down-regulated cells are still able to contact a dendrite of an untransfected neuron (phalloidin-labeled in red) by running on top of the dendrite (Fig. 7, inset 2). Because the total level of actin protein in both treated and untreated neurons was not significantly altered (see Fig. S1 C), the observed differences in staining pattern are presumed to reflect a rearrangement of F-actin. The pattern of G-actin, however, was not significantly altered as assessed by DNase I-staining (unpublished data). Collectively, these results demonstrate that the actin cytoskeleton in dendrites is severely affected by the Stau2 down-regulation.

The formation of synapses is critically dependent on the actin-based motility of dendritic protrusions (Zito et al., 2004). Furthermore, β-actin mRNA localizes to both axonal and dendritic sites of cultured hippocampal neurons (Bassell and Singer, 1997; Tiruchinapalli et al., 2003). We, therefore, analyzed levels of β-actin mRNA in cell bodies as well as the number of β-actin mRNA-containing particles in dendrites in si2-2 and mismatch shRNA-transfected neurons by FISH. Figure 8 A shows a Stau2 down-regulated hippocampal neuron (transfected cell expressing GFP, T) and an adjacent untransfected neuron (UT). In neuronal cell bodies, significantly lower FISH signals were detected in si2-2–transfected cells compared with untransfected cells (Fig. 8 A, see also enlarged cell bodies) and to misStau2-transfected neurons. To verify the nuclear integrity, DAPI staining was performed in transfected neurons after FISH (Fig. S2, available at http://www.jcb.org/cgi/content/full/jcb.200509035/DC1). Quantification of three independent experiments revealed a 23 ± 9% reduction of β-actin mRNA levels in the cell body only in si2-2–transfected neurons (P = 0.04, t test) in contrast to mismatch Stau2 transfected neurons (Fig. 8 A, top graph). Because Stau2 localizes to the dendritic compartment of neurons (Duchaine et al., 2002), we next analyzed whether the dendritic localization of β-actin mRNA is changed upon Stau2 down-regulation. The enlarged insets of the indicated dendritic regions (Fig. 8 A, dendrites) of both cells clearly display a difference in the number of localized β-actin mRNA puncta: a reduction by 37 ± 5% compared with values obtained for mismatch Stau2-transfected neurons (Fig. 8 A, bottom graph). To demonstrate that the reduced levels of β-actin mRNA upon Stau2 down-regulation were not related to unspecific RNAi effects, FISH was performed to detect GAPDH mRNA, which is restricted to cell bodies (Fig. 8 B) and to CaMKIIα mRNA, which is localized to dendrites (unpublished data). In contrast to the observed effects on β-actin mRNA, the Stau2 down-regulation did not alter the levels nor the localization pattern of both transcripts. In conclusion, these data suggest that Stau2 down-regulation affects the levels of β-actin containing RNPs in polarized neurons.

Stau2-deficient neurons display reduced mEPSC amplitudes

To reveal whether the morphological and biochemical alterations described in the previous paragraphs above are associated with functional consequences, we searched for changes in synaptic transmission. As the loss of PSD95 (Figs. 4 and 5) is suggestive of alterations in excitatory synapses, miniature excitatory postsynaptic currents (mEPSCs) through non-NMDA glutamate receptors were determined (Fig. 9). In cultures exposed to the si2-2 pSUPERIOR plasmid, the mEPSC amplitudes of transfected neurons were significantly smaller than those of nontransfected ones. In contrast, in cultures treated with the mismatch plasmid, there were no significant differences in mEPSC amplitudes between transfected and nontransfected neurons. Moreover, mEPSC amplitudes in si2-2–transfected cells were significantly smaller than those in mismatch-transfected cells. The frequencies of all the mEPSCs determined, however, were not different between si2-2–transfected and mismatch-transfected cells (0.55 Hz and 0.62 Hz, respectively; P > 0.1). Changes in amplitudes of mEPSCs reflect changes in postsynaptic receptor sensitivity, whereas mEPSC frequencies correspond to the probability of presynaptic vesicle exocytosis (Scanziani et al., 1992). Accordingly, the present results indicate that Stau2 down-regulation impairs excitatory synaptic transmission primarily through interference with the responsiveness of postsynaptic glutamate receptors.

Discussion

The double-stranded RNA-binding protein Staufen plays an essential role in Drosophila oogenesis, early embryonic patterning, and in establishing cellular asymmetry in neuroblasts (Roegiers and Jan, 2000). Despite a plethora of information on the roles of Staufen in Drosophila, the functions of the mammalian homologues are still largely unknown.
Stau2 is preferentially expressed in the central nervous system and here particularly in neurons (Duchaine et al., 2002), where it is present during all stages of neuronal development and in mature neurons (Fig. S1 A and unpublished data). Previous work has implicated Stau2 in dendritic mRNA transport, which is assumed to occur solely in the cytoplasm (Roegiers and Jan, 2000; Belanger et al., 2003; Macchi et al., 2004; Miki and Yoneda, 2004; Monshausen et al., 2004). A more detailed analysis, however, provided the first evidence that both Stau1 (Martel et al., 2006) and two isoforms of Stau2, Stau262 and Stau259 (Macchi et al., 2004; Miki and Yoneda, 2004), shuttle between the nucleus and the cytoplasm using separate export pathways, suggesting distinct roles for the different Stau2 isoforms (Kiebler et al., 2005).

Aside from these indirect observations, no direct function has been assigned to any of the mammalian Staufen proteins. Because they are assumed to play a role in dendritic mRNA transport, a process generally assumed to contribute to synaptic plasticity (Steward and Schuman, 2001), we decided to investigate the function of the brain-specific Stau2 in polarized hippocampal neurons using an RNAi approach. Down-regulation of Stau2 caused (1) a loss of dendritic spines and the appearance of extended filopodia; (2) a drastic reorganization of the actin cytoskeleton in dendrites; (3) a significant reduction in β-{actin} RNA expression level in both the cell body and in dendrites of Stau2 down-regulated mature neurons; and (4) an attenuation of excitatory synaptic transmission due to a decreased postsynaptic responsiveness.

Dendritic spines are morphological specializations that protrude from the main shaft of dendrites contacting presynaptic nerve terminals (Chicurel and Harris, 1992). Although their precise function is still unclear, the generally accepted hypothesis has been put forward that “spines create a micro compartment with a range of properties that enable them to operate as a multifunctional integrative unit” (Shepherd, 1996). Dendritic spines can thereby act as semi-autonomous chemical compartments to segregate postsynaptic responses (e.g., elevated calcium) to spatially and temporally modify molecules and to newly synthesize proteins upon synaptic activation. The formation and maintenance of dendritic spines are important for both neurogenesis and neuronal activity in the mammalian brain (Hering and Sheng, 2001; Yuste and Bonhoeffer, 2004). Considerable progress has been made toward identifying the molecules that might control dendritic spine growth and maturation.
Principally, the newly identified proteins fall into four categories:

1. Membrane proteins (e.g., glutamate receptors, cell adhesion molecules);
2. Scaffold proteins (e.g., PSD95, Shank, Homer);
3. Cytoskeletal-binding/regulating proteins (e.g., actin, drebrin, spinophilin, SPAR); and
4. Cytoplasmic proteins (e.g., kinases/phosphatases and other enzymes).

Recently, two other RNA-binding proteins have been implicated in dendritic spine morphogenesis, the Fragile X mental retardation protein (FMRP) and translocated in liposarcoma (TLS) (Antar and Bassell, 2003; Fujii et al., 2005). Both in Fragile X mental retardation patients (Purpura, 1974) and in adult Fmr1 knockout mice (Comery et al., 1997), unusually long and thin dendritic spines with increased density were observed. The putative functional consequences of this phenotype, e.g., on learning and memory, are currently under investigation. The increased dendritic spine density may be attributed to the absence of an activity-dependent translational repression by FMRP (Antar and Bassell, 2003). TLS, a component of heterogeneous nuclear ribonucleoprotein complexes and a nucleocytoplasmic shuttling protein, accumulates in spines at excitatory synapses upon mGluR5 activation. Hippocampal neurons derived from tls knockout mice, which die shortly after birth, also exhibited abnormal spine morphology: lower spine density and filopodia-like thin and long cytoplasmic protrusions (Fujii et al., 2005). A third RNA-binding protein, the zipcode binding protein 1 (ZBP1), is involved in localization of the β-actin message to growth cones of developing neurons and to dendrites of mature hippocampal neurons, respectively. This protein has been found to translocate from dendritic shafts into dendritic spines upon synaptic activity (Tiruchinapalli et al., 2003). Whether it is involved in dendritic spine morphogenesis, however, is unclear at present. Our studies provide first evidence that another conserved RNA-binding protein, the brain-specific Stau2, is crucial to dendritic spine formation and maintenance, suggesting that the function of RNA-binding proteins is essential to this process.

How could a defect in Stau2 cause impairment in dendritic spine morphogenesis? We have recently shown that Stau2 assembles into RNPs that move along microtubules into dendrites localizing in the proximity of the dendritic spines (Duchâne et al., 2002; see also Fig. 2). Stau2 particles, however, do not colocalize with PSD95, a postsynaptic marker, but instead are restricted to the dendritic shaft (see Fig. 2). It is, however, possible that synaptic stimulation causes a translocation of Stau2 RNPs from the dendritic shaft to dendritic spines, as reported for TLS, FMRP, and ZBP1 (Antar and Bassell 2003; Tiruchinapalli et al., 2003; Fujii et al., 2005). This will be subject to future investigation.

It is interesting to note that the longest Stau2 isoform, Stau262, displays a greater ability to rescue the observed loss of dendritic spines in Stau2 down-regulated neurons. This ties in with previous findings indicating what might be distinct roles of the different Stau2 isoforms in mammalian cells. The 62-kD isoform has been shown to preferentially accumulate in the nucleolus upon down-regulation of exportin-5 (Macchi et al., 2004). Because exportin-5 has been shown to be the export factor for microRNAs from the nucleus (Yi et al., 2003; Lund et al., 2004), this suggests a possible involvement of Stau262 in microRNA trafficking and translational control at the synapse (Kiebler et al., 2005).

There is currently very little information on the composition of endogenous mammalian Stau2 RNPs. This is in sharp contrast to the more ubiquitously expressed Stau1 RNPs, for which both interacting proteins and putative cargo RNAs have recently been reported (Ohashi et al., 2002; Mallardo et al., 2003; Brendel et al., 2004; Kanai et al., 2004; Villace et al., 2004). To our knowledge, not a single RNA has been identified as a bona fide cargo for Stau2. Our findings that down-regulation of Stau2 results in a reorganization of the actin cytoskeleton in dendrites and also affects the levels of β-actin mRNA in both
the cell body and the dendrites allow us to draw two important conclusions. First, there is a yet to be identified link between Stau2 and the actin cytoskeleton. It is particularly interesting to note in this context that F-actin, consisting of α- and γ-isofoms of actin, is highly concentrated in dendritic spines and that the actin cytoskeleton (Star et al., 2002) plays an important role in activity-dependent blockade of dendritic spine motility (Matus, 2005). Second, Stau2 may bind to β-actin RNA, thereby influencing either its stability and/or its dendritic transport. It is tempting to speculate that the down-regulation of Stau2 may cause a reorganization of the (dendritic) actin cytoskeleton by either affecting the stability of Stau2-interacting transcripts (e.g., β-actin) or by controlling the translation of transcripts coding for key players in the observed actin dynamics. There are several lines of evidence that support this notion. A Staun-specific mRNA decay pathway has recently been discovered as a means for cells to down-regulate the expression of transcripts bound by Staun (Kim et al., 2005). In addition, Drosophila Staufen functions in translational derepression of oskar mRNA once the mRNA has been localized to the posterior pole (Kim-Ha et al., 1991, Micklek et al., 2000). Furthermore, a recent study provided first direct evidence that Staun may play a similar role in mammals by facilitating translation initiation (Dugre-Brisson et al., 2005). The challenge will now be to characterize a possible molecular mechanism of how Staun may affect the β-actin mRNA stability and/or regulate local translation of β-actin.

The link between Staun2 and the actin cytoskeleton may provide the basis for the functional alterations observed after down-regulation of Staun2. On one hand, the morphology of dendritic spines clearly depends on the presence of F-actin (Matus, 2000) and actin depolymerization leads to a loss of spines (Allison et al., 1998). On the other hand, the geometry of spines is a major determinant of the responsiveness of synaptic non-NMDA glutamate receptors (Matsuzaki et al., 2001). Thus, the reduction of mEPSC amplitudes correlates well with the molecular and morphological changes of Staun2 down-regulation and thus unveils this protein as a regulator of synaptic efficacy.

Materials and methods

shRNAs and constructs

Primers complementary to two distinct regions of rat Staun2 were cloned BgIII and HindIII into both the pSUPER and pSUPERIOR vectors (Oligoen- gine; Brummelkamp et al., 2002). The sequences of the primers (Table S1, available at http://www.jcb.org/cgi/content/full/jcb.200509035/DC1) used in this study are available upon request.

The GFP-PDS95 construct (Marrs et al., 2001) was provided by Dr. M. Dailey (University of Iowa, Iowa City, IA) with the permission of Dr. D. Breid (University of California, San Francisco, San Francisco, CA). To avoid cotransfection of too many plasmids, PDS95 was cloned in frame with the GFP DNA into the pSUPERIOR vector that also contains the Staun2 shRNA (si2-2). The cDNA (an EYFP variant) plasmid was provided by Dr. Virginie Georget (CNRS, Monpellier, France). The photo-activatable (PA) GFP (Patterson and Lippincott-Schwartz, 2002) was provided by Dr. Jennifer Lippincott-Schwartz (National Institutes of Health, Bethesda, MD). The mutant version of Staun2 (dn2) was created as described in Lang et al. (2001).

Semi-quantitative PCR

RT-PCR was performed on total RNA isolated from cultured hippocampal neurons at different days in vitro (0, 3, and 23) using the RNeasy Kit (QIAGEN). The cDNAs were then amplified in the same PCR reaction and different numbers of PCR cycles were tested to ensure that amplification was not at the level of saturation.

HeLa cells, hippocampal cultures, and transient transfections

HeLa cells were cultivated and transfected as described in Macchi et al. (2004). Rat hippocampal neurons were cultured (Goetze et al., 2003) and transiently transfected (Goetze et al., 2004) with the plasmids expressing citrine together with pSUPER or pSUPERIOR vectors. Neurons were fixed with 4% PFA d after transfection. For PDS95 experiments, 15 DIV neu- rons were cotransfected with vectors coding for GFP-PDS95 and si2-2, mis-Staun2, or dn2 in the ratio of 1:3 to avoid overexpression of GFP-PDS95.

Immunocytochemistry and fluorescence microscopy

The following antibodies (incubation at RT for >1 h) were used: immunopurified rabbit anti-Stau1 antibodies (1 μg/ml); anti-Stau2 antibodies (1 μg/ml); monoclonal anti-PDS95 (1:1,000; Sigma-Aldrich) and polyclonal anti-synapsin1 (1:1,500; Chemicon International); Cy3-coupled goat anti-mouse and anti-rabbit IgG antibodies (1:2,000) were used as secondary antibodies (Dianova). Phalloidin staining was performed as described in Goetze et al. (2004). Fluorescent images were acquired (Goetze et al., 2004) using Axiosvert 200M, Axiosvert 100TV, and Axioptophot microscopes (all Carl Zeiss Micromaging, Inc.) equipped with the following objectives: 40× PlanApot oil immersion, 1.2 NA, or 63× PlanApot oil immersion, 1.4 NA (both Carl Zeiss MicroImaging, Inc.) and the following CCD cameras: Olympus F-view2 (Soft Imaging System), Spec-10 LN-1300 and CoolSnap HQ (both Princeton Instruments/Roper Scientific) and the following soft- ware: MetaMorph 6.3 (Universal Imaging Corp.) or AnalySIS Five (Soft Imaging System) and assembled using Adobe Photoshop 7.0. Pictures were not modified other than adjustments of scaling, levels, brightness, and contrast.

Data analysis

To determine the length of dendritic spines, 15–30 EYFP-positive dendrites were randomly selected for each condition and the number and length of all protrusions was manually determined using MetaMorph 5.6. For GFP- PDS95-expressing cells, 10 cells per condition were analyzed. Only GFP- PDS95-positive puncta that reside beside the dendritic shaft were counted and expressed as puncta μm dendrite length using Microsoft Excel. Cells expressing high levels of GFP-PDS95 were discarded. For statistical analysis, t test was applied using Microsoft Excel, P values <0.001 (***) were considered as highly significant. The experimenter was not aware of the experimental conditions.

To quantify β-actin mRNA levels, the fluorescence intensities of si2-2 and mis-transfected cell bodies were measured and normalized to the intensities of adjacent, untransfected neurons using MetaMorph 5.6. Three independent experiments with 15 cells per condition were evaluated. Den- dritic particles were manually counted and the numbers per cell compared between si2-2 and mis-transfected neurons.

Electrophysiological recordings of miniature excitatory postsynaptic currents

mEPSCs were determined in whole-cell patch-clamp recordings at room temperature (20–24°C) on neurons at 18 DIV using an Axopatch 200B amplifier and the PClamp 6.0 hard- and software (Axon Instruments; see Boehm and Betz, 1997). The bathing solution contained [in mM] NaCl [140], KCl (6), CaCl2 (3), MgCl2 (2), glucose (20), and Heps (10), and was adjusted to pH 7.4 with NaOH. Tetrodotoxin (TTX; 0.5 μM) and bicuculline methiodide (30 μM) were added to suppress action potential propagation and miniature inhibitory postsynaptic currents, respectively. Neurons were continuously superfused using a DAD-12 (Adams and List) application system. Electrodes were pulled from borosilicat glass capillaries (Science Products) using a Flaming-Brown puller (Sutter Instruments) to yield tip resistances of 4.5–5.5 MΩ and were filled with a solution containing (in mM) KCl [140], CaCl2 [1], EGTA [10], Heps [10], Mg-ATP [2], and Li-GTP [2], adjusted to pH 7.3 with KOH.

3 d after exposure to plasmids, mEPSCs were recorded from either transfected or nontransfected cells present within the same culture dish for periods of time sufficiently long to obtain at least 25 consecutive events. Thereafter, 10 μM cyanos-3,3-dihydroxy-7-nitroquinoxaline (CNQX) was applied, which blocks all mEPSCs in the presence of Mg2+ (Boehm and Betz, 1997).
mEPSCs were evaluated using the Mini Analysis Program (Synaptosoft Inc.) and detection thresholds were adjusted for each cell by analysis of traces obtained in the presence of 10 μM CNQX. mEPSCs and their inter-event intervals were tested for normal distribution by a Kolmogorov-Smirnov test and then compared by a one-way analysis of variance. The results show arithmetic means ± SEM, and P values below 0.05 were taken as indication of statistical significance.

**FISH**

Endogenous β-actin mRNA was detected by two different approaches. First, a 500-bp RNA probe complementary to bases 21–520 of rat β-actin mRNA (NM 031144) was used according to Thomas et al. (2005). After hybridization at 52°C, cells were blocked and the probes were detected using rhodamine-labeled anti-Dig Fab fragments (Roche) according to the manufacturer’s instructions. Alternatively, a mix of four antisense oligonucleotides was applied (Bassell et al., 1998). These oligonucleotides were then modified with digoxigenin at the 3′-end by terminal transferase (according to the manufacturer’s instructions; Roche). FISH was performed using a GAPDH antisense probe (M17701, nucleotides 4–1233) as described in Macchi et al. (2003).

**Western blotting**

Neurons were transfected by nucleoporation (Amaxa) with a total of 3 μg DNA (ratio of the shRNA and citrine was 1:1) or Dharmacon oligos alone according to the manufacturer’s specifications (program O-03) with the following modifications: neurons were plated directly in growth medium and petri dishes were coated with 0.1 mg/ml poly-L-lysine in borate buffer (Goetze et al. 2003).

**Online supplemental material**

Fig. S1: (A) Semi-quantitative PCR performed on RNA extract from E17 hippocampal neurons at different DIV. (B) RNA for Sta2 in HeLa cells. (C) Western blot of nucleoporated neurons. (D) Quantitative analysis of the length of all protrusions. Fig. S2: Integrity of nuclei in transfected neurons. Table S1: List of oligonucleotides used in this study. Online supplemental material available at http://www.jcb.org/cgi/content/full/jcb.200509035/DC1.

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