Dynamic remodeling of scaffold interactions in dendritic spines controls synaptic excitability

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Scaffolding proteins interact with membrane receptors to control signaling pathways and cellular functions. However, the dynamics and specific roles of interactions between different components of scaffold complexes are poorly understood because of the dearth of methods available to monitor binding interactions. Using a unique combination of single-cell bioluminescence resonance energy transfer imaging in living neurons and electrophysiological recordings, in this paper, we depict the role of glutamate receptor scaffold complex remodeling in space and time to control synaptic transmission. Despite a broad colocalization of the proteins in neurons, we show that spine-confined assembly/disassembly of this scaffold complex, physiologically triggered by sustained activation of synaptic NMDA (N-methyl-d-aspartate) receptors, induces physical association between ionotropic (NMDA) and metabotropic (mGlu5a) synaptic glutamate receptors. This physical interaction results in an mGlu5a receptor–mediated inhibition of NMDA currents, providing an activity-dependent negative feedback loop on NMDA receptor activity. Such protein scaffold remodeling represents a form of homeostatic control of synaptic excitability.

Introduction

Protein–protein interactions play key roles in cellular processes. Identifying such multiprotein complexes has been a major issue in the discovery of key biological pathways. Indeed, in their natural environment, membrane receptors are associated with scaffolding proteins that link them to their intracellular signal transduction pathways and cytoskeleton. Such receptor-associated scaffolds are relatively stable structures, but exchange of individual adaptor proteins can occur at a fast time scale and in a highly regulated manner, which provides fine tuning, speed, and specificity of the receptor signaling (Zeke et al., 2009). Therefore, understanding how proteins are activated as free molecules or part of complexes is an essential biological concern. Currently, the molecular detail of the dynamics of these interactions and the roles that they play in various cellular functions are poorly defined because of the dearth of methods for acutely and specifically controlling the binding interactions.

For instance, at brain synapses, scaffolding proteins function not only as anchors but also as signaling proteins for neurotransmitter receptors. As synapses are dynamic structures, it is a fundamental issue to study the dynamics of such synaptic receptor scaffolds and their role in neurotransmission. Synaptic transmission involves neurotransmitter receptors and ion channels. Their targeting, functioning, and dynamic exchanges at synapses depend on their interaction with synaptic scaffolding proteins (Renner et al., 2008). Glutamatergic neurotransmission in the mammalian brain is mainly mediated by the ligand-gated AMPA(2-amino-3-(3-methyl-1-oxo-1,2-oxazol-4-yl)propanoic acid) and kainate receptor channels and modulated by NMDA (N-methyl-d-aspartate) receptor channels and G protein–coupled metabotropic receptors (mGlu). Interestingly, group I mGlu...
receptor (mGlu1 and mGlu5) and NMDA receptors are physically linked together in the postsynaptic density by a Homer protein–containing complex (Brakeman et al., 1997; Scannevin and Huganir, 2000). Functional interaction between the NMDA and group I mGlu receptors has been extensively studied (Gerber et al., 2007; Homayoun and Moghaddam, 2010), but whether dynamic exchange of Homer proteins controls functional cross talk between those receptors has received little attention (Bertaso et al., 2010).

The Homer family of postsynaptic proteins displays an EVH1 (Ena/Vasp homology) N-terminal domain, which recognizes a proline-rich sequence (PPxF) of protein partners. The long forms of Homer proteins (Homer1b, Homer1c, Homer2, and Homer3) display a central hinge region followed by a C-terminal coiled-coil domain that is organized in two separate regions, CC1 and CC2 (Hayashi et al., 2006). These proteins are constitutively expressed in neurons and other cell types. They form a tetrameric hub structure composed of two anti-parallel dimers at the postsynaptic density (Hayashi et al., 2006). This structure confers slow turnover rates and great efficiency in coordinating dendritic spine functions. Shank proteins are major components of the postsynaptic density that are assembled in high-order complexes through self-association of their sterile α-motif C-terminal domain. Together with Homer multimers, they are major constituents of a platform that cross-links group I mGlu receptors to the guanylate kinase–associated protein (GKAP)–PSD95–NMDA receptor assembly in dendritic spines (Baron et al., 2006). The short form of Homer proteins, Homer1a, also displays an EVH1 domain but lacks a coiled-coil domain. Therefore, this protein can virtually bind to the same targets as the long forms of Homer proteins but cannot multimerize. This confers to Homer1a dominant-negative properties and the ability to disrupt Homer-associated multiprotein complexes. In contrast to the long forms of Homer proteins, Homer1a is an immediate early gene that is transiently expressed after elevated neuronal activity or intake of drug of abuse such as cocaine, amphetamine, LSD, phencyclidine, and nicotine (Xiao et al., 2000; Fagni et al., 2002; Szumlinski et al., 2006, 2008). Homer1a plays fundamental physiological functions, such as modulating synaptic plasticity and temporal encoding of spatial memory (Celikel et al., 2007) or enabling homeostatic scaling (Hu et al., 2010).

Because of its dominant-negative properties, Homer1a is a viable mean that may trigger dynamic changes in the association/dissociation of mGlu receptors to the GKAP–PSD95–NMDA receptor assembly. Therefore, it is fundamental to depict the spatiotemporal dynamics of mutually exclusive interactions of long and short forms of Homer proteins with mGlu receptors. Bioluminescence resonance energy transfer (BRET) is a very sensitive technology that became in the past decade a technology of choice to study the dynamic of protein–protein interactions in living cells (see Boute et al. [2002] and Pfleger and Eidne [2006] for reviews about BRET). In this assay, the efficacy of the energy transfer depends on the close proximity (<10 nm) and orientation of the donor and acceptor entities. The mean radius of proteins being 5 nm, the occurrence of resonance energy transfer is interpreted as a strong indication that the proteins attached to the energy donors and acceptors, respectively, are indeed in direct contact. We recently adapted BRET to single-cell imaging analysis to study subcellular localization of protein–protein interactions under microscope in living cells (Coulon et al., 2008; Perroy, 2010). Here, we investigated by single-cell BRET imaging the spatiotemporal remodeling of the interactions between Homer proteins and mGlu5a receptor in cultured hippocampal neurons and its consequence on NMDA receptor function. We found that competition between Homer1a and multimeric Homer proteins on mGlu5a receptor binding is virtually restricted to dendritic spines. Such a scaffold remodeling triggers a direct physical interaction between mGlu5a and NMDA receptors and inhibition of NMDA currents. Our data also evidence that such a regulation occurs after sustained activation of synaptic NMDA receptors to restore synaptic NMDA current. Thus, this remodeling controls synapse excitability. To our knowledge, this is the first study showing temporal dynamic remodeling of a multiprotein scaffold and its function at a subcellular level in living cells.

**Results**

Two different adaptor proteins, the long and short Homer isoforms, competitively interact with mGlu5a receptor in living cells

The proline-rich Homer ligand domain (PPxFr) identified on mGlu5a receptor indifferently communoprecipitates with the short and long forms of Homer (Tu et al., 1998), suggesting that competitive interaction may occur between the two Homer isoforms. We investigated the modality of these mutually exclusive interactions in HEK-293 living cells by BRET. We fused the C terminus of mGlu5a receptor to the energy donor *Renilla luciferase* (Rluc8) and the N terminus of the long Homer3 or short Homer1a protein to the acceptor YFP (Myc-mGlu5a–Rluc8, YFP-Homer, and YFP-Homer1a, respectively). The obtained tagged proteins were functional (Fig. S1, A and B). Under the condition of a constant level of Myc-mGlu5a–Rluc8 expression, BRET signal increased hyperbolically as a function of YFP-Homer1a or YFP-Homer expression level (Fig. 1 A). Saturation of the BRET signal when all the donor was linked to the acceptor indicated a specific interaction between the mGlu5a receptor and Homer proteins. For a constant donor/acceptor ratio, the BRET signal between Myc-mGlu5a–Rluc8 and either YFP-Homer1a or YFP-Homer remained constant whatever the total level of protein expression (Fig. 1 B). By opposition, the point mutant Myc-mGlu5a–P1124K–Rluc8, which could not interact with Homer proteins (Tu et al., 1998), did not display BRET signal neither with YFP-Homer1a nor YFP-Homer (Fig. 1 A). NMDA receptor (NR1A–Rluc + NR2B) and YFP-Homer proteins did not display BRET signal either, confirming the specificity of interaction between Homer proteins and the mGlu5 receptor.

To monitor competition between Homer1a and the long form of Homer proteins for the binding to the mGlu5a receptor in the same cell, we took advantage of the distinct spectral properties of two luciferase substrates, coelenterazine H and DeepBlueC coelenterazine (see Materials and methods). The coexpression of Homer1a slightly reduced the binding of cotransfected...
Homer3 to the receptor (Fig. 1, C and D). Reciprocally, Homer3 expression impaired the interaction between Homer1a and mGlu5a receptor but with significantly higher efficacy (Figs. 1 [E and F] and S1 [C–F]). Thus, concomitant detection of Homer1a and Homer3 interactions with mGlu5a receptor in cells co-expressing the three partners revealed that the competitive binding between the two Homer proteins on mGlu5a receptor occurred in living cells. The shift in interaction between mGlu5a and Homer induced by the presence of a concurrent Homer isoform emphasized the apparent higher affinity of the receptor for the multimeric Homer than for the monomeric Homer1a isoform. Both long multimeric isoforms of Homer tested (Homer3 and Homer1c) displayed similar affinity for the mGlu5a receptor (in all the following experiments, the multimeric Homer3 was used and referred to as Homer; Fig. S1 G).

In living neurons, the competition between long and short Homer isoforms on mGlu5a is confined to dendritic spines

We further studied mGlu5a receptor–Homer interactions in cultured hippocampal neurons by BRET imaging. The highest BRET signals between mGlu5a-Rluc8 and the multimeric form of Homer, YFP-Homer, were found in the neurites, as compared with the cell body. Despite a similar mean BRET intensity, quantification of the high SD indeed indicates a clusterization in neurites (Fig. 2 A). We then compared BRET signals in the dendritic spine and shaft. Spines were chosen according to their morphological criteria using the YFP-Homer fluorescence: a protrusion composed of a large spine head (diameter ranging from 0.5 to 1.0 µm) connected to the dendrite via a membranous neck. BRET images revealed the highest intensity of BRET signals between mGlu5a-Rluc8 and YFP-Homer confined to spines (image 535/480 in Fig. 2 [B–D]). Interestingly, this occurred despite colocalization and equal abundance of the two proteins in both the dendritic shaft and spine (image Em480 for mGlu5a-Rluc8 and image GFP for YFP-Homer in Fig. 2 B). In contrast to the interaction between multimeric Homer and mGluR5, the interaction between the mGlu5a-Rluc8 and the monomeric form, YFP-Homer1a, was equally distributed in the cell body and neurites (Fig. 2 A). Importantly, the long-term expression of transfected Homer1a induced dramatic decrease in spine number and size, which was consistent with the previously described inhibitory effect of the protein on synaptic transmission (Sala et al., 2003). This effect on dendritic spines hampered...
reliable experiments of precise dendritic localization and physical interaction between mGlu5a-Rluc8 and YFP-Homer1a.

To bypass this long-term effect of Homer1a, the protein was conjugated to the cell membrane transduction domain of the HIV-1 TAT protein (TAT-Homer1a). TAT-conjugated proteins can cross the plasma membrane, thus allowing their acute cell internalization (Dietz and Bähr, 2005). We verified that this also applied to TAT-Homer1a (Fig. S3). A 10-min perfusion of TAT-Homer1a, but not a TAT-HomerW24Y protein (a point mutation that selectively abolished the interaction of Homer1a with mGlu5a; Fig. S1 H; Beneken et al., 2000), decreased the BRET signal between mGlu5a-Rluc8 and YFP-Homer in a dose- and time-dependent manner (Fig. 3 A). Consistently, BRET imaging revealed that the spine-confined basal interaction between YFP-Homer and mGlu5a-Rluc8 was disrupted by acute perfusion of TAT-Homer1a but not a TAT-HomerW24Y protein (Fig. 3 B). In basal condition, BRET pixel distribution in dendritic shaft versus spines, expressed as a function of BRET intensity, further showed the existence of high-intensity BRET signals between the receptor and Homer in spine solely, whereas TAT-Homer1a shifted the pixel distribution in the spine to lower BRET values undistinguishable from the basal signal in the shaft (in the presence of Homer1a, BRET ratio in the spine was shifted from 364 + 57% to 101 + 19% of mean BRET in the shaft; n = 8; Fig. 3, C and D). These experiments put emphasis on the efficiency of Homer1a to disrupt the association of mGlu5a receptor with multimeric forms of Homer specifically in the spine.

Dynamics of mGlu5 receptor–Homer complex control physical and functional cross talk between mGlu5a and NMDA receptors in hippocampal neurons

In a heterologous expression system, NMDA and mGlu5a receptors can directly interact and display constitutive mutual inhibition (Perroy et al., 2008). In neurons, however, the constraints that result from the link between the C terminus of these receptors with the Homer-Shank-GKAP-PSD95 scaffold might preclude the direct mGlu5a–NMDA receptor association. Consistent with this hypothesis, although Rluc8-mGlu5a (Em480 image in Fig. 4 A) and YFP-NR1A + NR2B subunits (GFP image in Fig. 4 A) clearly colocalized in the dendritic shaft and spine, BRET signals between these tagged proteins remained close to noise in both cell compartments (control condition 535/480 image in Fig. 4 A). This suggested that the NMDA and mGlu5a receptors did not interact in control hippocampal neurons, although both receptors were present in the same dendritic spine. We reasoned that disassembly of the synaptic multimeric Homer–mGlu5a receptor complex by Homer1a would allow physical and functional interactions between NMDA and mGlu5a receptors. Consistent with this hypothesis, after a 10-min incubation with TAT-Homer1a (50 nM), BRET spots of high intensity appeared in spines (TAT-Homer1a condition; 535/480 image in Fig. 4 A), thus highlighting the occurrence of confined mGlu5a and NMDA receptor putative physical interactions. In basal condition, BRET pixel distribution did not differ in the dendritic shaft versus spines. On the other hand, two distinct
directly interact, resulting in inhibition of NMDA current (Perrey et al., 2008), we hypothesized that the present Homer1a-induced inhibition of NMDA current could result from disruption of endogenous mGlu5a receptor–multimeric Homer complexes by Homer1a allowing physical interaction of mGlu5a with NMDA receptors. To test this hypothesis, we used the Homer1a point mutant, HomerW24Y, which cannot interact with mGlu5a (Fig. S1 H) and therefore could not disrupt the interaction between mGlu5a and the multimeric Homer (Fig. 3). This Homer1a mutant had no effect on whole-cell NMDA currents (Fig. 5 A), showing that to inhibit NMDA currents, Homer1a needs to interact with mGlu5a receptor. This mGlu5a–Homer1a interaction would relax mGlu5a from the physical constraint of the scaffold. We also used an alternative manner to disrupt the scaffold, achieved by coexpression of the C terminus of the mGlu5a receptor, which quenched mGlu5a receptor partners (Mao et al., 2005). This led to similar NMDA current inhibition (55.3 ± 5.3% decrease; n = 8; Fig. 5 B) and prevented additional effects of Homer1a on NMDA current (Fig. 5 B). By opposition, distributions clearly appeared after TAT-Homer1a incubation (but not TAT-HomerW24Y), with the highest- and lowest-pixel intensities in spines and the dendritic shaft, respectively (Fig. 4 B). Statistical analyses further confirmed such a Homer1a-induced spine-restricted interaction between Rluc8-mGlu5a and YFP-NR1a + NR2B, as the basal BRET ratio in spine over shaft was shifted from 1.05 ± 0.24 to 1.77 ± 0.12 (n = 8) in the presence of Homer1a (Fig. 4 C). These data show that although mGlu5a and NMDA receptors colocalized in neurons, the receptors were in sufficient proximity to directly interact with each other, only in the presence of Homer1a and specifically in spines.

We further investigated the functional consequences of such a protein scaffold remodeling and consequent physical interaction between receptors on NMDA currents. Interestingly, in nontransfected hippocampal neurons, whole-cell NMDA currents were strongly decreased after TAT-Homer1a exposure (57.7 ± 7.1% decrease; n = 8; Fig. 5 A). Based on previous observations showing that, in HEK cells (i.e., in the absence of scaffolding protein expression), NMDA and mGlu5 receptor directly interact, resulting in inhibition of NMDA current (Perrey et al., 2008), we hypothesized that the present Homer1a-induced inhibition of NMDA current could result from disruption of endogenous mGlu5a receptor–multimeric Homer complexes by Homer1a allowing physical interaction of mGlu5a with NMDA receptors. To test this hypothesis, we used the Homer1a point mutant, HomerW24Y, which cannot interact with mGlu5a (Fig. S1 H) and therefore could not disrupt the interaction between mGlu5a and the multimeric Homer (Fig. 3). This Homer1a mutant had no effect on whole-cell NMDA currents (Fig. 5 A), showing that to inhibit NMDA currents, Homer1a needs to interact with mGlu5a receptor. This mGlu5a–Homer1a interaction would relax mGlu5a from the physical constraint of the scaffold. We also used an alternative manner to disrupt the scaffold, achieved by coexpression of the C terminus of the mGlu5a receptor, which quenched mGlu5a receptor partners (Mao et al., 2005). This led to similar NMDA current inhibition (55.3 ± 5.3% decrease; n = 8; Fig. 5 B) and prevented additional effects of Homer1a on NMDA current (Fig. 5 B). By opposition,
the mGlu5a–C terminus point mutant (P1124K), which cannot interact with Homer proteins, had no effect on the NMDA currents and did not impair their inhibition by Homer1a (Fig. 5 B). Disengagement of the mGlu5a receptor would favor its direct interaction with NMDA receptor and functional blockade of NMDA receptors. Accordingly, depletion of mGlu5a receptor expression by specific short hairpin RNAs (shRNAs) significantly reduced the TAT-Homer1a–induced inhibition of NMDA currents (Fig. 5 C). Importantly, the potency of Homer1a to induce inhibition of NMDA currents was correlated to the amount of mGlu5a receptor expression (Fig. 5, C and D). To rule out unspecific targets of the mGlu5 shRNAs, we verified that the loss of Homer1a-induced inhibition of NMDA currents could be rescued by overexpression of the mGlu5a receptor (Fig. 5 E). Finally, blocking the activity of mGlu5 receptor with a specific antagonist, MPEP (2-methyl-6-(phenylethynyl)-pyridine; 10 µM), was not sufficient to abolish the Homer1a-dependent suppression of NMDA currents (Fig. 5 F), suggesting that the removal of mGlu5a protein was required. Collectively, these results showed that inhibition of NMDA currents by Homer1a requires the interaction of Homer1a with mGlu5. Homer1a-induced dissociation of the mGlu5a receptor from multimeric Homer complex allowed, in turn, association between mGlu5a and NMDA receptors and inhibition of the NMDA current.

Molecular Homer–mGlu5 receptor complex reorganization occurs after sustained activation of synaptic NMDA receptors

Homer1a protein expression is very low or virtually absent in resting neurons. Elevated neuronal activity induced by psycho-stimulants (Brakeman et al., 1997) or sustained NMDA receptor stimulation (Sato et al., 2001), which eventually results in long-term potentiation (LTP) of synaptic transmission (Kato et al., 1997), can induce expression of the protein in neurons. Therefore, we examined whether Homer1a-induced mGlu5a–NMDA receptor interaction occurred after NMDA receptor–sustained activity. As previously shown (Lu et al., 2001; Park et al., 2004), prolonged stimulation of NMDA receptors by the coagonist glycine (200 µM; 3 min) successfully induced LTP in primary culture of hippocampal neurons (Figs. 6 [A–C] and S4). Indeed, the glycine treatment significantly increased the amplitude and frequency of miniature excitatory postsynaptic currents (mEPSCs), and this effect remained stable for >60 min after glycine washout (mEPSC frequency and amplitude were increased by 40 ± 10 and 34 ± 7% [mean ± SEM; n = 8], respectively; Fig. 6 B). Consistently, glycine treatment also increased the size of the spine head and the level of AMPA receptors expressed at the cell surface (Fig. S4, B and C). Interestingly, this sustained activation of synaptic NMDA receptor successfully triggered Homer1a transcription and expression (Fig. 6, D and E). We found that sustained activation of synaptic NMDA receptor (a 3-min application of glycine/strychnine followed by washout of the drugs) also triggered BRET signals between NMDA (YFP-NR1A + NR2B) and Rlu8-mGlu5a receptors in the spine. The BRET was detectable 30 min after the glycine application and persisted for at least 60 min (Fig. 6 F). Such a kinetic correlated with the time course of Homer1a induction (Fig. 6 E). To characterize the effect of glycine treatment on synaptic AMPA and NMDA receptors, we analyzed the fast and slow components of mEPSCs (Fig. 6 C), which are carried by AMPA and NMDA currents, respectively (Fig. S4 A). The glycine treatment increased the amplitude of the synaptic AMPA component of mEPSCs for at least 60 min (which was consistent with the aforementioned increase in mEPSCs amplitude). The NMDA component of mEPSCs also strongly increased but only transiently. Indeed, the current progressively recovered to its control value (Fig. 6 C). Thus, after sustained activation of synaptic NMDA receptor, there is a strong temporal correlation between Homer1a induction, mGlu5a–NMDA receptor interaction in the spine head, and inhibition of mEPSC NMDA receptor component (Fig. 6). All of these evidences favor the hypothesis of a role of the Homer1a-dependent mGlu5–NMDA receptor interaction to inhibit synaptic NMDA current.
To further examine the direct implication of Homer1a in synaptic mGlu5a–NMDA receptor interaction and inhibition of synaptic NMDA current, we perfused the TAT-Homer1a protein immediately after glycine application. Remarkably, the TAT-Homer1a, but not TAT-HomerW24Y, decreased NMDA synaptic currents 10 min after glycine washout (Fig. 7 A). This delay corresponded to the time required for the TAT-Homer1a protein to enter the cell and to abolish BRET signals between Homer and mGlu5a receptor (Fig. 3 A). By opposition, the knockdown of Homer1a by a mix of two specific siRNAs (see Materials and methods) blocked the induction of Homer1a expression after sustained activation of synaptic NMDA receptors (Fig. S5) and abolished the recovery of synaptic NMDA current (Fig. 7 B). However, this siRNA-induced loss of post-synaptic NMDA current inhibition was rescued by perfusion of TAT-Homer1a at the end of the experiment. These electrophysiological experiments were systematically correlated to BRET imaging between mGlu5a and NMDA receptors. In the presence of TAT-HomerW24Y, which does not interact with mGlu5a receptor, no BRET signal was detected 10 min after glycine washout. By opposition, TAT-Homer1a treatment induced BRET signals between mGlu5a and NMDA receptors in the spine (Fig. 7 A). On the other hand, knockdown of endogenous Homer1a by siRNA abolished BRET signals between the two receptors 30 min after glycine treatment (inset in Fig. 7 B). These results strongly suggest that induction of Homer1a by sustained activation of synaptic NMDA receptors can trigger physical and functional interaction between mGlu5a and NMDA receptors, thus leading to down-regulation and recovery of synaptic NMDA currents while leaving synaptic AMPA current potentiation unaffected.

Discussion

Several studies have suggested that the temporal and spatial dynamics of protein–protein interactions is crucial to specify synaptic membrane receptor and channel signaling (Sala et al., 2001; Fagni et al., 2002; Renner et al., 2008; Zeke et al., 2009; Sainlos et al., 2011). Thanks to recent development in single-cell BRET imaging (Coulon et al., 2008; Perroy, 2010), we have examined this issue by studying the competitive binding of the monomeric Homer1a and multimeric Homer with the neurotransmitter mGlu5a receptor at synapses of living neurons. We found that the competitive interactions between mGlu5a and Homer1a...
the long-term expression of transfected Homer1a prevented
the direct analysis of the BRET between Homer1a and mGlu5a
receptor in spines. However, it is important to note that the
competition between TAT-Homer1a and Homer to interact
with the receptor in spines indeed attested the occurrence of
Homer1a–mGlu5a interaction in the spine as well (Fig. 3, B–D).
The occurrence of Homer1a–mGlu5a interaction in the spine
was further supported by the spine-confined interaction between
mGlu5a and NMDA receptors after Homer1a expression
induced by glycine stimulation (Fig. 7 B). These observations
further support the notion that competition between long and
short Homer isoforms on mGlu5 receptors at synaptic sites may
control neurotransmission.

Competition between the monomeric Homer1a and multi-
meric Homer proteins on mGlu5 receptor depends on the level
of Homer1a expression, the relative affinity of the Homer pro-
teins for their target, and the subcellular localization of these
partners. The apparent higher affinity of multimeric versus mono-
meric Homer for the mGlu5a receptor might be explained by
the dimeric state of the receptor and Homer proteins was restricted to specific subcellular compartments (dendritic spines), precisely where synaptic transmission takes place. Interaction with Homer1a and disso-
ciation with Homer resulted in mGlu5a–NMDA receptor asso-
ciation and NMDA current inhibition. We further showed that a
sustained activation of synaptic NMDA receptors triggered the
expression of endogenous Homer1a, interaction between syn-
aptic mGlu5a and NMDA receptors, and inhibition of postsyn-
aptic NMDA currents. These results provide, for the first time,
a physiological role for dynamic remodeling of a receptor scaf-
dfold (the postsynaptic glutamate receptor scaffold) and its
cellular function (the control of synaptic excitability; Fig. 8).

Despite nonpreferential distribution of the transfected Homer protein and mGlu5 receptor in mature hippocampal neu-
rons, we found that the mGlu5a receptor interacts with Homer
exclusively in spines. Consistent with this finding, transfection of
long or short Homer isoforms results in spine enlargement or
drastic reduction of spine density, respectively, in hippocampal
neurons (Sala et al., 2001; Szumlinski et al., 2005; Tappe et al.,
2006; Jaubert et al., 2007). This drastic loss of spines as a result
of the long-term expression of transfected Homer1a prevented
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of Homer1a expression, the relative affinity of the Homer pro-
teins for their target, and the subcellular localization of these
partners. The apparent higher affinity of multimeric versus mono-
meric Homer for the mGlu5a receptor might be explained by
the dimeric state of the receptor, which would favor cooperative
binding of the multimeric over monomeric Homer isoform (Sainlos et al., 2011). Nevertheless, native Homer1a, even at a relatively low level, can affect group I mGlu receptor signaling in neurons (Kammermeier, 2008). Consistent with this result, the displacement of multimeric Homer interaction with the mGlu5a receptor by coexpressed Homer1a was quite efficient. In light of these results, sufficient Homer1a expression would be required to displace Homer–mGlu5a receptor interaction, and this may restrain the phenomenon to particular conditions, such as induction of synaptic plasticity (Ronesi and Huber, 2008) or after drug-of-abuse intake, epilepsy, or chronic pain (Tappe et al., 2006; Szumlinski et al., 2008).

Our results also show that the delicate balance of Homer protein interactions would control mGlu5a receptor functions. Thus, interaction of Homer1a with mGlu5a receptor triggers a direct inhibition of NMDA channel by mGlu5a receptor. The functional modulation of NMDA receptor channels by group I mGlu receptors is highly debated. Both synergism (Aniksztejn et al., 1992; Harvey and Collingridge, 1993; Doherty et al., 1997; Ugolini et al., 1997; Awad et al., 2000; Attucci et al., 2001) and mutual antagonism (Anwyl, 1999; Bortolotto et al., 1999; Kotecha et al., 2003; Perroy et al., 2008; Bertaso et al., 2010) have been observed in neurons of various brain regions. The mGlu5a receptor is physically linked to the Shank–GKAP–PSD95–NMDA receptor complex by multimeric Homer proteins. Herein, we suggest that competition between monomeric Homer1a and multimeric Homer on the binding domain of mGlu5 receptor would disrupt the interaction between this receptor and the PSD95–GKAP–Shank–Homer scaffold complex, thus allowing the mGlu5 receptor to directly interact with and inhibit the NMDA receptor. The dual role of group I mGlu receptors on NMDA receptors in neurons may rely on the presence or absence of Homer1a and on the integrity of the mGlu5–Homer–Shank–GKAP–PSD95–NMDA receptor complex. By disrupting the scaffolding complex, Homer1a may affect mGlu5a as well as NMDA receptor complex localization. Studies are currently in progress in our laboratory to further address the precise movement of glutamate receptors and their rearrangement in the postsynaptic density.

Homer1a expression is regulated by neuronal activity (Brakeman et al., 1997; Kato et al., 1997). Here, we could induce Homer1a expression by sustained activation of synaptic NMDA receptors in neurons may rely on the presence or absence of Homer1a and on the integrity of the mGlu5–Homer–Shank–GKAP–PSD95–NMDA receptor complex. By disrupting the scaffolding complex, Homer1a may affect mGlu5a as well as NMDA receptor complex localization. Studies are currently in progress in our laboratory to further address the precise movement of glutamate receptors and their rearrangement in the postsynaptic density.

Figure 7. After activation of synaptic NMDA receptors, Homer1a is necessary and sufficient to induce mGlu5a–NMDA interaction and inhibition of NMDA receptor. (A and B) Mean of 50 mEPSCs recorded at different times before, during, and after the application of glycine (top). The graphs represent the mean (±SEM; n = 8) of AMPA and NMDA components of mEPSCs (middle). BRET images were obtained at the indicated times after washout of glycine (bottom). Calibration bars apply to A and B. [A] TAT-Homer/W24Y (black traces) or TAT-Homer1a (green traces) was perfused immediately after glycine application. Note that TAT-Homer1a accelerated the inhibition of the NMDA component of mEPSCs after washout of glycine, as compared with the inactive TAT-Homer/W24Y. Asterisks indicate that NMDA current is significantly different in TAT-Homer1a and TAT-Homer/W24Y conditions at the same time after glycine application. BRET images show that interaction between mGlu5a and NMDA receptor in the presence of TAT-Homer1a (but not TAT-Homer/W24Y) occurs in spines at the same time as postsynaptic NMDA current is inhibited. (B) 2 d before electrophysiological recordings, neurons were transfected with control siRNA (black traces) or Homer1a siRNA (red traces). Note that Homer1a siRNA (but not control siRNA) prevented the recovery of NMDA current. Asterisks indicate that NMDA current is significantly different in Homer1a siRNA and control siRNA conditions at the same time after glycine application. TAT-Homer1a perfusion restored the inhibition of postsynaptic NMDA currents. 30 min after washout of glycine, BRET images show that Homer1A siRNA (but not control siRNA) prevented mGlu5a–NMDA receptor interaction in the spine.
Dramatic consequences. Such a Homer1a-induced negative molecular control of synaptic excitability could therefore have been shown that less mGlu5 receptors are associated with the herein-identified multimeric Homer isoforms, and this could be the molecular mechanism of human Fragile X mental retardation syndrome, it has been shown that glycine application. Note that TAT-Homer1a abolished the glycine-induced NMDA current increase as well as AMPA current potentiation, as compared with the inactive TAT-HomerW24Y. Asterisks indicate that NMDA current is significantly different in TAT-Homer1a and TAT-HomerW24Y conditions at the same time after glycine application.

This work highlights the importance of the association/dissociation dynamics of multiprotein complexes in receptor functions and cell physiology. Neurotransmitter and hormone receptors can no longer be seen as cell surface–isolated entities. Regulations of receptor signaling by dynamic changes in receptor-associated complex that we described here can be taken as a template to study other high-order modulatory mechanisms in various systems. Thus, similar remodeling of multiprotein assemblies by environmental factors would define a given cell status, which in turn would influence subsequent cellular responses, depending on the history of the cell.

**Materials and methods**

**Plasmids, shRNA, and siRNA**

DNA plasmids containing the ORF for Myc-mGlu5a-RLuc8, Homer1a, Homer3, or the NR2B subunit of NMDA receptors were encoded under control of cytomegalovirus promoter in pcDNA3.1-Myc-mGlu5a-RLuc8, pRK5-Homer1a, pRK5-Homer3, or p3apA-e2-NR2B, respectively, as previously described (Ango et al., 1999; Coulon et al., 2008; Perroy et al., 2008). Homer proteins tagged at their N terminus with either YFP or GFP2 were used for BRET experiments. The coding sequences of Homer1a or Homer3 were added in-frame to the 3' end coding sequence of mGlu5a, mGlu5a, luct8, Homer1a, luct8, Homer1a, pcDNA3.1-YFP-Homer1a, pcDNA3.1-YFP-Homer3, and pcDNA3.1-GFP2-Homer1a. For BRET experiments between receptors, tags were added in the extracellular N terminus part of the receptors to avoid any interference with the protein interactions on their cytosolic tail. The RLuc8 tag (a gift from A. De and A. Loening, Stanford University, Stanford, CA) was added in-frame between the 3' end of the signal peptide and the N terminus of mGlu5a receptor to obtain pRK5-RLuc8-mGlu5a. The YFP-NR1A construct was engineered by inserting a YFP cDNA fragment in-frame with the NR1-1a subunit after the predicted sequence for signal peptide (MSTMHLTLAFLPSCSFARAA) to obtain the p-YFP-NR1a plasmid. pRK5-cherry-CD4-mGlu-Cterm was

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**Figure 8.** Model of molecular scaffold remodeling and NMDA–mGlu5a receptor cross talk to control synaptic excitability. (A) Under basal condition, multimeric forms of Homer cross-link group 1 mGlu receptors to the GKAP–PSD95–NMDA receptor complex in the spine and prevent mGlu–NMDA receptor interaction. In this condition, mGlu5a and NMDA receptors do not directly interact. (B) Intense neuronal activity triggers Homer1a expression, which competes with multimeric forms of Homer on the mGlu5a receptor C terminus, resulting in the disruption of the interaction between mGlu5a receptor and GKAP–PSD95–NMDA receptor complex. (C) Homer1a would trigger disengagement of mGlu5a from the multimeric Homer complex, thus allowing association of mGlu5a with NMDA receptor in spines. In this condition, mGlu5a receptors directly inhibit NMDA receptors.

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**Figure 9.** Preapplication of TAT-Homer1a precludes the induction of LTP by activation of synaptic NMDA receptors. Mean of 50 mEPSCs recorded at different times before, during, and after the application of glycine (top). The graph represents the mean ±SEM; n = 8) of AMPA and NMDA components of mEPSCs. TAT-HomerW24Y (black traces) or TAT-Homer1a (blue traces) was perfused at the beginning of the experiment before glycine application. Note that TAT-Homer1a abolished the glycine-induced NMDA current increase as well as AMPA current potentiation, as compared with the inactive TAT-HomerW24Y. Asterisks indicate that NMDA current is significantly different in TAT-Homer1a and TAT-HomerW24Y conditions at the same time after glycine application.

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**Table:**

<table>
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<th>Condition</th>
<th>AMPA Current</th>
<th>NMDA Current</th>
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<tr>
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<td>50 pA</td>
<td>30 pA</td>
</tr>
<tr>
<td>TAT-Homer1a</td>
<td>40 pA</td>
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</tr>
<tr>
<td>TAT-HomerW24Y</td>
<td>60 pA</td>
<td>50 pA</td>
</tr>
</tbody>
</table>

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**Figure:**

- **A**: Basal transmission
- **B**: Sustained neuronal activity
- **C**: Scaffold remodeling-induced receptor cross-talk.
generated by PCR amplification of the DNA coding for the C-terminal tail of mGlu5a, which was then subcloned in-frame with the 3′ end of the DNA coding for the ectodomain and transmembrane domain of CD4. The Homer1α coding sequence was fused to the coding sequence of the Tat-permeant peptide to obtain pET-TAT-His-Homer1α. To engineer pcDNA3.1-Myc-mGlu5a-P1124K, we used primers containing the point mutations coding for P1124K, pcDNA3.1-YFP-HomerW24Y, and pET-TAT-His-HomerW24Y, as previously described (Roussignol et al., 2005).

BRET imaging

BRET imaging has been previously described (Coulon et al., 2008; Perroy et al., 2003). In brief, transfected cells were fixed with 4% PFA at 4°C for 20 min, permeabilized with 0.15% Triton X-100 for 3 min, incubated with Cy3-conjugated secondary antibody (Jackson ImmunoResearch Laboratories, Inc.) for 1 h at room temperature. Cells were washed and incubated with Cy3-conjugated secondary antibody (Jackson ImmunoResearch Laboratories, Inc.) for 1 h at room temperature. Cells were then observed under a microscope (Axioimager Z1; Carl Zeiss). Quantification of the immunostaining of endogenous mGlu5 (histogram in Fig. 5 D) was performed on neurons transfected with shRNA1 or shRNA2 and on nontransfected neurons in the same dish. For each condition, we measured the mean fluorescence intensity and substracted the noise measured in an adjacent equivalent area with no cell to obtain the fluorescence intensity and net fluorescence. The net fluorescence was expressed as a percentage of the expression of mGlu5a in the terminal condition, shown as net FluorshRNA/net Fluorc terminal × 100.

Analysis of the expression level of Homer1α

We extracted total RNA from hippocampal neurons with TRIzol reagent (Invitrogen) according to the manufacturer’s instructions. RT-PCR analysis of total RNA was performed with random hexamer oligonucleotides for reverse transcription. Sequences of the primers used for the determination of Homer1α expression levels are Homo1α-430F (5′-GGTGGAATTCCTGAGTACTGCGATGAGGTCCTGAGTACTCACGTACG-3′) and Homo1α-480R (5′-CGCTCGCACAGGCATCATCAACCTGACG-3′).
The level of expression of Homer1a was normalized to the geometric mean of GAPD, B2M, and Gus, according to the formula $X_{\text{geom}} = \frac{1}{\sqrt{R1 \times R2 \times R3}}$, where $R$ is the threshold cycle, and $R1$, $R2$, and $R3$ are the reference genes (X denotes Homer1a, and R1, R2, and R3 denote GAPD, B2M, and Gus, respectively).

**Western blot analyses**

Protein samples were resolved on 7.5% PAGE, transferred to nitrocellulose, and subjected to immunoblotting using a rabbit anti-Homer antibody (1:1,000; Synaptic Systems). The nitrocellulose was then incubated with anti-rabbit/HRP conjugate (1:10,000; GE Healthcare) for 30 min and developed using a chemiluminescence kit (RENAISSANCE; PerkinElmer). To quantify the level of Homer protein (Figs. 6E, S1C, and S5C), we measured the mean intensity of the Homer bands and display different relative apparent affinity for the mGlu5a receptor.

**Statistical analyses**

Analyses were performed using Prism software (GraphPad Software). Statistical analyses were performed with the nonparametric Kruskal–Wallis test for more than two independent samples or with the Friedman test for paired samples with a p-value risk threshold of 5 or 10%.

**Supplemental materials**

**Quantification of cell surface receptor expression using ELISA.** Cells expressing MGLU5a–GFP-C or MGLU5a–GFP-C-Δcarboxy were fixed with 4% PFA, washed, and incubated with PBS plus 5% FBS for 1 h. Cells were blocked with PBS plus 5% FBS for 1 h. After a 30-min reaction with mouse IgG anti-Myc (1:200; Molecular Probes) primary antibody, goat anti–mouse antibody coupled to HRP (1:500; Jackson ImmunoResearch Laboratories, Inc.) was applied for 30 min. The secondary antibody was detected and quantitatively quantified by chemiluminescence (SuperSignal West Femto; Thermo Fisher Scientific) using a luminiscence counter (Wallac VICTOR2; PerkinElmer).

**Cell surface receptor immunoaffinity**

DV14 hippocampal neurons transfected with GFP-GluR1 were incubated with rabbit anti-GFP (Invitrogen) for 20 min at 10°C to label surface AMPA receptors. After PBS washing, cells were fixed with 4% PFA. Cells were washed and incubated with Cy3-conjugated secondary antibody (Jackson ImmunoResearch Laboratories, Inc.) for 1 h at room temperature. Cells were then observed under a microscope (Axioimager Z1) equipped with appropriate epifluorescence and filters (GFP, 475/50 and 530 ± 50 nm for excitation and emission, respectively).

**Intracellular Ca²⁺ measurements.** Transfected HEK293 cells were seeded in polyornithine-coated, black-walled, clear-bottom 96-well plates seeded in polyornithine-coated, black-walled, clear-bottom 96-well plates. Statistical analyses were performed with the nonparametric Kruskal–Wallis test for more than two independent samples or with the Friedman test for paired samples with a p-value risk threshold of 5 or 10%.

**References**


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Tagged Homer1a and Homer are functional and display different relative apparent affinity for the mGlu5a receptor. (A and B) Homer-induced modulation of mGlu5a receptor cell surface expression and functional coupling to intracellular Ca\(^{2+}\) stores. 24 h after transfection with DNA coding for the indicated proteins, HEK293 cells were split in two distinct 96-well plates and grown for 24 supplementary hours. One plate was used for live calcium experiments, and the second one was fixed to perform surface ELISA to quantify the expression of the receptor at the cell surface in the same conditions. (A, top) YFP-Homer3 fluorescence acquired in a microplate reader. (middle) mGlu5a-Rluc8 luminescence measured in the presence of DeepBlueC coelenterazine. These measurements translate total expression of the tagged proteins. (bottom) ELISA quantification of cell surface receptor. Note that Homer3, but not Homer1a, decreased cell surface localization of mGlu5a receptor. (B) HEK293 cells were transfected with mGlu5a receptor in combination or absence of Homer1a or Homer3. (top) A representative experiment showing the kinetics of intracellular Ca\(^{2+}\) release induced by the mGlu5a receptor agonist DHPG (100 µM). (bottom) Maximal DHPG-induced Ca\(^{2+}\) release measured in the indicated transfection conditions and normalized (right) or not (left) to the receptor cell surface expression. Note that for a given level of mGlu5a-Rluc8 expression, YFP-Homer, but not YFP-Homer1a, decreased cell surface expression of the receptor and significantly increased mGlu5a receptor–induced intracellular Ca\(^{2+}\) release. These results corroborate a previous study (Tu et al., 1998) and indicate that the tagged proteins were functional. (A and B) Each bar of the histogram is the mean ± SEM of five experiments. *p < 0.05. (C–F) Correlation between protein expression and fluorescence emission of YFP-Homer1a or YFP-Homer3 to quantify the relative affinities of Homer proteins for the mGlu5a receptor. (C) Western blots were obtained using an anti-YFP antibody to quantify protein expression level (YFP-Homer1a or YFP-Homer3) in HEK293 cells transfected with increasing amounts of expression plasmid. (top) A representative Western blot out of three repeats. Homer protein expression was divided by the expression of actin as a control for protein loading. The Homer/actin ratio (mean ± SEM) was quantified on three repeated experiments and expressed as a function of DNA quantity. (D) Fluorescence emission of YFP-Homer1a or YFP-Homer3 was expressed as a function of protein expression (YFP-Homer/actin). Note that for an equivalent level of protein expression, YFP-Homer3 fluorescence was 2.8-fold higher than YFP-Homer1a. a.u., arbitrary unit. (E) Cells were cotransfected with a constant concentration of mGlu5a-Rluc8 and increasing concentrations of YFP-Homer1a or YFP-Homer3 plasmids. The BRET signal was expressed as a function of Homer/mGlu5a protein expression. Fluor, fluorescence; Lum, luminescence. (F) Each bar of the histogram indicates the apparent affinity (kD) of the interaction calculated from titration curves (see E) in cells transfected with mGlu5a-Rluc8 and YFP-Homer1a or YFP-Homer3. Two populations of values can be distinguished, depending on the Homer variant transfected. Each bar of the histogram indicates the apparent affinity (kD) of the interaction calculated from titration curves (one site binding hyperbola) ± SEM of kD. (G and H) Relative affinity of Homer proteins and mutant for the mGlu5a receptor. HEK293 cells were cotransfected with constant concentration of mGlu5a-Rluc8 and increasing concentrations of YFP-Homer1c or YFP-Homer3 [Q] or YFP-Homer1a or YFP-HomerW24Y [H] plasmids. The BRET signal is expressed as a function of Homer/mGlu5a protein expression ratio. The affinity of a given protein–protein interaction is indicated by the protein level required to reach the BRET\(_{50}\) value. This value is obtained when 50% of the Rluc8-tagged donor protein is linked to the YFP-tagged acceptor protein. The BRET signal between two partners is classically expressed as a function of the donor and acceptor expression levels measured by luminescence and fluorescence of the cells, respectively (see Materials and methods). However, it is important to note that the fluorescence emission differed from YFP-tagged Homer3 and Homer1a. Therefore, for comparative studies, BRET signals were expressed as a function of donor and acceptor expression levels rather than as a function of fluorescence. Western blot quantification and fluorescence measurements revealed that for a given level of protein expression, YFP-Homer3 generated a 2.8-fold higher fluorescence intensity than YFP-Homer1a [C and D]. Thus, the fluorescence measured with YFP-Homer1a was multiplied by 2.8 to obtain the so-called corrected fluorescence/luminescence ratio that rigorously reports the BRET value as a function of protein expression (E and F). To compare the relative affinity of Homer proteins for mGlu5a receptor, we measured the protein level required to reach the BRET\(_{50}\) value. mGlu5a-Rluc8 displayed a BRET\(_{50}\) fluorescence/luminescence value of 5.3 ± 0.2 with YFP-Homer1a and 1.8 ± 0.3 with YFP-Homer (E and F), suggesting that Homer3 has a 2.9-fold higher affinity than Homer1a for mGlu5a. Please note that here and in the following figures, Homer3 is referred to as Homer.
Figure S2. **Tagged mGlu5a and NMDA receptors are functional in neurons.** (A) DIV14 hippocampal neurons transfected with YFP-mGlue5a were fixed in nonpermeabilizing conditions. YFP fluorescence (left) revealed the total expression of the receptor. A rabbit anti-GFP antibody combined with a Cy3-conjugated secondary antibody was used to reveal the receptor expressed at the cell surface (middle). Note that the addition of the tag did not impair the adequate expression of the mGlu5 receptor. (B) Neurons were transfected with YFP-NR1A and Rluc-NR2B. The pictures show expression of YFP-NR1A (GFP) and BRET signals generated by the two tagged proteins (535/480). Note that YFP-NR1A and Rluc-NR2B form a complex localized in the soma, neuritic processes, and spines. Boxed areas are magnified below each image. (C) Mean BRET signal (535/480) between mGlu5a-Rluc8 and YFP-Homer proteins in neurons displaying a similar ratio of acceptor/donor expression level (GFP fluorescence [Fluo]/Em480 = 0.5 ± 0.05) but a different total amount of protein expression (fluorescence ranging from a 2,500 to 25,500 count). Note that for a constant acceptor/donor ratio, the BRET signal remained constant whatever the total expression of the YFP-tagged partner.
Figure S3. Purification of TAT-Homer1a protein, validation of the protein penetration, and absence of change in dendritic spine density in hippocampal neurons. (A) Purification of TAT-Homer1a using Ni-NTA resin in denaturing condition. SDS-PAGE gel was stained with Coomassie blue. MM, molecular mass; S, supernatant BL21 (DE3); FT, flowthrough 3 h after IPTG induction; E, TAT-Homer1a, pH 4.5, elution fraction. (B) Western blot using anti-Homer antibody was performed on the purified TAT-Homer1a protein (P) or from cellular extracts of DIV14 hippocampal neurons before (time 0) and after a 10- and 30-min incubation with 50 nM TAT-Homer1a. Note that a 10-min incubation of the neurons with 50 nM TAT-Homer1a was sufficient to allow penetration of the TAT-protein into the cell. (C) DIV14 hippocampal neurons transfected with GFP were treated with 50 nM TAT-Homer1a for 0, 15, 30, and 60 min before fixation. The graph represents dendritic spine density measured in 10 neurons at each time. Note that acute perfusion of TAT-Homer1a did not affect dendritic spine morphology or density. Error bars are SEM.
Figure S4. **Glycine activation of synaptic NMDA receptors.** (A, left) Mean trace of mEPSCs recorded in control condition (before glycine application). In the presence of the NMDA antagonist AP5 (100 µM), the mean mEPSC displayed only the fast AMPA current component (black trace; AP5). This component was subtracted from the control trace to obtain the NMDA component (gray trace on the right; control-AP5). According to this analysis, the AMPA component was measured at the mEPSC peak amplitude and the NMDA component 7 ms later. (B) Increase in spine size after glycine application. DIV14 hippocampal neurons transfected with GFP were exposed to glycine (200 µM for 3 min) or not (control). Spine size was quantified 30 min after the treatment. (C) Increase in surface AMPA receptor immunostaining after glycine application. Hippocampal neurons expressing GFP-GluR1 were fixed and incubated with an anti-GFP antibody and a red fluorescent secondary antibody under nonpermeabilizing conditions to label surface GluR1 subunits in control and glycine condition. Cell surface immunostaining of GluR1 was normalized to the total subunit expression assessed by GFP fluorescence. (B and C) Each value is the mean ± SEM of 10–20 spines taken from 10 neurons. Asterisks indicate significant differences at P < 0.05.
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Figure S5. Specificity of siRNA targeted against Homer1a. (A) Western blot (with a rabbit anti-GFP antibody; reference no. A11122; Invitrogen) showing decreased Homer1a expression in HEK cells transfected with YFP-Homer1a and Homer1a siRNA but not control siRNA. (B and C) Hippocampal neurons were transfected at DIV11 with Homer1a siRNA or control siRNA. Homer1a mRNA (B) and protein levels (C) were quantified at DIV14 by quantitative PCR and Western blot, respectively. (B) Basal Homer1a mRNA and Homer1a mRNA variation 60 min after glycine application with control siRNA or Homer1a siRNA. Each bar of the histogram is the mean ± SEM of three experiments. *, P < 0.05. (C) Western blot (using a rabbit anti–pan-Homer1 antibody (reference no. 160003; Synaptic Systems; left) showing glycine-induced Homer1a expression in the presence of Homer1a siRNA or control siRNA. No variation was detected for the Homer long isoform. The data shown are from a single representative experiment out of three repeats. Note that Homer1a siRNA decreased basal Homer1a mRNA (B) and protein expression (C) and blocked glycine-induced Homer1a expression.