Neurotransmitter release regulated by a MALS–liprin-α presynaptic complex

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Synapses are highly specialized intercellular junctions organized by adhesive and scaffolding molecules that align presynaptic vesicular release with postsynaptic neurotransmitter receptors. The MALS/Veli–CASK–Mint-1 complex of PDZ proteins occurs on both sides of the synapse and has the potential to link transsynaptic adhesion molecules to the cytoskeleton. In this study, we purified the MALS protein complex from brain and found liprin-α as a major component. Liprin proteins organize the presynaptic active zone and regulate neurotransmitter release. Fittingly, mutant mice lacking all three MALS isoforms died perinatally with difficulty breathing and impaired excitatory synaptic transmission. Excitatory postsynaptic currents were dramatically reduced in autaptic cultures from MALS triple knockout mice due to a presynaptic deficit in vesicle cycling. These findings are consistent with a model whereby the MALS–CASK–liprin-α complex recruits components of the synaptic release machinery to adhesive proteins of the active zone.

Introduction

Synaptic transmission requires precise alignment of pre- and postsynaptic specializations. On the presynaptic side, synaptic vesicles containing neurotransmitters must be aligned and docked at active zones, where vesicles fuse with the presynaptic membrane for secretion (Südhof, 2004). On the postsynaptic side, neurotransmitter receptors must be clustered together with relevant signal transduction machinery to respond to released transmitters. Recent studies have begun to elucidate the molecular machinery responsible for the organization of synaptic junctions. Adhesion molecules that span the synaptic cleft function in both stabilization and definition of the presynaptic active zone and postsynaptic specialization (Ichtchenko et al., 1995; Fannon and Colman, 1996; Flanagan and Vanderhaeghen, 1998). Cytosolic molecules associated with these adhesive factors help position synaptic vesicles and neurotransmitter receptors on their respective sides of the synapse (Hata et al., 1996; Torres et al., 1998; Perego et al., 2000).

One such set of modular scaffolding proteins comprises a ternary complex of MALS/Veli (mammalian LIN-7/vertebrate homologue of LIN-7), CASK (peripheral plasma membrane protein), and Mint-1 (munc-18 interacting protein 1), which are vertebrate homologues of a complex first identified in Caenorhabditis elegans that mediates vulval development (Kaech et al., 1998). In mammalian brain, the MALS–CASK–Mint-1 complex occurs on both sides of synaptic junctions and is thought to serve distinct roles in these two locations. Presynaptically, this complex links to neurexin (Hata et al., 1996), an adhesion molecule that binds across the synapse to postsynaptic neuroligin (Ichtchenko et al., 1995). Furthermore, Mint-1 associates with Munc18-1, an essential component of the synaptic vesicle fusion machinery (Okamoto and Südhof, 1997). Postsynaptically, MALS binds to the N-methyl-D-aspartate (NMDA)–type of glutamate receptors (Jo et al., 1999) and is reported to transport NMDA receptor vesicles along microtubules (Setou et al., 2000).

Genetic studies have failed to establish the essential roles of the MALS–CASK–Mint-1 complex in brain. Three MALS genes exist in mammals (Borg et al., 1998; Butz et al., 1998; Jo et al., 1999), and targeted disruption of MALS-1 and MALS-2 leads to compensatory up-regulation of MALS-3 in the CNS (Misawa et al., 2001). Mint-1 mutant mice show no defects in...
excitatory synaptic transmission and only a subtle defect in inhibitory synaptic transmission (Ho et al., 2003). Also, no synaptic analysis has been reported for CASK knockouts that die at birth due to midline defects (Laverty and Wilson, 1998).

Several molecules that mediate synapse development have been identified through invertebrate genetic studies. For example, mutation of C. elegans syd-2 disperses presynaptic active zones (Zhen and Jin, 1999). A similar structural defect occurs in flies lacking the Drosophila melanogaster syd orthologue liprin-α, which exhibits a concomitant decrease in synaptic transmission (Kaufmann et al., 2002). Liprin-α binds to a receptor protein tyrosine phosphatase, Dlar (Serra-Pages et al., 1998), suggesting a model whereby liprin-α and Dlar cooperate to organize presynaptic active zones. How liprin-α links to the synaptic vesicle machinery remains uncertain.

To define the essential roles for the MALS complex in mammals, we purified the MALS complex from brain. Isolation of the MALS complex revealed an association with a family of cytoskeletal and presynaptic adhesion molecules. Importantly, we found liprin-α1, -α2, -α3, and -α4 in the MALS complex. Association with this complex is mediated through the SAM domains in liprin-α and an NH2-terminal region in CASK. Using the sterile α motif (SAM) domains of liprin-α as a dominant negative, we disrupted the MALS–liprin complex in dissociated neurons. To understand the function of the MALS complex, we generated mutant mice lacking all three MALS genes. Mice lacking any single gene were viable and fertile. However, mice lacking all three MALS genes died within one hour of birth. This perinatal lethality is associated with impaired presynaptic function, reflecting the presynaptic deficits of invertebrates lacking liprin-α orthologues. These studies establish a crucial role for the MALS complex in synaptic vesicle exocytosis and implicate liprin-α in this process.

**Results**

**Proteomic characterization of the MALS complex in brain**

To identify molecular roles for MALS, we assessed the composition of the MALS protein complex. We performed preparative immunoprecipitation of MALS-3 from brain homogenates and used MALS-3 knockout mice (Fig. S1, available at http://www.jcb.org/cgi/content/full/jcb.200503011/DC1) as a powerful control. A series of protein bands were present in the MALS-3 immunoprecipitation that were absent in precipitations from MALS-3 knockouts. Several known components of the MALS-3 complex were identified, including neurexin, CASKIN, NMDA receptor 2B, Mint-1, and PALS-1, which is a protein associated with lin-7 (Fig. 1 A). Silver staining of immunoprecipitates showed specific bands at 140, 120, and 105 kD (Fig. 1 A). Mass spectrometry indicated that the 105-kD band corresponds to CASK, the 120-kD band corresponds to SAP-97, and the 140-kD band contained Mint-1, as well as liprin-α2, -α3, and -α4 (Fig. 1 A). Western blotting confirmed the efficient commnunoprecipitation of CASK, Mint-1, and liprin-α1 and -α2 (Fig. 1 B).

**Interaction of liprin-α with the MALS complex**

Liprin-α mutants in D. melanogaster (and syd mutants in C. elegans) display impaired synaptic vesicle exocytosis. Our discovery that liprin-α binds to the MALS–CASK complex is novel. Consistent with this, MALS, CASK, and liprin-α2 were enriched in synaptic biochemical fractionations of brain extracts (Fig. 1 C). Furthermore, MALS partially colocalized with liprin-α2 and the presynaptic marker synaptophysin in cultured hippocampal neurons (Fig. 1, D and E).

Liprin-α proteins contain conserved coiled-coil regions, three SAM domains, and a COOH-terminal region that binds to

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**Figure 1. Identification of a neuronal protein complex containing MALS and liprin-α.** (A) Immunoprecipitation of MALS-3 from brain extracts showed a series of bands in heterozygote (H) that were absent from MALS-3 knockout (K). Bands were identified by MS/MS obtained using a micro-ionspray source attached to a mass spectrometer (red) and confirmed by Western blotting (black). Molecular weights are presented in blue and Mint-1 degradation products are shown with asterisks. (B) Western blotting of heterozygote and knockout brain extracts immunoprecipitated for MALS-3 shows specific association of CASK, Mint-1, liprin-α1, and -α2 with MALS-3. (C) Western blotting shows that MALS-3, CASK, and liprin-α2 are highly enriched with synaptophysin (Synphy) in the synaptosome (Syn) fraction and PSD-95 in PSD fractions. (D and E) Hippocampal cultures (28 DIV) were stained for MALS, liprin-α2, and synaptophysin. Immunostaining reveals that both liprin-α2 (D) and synaptophysin (E) partially colocalize with MALS (arrowheads). Bar, 20 μm.
certain PDZ domains (Fig. 2 B). Using immunoprecipitation analysis and the yeast two-hybrid system, we found that MALS-1 does not directly bind to liprin-α2 (Fig. 2, A [top left] and C). We therefore asked whether other core components of the MALS complex might directly associate with liprin-α2. Indeed, CASK, but not Mint-1, bound to liprin-α2 directly (Fig. 2 A, bottom left and top right). Furthermore, we found that CASK can link liprin-α2 to a MALS-1 complex (Fig. 2 A, bottom right). These biochemical associations also redirect protein distribution in transfected cells, and all three MALS isoforms can associate with CASK to form MALS–CASK–liprin-α complexes (Figs. 1 and 2; unpublished data).

To define the site for interaction between liprin-α2 and CASK, we used the yeast two-hybrid system. We found that full-length CASK readily bound to full-length liprin-α2 (Fig. 2 C). This binding was mediated specifically by the first SAM domain in liprin-α2. Deletion analysis of CASK showed that the CAM kinase (CaMK) and first L27 domain of CASK were necessary for binding. We were unable to map this interaction further, suggesting that the binding domain may require large sequences for proper folding.

**Targeted disruption of MALS-3 and breeding of MALS-deficient mice**

To examine the essential roles for MALS in this complex, we targeted disruption of MALS-3. Our targeting vector replaced exons 3, 4, and 5 of MALS-3 with a neomycin cassette (Fig. S1, A–C). After targeted disruption in embryonic stem cells, we generated MALS-3–deficient mice. MALS-3 mutant mice were born at the expected Mendelian ratios and displayed no overt behavioral abnormalities. Western blotting showed a complete absence of MALS-3 protein in the knockout (Fig. S1 D). Histological inspection of brain showed no gross anatomical abnormalities. As previously reported (Misawa et al., 2001), MALS-3 occurs diffusely in numerous neuronal populations in the brain (Fig. S1 E). Furthermore, expression of MALS-3 is up-regulated, especially in the dentate gyrus region of the hippocampus, in MALS-1/2 double knockout mice (Fig. S1 E).

We interbred MALS-3 knockout mice with the previously generated MALS-1/2 mutants, which yielded 27 possible genotypes. These compound genotypes are presented in Fig. 3 A. We found that most mice lacking both MALS-1 and -3 died shortly after birth, whereas mice lacking MALS-1 and -2 were viable and fertile. Mice lacking MALS-2 and -3 and heterozygous for MALS-1 died during the second postnatal week. Finally, mice lacking all three MALS isoforms exhibited irregular, labored breathing and died within one hour of birth. The complete absence of MALS is not associated with embryonic lethality, as the predicted Mendelian ratio of fetuses was found when a caesarian section was performed at embryonic day 18 (Fig. 3 B).
Disruption of the MALS–CASK–liprin-α complex

MALS triple knockout (TKO) mice appear anatomically normal at birth; however, their perinatal death and difficulty breathing suggest neurological deficits. To assess whether components of the MALS complex or other synaptic proteins show quantitative expression differences, we performed Western blotting in the MALS TKO mice as compared with MALS-1/2 knockout mice, which were phenotypically normal, or wild type (WT). We found that CASK levels are dramatically decreased in the MALS TKO, whereas levels of all other assayed synaptic proteins were normal in the TKO mice (Fig. 4, A and B). We also found that the synaptic localization of CASK, but not other synaptic markers, was partially disrupted in TKO neuronal cultures (Fig. 4, C and D).

Liprins play important roles in synaptic development and function. Because we did not detect any change in liprin-α amount or localization (unpublished data), we suspected that the MALS–CASK complex may be a downstream effector for liprin-α’s presynaptic function. To test this hypothesis, we generated dominant-negative liprin-α constructs consisting of the SAM domains fused to GFP in the PSCA1 Semliki Forest viral vector to disrupt the liprin-α–CASK interaction. Infection of neurons with Semliki virus expressing GFP alone showed that >90% of neurons were infected and that neither the virus nor GFP affected MALS distribution (Fig. 5 A). However, expression of the liprin dominant-negative (GFP-SAM) misdirected MALS to nonsynaptic sites and significantly disrupted synaptic localization of MALS (Fig. 5 B). These results suggest that liprin-αs are upstream of MALS and may function, at least partially, through their interaction with the MALS–CASK complex.

MALS-deficient mice have deficient neurotransmitter release

Because of the perinatal death of MALS TKO mice, we were unable to assess electrophysiological parameters in forebrain neurons. Therefore, we generated microisland neuronal cultures from these mice to assess synaptic function. Individual neurons in such cultures are grown on isolated dots of substrate and form functional autaptic synapses. Because liprin-αs are necessary for proper synapse differentiation, we examined the morphology and number of synapses in autapses from TKO mice. We found that neurons from MALS TKO formed autaptic synapses in which presynaptic synaptophysin was juxtaposed to postsynaptic density (PSD)-95 (Fig. 6 A). The density of synapses in the TKO was comparable to WT (Fig. 6 B);
however, the distribution of synaptic areas in the TKO was shifted to slightly larger sizes (Fig. 6 C).

Electrophysiological experiments demonstrated that excitatory postsynaptic currents (EPSCs) in the MALS TKO cultures were profoundly reduced relative to WT (Fig. 7 A). Furthermore, the rate and degree of EPSC depression during high frequency stimulation (10 Hz) was enhanced in the MALS TKO autapses (Fig. 7 B), suggesting that the MALS–liprin–isoforms plays a role in presynaptic vesicle cycling. Because MALS mutant mice die around birth, structural analyses of mature synapses are not feasible. However, the magnitude and distribution of miniature EPSCs was the same in autapses prepared from WT and MALS TKO mice (Fig. 7 C, D).

**Discussion**

**MALS proteins are essential**

This study establishes MALS as an essential protein family involved in neurotransmitter release. MALS are components of a large presynaptic protein complex that includes scaffolding proteins, adaptor proteins, and adhesion molecules (Butz et al., 1998). Importantly, we find that liprin-α isoforms are components of this complex. Because liprin-α orthologues define the dimensions of the active zone in invertebrate synapses (Zhen and Jin, 1999; Kaufmann et al., 2002), the MALS complex has the potential to link adhesion molecules to the exocytotic machinery.

Although each strain of individual MALS knockouts is viable and fertile, certain combinations are synthetically lethal. Mice lacking all three MALS isoforms die within one hour of birth and have a severe breathing defect. This defect resembles the phenotype of mice lacking all three neurexin isoforms (Missler et al., 2003), which are also part of the MALS complex (Hata et al., 1996). Previous studies showed that MALS can bind to the COOH termini of proteins typical for morphological development, including β-catenin and epidermal growth factor receptors (Garcia et al., 2000; Perego et al., 2000; Shelly et al., 2003). That MALS TKO mice show no gross external abnormalities suggests that MALS does not play general
roles in tissue morphogenesis. Detailed histological evaluation may, however, reveal specific tissues whose development requires the MALS complex.

**Presynaptic defect in MALS mutants**

The perinatal lethality and labored breathing of MALS TKO mice are phenotypes often seen in mice with impaired synaptic transmission. Consistent with this, we found a profound presynaptic defect in these mutants. No change in the mEPSC amplitude distribution and no change in the ratio of AMPA/NMDA receptor–mediated currents were observed. In contrast to normal postsynaptic function, high-frequency stimulation produced an accelerated and more pronounced synaptic depression, suggesting greater depletion of vesicles in the readily releasable pool of MALS TKO mice. These results also imply that the MALS–CASK–liprin-α complex helps determine the size of the releasable pool and is important for replenishing this pool from the reserve pool.

**Assembly of the MALS protein complex**

The presynaptic defects in MALS TKO mice are paralleled by the association of MALS with a large presynaptic complex. Numerous modular protein interaction interfaces assemble this complex. The membrane-associated guanylate kinase CASK directly binds to many components and therefore constitutes the core. MALS uses its coiled-coil L27 domain to bind to the second of two L27 domains in CASK (Lee et al., 2002). The first L27 domain in CASK associates with the NH2-terminal L27 domain of SAP-97 (Lee et al., 2002). Neuroxin binds to the PDZ domain of CASK (Hata et al., 1996) and Mint-1 binds to the CaMK domain of CASK (Butz et al., 1998; Borg et al., 1999). Furthermore, we find that liprin-α proteins associate with the NH2-terminal region of CASK, which includes the CaMK domain and the first L27 region. Previous studies showed that liprin-α proteins also bind to LAR-family receptor protein tyrosine phosphatase (Serra-Pages et al., 1998) and to the Rab3A binding protein RIM1α (Schoch et al., 2002). Our failure to detect LAR or RIM proteins in the MALS complex may suggest that interaction of CASK with the SAM domains of liprin-α occludes association with these other presynaptic molecules.

The liprin protein family comprises seven liprin isoforms that are subdivided into the α- and β-type. We identified only liprin-α family members as part of the MALS complex. The SAM1 domain of liprin-α mediates their interaction with CASK. These domains are highly conserved between liprin-α proteins, sharing >90% identity. In contrast, liprin-α SAM1 domains share <45% identity with the most homologous liprin-β member. The SAM1 domain of liprin-α is evolutionarily conserved; mammalian liprin-α share >90% identity with orthologues in *D. melanogaster* and *C. elegans*, which suggest that the liprin-α–CASK interaction is likely conserved.

**Potential mechanisms for MALS complex regulating transmitter release**

Our discovery that the MALS complex contains liprin-α proteins can explain how this complex participates in synaptic vesicle exocytosis. Genetic analysis of invertebrates shows that liprin-α in *D. melanogaster* and its homologue *syd* in *C. elegans* control presynaptic function and morphology (Zhen and Jin, 1999; Kaufmann et al., 2002). In addition to these developmental defects, these mutants show decreased synaptic transmission resembling that seen in the MALS TKO. Because the mammalian genome contains four liprin-α isoforms (Serra-Pages et al., 1998), functional analyses are difficult. Some biochemical work suggests that mammalian liprin-α proteins may be postsynaptic and regulate AMPA receptors through the glutamate receptor interacting protein GRIP (Wyszynski et al., 2002). *lin-10* also has been shown to regulate GLR-1 in *C. elegans* (Rongo et al., 1998). MALS and liprin-α are also enriched in PSD fractions from rat brain (Fig. 1 C) and partially colocalize with PSD-95 in cultured hippocampal neurons (Fig. S2, available at http://www.jcb.org/cgi/content/full/jcb.200503011/DC1). We cannot rule out the possibility that postsynaptic MALS may contribute to the synaptic defect in the MALS TKOs, but our failure to detect GRIP or AMPA receptors in the MALS complex suggests no role for postsynaptic liprin-α in our analysis. Because MALS mutant mice die around birth, conditional mutants of the MALS may be required to evaluate roles for this complex in synaptic morphogenesis.

This study provides the first evidence that the MALS complex plays an important role in controlling transmitter release at excitatory synapses in brain. The myriad of interactions for the core MALS–CASK complex has suggested diverse roles; however, decisive genetic evidence has been lacking. Our work is consistent with a model whereby this complex recruits components of the synaptic release machinery to adhesives proteins of the active zone. According to this proposal, the MALS–CASK complex would couple extracellular synaptic interactions to the intercellular organization of the presynaptic secretory machinery.

**Materials and methods**

**Antibodies**

Isoform-specific and pan antibodies against MALS-1-, 2-, and 3- were generated in rabbits as described previously (Misawa et al., 2001). Mouse anti–liprin-α1 [C3-77] and α2 [243-252] antibodies have also been described previously (Serra-Pages et al., 1998). Mouse anti-CASK, MINT, ZO-2, Sec8, β-catenin, and N-cadherin were all purchased from Transduction Labs. Munc-18, Rab3, and neurologin antibodies were purchased from Synaptic Systems GmbH. Rabbit anti-CASK and antisynaptophysin were obtained from Zymed Laboratories. The mouse anti–Erb-B4 antibody was purchased from Lab Vision/Neomarkers and anti–PSD-95 antibody was obtained from Affinity BioReagents, Inc. The mouse anti-GluR 2/4 antibody was purchased from Chemicon International and rabbit synaptophysin was obtained from Sigma-Aldrich.

**Immunoprecipitations**

Using a Potter homogenizer (Braun), adult mouse brains from either MALS-3 heterozygote or knockout mice were homogenized in three volumes of STE buffer (320 mM sucrose, 20 mM Tris, pH 8.0, and 2 mM EDTA) containing 10 μg/ml leupeptin and 200 μg/ml PMSF. Homogenates were spun at 20,000 g for 1 h and pellets were resuspended in TET buffer (20 mM Tris, pH 8.0, 1 mM EDTA, and 1.3% Triton X-100) containing 10 μg/ml leupeptin and 50 μg/ml PMSF. After rehomogenization with a Potter homogenizer and a 1-h incubation at 4°C, the lysates were spun at 100,000 g for 1 h. The supernatant was collected and preclarified with protein A–Sepharose (GE Healthcare) for 1 h at 4°C. Preclarified lysates were immunoprecipitated with 10 μg MALS-3 antibody or control rabbit IgG for 2 h at 4°C. To collect immunoprecipitated protein complexes,
80 μl of a 50% protein A-Sepharose slurry was added to the lysates and incubated for 1 h at 4°C. Immunoprecipitates were washed extensively and loaded onto SDS-PAGE to separate the proteins. Gels were either silver stained or transferred to nitrocellulose for Western blotting. Immunoprecipitations from COS cells were performed similarly, except that the cells were directly lysed in TET buffer and spun at 20,000 g for 10 min, and supernatants were collected.

**Immunocytochemistry**

Hippocampal cultures grown on poly-lysine–treated coverslips were fixed with 4% PFA on ice for 10 min followed by methanol at −20°C. After thorough washing with PBS containing 0.1% Triton X-100 (PBSX), cells were blocked with PBSX containing 3% normal goat serum (blocking solution). Immunostudies were incubated for 2 h at RT or 4°C overnight in blocking solution. Cells were washed three times with PBSX and incubated with secondary antibodies in blocking solution for 1 h at RT. Cells were washed with PBSX and mounted onto slides with Fluoromount-G (Southern Biotechnologies Associates, Inc.).

Colocalization experiments in neurons were performed using images acquired from a confocal microscope (model LSM510; Carl Zeiss Microlmaging, Inc.) and analyzed using image analysis software (MetaMorph). Neurons were chosen randomly for quantification. For all images, thresholds were set at a predetermined level and colocalization values were obtained using MetaMorph software. Statistical significance was determined by an unpaired t test.

**Nano-LC-ESI-Qq-TOF tandem mass spectrometry (MS) analysis**

Individual gel bands were reduced with 10 mM dithiothreitol at 56°C for 1 h followed by alkylation with 55 mM iodoacetamide for 45 min at RT. The proteins were digested overnight with 12 ng/μl trypsin at 37°C. Peptides were extracted with a 50% acetonitrile/5% formic acid solution. The peptides were dried down and resuspended in 0.1% formic acid, and a 50% acetonitrile/5% formic acid solution. The LC eluent was coupled to a micro-ionspray source attached to a mass spectrometer (model QSTAR Pulsar; MDS Sciex). Peptides were analyzed in positive ion mode. MS spectra were acquired for 1 s, followed by 3-s MS/MS on the most intense multiply charged peak.

**Subcellular fractionation**

Subcellular fractions of rat brain were prepared by differential centrifugation. Brains were homogenized in buffer containing 320 mM sucrose and 10 mM HEPES-NaOH, pH 7.4. Homogenate (C, crude lysate) was centrifuged for 10 min at 1,000 g to produce a pellet. The supernatant was centrifuged at 13,800 g for 10 min to produce a pellet (P13.8) and supernatant (P100, crude synaptosomal vesicle pellet) and supernatant (S100, crude cytosolic synaptonal supernatant). Synaptosomal and PSD fractions were isolated by a discontinuous sucrose gradient centrifugation using P13.8. The pellet was extracted twice with ice cold 0.5% Triton X-100 (synaptonal) and then centrifuged to obtain the PSD pellet.

**Cell culture and transfections**

Hippocampal cultures were prepared as described previously (Tomita et al., 2003). In brief, hippocampi were dissected from 17- and 18-day-old embryos, digested with papain solution and plated at a density of 5 × 10^4 neurons/well in 24-well dishes. Neurons were cultured in Neurobasal media (GIBCO BRL) supplemented with B27, penicillin, and 100 U/ml streptomycin according to the manufacturer’s protocol (GIBCO BRL). Neurons were cultured in Neurobasal media (GIBCO BRL) supplemented with B27, penicillin, streptomycin, and L-glutamine according to the manufacturer’s protocol (GIBCO BRL). Neurons were chosen randomly for quantification. For all immunocytochemical studies, the following antibodies were used: anti-GFP (1:500; Abcam), anti-CASK (1:500; Santa Cruz), anti-PSD-95 (1:500; Synaptic Systems), anti-NeuN (1:500; Millipore), and anti-rat IgG (1:1,000; Jackson ImmunoResearch). Cells were incubated with secondary antibodies in blocking solution for 1 h at 4°C. After thorough washing with PBS containing 0.1% Triton X-100, neurons were incubated with secondary antibodies in blocking solution for 1 h at RT. Cells were blocked with PBSX and mounted onto slides with Fluoromount-G (Southern Biotechnologies Associates, Inc.).

**Yeast two-hybrid**

Yeast co-transformation was performed according to the manufacturer’s protocol (CLONTECH Laboratories, Inc.) with the yeast strain AH109. Binding was assessed by quantification of colonies transformed with the indicated plasmids on -L-WHI plates. Interactions were scored as positive (+) if more than 50% individual colonies were observed or negative (-) if no colonies were present on the -L-WHI plate. Control plates (-LW) were used to verify transformation efficiency.

**Isolation of MALS-3 genomic DNA and construction of targeting vector**

A mouse MALS-3 cDNA probe was used to isolate bacterial artificial chromosome clones from a 129Sv/J mouse genomic library (Genome Systems, Inc.). The targeting vector was constructed using the pPNT replacement vector. A 1.4-kb region downstream from the targeted exons was PCR-amplified, digested with XhoI and NotI, and subcloned into the XhoI–NotI sites of pPNT. Similarly, a 5-kb genomic region upstream from the targeted exons was PCR-amplified, digested with BamHI and XbaI, and inserted into the BamHI–XbaI sites of the pPNT vector. In the targeting vector, the third, fourth, and fifth exons (as well as the third and fourth introns of MALS-3) were replaced with a neocassette.

**Generation of MALS-3 null mice**

The targeting vector was linearized with BamHI and electroportioned into R1 embryonic stem cells. Clones resistant to G418 and gancyclovir were analyzed for recombination by PCR. To ensure proper homologous recombination, PCR-positive clones were further analyzed by Southern blotting using probes containing genomic sequences outside of the targeting vector and with a neoprobe. Properly targeted clones were injected into blastocysts from C57Bl6 (The Jackson Laboratory) mice and transferred to surrogate mothers. Male chimeras were mated with C57Bl6 females for transmission of the mutated allele through the germline. Heterozygous mice were interbred to generate MALS-3 null mice. The genotypes of these and subsequent backcrosses were determined by Southern blotting or PCR using allele-specific primers as follows: GGAAGAAATGTGAGTGCCCGCTTG and ACAGCGGAGACAGAATGTTCC for the WT allele; GCTAAAGCGCAGTCCGAGACTG and ACAGCGGAGACAGAATGTTCC for the targeted allele. The null phenotype was confirmed by Western blotting of brain homogenates with antibodies to MALS-3.

**Generation of MALS TKO mice**

Female MALS-1/2 null mice (Misawa et al., 2001) and male MALS-3 null mice were mated, generating MALS-1/2/3 triple heterozygous mice. Triple heterozygous mice were bred back to MALS-1/2 null mice, and MALS-1/2 double null and 3 heterozygous mice were selected. These mice were interbred to generate MALS-1/2/3 triple null mice. Genotyping for the MALS-1 and -2 targeted loci has been described previously (Misawa et al., 2001).

**Electrophysiology**

Microdial cultures were prepared as described previously (Bekkers and Stevens, 1991; Augustin et al., 1999). For whole cell voltage-clamp recordings in autaptic culture (10–18 days in vitro [DIV]), patch pipette solutions contained the following: 135 mM potassium glutamate, 10 mM HEPES, 1 mM EGTA, 4.6 mM MgCl2, 4 mM NaATP, 15 mM creatine phosphate, 50 μM phosphocreatine kinase, pH 7.3, and 300 mM Nmos. The extracellular solution contained 140 mM NaCl, 2.4 mM KCl, 10 mM Heps, 10 mM glucose, 4 mM CaCl2, 4 mM MgCl2, pH 7.3, and 300 mM Nmos. To determine the ratio of AMPA/NMDA EPSCs, MgCl2 was omitted from the extracellular solution; the patch pipette and extracellular solutions were prepared as described previously (Tovar and Westbrook, 1999). Cells were held at −70 mV and stimulated at 0.1 Hz with a 1–4 ms 80 mV depolarizing current pulse. Pyramidal cells were distinguished based on the decay kinetics of the evoked current and by application of 10 μM CNQX at the end of the experiment.

**Immunohistochemistry**

Adult mice were anesthetized with pentobarbital and perfused with 4% PFA in 0.1 M phosphate buffer. The brain was removed and immersed in the same fixative for 4 h at 4°C and then cryoprotected in 20% sucrose in PBS.
overnight at 4°C. 35-μm free-floating sections were cut on a sliding microtome. Endogenous peroxidase activity was inactivated by incubating brain sections in 0.5% H2O2 for 10 min. Sections were blocked for 1 h in PBS containing 3% normal goat serum and then incubated in the same buffer containing diluted 0.1 μg/ml MALS-3 antibody for 2 d at 4°C. Immunohistochemical staining was performed with an avidin/biotin/peroxidase system (ABC Elite, Vector Laboratories) and DAB (Vector Laboratories).

Online supplemental material
Fig. S1 shows the targeted disruption of the MALS-3 gene. Fig. S2 shows online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.200503011/DC1.

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