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The X-linked microtubule-associated protein, Mid1, regulates axon development

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Abstract

Opitz syndrome (OS) is a genetic neurological disorder. The gene responsible for the X-linked form of OS, *MID1*, encodes an E3 ubiquitin ligase that regulates the degradation of the catalytic subunit of protein phosphatase 2A (PP2Ac). However, how Mid1 functions during neural development is largely unknown. In this study, we provide data from *in vitro* and *in vivo* experiments suggesting that silencing Mid1 in developing neurons promotes axon growth and branch formation, resulting in a disruption of callosal axon projections in the contralateral cortex. In addition, a similar phenotype of axonal development was observed in the *Mid1* knockout mouse. This defect was largely due to the accumulation of PP2Ac in Mid1-depleted cells as further down-regulation of PP2Ac rescued the axonal phenotype in both *in vitro* and *in vivo* experiments. Together, these data demonstrate that Mid1-dependent PP2Ac turnover is important for normal axonal development and dysregulation of this process may contribute to the underlying cause of OS.

Significance

The gene responsible for the X-linked form of Opitz syndrome (OS), *MID1*, encodes an E3 ubiquitin ligase and was reported to guide the degradation of the catalytic subunit of protein phosphatase 2A (PP2Ac). But whether and how it is involved in neural development is unclear. We demonstrate here Mid1-dependent PP2Ac turnover is involved in axon development. Knocking down or knocking out Mid1 not only promotes axon growth and branching *in vitro*, but also accelerates axon elongation and disrupts the pattern of callosal projection in mouse cortex. These defects can be reversed by down-regulating the accumulated PP2Ac in Mid1-depleted cells. Dysfunction of this Mid1-PP2Ac pathway may underlie neural symptoms of OS patients.

\Body

Mental retardation (MR) is a neurological disorder typically associated with brain malformation and intellectual disability. Gene mutations on the X chromosome can lead to different types of syndromic and non-syndromic forms of MR, which are collectively termed X-linked mental retardation (XLMR) (1) . The genes associated with XLMR have diverse functions, such as transcriptional regulation and neuronal morphogenesis (2, 3). Opitz G/BBB syndrome (Opitz syndrome; OS) is a genetically heterogeneous disorder characterized by distinctive facial and genital features, as well as a spectrum of variably penetrant phenotypes, including structural heart defects, structural brain anomalies, intellectual disability, and developmental delay (4). The gene responsible for the X-linked form of OS has been identified and named *Midline*-1 (*MID1*) (5). *Mid1* encodes a 667-amino acid protein of the RBCC/TRIM family, and has been

shown to exhibit E3 ligase activity (6). The Mid1 protein is highly conserved between rodents and human(7), and its transcript is expressed ubiquitously in embryonic tissues, with the highest levels observed in the progenitor cells of the central nervous system and where cell proliferation is active (7, 8). Full length Mid1 protein is associated with microtubules (9, 10), and the most frequently reported cases of mutations or deletions in Mid1 occur at its C-terminus (11), which is known to disrupt its association with microtubules, leading to the clustering of truncated Mid1 (9). Additional researches have implicated Mid1 in the development of *C.elegans* (12, 13), *Xenopus* (14) and chicken (15). However, whether and how Mid1 plays a role in the development of the mammalian central nervous system, and especially in neuronal development, remains largely unknown.

Previous studies revealed that Mid1 has multiple binding partners (16-18), including the α4 subunit of the major cellular phosphatase PP2A. It guides the degradation of the catalytic subunit in the PP2A complex (PP2Ac), and is associated with microtubules (16). Recently, the Mid1-PP2Ac complex has been shown to be involved in asthma (19) and in regulating mRNA translation (20). Here, we report that Mid1-dependent turnover of PP2Ac is required for proper axonal development, specifically for the control of axonal growth speed and branch formation. We reported that Mid1 is highly expressed in the cerebral cortex during development and enriched in the axon segment of developing neurons. Silencing Mid1 in cultured neurons increased axonal growth and branch formation, while down-regulation of Mid1 in the developing cortex accelerated callosal axon growth, and altered the projection pattern of callosal axons in the contralateral hemisphere. In addition, a similar defect of axon development was observed in *Mid1*

knockout (KO) mice. Consistent with an observed increase in PP2Ac levels following loss of Mid1, knockdown of PP2Ac in Mid1-depleted cells rescued the axonal phenotypes both *in vitro* and *in vivo*. Here, we report the first demonstration of the importance of Mid1-regulated PP2Ac turnover in axon development, and provide a possible mechanism underlying the pathological outcomes observed in OS.

Results

Mid1 is expressed in the developing brain and enriched in the axonal segment of developing neurons.

Real-time PCR showed that *Mid1* mRNA was strongly expressed, and at similar levels from embryonic day (E) 14 to adult in the mouse cerebral cortex (Fig. S1A). Similarly, the level of Mid1 protein remained relatively high throughout development and peaked between E15 and postnatal day (P) 3, and then slightly decreased at later postnatal stages (Fig. S1B). *In situ* hybridization demonstrated that *Mid1* mRNA was abundant in the ventricular/subventricular zone (VZ/SVZ) at E15, and extended to the cortical plate (CP) at E18 (Fig.1A and Fig. S1C). After birth, *Mid1* mRNA was primarily located in the cerebral cortex, olfactory bulb, hippocampus and cerebellum (Fig. S1C), and it was mainly expressed in cortical layers II/III and VI at P7 and P14 (Fig. 1A).

Previous research reported that Mid1 is a microtubule-associated protein (9). Consistently, we found that ectopic GFP-tagged Mid1 co-localized with tubulin in COS7 cells, while overexpressing a C-terminus truncated form Mid1ΔCTD-GFP led to clustered punctate expression in the cytoplasm (Fig. S1D). Furthermore, endogenous Mid1 could be co-immunoprecipitated (co-IP) with tubulin in cultured cortical

neurons (Fig. 1C), indicating that Mid1 was also associated with microtubules in neurons. In polarized neurons, the endogenous Mid1 was mainly located in the soma and axons, but was relatively low in the dendrites (Fig. 1B). Normalizing the intensity of Mid1 staining to that of ectopic GFP revealed that the Mid1 staining in axons was about 4-fold greater than that in dendrites (Fig. 1D), suggesting a potential role for Mid1 in axonal development.

Depletion of Mid1 promotes axon growth and branch formation *in vitro*. Mutations of *MID1* are known to underlie the X-linked form of OS, which is characterized by midline abnormalities, including brain malformations such as agenesis of the corpus callosum (AgCC) (21). To investigate how the loss of Mid1 impacted upon neurons, we down-regulated Mid1 in cultured neurons using RNAi strategy. First, we confirmed that the Mid1 RNAi construct was specific and sufficient to down-regulate endogenous Mid1 protein through western blotting and immunostainning (Fig. S2A and Fig. S2B). Neurons transfected with the Mid1 RNAi showed a significant increase in total axon length, length of the longest axon, and the number of axon terminals, compared to control cells (Fig. 2A and Fig. 2B), indicating increased axon growth and branching. Sholl analysis further confirmed this increased axonal complexity in the Mid1 RNAi transfected neurons (Fig. S2C). However, the establishment of neural polarity appeared to be unaffected (Fig. S2F). To rule out off-target effects, a plasmid encoding the rat Mid1 protein (rMid1) was co-transfected with the Mid1 RNAi to restore Mid1 protein expression (Fig. S2A and Fig. S2B). As predicted, the axon length and branch number were restored to control levels, indicating a complete functional rescue and therefore demonstrating the specificity of the Mid1 RNAi construct (Fig. 2A and Fig.

2B). In contrast, the dendritic morphology of transfected neurons showed little difference among the three groups (Fig. S2D). To examine whether the axonal phenotype in Mid1 down-regulated neurons was observed only in cortical neurons, we repeated the above experiment in cultured hippocampal neurons. In a similar manner, knocking down Mid1 resulted in increased axonal growth and branching, while co-transfecting Mid1 rescued this effect (Fig. S2E). Thus Mid1 functions specifically to regulate axon growth, rather than neuronal polarity or dendrite morphogenesis in cultured neurons.

To further dissect how Mid1 affects axon growth, time-lapse imaging was carried out in cultured neurons. We found that knocking down Mid1 promoted axon elongation, while co-expressing rMid1 restored this phenotype (Fig. 2C and Fig. S2G). By measuring the change of neurite length and branch number over 180 minutes, we showed that down-regulating Mid1 increased the speed of axonal growth and the rate of axon branching, without affecting dendrites (Fig. 2D and Fig. S2H). Furthermore, replenishing rMid1 restored the growth speed and branching rate of axons to control levels (Fig. 2D).

Silencing Mid1 accelerates callosal axon growth and branching. To determine the role of Mid1 during neuronal development *in vivo*, we performed *in utero* electroporation of the Mid1 RNAi and GFP into a subpopulation of neural progenitor cells at E15 and analyzed brain slices at different developmental stages. First, we validated the knockdown efficacy of Mid1 RNAi *in vivo*. We sorted the GFP-positive cells from electroporated mouse brains at P0 by fluorescent activated cell sorting (FACS). Both the GFP-positive and GFP-negative cells were subjected to western blotting in control and Mid1 RNAi animals. The result showed that GFP-positive cells in Mid1 RNAi electroporated animals had dramatically decreased Mid1

expression, compared with both GFP-positive/pSUPER cells and GFP-negative cells (Fig. S3A). Although *Mid1* mRNA was highly expressed in the VZ/SVZ, the BrdU incorporation experiment showed that down-regulating Mid1 did not affect neural precursor cell proliferation (Fig. S3B). In addition, by examining the brain slices from P3 mice, we found little influence of depleting Mid1 on neuronal migration and dendritic arborization (Fig. S3C and Fig. S3D). Moreover, Cux1 and Satb2 staining confirmed that the neuronal identity of callosal neurons was not affected by silencing Mid1 (Fig. S3E).

To determine the role of Mid1 in axon development *in vivo*, we assessed callosal axon growth and projection at different postnatal stages. In the control group at P4, callosal axons originating from electroporated neurons had crossed the midline and axon bundles were restricted to the corpus callosum (CC). In mice of the same age that were transfected with the Mid1 RNAi, the axon terminals were positioned further away from the midline, indicating accelerated axon elongation (Fig. 3A and Fig. S4A). Quantitative analysis revealed that the length of axons in the CC was significantly increased in the Mid1 RNAi group (Fig. 3D). Co-transfecting the rescue construct encoding rMid1 restored this phenotype (Fig.3A and Fig.3D). In P7 mice from the control group, axons terminated predominantly in the area beneath the S1 (primary somatosensory cortex) and S1/S2 (secondary somatosensory cortex) border of contralateral cortex, with some projections in S2 and the entorhinal cortex (Etc). Suppressing Mid1 expression promoted callosal axon growth to most regions in particular with more axons invading S2 and Etc (Fig. 3B and Fig. S4B). The axon length was increased by about 30% (Fig. 3E). Replenishing rMid1 also rescued these phenotypes (Fig. 3B and Fig. 3E). These data suggest that down-regulating Mid1 in

callosal projection neurons promotes axon growth and branching *in vivo*, which is consistent with the *in vitro* phenotypes.

Depleting Mid1 affects callosal axon projection pattern in the contralateral hemisphere. Callosal axons leave the contralateral white matter and start to grow into the cortical plate at P6. This process is completed by P12, when a dense projection of callosal axons forms at the S1/S2 border that arborizes predominantly in layers 5 and 2/3 (22). In our study, a dense collection of callosal axon terminals was observed at the S1/S2 border, with minor axon projections existing in S2 and Ect at P14 in control animals (Fig. 3C and Fig. S4C), consistent with previous report (22). In Mid1-depleted neurons, however, the axon projection to the S1/S2 border was largely decreased and a dense collection of axon terminals was observed in S2 and Etc (Fig. 3C and Fig. S4C). For quantification, we devised a parameter axon distribution index (ADI) to demonstrate the axon terminal distribution in the contralateral hemisphere (Fig. S5A). From this analysis, depletion of Mid1 dramatically increased the ADI value (Fig. 3F), indicating a shift of axon terminal distribution with less in S1 and more in S2 and Etc (Fig. 3C). A similar phenotype was also observed in brain slices from P30 mice, indicating this phenotype was not transient and was maintained during development (Fig. S5C). Co-expression of rMid1 restored the axon projection pattern, as the dense region of axon terminals shifted back toward the S1/S2 border (Fig. 3C) and the ADI value returned to a level similar to that of control animals (Fig. 3F).

These changes in axon projection may result from an altered response to axon guidance cues. Thus we tested whether depleting Mid1 changed the response of growth cones to guidance cues whose roles are

well established in callosal axon pathfinding. By performing the growth cone turning assay (23), we found that depleting Mid1 had no obvious effect on the turning response of growth cones to attraction or repulsion molecules Netrin-1 and Wnt5a (Fig. S6A – Fig. S6C). In addition, Slit2-induced growth cone collapse was also unaffected in Mid1 RNAi cultures compared to controls (Fig. S6D and Fig. S6E). In addition, we investigated whether the phenotype was general or specific to the somatosensory cortex by examining coronal sections at Bregma -1.94 mm, where the S2 region becomes the AuV (secondary auditory cortex, ventral). Consistent with what we observed in the S1/S2 region, enhanced axon distribution was also observed in the AuV in the Mid1 RNAi group (Fig. S5D). This result indicated that accelerated axon growth is a general phenotype of Mid1-depleted cells *in vivo*. Thus the abnormal projection pattern of callosal axons was probably caused by enhanced axon growth and branching in a cell autonomous manner. Taken together, our data suggest that loss of Mid1 leads to aberrant axonal arborization of callosal projection neurons in the cerebral cortex, which may result from accelerated axon growth and branching.

Accumulation of PP2Ac in Mid1-depleted cells mediates defects in axonal development. Mid1 has been identified as an E3 ligase of PP2Ac, by binding to its regulatory subunit α4, and a marked accumulation of PP2Ac protein has been observed in fibroblast cells from OS patients (16). A previous study in cultured neurons has shown that PP2Ac is expressed in axons (27). Consistent with these work, we found that knocking down Mid1 increased the protein level of PP2Ac, which could be reversed by additional expression of rMid1 (Fig. 4A). We also found that down-regulating Mid1 in cultured cortical neurons led to

increasing PP2Ac staining in the axon shaft, compared with adjacently non-transfected cells (Fig. S7B). Simultaneously, the RNAi transfected cells exhibited increased acetylated-tubulin (Ac-tubulin) in axons, with the tyrosinated-tubulin (Tyr-tubulin) unchanged (Fig. S7C), indicating an altered balance between stabilized and dynamic tubulin, which may contribute to the excessive axon growth in Mid1-depleted cells. In contrast, overexpression of Mid1 caused a ~50% reduction of endogenous PP2Ac (Fig. 4A). Consistently, PP2A activity increased in Mid1-depleted neurons, whereas overexpressing Mid1 led to its decrease (Fig. S7A). Thus Mid1 negatively regulates the protein level and catalytic activity of PP2Ac in neurons. To determine whether the up-regulation of PP2Ac protein after knocking down Mid1 was a consequence of decreased protein turnover by ubiquitin-proteasome system (UPS), we treated neurons with the proteasome inhibitor MG132. We found MG132 treatment increased the protein level of endogenous PP2Ac in control neurons. In contrast, this accumulation was not obvious in Mid1-depleted cells (Fig. S7D). Furthermore, we performed IP with PP2Ac antibody and detected the ubiquitinated PP2Ac using poly-ubiquitin antibody. The results showed that down-regulating Mid1 caused a decrease in poly-ubiquitinated PP2Ac (Fig. S7D), supporting the notion that Mid1 acts as an E3 ligase to mediate the ubiquitination and degradation of PP2Ac. To further confirm the relationship between Mid1 and PP2Ac, we performed co-IP in cell lines and cultured cortical neurons. Consistent with previous reports (16, 17, 24), Mid1 and PP2Ac exist in a protein complex when Mid1, α4 and PP2Ac were expressed in HEK293 cells (Fig. S7E). Similarly, PP2Ac and α4 antibody could co-IP endogenous Mid1 and PP2Ac in cultured

neurons, while the control GFP antibody failed (Fig. 4B). These data indicate that Mid1, PP2Ac, and α4 form a complex in neurons and Mid1 acts as an E3 ligase to regulate the protein turnover of PP2Ac.

As a major protein phosphatase, PP2A is required in axonogenesis, and involved in axon guidance in *C.elegans* (25, 26). However, whether Mid1 affects axon growth through PP2A signaling is not known. In cultured neurons, we observed that overexpressing PP2Ac promoted axon outgrowth and branching, similar to the phenotype of Mid1-depleted neurons (Fig. 4C and Fig. 4D). In addition, co-transfecting Mid1 RNAi and PP2Ac RNAi (Fig. S7F) prevented the excessive axon growth found in the Mid1 RNAi group (Fig. 4C and Fig. 4D) and chronically inhibiting PP2A activity with okadaic acid (OA) in Mid1-depleted neurons also restored the axonal length and number of axonal terminals to the control levels (Fig. 4C and Fig. 4D). Similarly, overexpression of PP2Ac *in vivo* also mimicked the phenotype observed in the Mid1 RNAi-transfected brains (Fig. 4E). And introducing a PP2Ac RNAi construct successfully restored axonal growth and projection pattern, as a dense bundle of axon terminals were observed at the S1/S2 border with few projecting to the S2 region (Fig. 4E and Fig. 4F). Thus aberrant axon phenotypes that resulted from Mid1 knockdown were predominantly due to the accumulation of PP2Ac in the cells.

Corpus callosum development is abnormal in *Mid1* KO mice. Given that knockdown of Mid1 resulted in increased axon outgrowth both *in vitro* and *in vivo*, we next sought to determine whether a similar axonal phenotype existed in *Mid1* KO mice (27). Immunoblotting showed that the Mid1 protein was undetectable in the mutant animals, accompanied by the increase of PP2Ac protein (Fig. S9E). By comparing the morphology of cortical neurons cultured from WT and KO mice cortices, we found the axon length and

branch number increased in KO neurons, which is consistent with the RNAi experiment (Fig. S8A). Similarly, expressing rMid1 or PP2Ac RNAi restored the excessive axonal growth and branching (Fig. S8A). Additionally, by performing *in utero* electroporation, we found that cell proliferation, neuronal migration, and dendritic arborization were unchanged in the *Mid1* KO mice cortex (Fig. S9A - Fig. S9C). Immunostaining with specific cortical neuron markers further confirmed that *Mid1* loss-of-function did not affect cell fate determination or neuronal migration (Fig. S9D).

To examine whether genetic ablation of *Mid1* resulted in abnormal axon development, we first employed diffusion MRI tractography to examine the integrity of the CC in *Mid1* KO mice and their WT littermates, and found no obvious difference (Fig. 5A). From the whole brain tractography, streamlines passing through the CC were extracted for comparison, but no morphological differences were observed between the genotypes (Fig. 5A). No difference was observed in the number of voxels, nor the number streamlines alone or when normalized to the CC voxel volume (Fig. 5B). These data suggest that loss of Mid1 does not change gross CC morphology in adult mice. As the diffusion MRI method could not determine the growth rate of developing axons or provide precise information regarding the exact position of axonal projections, we used electroporation to examine callosal axon development in *Mid1* KO mice. We found that the callosal axons in KO mice had grown further into the contralateral hemisphere than those in their WT littermates at P4 (Fig. 5C). At P14, compared to the WT littermates, axon distribution was altered in *Mid1* KO mice, as a greater number of axon terminals, with a wider distribution, were observed in both the S1 and S2 regions but not restricted at the S1/S2 border (Fig. 5D). Consistently, the ADI of KO mice was

significantly increased (Fig. 5E). Meanwhile, we performed anterograde and retrograde tracing experiments to confirm the phenotype. When the retrograde tracer cholera toxin B subunit (CTb) was injected into S2, most of the labeled cell bodies were located in the contralateral S2 in WT animals with some cell bodies in the contralateral S1 region of KO animals (Fig. S10A), suggesting that S2 also contained axon terminals from callosal projection neurons in the contralateral S1 area. On the other hand, when the anterograde tracer biotinylated dextran amines (BDA) was injected into S1, most axon terminals were seen in the contralateral S1 in WT animals; while in KO animals, axon terminals distributed in both S1 and S2 areas (Fig. S10B). Collectively, Mid1 KO caused a broader distribution of the contralateral axon projection pattern, consistent with the knockdown experiment.

As the PP2Ac protein and PP2A activity were increased in *Mid1* KO mice brain lysates (Fig. S9E and Fig. S9F), in order to test whether this causes abnormal callosal axonal development, we introduced PP2Ac RNAi into *Mid1* KO mice, which successfully restored the axonal projection pattern (Fig. 5D), as well as the ADI value (Fig. 5E).

Interestingly, overexpression of the C-terminal truncated form of Mid1 (Mid1ΔCTD), which is common in OS patients, in either Mid1 KO cells or by electroporation into mice led to phenotypes that were different from those generated solely by gene KO. Not only did Mid1ΔCTD reverse the effect but further decrease axonal length and branching number *in vitro* (Fig. S8A), impair neuronal migration and cause an obvious decrease in axon terminals in contralateral cortex *in vivo* (Fig. S8B). This result indicated that Mid1ΔCTD may cause accumulated toxicity in the cells, and further impair neuronal migration and axon development.

Discussion

Various mutations of *MID1* have been identified in human patients with X-linked OS since the 1990s (28), and it has been reported as an E3 ligase for PP2Ac (16). However, the role of Mid1 in mammalian neural development and function is largely unknown. Here, we described a novel role for Mid1 in axon development. We provided evidence to support the conclusion that Mid1-dependent PP2Ac turnover controls axon growth and branching *in vitro*, and regulates axon elongation and projection *in vivo.*

Correct axonal connections are required for normal neural function (29). It has recently been shown that depleting *FGF13*, another XLMR candidate gene, increases callosal axon branching in the rodent cortex (30), indicating that abnormal axonal branching and targeting may underlie some XLMR. We demonstrate here that depleting Mid1 causes a dramatic axon overgrowth both in cultured cells and *in vivo,* indicating that Mid1 may act as an inhibitory factor to regulate axon growth to ensure precise structural and functional patterning, which is crucial for proper circuit formation.

As OS patients often have defects associated with midline development, including agenesis of the corpus callosum (21), we initially expected *Mid1* KO mice to display midline abnormalities of the CC. However, DTI analysis proved this was not the case, with the gross structure of CC found to be normal (Fig. 5A and Fig. 5B). Furthermore, no obvious midline defects were observed in these *Mid1*-deficient mice, nor in a *Mid1* KO line generated by another group (31). This discrepancy between human symptoms and animal phenotypes may result from different regulatory mechanisms in different species. Specifically, Mid2, a close homolog of Mid1 (32, 33), may play a redundant role and compensate for the effect of Mid1 deletion

(14, 34). In addition, many mutations identified in OS patients are located in the C-terminal region of the protein (11), which causes Mid1 to dissociate from the microtubules and form clusters (9, 17) (Fig. S1D). Interestingly, overexpressing Mid1ΔCTD could not rescue the phenotypes caused by deleting *Mid1*, but resulted in different defects *in vitro* and *in vivo* (Fig. S8A and Fig. S8B). We speculate that the reversed effect of Mid1ΔCTD in cultured neurons was not due to its ability to rescue the phenotype; instead, Mid1Δ CTD possibly has a gain-of-function consequence that causes accumulated toxicity in the cells, which further impairs neuronal migration and axon development *in vivo*.

Increasing evidence has demonstrated that remodeling of the cytoskeleton plays important roles in various aspects of brain development (35). Several genes associated with MR have also been found to be involved in cytoskeletal processes (30, 36), indicating a common pathological mechanism may underlie different human disorders. As PP2A is a major phosphatase and microtubule dynamics are widely regulated by protein phosphorylation and dephosphorylation (37), it is reasonable to hypothesize that Mid1 plays a role in neural development by modulating the cytoskeletal structure. In individuals with OS, most mutations in the *MID1* gene result in disruption of the normal distribution of protein along the microtubules, supporting the notion that functional MID1 is required along the length of the cytoskeleton (21). Indeed, subsequent studies have shown that in OS the normal regulated turnover of PP2Ac along the microtubules is perturbed, leading to other microtubule-associated proteins being caught in an abnormal phosphorylation state (16), which in turn may affect microtubule polymerization and stability. Recently, mTORC1 signaling, which is also involved in cytoskeletal remodeling, was identified as a downstream component of the

Mid1-PP2Ac pathway (38). Further investigation should therefore be focused on elucidating the downstream molecular events triggered by Mid1-directed PP2Ac regulation.

On the other hand, Madd-2, the homolog of Mid1 in *C. elegans*, has recently been shown to play a role in axon guidance through the Netrin/DCC pathway (12, 13). Although the response of growth cone to Netrin-1, Wnt5a and Slit2 exhibit no significant difference between pSUPER and Mid1 RNAi transfected neurons (Fig. S6), it would be interesting to explore whether Mid1 regulates mammalian axon development via other guidance cues.

Materials and Methods

For details, see Supporting Materials and Methods

Animals. *Mid1* mutant mice were a kind gift from Prof. Timothy Cox, were genotyped as described previously(27). We also used female ICR and C57BL/6 mice in *in utero* electroporation experiments. The morning of vaginal plug was considered to be E0.5. All experimental procedures using animals were approved by the animal care and use committee of the Institute of Neuroscience, Chinese Academy of Sciences.

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Figure Legends

Fig. 1. Mid1 is expressed in the developing cortex and enriched in axons. (A) Expression of *Mid1* mRNA in the developing mouse cortex. CP: cortical plate; IZ: intermediate zone; VZ: ventricular zone; SVZ: subventricular zone; I-VI: cortical layer I-VI; WM, white matter. (B) Mid1 is associated with microtubules and mainly located in axons. Double staining of Mid1 and the indicated markers were performed in polarized neurons at 3 days *in vitro* (DIV). (C) Mid1 is associated with tubulin in neurons. Co-immunoprecipitation was performed on lysate from cultured cortical neurons at 4 DIV with tubulin antibody. Mouse IgG was used as control. Mid1 and tubulin were detected with specific antibodies. (D) Mid1 is enriched in the axon segment. GFP-transfected neurons were stained for Mid1 at 3 DIV. Relative immunofluorescence intensity of Mid1 in axons and dendrites was quantified. The ratio of the intensity of Mid1 to GFP in dendrites was taken as 1. Results are shown as mean±SEM. 14 neurons were analyzed. ***$p<0.001$. Student's t-test. Scale bars in A, 200 μm, B and D, 20 μm.

Fig. 2. Knockdown of Mid1 promotes axon growth and branching *in vitro*. (A) Representative images of neurons transfected with GFP and the constructs indicated. At 4 DIV, the neurons were stained for GFP and Tau1 to visualize the morphology of whole cells and axons. (B) Quantification of total axonal length, longest axon length and number of axonal terminals in neurons transfected with pSUPER, Mid1 RNAi and Mid1 RNAi plus rMid1. More than 100 neurons from four independent experiments were analyzed in each group, data are shown as mean±SEM, ***p<0.001. Student's t-test. (C) Dynamics of axonal tips. Neurons transfected with the plasmids indicated were imaged for 180 min at 2 DIV. Right panels are higher magnification images of the boxed regions at the time points indicated. Magnified images of the dashed box region are shown in Fig. S2F. (D) Quantification of neurite dynamics. The change of axon length and number of axon terminals over 180 min was measured and shown as mean±SEM. n = 48 in pSUPER group, n = 74 in Mid1 RNAi group, n = 87 in Mid1 RNAi+rMid1 group, *p<0.05, **p<0.01. t-test. Scale bars, 20 μm.

Fig. 3. Silencing Mid1 accelerates callosal axons growth and changes their projection pattern. (A-C) The constructs pSUPER, Mid1 RNAi or Mid1 RNAi plus rMid1 were co-electroporated with GFP into the ventricles of E15 mice. Animals were sacrificed at different developmental stages. Brain slices at the level of Bregma -1.58 mm were stained with Hoechst and GFP antibodies to visualize the callosal axons. Arrows indicate the location of axon terminals. The S1/S2 border is labeled with white lines. Scale bar, 500 μm. S1: primary somatosensory cortex; S2: second somatosensory cortex. Ipsi: ipsilateral side to electroporation; contra: contralateral side to electroporation. (D-F) Quantitative analysis of callosal axon

length and axon distribution index. Results are shown as mean±SEM. At P4, n = 4 in each group; at P7 and P14, n = 5-7 in each group. **p<0.01. Student's t-test.

Fig. 4. PP2Ac accumulation mediates the axon abnormality following Mid1 down-regulation. (A) Mid1 negatively regulates the protein level of PP2Ac. Cortical neurons electroporated with the constructs indicated were harvested and subjected to immunoblotting at 4 DIV. For quantification, GAPDH was used as the loading control. n = 3 in each group. *p<0.05. Student's t-test. (B) Mid1 and PP2Ac interact in cultured neurons. Cortical neurons were harvested at 4 DIV and immunoprecipitation was performed with the antibodies indicated. Mid1 and PP2Ac were detected with specific antibodies. (C) Representative images of neurons transfected with different constructs at 4 DIV. GFP was amplified by immunostaining to visualize the cell morphology. (D) Quantitative analysis of the total axonal length and number of axonal terminals. Results are shown as mean±SEM. More than 100 neurons from four independent experiments were analyzed in each group. ***p<0.001. Student's t-test. (E) Representative images of brain slices at the level of Bregma -1.58 mm from P14 animals transfected with indicated constructs. The projection patterns of callosal axons were shown by GFP staining. (F) The axon distribution index of brain slices from P14 mice in different groups. n = 6-7 in each group. ***p<0.001, compared with Mid1 RNAi. t test. Scale bar in C, 20 μm, E, 500 μm.

Fig. 5. Corpus callosum development is abnormal in *Mid1* KO mice. (A) Comparison of the corpus callosum (CC) between *Mid1* KO and WT adult mice using DTI. Top panels show representative whole brain streamlines in a lateral-sagittal view of WT and KO mice. Bottom panels show CC streamlines in a

dorsal view of WT and KO mice. Streamline color follows the following orientation code: green, mediolateral; red, rostrocaudal; blue, dorsoventral. (B) The volume of the CC was measured by voxel number, the number of streamlines and the number of streamlines per voxel. n = 3 in each group. (C) Callosal axon growth is accelerated in *Mid1* KO mice. The GFP plasmid was electroporated into neuronal progenitors at E15 and GFP staining was performed in brain slices of P4 animals. Arrows indicate the axon terminals within the corpus callosum. (D) Callosal projections are abnormal in *Mid1* KO mice. GFP or PP2Ac RNAi constructs were electroporated at E15. Brain slices (Bregma -1.58 mm) from P14 *Mid1* KO mice and their WT littermates were stained for GFP to visualize the callosal projection. (E) Statistical analysis of axon distribution index in (D). Results are shown as mean±SEM. n = 7-8 in each group. ***p<0.001, compared to WT; ###p<0.001, compared to KO. Student's t-test. Scale bar in A, 1 mm, C and D, 500 μm.