

Rac GEF Dock4 interacts with cortactin to regulate dendritic spine formation

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ABSTRACT In neuronal development, dendritic spine formation is important for the establishment of excitatory synaptic connectivity and functional neural circuits. Developmental deficiency in spine formation results in multiple neuropsychiatric disorders. Dock4, a guanine nucleotide exchange factor (GEF) for Rac, has been reported as a candidate genetic risk factor for autism, dyslexia, and schizophrenia. We previously showed that Dock4 is expressed in hippocampal neurons. However, the functions of Dock4 in hippocampal neurons and the underlying molecular mechanisms are poorly understood. Here we show that Dock4 is highly concentrated in dendritic spines and implicated in spine formation via interaction with the actin-binding protein cortactin. In cultured neurons, short hairpin RNA (shRNA)-mediated knockdown of Dock4 reduces dendritic spine density, which is rescued by coexpression of shRNA-resistant wild-type Dock4 but not by a GEF-deficient mutant of Dock4 or a truncated mutant lacking the cortactin-binding region. On the other hand, knockdown of cortactin suppresses Dock4-mediated spine formation. Taken together, the results show a novel and functionally important interaction between Dock4 and cortactin for regulating dendritic spine formation via activation of Rac.

Monitoring Editor
Paul Forscher
Yale University

Received: Nov 2, 2012
Revised: Feb 13, 2013
Accepted: Mar 18, 2013

INTRODUCTION

Dendritic spines are specialized protrusions found at dendrite postsynaptic regions of excitatory neurons in mammalian CNS (Harris and Kater, 1994), and spine morphology is directly linked to synaptic strength, stability, cell-surface receptor number, and neurotransmitter sensitivity (Kasai *et al.*, 2003). Abnormalities of spine morphology and density are associated with various neuropsychiatric disorders, such as autism spectrum disorders (ASDs), mental retardation, and schizophrenia (Lin and Koleske, 2010; Penzes *et al.*, 2011).

Filamentous actin (F-actin) is highly concentrated in dendritic spines and provides essential structural support for dendritic spine morphology (Matus *et al.*, 1982). Rho-family small GTPases, includ-

ing Rho, Rac, and Cdc42, play key roles in the regulation of F-actin organization, and these proteins also contribute to the determination of spine morphology (Tashiro *et al.*, 2000). In particular, Rac1 and RhoA have antagonistic roles in the regulation of spine formation. Activation of Rac1 promotes spine formation, growth, and maintenance, whereas activation of RhoA causes spine retraction and decreases spine density (Newey *et al.*, 2005). Several modulators of actin cytoskeletal dynamics, including p21-activated kinase, LIM kinase, insulin receptor substrate p53 (IRSp53), WASP-family verprolin-homologous protein, and Arp2/3 complex, have been implicated in the downstream signaling of Rac in the regulation of spine morphology (Meng *et al.*, 2002; Choi *et al.*, 2005). Rho GTPases are activated by guanine nucleotide exchange factors (GEFs) and are inactivated by GTPase-activating proteins (GAPs), and recent studies reported that GEFs and GAPs are involved in the regulation of dendritic spine formation (Tolias *et al.*, 2011). However, precise spatiotemporal regulation by different GEFs and GAPs is unclear.

Dock4 is a member of the Dock180-related Rho-GEF protein family and specifically activates Rac (Côté and Vuori, 2002; Meller *et al.*, 2005; Hiramoto *et al.*, 2006). DOCK4 was originally identified as a gene deleted during tumor progression (Yajnik *et al.*, 2003), and recent studies report that DOCK4 is a candidate gene for susceptibility to several neuropsychiatric disorders, including autism,

This article was published online ahead of print in MBoC in Press (<http://www.molbiolcell.org/cgi/doi/10.1091/mbc.E12-11-0782>) on March 27, 2013.

The authors declare that there are no conflicts of interest regarding this article.

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Abbreviations used: ASD, autism spectrum disorder; DHR, Dock-homology region; DIV, days in vitro; F-actin, filamentous actin; GEF, guanine nucleotide exchange factor; SH3, Src-homology 3; shRNA, short hairpin RNA.

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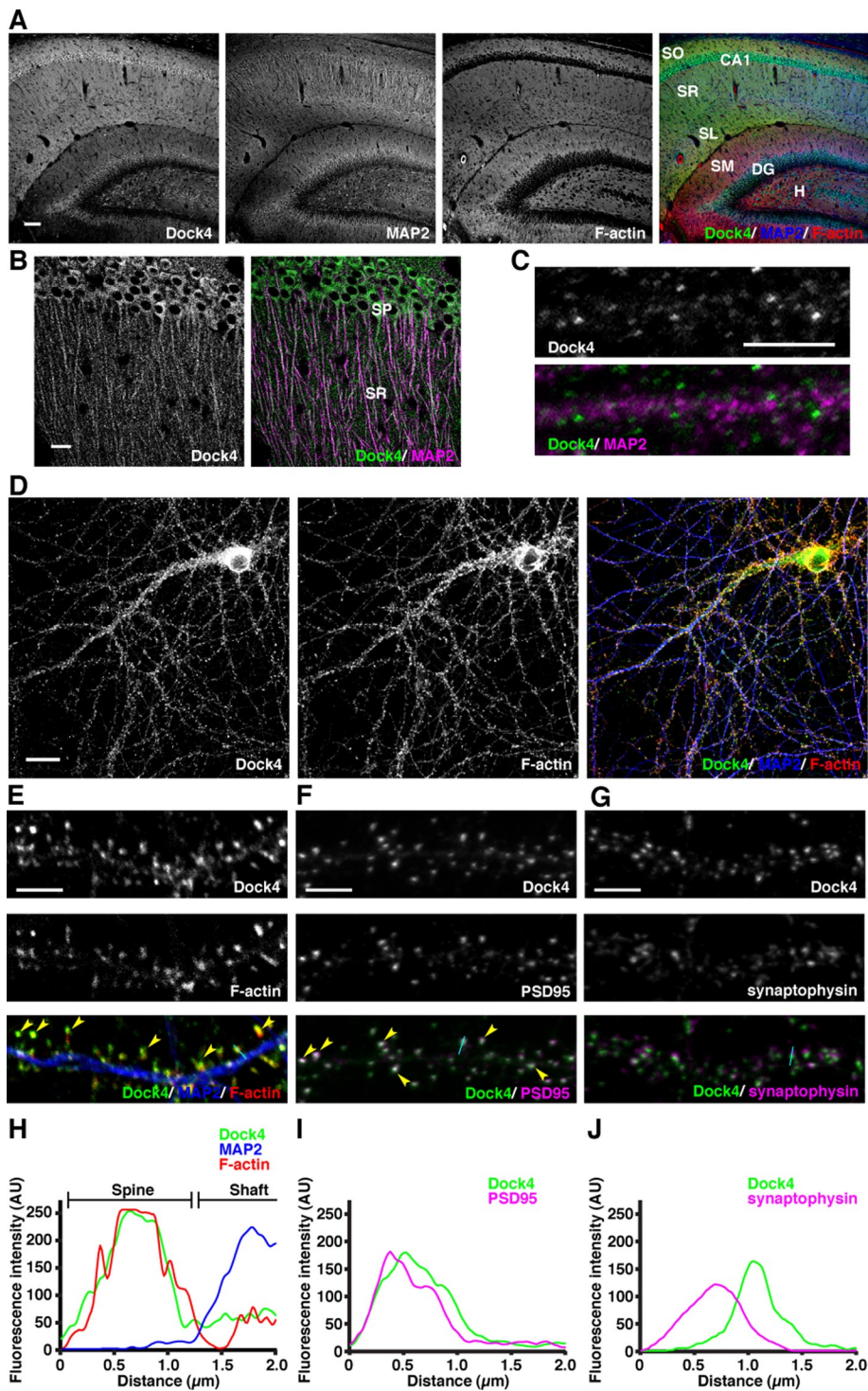


FIGURE 1: Subcellular localization of Dock4 in hippocampal neurons. (A–C) Frozen coronal sections of postnatal day 20 rat brain were incubated with anti-Dock4 antibody, anti-MAP2 antibody, and phalloidin to stain F-actin. (A) Low-magnification images of the hippocampus. Green, blue, and red indicate Dock4, MAP2, and F-actin staining, respectively. (B, C) High-magnification images of the pyramidal neurons of the CA1 region. Green and magenta indicate Dock4 and MAP2 staining, respectively. Scale bars, (A) 100 μm , (B) 20 μm , (C) 5 μm . DG, dentate gyrus; H, hilus; SL, stratum lacunosum; SM, stratum moleculare; SO, stratum oriens; SP, stratum pyramidale; SR, stratum radiatum. (D–G) Primary cultured rat hippocampal neurons were fixed at 15 DIV and then stained with indicated antibodies and phalloidin. (D, E) Green, blue, and red indicate Dock4, MAP2, and F-actin staining, respectively. (F) Green and magenta indicate Dock4 and PSD95 staining, respectively. (G) Green and magenta indicate Dock4 and synaptophysin staining, respectively. Arrowheads indicate the dendritic spines where Dock4 colocalized with

dyslexia, and schizophrenia (Maestrini *et al.*, 2010; Pagnamenta *et al.*, 2010; Alkelai *et al.*, 2012). Dock4 forms a complex with ELMO, and the ELMO–Dock4 complex serves as a functional GEF for Rac to promote cell migration in fibroblasts and breast cancer cells (Hiramoto *et al.*, 2006; Hiramoto-Yamaki *et al.*, 2010). On the other hand, Dock4 is highly expressed in rat brain, particularly in the hippocampus during late developmental stages and adulthood, and in cultured hippocampal neurons, Dock4 positively regulates dendritic growth and branching (Ueda *et al.*, 2008). However, its roles and their molecular mechanisms are largely unknown. In the present study, we provide evidence for a novel role of Dock4 in the regulation of dendritic spine development in hippocampal neurons. We also identify the actin-binding protein cortactin as a novel binding partner of Dock4. Cortactin is well known to regulate branching and stabilization of actin filaments (Weaver *et al.*, 2001) and is also implicated in spine morphogenesis and activity-dependent remodeling of spines in neurons (Hering and Sheng, 2003; Iki *et al.*, 2005; Chen and Hsueh, 2012). Our studies show that Dock4 localizes to dendritic spines and regulates spine formation through interaction with cortactin and activation of Rac.

RESULTS

Dock4 is localized to dendritic spines in hippocampal neurons

We previously reported that Dock4 mRNA is highly expressed in rat hippocampus and the expression level of Dock4 protein is up-regulated during late developmental stages, when accelerated dendritic growth and spinogenesis occur in cultured hippocampal neurons (Ueda *et al.*, 2008). To investigate the subcellular localization of Dock4 in hippocampal neurons, we first examined the distribution of Dock4 in the postnatal day 20 rat hippocampus. Immunofluorescence staining of tissue sections with anti-Dock4 antibody revealed that Dock4 was expressed in the hippocampal neurons in the cornu ammonis (CA) fields and the dentate gyrus (DG) region (Figure 1A, green). The same section was also labeled with MAP2 (blue) and F-actin (red). In the CA1 region of hippocampus, punctate Dock4 fluorescence (green) was observed along MAP2-positive

F-actin or PSD95, respectively. Scale bars, (D) 20 μm , (E–G) 5 μm . (H–J) Fluorescence intensity profiles along cyan lines drawn in E–G were measured in corresponding channels.

dendrites (magenta) of hippocampal neurons (Figure 1, B and C). Next we immunostained primary cultured rat hippocampal neurons at 15 d in vitro (DIV) and showed that Dock4 was widely distributed throughout the cell body and dendrites (Figure 1D). In particular, Dock4 fluorescence signals largely overlapped with those of F-actin and a postsynaptic marker PSD95 and were closely apposed to a presynaptic marker, synaptophysin (Figure 1, E–G). Fluorescence intensity analyses along cyan lines drawn in Figure 1, E–G, confirmed that the Dock4 fluorescence peak was entirely matched by the F-actin peak and the PSD95 peak but not the synaptophysin peak (Figure 1, H–J). Taken together, these results show the postsynaptic spine localization of Dock4 in hippocampal neurons.

Knockdown of Dock4 reduces dendritic spine density

To examine the physiological roles of Dock4 in dendritic spines, we performed RNA interference–mediated knockdown of Dock4 in cultured hippocampal neurons. We generated three short hairpin RNA (shRNA) expression vectors designed to target three different regions of mouse Dock4 cDNA (see *Materials and Methods*). Dock4 shRNA-1500 and -3685 (shDock4 #1 and #2, respectively) effectively reduced the level of Flag-tagged mouse Dock4 expressed in HEK293T cells, whereas Dock4 shRNA-114 had no effect. Therefore we used Dock4 shRNA-114 as a control shRNA (shControl; Figure 2A). Similarly, shDock4 #1 and #2 effectively reduced the intensity of endogenous Dock4 immunolabeling in cultured rat hippocampal neurons (green fluorescent protein [GFP]–positive neurons) compared with that of nearby untransfected neurons, but shControl did not (Figure 2, B and C). To examine the effects of Dock4 shRNAs on spine morphology, we cotransfected cultured hippocampal neurons with enhanced yellow fluorescent protein (EYFP) and shRNAs at 11 DIV and fixed and imaged them at 15 DIV. Expression of shControl did not affect the dendritic spine formation compared with that observed in neurons transfected with EYFP alone. However, expression of the effective Dock4 shRNAs impaired spine formation (Figure 2, D–G). Quantitative evaluations of protrusion density showed that expression of shControl had little effect on the number of dendritic protrusions (EYFP alone, 5.32 ± 0.23 spines and 0.88 ± 0.06 filopodia/10 μm ; shControl, 5.59 ± 0.22 spines and 0.98 ± 0.06 filopodia/10 μm), whereas expression of shDock4s significantly decreased spine density (#1, 3.38 ± 0.16 ; #2, 3.59 ± 0.17 ; Figure 2H). The number of dendritic filopodia also tended to decrease in Dock4-knockdown neurons (#1, 0.77 ± 0.05 ; #2, 0.81 ± 0.06 ; Figure 2H). These results suggest that Dock4 is required for dendritic spine formation in hippocampal neurons.

Rac GEF activity is required for Dock4-mediated spine formation

Dock4 contains two conserved regions among the Dock180-related proteins, Dock-homology region 1 (DHR-1) and DHR-2 domains, and the DHR-2 domain of Dock4 catalyzes the nucleotide exchange activity for Rac (Côté and Vuori, 2002; Meller et al., 2005; Hiramoto et al., 2006). To examine whether the GEF activity toward Rac is required for Dock4-mediated spine formation, we generated shRNA-resistant constructs of Dock4 (Dock4-res; Figure 3A) to restore the expression of Dock4 in knockdown cells (Figures 2A and 3C). Coexpression of Dock4-res-WT in hippocampal neurons completely rescued the reduction of protrusion density by shDock4 #1 (shControl, 6.14 ± 0.23 spines and 1.11 ± 0.06 filopodia/10 μm ; shDock4 #1, 3.54 ± 0.15 spines and 0.84 ± 0.05 filopodia/10 μm ; shDock4 #1 + res-WT, 6.24 ± 0.24 spines and 1.01 ± 0.06 filopodia/10 μm ; Figure 3, D–F and I), whereas coexpression of Dock4-res-AAA, which is defec-

tive in GEF activity toward Rac (Figure 3B; Hiramoto et al., 2006), did not (3.27 ± 0.22 spines and 0.74 ± 0.06 filopodia/10 μm ; Figure 3, G and I). These results suggest that Dock4 positively regulates dendritic spine formation through activation of Rac in hippocampal neurons.

Knockdown of ELMO2 reduces dendritic spine density

We previously reported that Dock4 interacts with ELMO through the N-terminal region, including Src-homology 3 (SH3) domain, and the ELMO–Dock4 complex serves as a functional GEF for Rac in intact cells (Hiramoto et al., 2006). Among the ELMO subfamily proteins, ELMO2 is mainly expressed in the developing hippocampus, and Dock4 interacts with ELMO2 in cultured rat hippocampal neurons (Katoh et al., 2006; Ueda et al., 2008). To examine whether ELMO2 is also implicated in spine formation, we generated an effective shRNA against ELMO2 (shELMO2; Figure 4A) and evaluated the effect of ELMO2 knockdown on spine formation. Knockdown of ELMO2 in hippocampal neurons significantly reduced spine density (shControl, 5.44 ± 0.14 spines and 0.75 ± 0.06 filopodia/10 μm ; shELMO2, 3.85 ± 0.17 spines and 0.67 ± 0.05 filopodia/10 μm ; Figure 4, B and C). These results suggest that ELMO2 is also involved in dendritic spine formation in hippocampal neurons.

The C-terminal, proline-rich region is required for Dock4-mediated spine formation

To further investigate the regulatory mechanisms of Dock4 in dendritic spine formation, we next used a deletion mutant of Dock4 lacking the C-terminal, proline-rich region (Dock4- ΔC ; Figure 3B). Coexpression of Dock4-res- ΔC failed to rescue the reduction of spine density by shDock4 #1 (4.12 ± 0.17). Instead it increased the number of dendritic filopodia (1.70 ± 0.09 ; Figure 3, H and I). Thus the C-terminal, proline-rich region of Dock4 plays a role in Dock4-mediated spine formation.

Dock4 binds to cortactin through the C-terminal, proline-rich region

Because the C-terminal, proline-rich region of Dock4 is critical for its function, we next screened Dock4-binding proteins by yeast two-hybrid system from adult rat brain cDNA library using the C-terminal region of Dock4 (amino acids 1602–1978) as bait and isolated a C-terminal fragment of cortactin (amino acids 403–546, cortactin-CT; Figure 5A) containing the SH3 domain as a potential binding partner. Cortactin is well known as a regulator of actin polymerization and stabilization in various cells (Wu and Parsons, 1993; Uruno et al., 2001; Weaver et al., 2001) and also known as a regulator of the dendritic spine formation in neurons (Hering and Sheng, 2003). To confirm the interaction between cortactin and Dock4, we expressed Flag-Dock4 in HEK293T cells and used a pull-down assay with recombinant glutathione S-transferase (GST)–fused cortactin or its mutants (Figure 5A). Wild-type cortactin (cortactin-WT) and its C-terminal fragment containing the SH3 domain (cortactin-SH3) bound Dock4, whereas a mutant lacking the SH3 domain (cortactin- ΔSH3) or containing a mutation in the SH3 domain (cortactin-W525K, which lost the ability to bind proline-rich ligands; Kinley et al., 2003) did not (Figure 5B). Thus cortactin interacts with Dock4 through the SH3 domain. Dock180, another member of Dock family of proteins, also has a proline-rich region at the C-terminus (Côté and Vuori, 2002). To determine whether Dock180 also interacts with cortactin, we transiently transfected HEK293T cells with Myc-cortactin-CT and Flag-Dock4 or Flag-Dock180, together with their constitutive binding partner

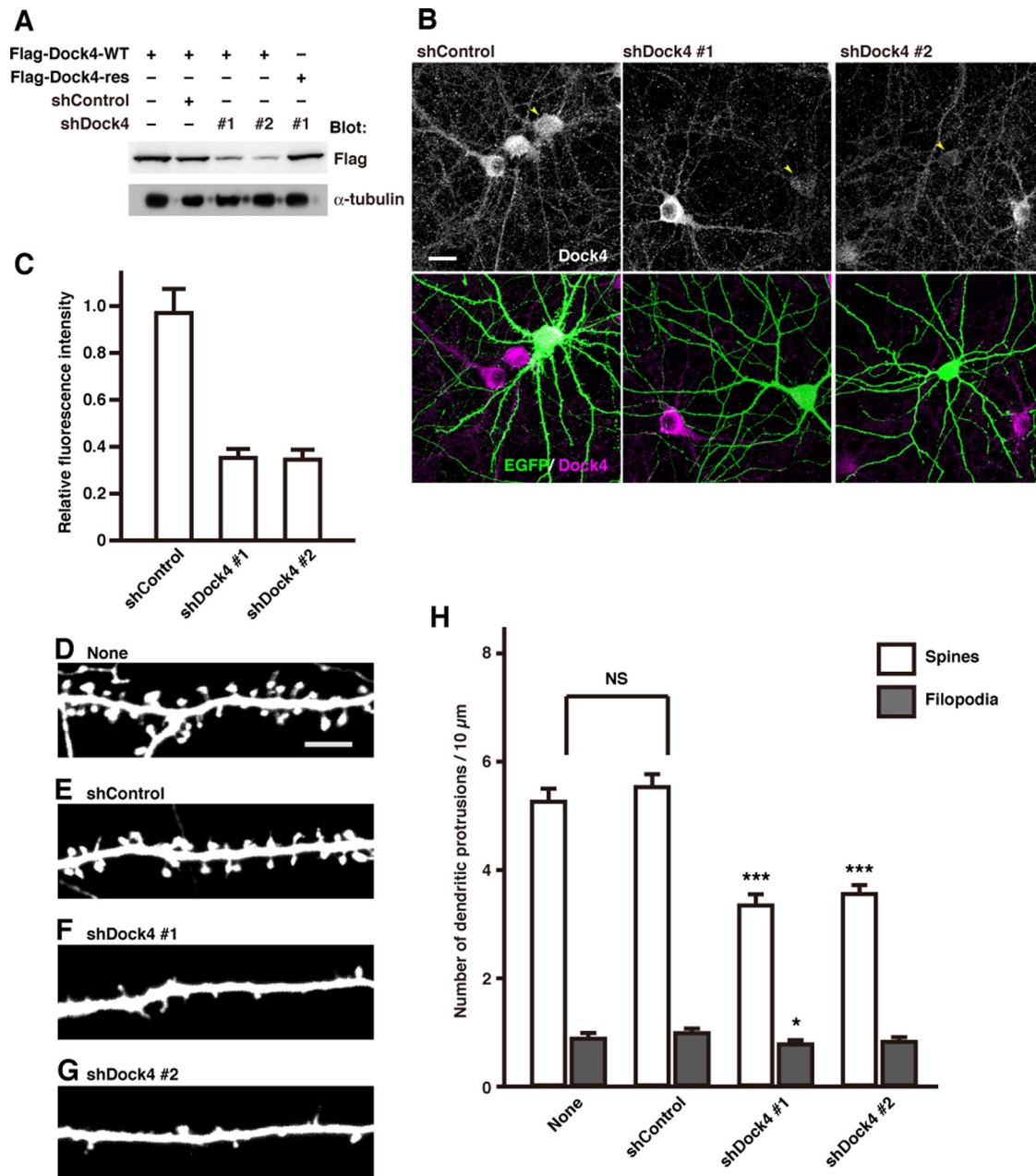


FIGURE 2: Knockdown of Dock4 suppresses dendritic spine formation. (A) Cell lysates from HEK293T cells cotransfected with indicated shRNAs (ineffective shControl or effective shDock4 #1, #2) and Flag-tagged, wild-type Dock4 (Dock4-WT) or shDock4 #1-resistant form of Dock4 (Dock4-res) were analyzed by immunoblotting with antibodies against Flag and α -tubulin. (B) Knockdown of endogenous Dock4 in hippocampal neurons. Primary cultured rat hippocampal neurons were cotransfected with EGFP and the indicated shRNA expression vector at 11 DIV. At 4 d after transfection, neurons were fixed and stained with antibody against Dock4 (magenta). Arrowheads indicate the transfected cells. Scale bar, 20 μ m. (C) Quantification of the knockdown efficiency. Under the same conditions as those in B, the Dock4 fluorescence intensity in the cell bodies of the EGFP-positive transfected cells relative to that of nearby untransfected cells was measured. The data are mean \pm SE of 10 cells. (D–G) Cultured hippocampal neurons were cotransfected with EYFP and the indicated shRNA expression vector at 11 DIV and then fixed at 15 DIV. Morphology of dendrites is shown by EYFP fluorescence. Scale bar, 5 μ m. (H) Under the same conditions as those in D–G, the dendritic protrusions per 10 μ m of dendrite were counted. The data are mean \pm SE of 45 cells in three independent experiments. * $p < 0.05$; *** $p < 0.001$ (vs. shControl).

HA-ELMO2, and immunoprecipitated the cell lysates with anti-Myc antibody. Dock4 was coimmunoprecipitated with Myc-cortactin-CT, but Dock180 was not (Figure 5C). The reason for multiple bands in blots of Myc-cortactin-CT is unknown, but they were not detected in blots from cell lysates without Myc-cortactin-CT expres-

sion (data not shown). Among Dock180-related proteins, only Dock4 contains an amino acid sequence within the proline-rich region (amino acids 1796–1803: SPPVPPRP) that was similar to a predicted binding motif for the SH3 domain of cortactin (+PPXPXKP; Sparks et al., 1996), which could explain the difference in the ability

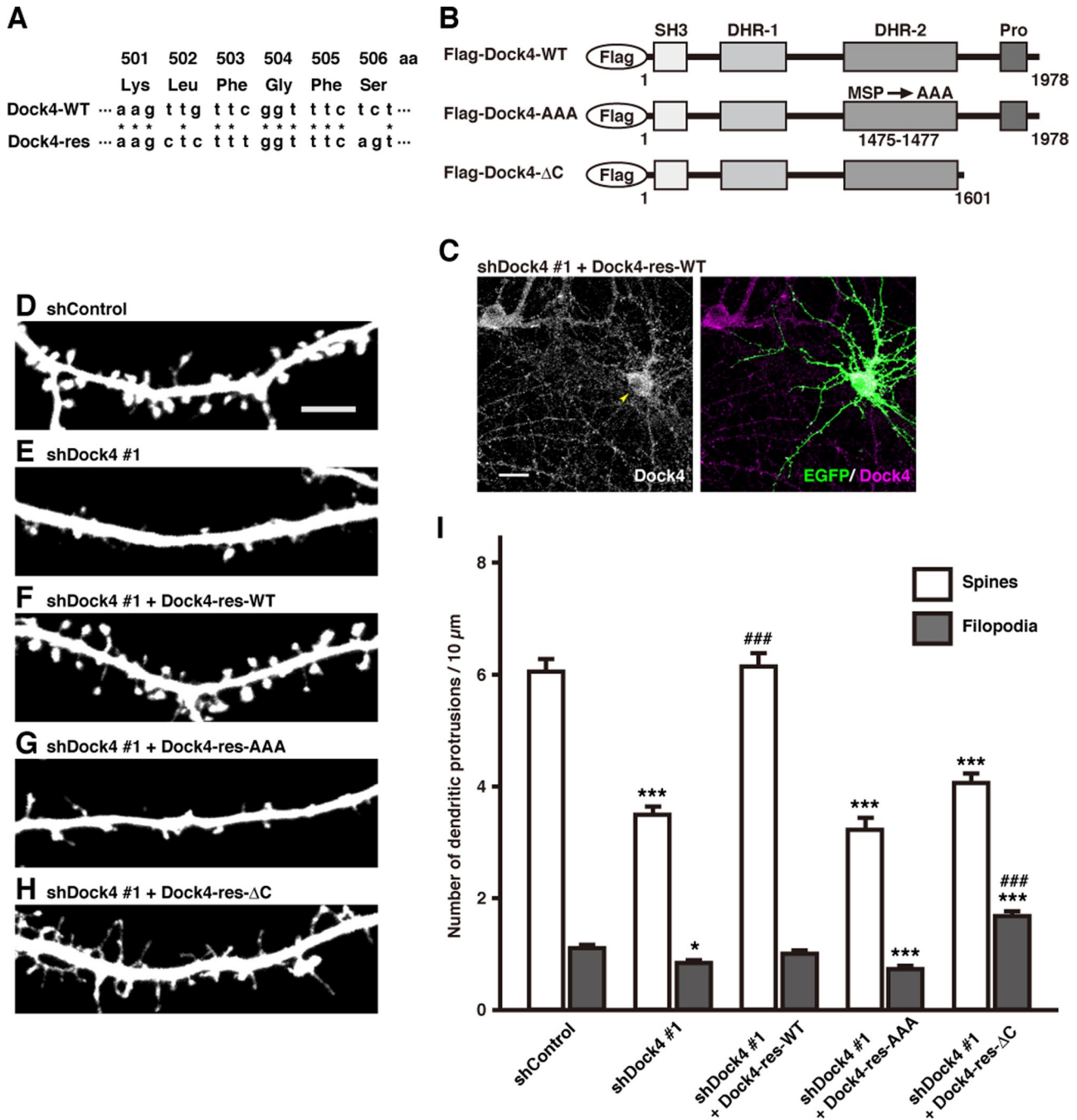


FIGURE 3: The GEF activity and the proline-rich region are required for Dock4-mediated spine formation. (A) Construction of shRNA-resistant Dock4 (Dock4-res) by silent mutagenesis. Sequence alignment of Dock4 and Dock4-res in the shDock4 #1 region is shown. Numbers indicate amino acid positions within the sequence, and asterisks indicate identical nucleotides. (B) Schematic diagram of Dock4 constructs used in this study. DHR, Dock-homology region; Pro, proline-rich region; SH3, Src-homology 3 domain. Numbers indicate amino acid positions in the sequence. (C) Primary cultured rat hippocampal neurons were cotransfected with EGFP, shDock4 #1, and Dock4-res-WT expression vector at 11 DIV. At 4 d after transfection, neurons were fixed and stained with antibody against Dock4 (magenta). Arrowheads indicate the transfected cells. Scale bar, 20 μ m. (D–H) Cultured hippocampal neurons were cotransfected with EYFP and the indicated plasmids at 11 DIV and then fixed at 15 DIV. Morphology of dendrite segments is shown by EYFP fluorescence. Scale bar, 5 μ m. (I) Under the same conditions as those in D–H, the dendritic protrusions per 10 μ m of dendrite were counted. The data are mean \pm SE of 45 cells in three independent experiments. * p < 0.05, *** p < 0.001 (vs. shControl), ### p < 0.001 (vs. shDock4 #1).

to bind to cortactin between Dock4 and Dock180. On the other hand, endogenous interaction between Dock4 and cortactin was observed in 16-DIV cultured rat hippocampal neurons by

immunoprecipitation with anti-Dock4 antibody (Figure 5D). Furthermore, immunofluorescence showed that endogenous cortactin, which was highly concentrated at dendritic spines, as reported

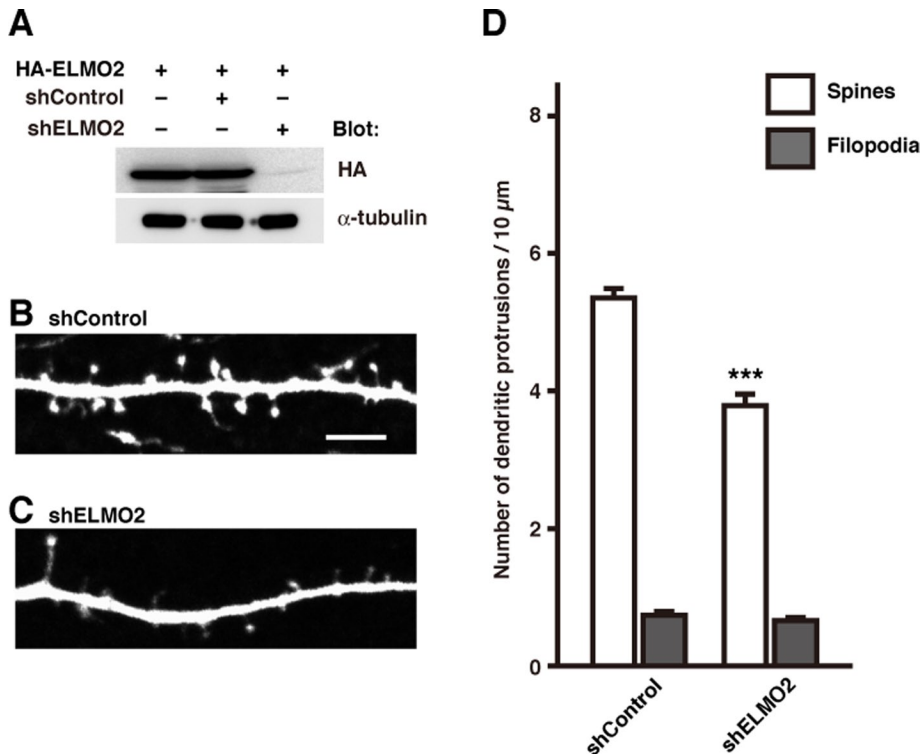


FIGURE 4: Knockdown of ELMO2 suppresses dendritic spine formation. (A) Cell lysates from HEK293T cells cotransfected with control or ELMO2 shRNA and HA-tagged ELMO2 were analyzed by immunoblotting with antibodies against HA and α -tubulin. (B, C) Cultured hippocampal neurons were cotransfected with EYFP and the indicated shRNA expression vector at 11 DIV and then fixed at 15 DIV. Morphology of dendrites is shown by EYFP fluorescence. Scale bar, 5 μ m. (D) Under the same conditions as those in B and C, the dendritic protrusions per 10 μ m of dendrite were counted. The data are mean \pm SE of 45 cells in three independent experiments. *** $p < 0.001$.

previously (Hering and Sheng, 2003), colocalized with Dock4 (Figure 5, E and F).

Cortactin is necessary for Dock4-mediated spine formation

To determine whether cortactin is involved in Dock4-mediated spine formation, we generated an effective shRNA against cortactin (shCTTN; Figure 6, A and B) to investigate the effect of cortactin knockdown on spine formation. Knockdown of cortactin in hippocampal neurons significantly reduced the spine density (shControl, 6.32 ± 0.28 spines and 1.00 ± 0.06 filopodia/10 μ m; shCTTN, 2.91 ± 0.18 spines and 0.91 ± 0.06 filopodia/10 μ m; Figure 6, C, D, and G), as previously reported (Hering and Sheng, 2003). We next assessed the effect of Dock4 overexpression on spine formation in hippocampal neurons. Cultured hippocampal neurons were cotransfected with Dock4 and ELMO2 together with shCTTN or shControl, and protrusion density was analyzed. Overexpression of Dock4 and ELMO2 with shControl led to an increase in spine density compared with that observed in neurons expressing shControl alone (7.90 ± 0.20 spines and 0.85 ± 0.05 filopodia/10 μ m; Figure 6, E and G). However, knockdown of cortactin completely suppressed the spine formation induced by overexpression of Dock4 and ELMO2. On the other hand, overexpression of Dock4 and ELMO2 in cortactin knockdown neurons increased filopodia density (3.53 ± 0.27 spines and 1.59 ± 0.08 filopodia/10 μ m; Figure 6, F and G). Of interest, these phenotypes are similar to those observed in neurons coexpressing Dock4-res- Δ C with shDock4. Taken together, these results suggest

that cortactin is required for Dock4-mediated spine formation.

The C-terminal, proline-rich region is required for spine localization of Dock4

To investigate the role of the C-terminal, proline-rich region of Dock4, we compared the distribution of Flag-Dock4-WT and Flag-Dock4- Δ C in dendrites of cultured hippocampal neurons. To minimize the effect of exogenous Dock4-WT or Dock4- Δ C on spine morphology, we fixed hippocampal neurons and stained them at 24 h after transfection (transfection at 14 DIV and fixation at 15 DIV). Flag-Dock4-WT was highly localized to spines and showed a similar distribution to that of endogenous Dock4, whereas Flag-Dock4- Δ C was observed in dendritic shafts (Figure 7, A and B). Fluorescence intensity analyses along magenta lines drawn in Figure 7, A and B, showed that the anti-Flag immunofluorescence peak of Dock4-WT was observed in the spine, whereas the peak of Dock4- Δ C was observed in the dendritic spine and shaft equally (Figure 7, C and D). On the other hand, cortactin localization to spines was unaltered by the expression of Dock4- Δ C. We also quantified the anti-Flag mean fluorescence intensity of the spine head and the dendritic shaft and expressed them as a ratio (spine/shaft fluorescence intensity). These quantitative analyses confirmed that Dock4- Δ C lost the specific localization to spines (Dock4-WT, 2.93 ± 0.23 ; Dock4- Δ C, 1.33 ± 0.21 ; Figure 7E). These results indicate that the C-terminal, proline-rich region of Dock4 is necessary for its localization to dendritic spines.

DISCUSSION

Dendritic spines are actin-rich structures, and regulation of the actin cytoskeletal reorganization is critical for dendritic spine formation and plasticity (Fischer *et al.*, 1998). The Rho-family GTPase Rac is well known as a molecular switch for signal transduction regulating the actin cytoskeleton in diverse cellular functions (Hall, 1998) and also as a key player in dendritic spine morphogenesis in excitatory neurons (Nakayama *et al.*, 2000; Tashiro *et al.*, 2000). In the present study, we show that the Rac activator Dock4 is localized in dendritic spines in hippocampal neurons and positively regulates spine formation. Our results suggest that both the Rac GFF domain and the C-terminal, proline-rich region of Dock4 play important roles in spine formation. We also find that the F-actin-binding protein cortactin interacts with the C-terminal, proline-rich region of Dock4 and is required for Dock4-mediated spine formation. Collectively our findings reveal a novel function of Dock4 in dendritic spines in hippocampal neurons.

Recent studies showed that several Rac GEFs are localized in dendritic spines and involved in spine morphogenesis (Tolias *et al.*, 2011). Among them, Kalirin-7 and Tiam1 form complexes with *N*-methyl-D-aspartate (NMDA) receptors, and their GEF activities are enhanced by calcium/calmodulin-dependent kinase II

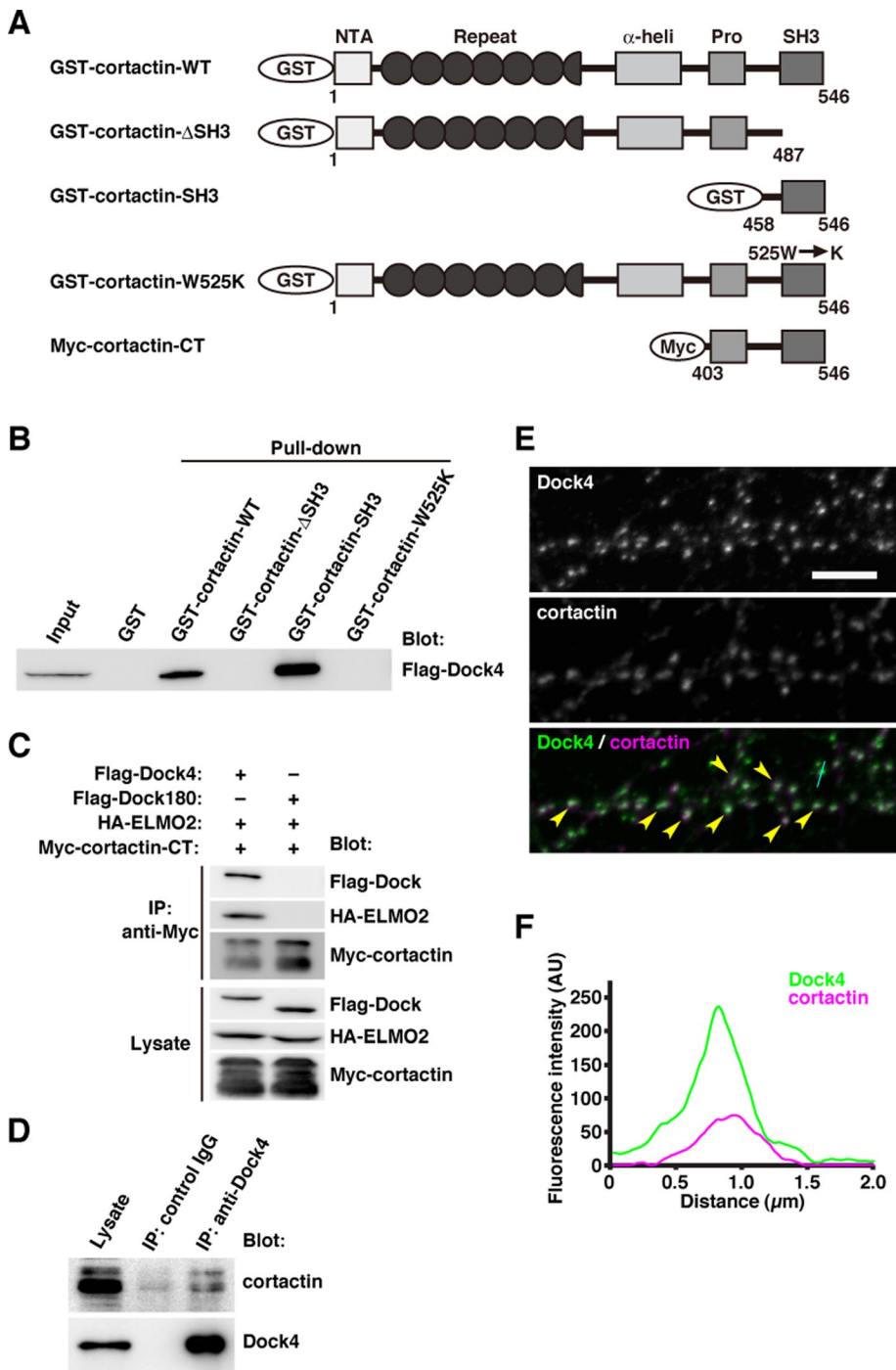


FIGURE 5: Cortactin is a novel binding partner of Dock4. (A) Schematic diagrams of cortactin constructs used in this study. NTA, N-terminal acidic region; Repeat, tandem repeat of 37-amino acid actin-binding domain; α -heli, α -helical region. Numbers indicate amino acid position in the sequence. (B) Cell lysates from HEK293T cells transfected with Flag-Dock4 were used in pull-down assay with GST or GST-fused cortactin proteins. (C) Cell lysates from HEK293T cells transfected with the indicated plasmids were immunoprecipitated with anti-Myc antibody, and bound proteins and lysates were analyzed by immunoblotting. (D) Cell lysates from cultured hippocampal neurons at 16 DIV were immunoprecipitated with anti-Dock4 antibody or control immunoglobulin G, and bound proteins and total cell lysates were analyzed by immunoblotting with anti-Dock4 and anti-cortactin antibodies. (E) Cultured hippocampal neurons at 15 DIV were fixed and double stained with anti-Dock4 (green) and anti-cortactin (magenta) antibodies. Arrowheads indicate the dendritic spines where cortactin colocalized with Dock4. Scale bar, 5 μ m. (F) Fluorescence intensity profiles along cyan line drawn in E were measured in corresponding channels.

(CaMKII)-mediated phosphorylation after glutamate stimulation of the NMDA receptor (Xie *et al.*, 2007; Tolias *et al.*, 2005). Kalirin-7 and Tiam1 are also translocated into the postsynaptic region by interacting with the EphB receptor after ephrinB ligand stimulation and enhance Rac activity in the spines (Penzes *et al.*, 2003; Tolias *et al.*, 2007). β PIX is recruited to spines by G-protein-coupled receptor kinase-interacting protein 1, and its GEF activity is also enhanced by CaMKI-mediated phosphorylation (Zhang *et al.*, 2003; Saneyoshi *et al.*, 2008). On the other hand, Dock4 forms a complex with the actin-binding protein cortactin in dendritic spines and regulates spine formation via activation of Rac. Therefore Dock4 and other Rac GEFs are targeted to dendritic spines by different systems and may generate spatiotemporally diverse regulation of Rac activity.

Cortactin binds to F-actin via the central tandem repeat region and to Arp2/3 complex via the N-terminal acidic region and promotes polymerization, branching, and stabilization of the actin cytoskeleton (Weed *et al.*, 2000; Uruno *et al.*, 2001; Weaver *et al.*, 2001). Cortactin is highly enriched in dendritic spines, where it colocalizes with F-actin and positively regulates spine formation (Hering and Sheng, 2003; Chen and Hsueh, 2012). Dock4 also colocalizes with F-actin and cortactin in spines, and Dock4-mediated spine formation requires cortactin. Cortactin interacts with the C-terminal, proline-rich region of Dock4, and deletion of this region causes a dramatic change in the localization of Dock4. Therefore the interaction with cortactin may play an important role in spine targeting of Dock4 because knockdown of cortactin results in the loss of dendritic spines. On the other hand, previous studies reported that cortactin interacts with various signaling molecules, such as N-WASP, WIP, Fgd1, ZO-1, and dynamin, through the C-terminal SH3 domain and contributes to diverse cellular processes, including cell migration, adhesion, and endocytosis (Daly, 2004; Ammer and Weed, 2008; Kirkbride *et al.*, 2011). Thus it is possible that cortactin functions as a scaffold protein to recruit these signaling molecules to the actin cytoskeleton. Of interest, the intracellular localization of cortactin is regulated by the activation of Rac1 in fibroblasts (Weed *et al.*, 1998). On the basis of these findings, we hypothesize that Dock4 may be recruited to the F-actin-rich region in dendritic spines via interaction with

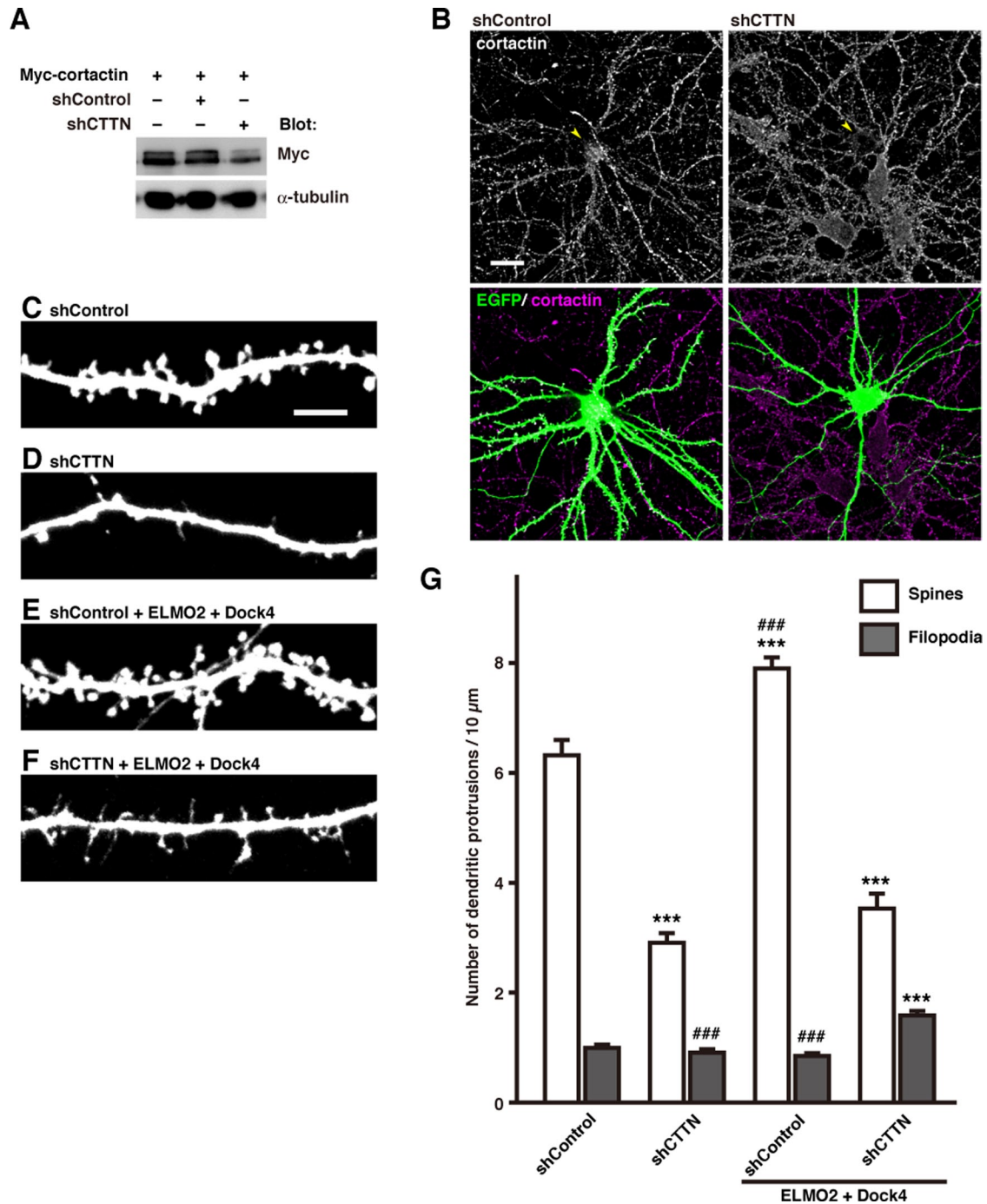


FIGURE 6: Cortactin is required for Dock4-mediated spine formation. (A) Cell lysates from HEK293T cells cotransfected with control or cortactin shRNAs and Myc-tagged cortactin were analyzed by immunoblotting with antibodies against Myc and α -tubulin. (B) Knockdown of endogenous cortactin in hippocampal neurons. Primary cultured rat hippocampal neurons were cotransfected with EGFP and the indicated shRNA expression vector at 11 DIV. At 4 d after transfection, neurons were fixed and stained with antibody against cortactin (magenta). Arrowheads indicate the transfected cells. Scale bar, 20 μ m. (C–F) Cultured hippocampal neurons were cotransfected with EYFP and the indicated plasmids at 11 DIV and then fixed at 15 DIV. Morphology of dendrite segments is shown by EYFP fluorescence. Scale bar, 5 μ m. (G) Under the same conditions as those in C–F, the dendritic protrusions per 10 μ m of dendrite were counted. The data are mean \pm SE of 45 cells in three independent experiments. *** $p < 0.001$ (vs. shControl), ### $p < 0.001$ (vs. shCTTN + ELMO2 + Dock4).

cortactin and promote actin polymerization via activation of Rac, which in turn recruits additional cortactin with Dock4 to the actin cytoskeleton, providing a positive feedback mechanism regulating the actin cytoskeleton by cortactin and Dock4 in dendritic spines.

Thin and long dendritic protrusions found in immature neurons are called dendritic filopodia. They are believed to be precursors of dendritic spines and important for initiation of synaptogenic contacts (Ziv and Smith, 1996). In this study, expression of a mutant of

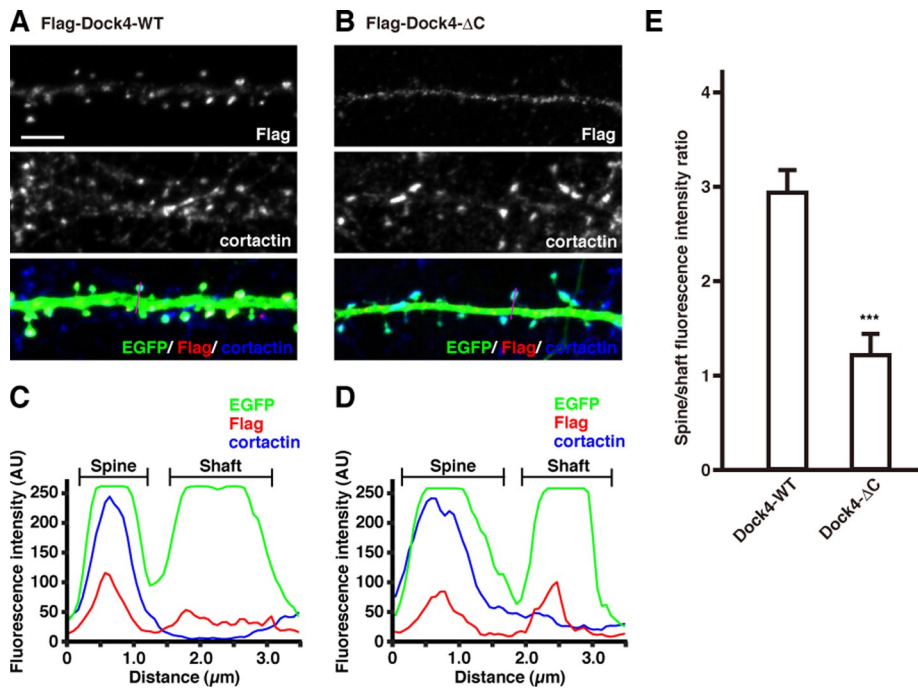


FIGURE 7: The proline-rich region is necessary for spine targeting of Dock4. (A, B) Primary cultured hippocampal neurons were cotransfected with ELMO2 and Flag-tagged Dock4-WT (A) or Dock4-ΔC (B) together with EGFP at 14 DIV and then fixed and stained at 15 DIV with antibody against Flag (magenta). Scale bar, 5 μm. (C, D) Fluorescence intensity profiles along magenta lines drawn in A and B were measured in corresponding channels. (E) Under the same conditions as those in A and B, relative anti-Flag fluorescence intensity ratio of spine/shaft normalized by EGFP fluorescence intensity was measured. The data are mean ± SE of 372 spines from 10 cells (Dock4-WT) and 270 spines from 10 cells (Dock4-ΔC). *** $p < 0.001$.

Dock4 lacking the cortactin-binding region in Dock4-knockdown neurons or overexpression of wild-type Dock4 in the absence of cortactin results in a decrease in the number of mushroom-shaped mature spines and an increase in the number of dendritic filopodia. These observations suggest that interaction between Dock4 and cortactin is necessary for spine maturation and/or mature spine maintenance. This is supported by a previous report that mutants of cortactin lacking the C-terminal region, which contains the Dock4-binding domain, significantly reduced the spine head width, even though these mutants can localize to dendritic spines (Hering and Sheng, 2003). On the other hand, it remains unclear whether Dock4 also regulates spine initiation. From the result that expression of Dock4 without cortactin interaction increases filopodia density, it is possible that Dock4 also regulates spine initiation by a cortactin-independent manner. Further investigations are required to determine at what stages (e.g., initiation, maturation, stabilization, maintenance, and plasticity) Dock4 is involved in spine formation and to understand how Dock4 regulates spine morphology in hippocampal neurons during development.

DOCK4 has been reported to be a susceptibility gene for several neuropsychiatric disorders, such as ASDs, dyslexia, and schizophrenia, by family-based, genome-wide association studies (Maestrini *et al.*, 2010; Pagnamenta *et al.*, 2010; Alkelai *et al.*, 2012). These disorders are believed to be associated with the disturbance of neuronal connectivity (Penzes *et al.*, 2011). ASDs make up a behaviorally defined syndrome characterized by deficits in social interaction, disruption of verbal and nonverbal communication, and the presence of repetitive, stereotyped behaviors (Lord *et al.*, 2000); they become established usually around 2–3 yr of age (Cox *et al.*, 1999). On the

other hand, schizophrenia is a mental disorder characterized by auditory and visual hallucinations, paranoia, delusions, blunted affect, avolition, and social withdrawal; it typically emerges in late adolescence or early adulthood (Lewis and Lieberman, 2000). Anatomical studies of hippocampal neurons have reported reduction in dendritic complexity and decrease in spine volume and number in individuals with autism and schizophrenia, respectively (Raymond *et al.*, 1996; Kolomeets *et al.*, 2005). Because Dock4 is involved in regulation of spine density in addition to its role in dendritic growth and branching in hippocampal neurons (Ueda *et al.*, 2008), dysfunction of Dock4 in dendrites during development might contribute to the pathogenesis of those psychiatric disorders. Further studies might allow us to better understand the biological mechanisms underlying these disorders and provide insights for new therapies.

MATERIALS AND METHODS

Antibodies and reagents

A rabbit polyclonal antibody against Dock4, which was used for immunoprecipitation, was obtained as described previously (Hiramoto *et al.*, 2006; Supplemental Figure S1A). The other antibodies were purchased commercially: a mouse monoclonal antibody against Dock4 used for immunoblotting and immunostaining (R6Y; Supplemental Figure S1B), a mouse monoclonal anti-Myc antibody (9E10), and a rabbit polyclonal antibody against cortactin (H-191; Santa Cruz Biotechnology, Santa Cruz, CA); a mouse monoclonal antibody against cortactin (4F11; Millipore, Billerica, MA); rabbit monoclonal antibodies against PSD95 (EP2652Y) and synaptophysin (YE269) and a rabbit polyclonal antibody against MAP2 (Abcam, Cambridge, MA); mouse monoclonal antibodies against Flag (M2) and α -tubulin (B-5-1-2; Sigma-Aldrich, St. Louis, MO); a rat monoclonal antibody against hemagglutinin (HA; 3F10; Roche, Indianapolis, IN); secondary antibodies conjugated to horseradish peroxidase (HRP; Dako, Carpinteria, CA); and secondary antibodies conjugated to Alexa Fluor 488, 555, and 647 (Invitrogen, Carlsbad, CA). F-actin was visualized with rhodamine-phalloidin (Invitrogen).

Plasmid constructs

The expression plasmid encoding Flag-tagged human Dock180 (pCXN2) was a gift from M. Matsuda (Kyoto University, Kyoto, Japan). EYFP expression vector (pCAG) was a gift from J. Miyazaki (Osaka University, Osaka, Japan) and T. Saito (Chiba University, Chiba, Japan). Flag-tagged mouse Dock4-WT, Dock4-AAA (M1475A, S1476A, P1477A), Dock4-ΔC (amino acids 1–1601), and HA-tagged rat ELMO2 were generated as described previously (Katoh and Negishi, 2003; Hiramoto *et al.*, 2006). EGFP was inserted into pCXN2. Mouse cortactin was obtained by reverse transcription PCR from mouse brain and subcloned into pCMV-Myc (Clontech, Mountain View, CA) or pGEX-4T-2 (GE Healthcare, Piscataway, NJ). Cortactin-ΔSH3 (amino acids 1–487), cortactin-SH3 (amino acids 458–546), and cortactin-W525K were generated by PCR-mediated

mutagenesis and subcloned into pGEX-4T-2. All shRNAs used in this study were expressed by using an shRNA expression vector, pSi-lencer-hygro (Ambion, Austin, TX). The shRNAs for Dock4 were designed to target 19 or 21 nucleotides of the mouse transcript (sh-Control, nucleotides 114–132, 5'-GTGCGACGGCTGGTACAGA-3'; shDock4 #1, nucleotides 1500–1518, 5'-GAAGTTGTTCCG-TTTCTCT-3'; shDock4 #2, nucleotides 3685–3705, 5'-GCCTA-CACTCTCCTGTTGTAT-3'). The shRNA for ELMO2 was designed to target 19 nucleotides of the mouse transcript (shELMO2, nucleotides 1998–2016, 5'-GGATATGTCCAGCGAGCTA-3'). The shRNA for cortactin was designed based on an shRNA sequence in a previous report (Hering and Sheng, 2003; shCTTN, nucleotides 330–348, 5'-GCACTGCTACAAGTGGAC-3'). The Dock4 shRNA-resistant constructs, Dock4-res, were obtained by introducing silent mutations within the target sequence of shDock4 #1 (nucleotides 1500–1518 were replaced with 5'-GAAGCTCTTTGTTTCAGT-3').

Immunohistochemistry

All rats used in this study were purchased from Japan SLC (Hamamatsu, Japan) and treated in accordance with the guidelines of the Animal Care and Use Committee of Graduate School of Bio-studies at Kyoto University. Postnatal day 20 Wistar rats were anesthetized and transcardially perfused. Isolated brains were fixed with 4% paraformaldehyde and then saturated with 30% sucrose in phosphate-buffered saline (PBS). Frozen brains were sliced in 30- μ m-thick coronal sections using a cryostat (CM3050S; Leica, Wetzlar, Germany). Sections were washed with PBS, permeabilized with 0.3% Triton X-100 in PBS for 15 min, and then blocked with PBS containing 2% goat serum and 0.15% Triton X-100 for 1 h at room temperature. The sections were incubated with the primary antibodies for 24 h at 4°C. After washing with PBS containing 0.1% Tween 20, the sections were incubated with the appropriate secondary antibodies and rhodamine-phalloidin for 24 h at 4°C. Then they were washed with PBS containing 0.1% Tween 20 and mounted with ProLong Gold Antifade Reagents (Invitrogen). Confocal images were acquired using a laser-scanning confocal imaging system (FLUOVIEW FV1000-D; Olympus, Tokyo, Japan) and a microscope equipped with spectral system (IX81-S; Olympus) with a 10 \times /numerical aperture (NA) 0.40 dry or a 60 \times /NA 1.35 oil objective (Olympus). The images were arranged and labeled using Photoshop (Adobe, San Jose, CA).

Cell culture and transfection

Primary hippocampal neurons were prepared from the hippocampi of embryonic day 19 (E19) Wistar rats as described previously (Ueda *et al.*, 2008) and seeded on 24-well culture plates containing glass coverslips (circular, 13 mm in diameter; Matsunami Glass, Osaka, Japan) coated with poly-L-lysine (Sigma-Aldrich) at a density of 3 \times 10⁴ cells in DMEM (Nissui Pharmaceutical, Tokyo, Japan) supplemented with 10% fetal bovine serum (FBS), 4 mM glutamine, 100 U/ml penicillin, and 0.1 mg/ml streptomycin and cultured under humidified air containing 5% CO₂ at 37°C for 5 h. Then culture medium was replaced with Neurobasal medium (Invitrogen) containing 2% B27 supplement (Invitrogen), 0.5 mM GlutaMAX (Invitrogen), 50 U/ml penicillin, and 0.05 mg/ml streptomycin, and neurons were cultured under humidified air containing 5% CO₂ at 37°C. Transient transfections were carried out at 11 or 14 DIV using Lipofectamine 2000 (Invitrogen) according to the manufacturer's instructions.

HEK293T cells were cultured in DMEM containing 10% FBS, 4 mM glutamine, 100 U/ml penicillin, and 0.1 mg/ml streptomycin under humidified air containing 5% CO₂ at 37°C, and transient transfections were carried out using Lipofectamine Plus (Invitrogen) according to the manufacturer's instructions.

Pull-down assay, immunoprecipitation, and immunoblotting

For GST pull-down assays, recombinant GST-fusion proteins were purified from *E. coli* as described previously (Kato *et al.*, 1998). HEK293T cells transfected with Flag-tagged Dock4 were lysed with the ice-cold cell lysis buffer (50 mM Tris-HCl, pH 7.5, 100 mM NaCl, 2 mM MgCl₂, 1% Triton X-100, 10 mM NaF, 1 mM Na₃VO₄, 1 mM phenylmethylsulfonyl fluoride [PMSF], 1 mM dithiothreitol, 10 μ g/ml aprotinin, and 10 μ g/ml leupeptin). Cell lysates were then centrifuged for 10 min at 16,000 \times g at 4°C. The supernatants were incubated for 10 min at 4°C with 10 μ g GST or GST-fused cortactin proteins and subsequently with glutathione-Sepharose beads for 1 h at 4°C. After washing with ice-cold cell lysis buffer, the bound proteins were analyzed by SDS-PAGE and immunoblotting.

For immunoprecipitation, HEK293T cells cotransfected with the indicated plasmids, or primary cultured hippocampal neurons were lysed for 10 min with ice-cold cell lysis buffer (50 mM Tris-HCl, pH 7.5, 100 mM NaCl, 2 mM MgCl₂, 1% Triton X-100, 10 mM NaF, 1 mM Na₃VO₄, 1 mM PMSF, 10 μ g/ml aprotinin, and 10 μ g/ml leupeptin). After centrifugation for 10 min at 16,000 \times g, the supernatants were incubated with indicated antibodies for 1 h, followed by incubation with protein G-Sepharose (GE Healthcare) for 1 h. Then the beads were washed with the cell lysis buffer, and the bound proteins were analyzed by SDS-PAGE and immunoblotting.

For immunoblot analysis, proteins were separated by SDS-PAGE and were electrophoretically transferred onto polyvinylidene fluoride membrane (Millipore). The membrane was blocked with 3% low-fat milk in Tris-buffered saline and then incubated with primary antibodies. The primary antibodies were detected with HRP-conjugated secondary antibodies and chemiluminescence detection kits (Chemi-Lumi One [Nacalai Tesque, Kyoto, Japan] or ECL Prime [GE Healthcare]). Images were captured using a LAS3000 analyzer (Fujifilm, Tokyo, Japan).

Immunofluorescence microscopy

Primary cultured hippocampal neurons on coverslips were fixed with 4% paraformaldehyde in PBS for 15 min. After residual paraformaldehyde had been quenched with 50 mM NH₄Cl in PBS, the cells were permeabilized with 0.2% Triton X-100 in PBS for 10 min and incubated with 10% FBS in PBS for 30 min to block nonspecific antibody binding. Then cells were incubated with primary antibodies in Can Get Signal Immunostain Immunoreaction Enhancer SolutionA (Toyobo, Osaka, Japan) for 1 h. After wash with PBS, cells were incubated with the appropriate Alexa-conjugated secondary antibodies and rhodamine-phalloidin for 1 h, washed with PBS, and mounted in ProLong Gold Antifade Reagents (Invitrogen). The Z-stacked images were acquired using a laser-scanning confocal imaging system (FLUOVIEW FV1000-D; Olympus) and a microscope equipped with spectral system (IX81-S; Olympus) with a 60 \times /NA 1.35 oil objective (Olympus; five planes with 0.52- μ m step width per stack; Figures 1, 5, and 7) or a laser-scanning confocal imaging system (EZ-C1 version 3.20 software; Nikon, Melville, NY) and a microscope (Eclipse TE2000-U; Nikon) with a 60 \times /NA 1.40 oil objective (Nikon) and a digital camera (DXM1200C; Nikon; six planes with 0.3- μ m step width per stack; Figures 2, 3, 4, and 6). The images were arranged and labeled using Photoshop (Adobe).

Image analysis and quantification

Quantification of dendritic protrusion density was performed using ImageJ software (National Institutes of Health, Bethesda, MD). Protrusions were manually counted along >250 μ m of total dendrite segments per neuron. In this study, dendritic spines were defined as protrusions with mushroom-shaped heads or stubby-shaped

structures, and dendritic filopodia were defined as headless protrusions. At least 45 neurons per experimental group were collected from three independent experiments, and statistical differences for multiple groups were assessed by one-way analysis of variance and Tukey's post hoc test using SPSS 16.0 software (IBM, Armonk, NY).

Quantification of spine/shaft fluorescence intensity ratio was performed using Photoshop software. Averages of anti-Flag immunofluorescence intensity of $>1 \mu\text{m}^2$ of the spine head (to eliminate immature spines) and the dendritic shaft areas and EGFP fluorescence intensity of the same areas were measured. Then anti-Flag fluorescence values were normalized with EGFP fluorescence values as a volume marker, and spine/shaft ratios were calculated.

Yeast two-hybrid screening

A rat cDNA library fused to the GAL4 activation domain of the pACT2 vector (Clontech) was screened using pGBKT/Dock4-CT (amino acids 1602–1978) as bait in the yeast strain AH109 according to the manufacturer's instructions. Interaction between the bait and library proteins activates transcription of the reporter gene *HIS3*, *Ade*, and *lacZ*. From 8.7×10^6 transformants, 323 colonies grew on selective medium lacking histidine and adenine and were also positive for β -galactosidase activity. One of those was found to encode the C-terminal 144 amino acids of cortactin. For the β -galactosidase filter assay, colonies of yeast transformants were transferred onto Hybond-N filter papers (Amersham Biosciences, Piscataway, NJ) and permeabilized in liquid nitrogen. Each filter was placed on a Whatman No. 2 filter paper that had been presoaked in Z buffer (60 mM Na_2HPO_4 , 40 mM NaH_2PO_4 , 10 mM KCl, 1 mM MgSO_4 , and 37.5 mM β -mercaptoethanol) containing 0.33 mg/ml 5-bromo-4-chloro-3-indoyl- β -D-galactopyranoside and was incubated at 30°C for 5–8 h.

ACKNOWLEDGMENTS

We thank M. Matsuda for the Dock180 expression plasmid and J. Miyazaki and T. Saito for the EYFP expression plasmid. This work was supported in part by Grants-in-Aid for Scientific Research from the Ministry of Education, Culture, Sports, Science and Technology of Japan: Scientific Research (B) 23370085 (to H.K.), 23390019 (to M.N.), Challenging Exploratory Research 24659031 (to H.K.), and Research Fellowship for Young Scientists (DC) 236767 (to S.U.).

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