

REVIEW



Extra-cell cycle regulatory functions of cyclin-dependent kinases (CDK) and CDK inhibitor proteins contribute to brain development and neurological disorders

Takeshi Kawauchi^{1,2,3}*, Mima Shikanai^{2,3} and Yoichi Kosodo⁴

¹Precursory Research for Embryonic Science and Technology (PRESTO), Japan Science and Technology Agency (JST), Saitama 332-0012, Japan

²Department of Physiology, Keio University School of Medicine, 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan

³Department of Anatomy, Keio University School of Medicine, 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan

⁴Department of Anatomy, Kawasaki Medical School, 577 Matsushima, Kurashiki 701-0192, Japan

In developing brains, neural progenitors exhibit cell cycle-dependent nuclear movement within the ventricular zone [interkinetic nuclear migration (INM)] and actively proliferate to produce daughter progenitors and/or neurons, whereas newly generated neurons exit from the cell cycle and begin pial surface-directed migration and maturation. Dysregulation of the balance between the proliferation and the cell cycle exit in neural progenitors is one of the major causes of microcephaly (small brain). Recent studies indicate that cell cycle machinery influences not only the proliferation but also INM in neural progenitors. Furthermore, several cell cycle-related proteins, including p27^{kip1}, p57^{kip2}, Cdk5, and Rb, regulate the migration of neurons in the postmitotic state, suggesting that the growth arrest confers dual functions on cell cycle regulators. Consistently, several types of microcephaly occur in conjunction with neuronal migration disorders, such as periventricular heterotopia and lissencephaly. However, cell cycle re-entry by disturbance of growth arrest in mature neurons is thought to trigger neuronal cell death in Alzheimer's disease. In this review, we introduce the cell cycle proteinmediated regulation of two types of nuclear movement, INM and neuronal migration, during cerebral cortical development, and discuss the roles of growth arrest in cortical development and neurological disorders.

Introduction

The balance between the proliferation and differentiation of progenitors determines the size of many organs, including the brain. The timing of the cell cycle exit of neural progenitors is important for the brain morphology and functions, as the defects result in several neurological disorders, including microcephaly (small brain) (Mochida & Walsh 2004; Bond & Woods 2006; Lizarraga *et al.* 2010; Miyata *et al.* 2010; Gruber *et al.* 2011). Furthermore, recent studies indicate that the regulation of cell cycle and

Communicated by: Mitsuhiro Yanagida **Correspondence:* takeshi-kawauchi@umin.ac.jp growth arrest may play some roles in subsequent differentiation and maturation steps of postmitotic neurons. Neural progenitors exhibit a cell cycle-dependent nuclear movement within the ventricular zone, named interkinetic nuclear migration (INM), which influences cell fate determination as well as neurogenesis, at least in zebrafish retina (Kosodo 2012). In addition, several cell cycle-related proteins have additional functions in the postmitotic neurons of the developing cerebral cortex (Frank & Tsai 2009). For example, the function of $p27^{kip1}$, a regulator for cell cycle exit, switches after growth arrest to regulate the migration and morphology of postmitotic neurons through actin cytoskeletal organization (Kawauchi *et al.* 2006). In mature neurons, the

disturbance of growth arrest, which induces cell cycle re-entry, eventually leads to cell death (Herrup & Yang 2007). Thus, growth arrest confers dual functions on cell cycle-related proteins, and disrupting growth arrest may be associated with neurodegenerative diseases. In this review article, we introduce the mechanisms for neurogenesis and neuronal maturation, particularly focusing on INM and neuronal migration, respectively, and discuss the possible roles of growth arrest in brain development and several neurological disorders, such as developmental and neurodegenerative diseases.

Neural progenitor cells in mammalian cerebral cortex

Neural progenitor cells, opposed to their offspring, postmitotic neurons, exhibit cell cycle progression and cell division during brain development. Before the onset of neurogenesis, neural progenitor cells expand their numbers by symmetric, proliferative division, that is, one progenitor cell produces two progenitor cells (also called 'self-renewal division'). After neurogenesis begins, the division mode switches to asymmetric division, that is, one progenitor cell produces one progenitor and one neuron or other type of progenitor (Gotz & Huttner 2005; Fietz & Huttner 2011). Currently, at least three types of neural progenitor cells have been identified in the developing mammalian cerebral cortex (Fig. 1A): apical progenitor, basal progenitor, and outer subventricular zone (OSVZ) progenitor (Fietz & Huttner 2011; Lui et al. 2011). An apical progenitor [also known as a neuroepithelial cell or radial glial cell (Gotz & Huttner 2005)] is an epithelial cell possessing two long processes along its apico-basal polarity and undergoes both symmetric, proliferative division and asymmetric, neurogenic division at the most apical end (ventricular side) of the ventricular zone (VZ) (Fig. 1A, green). A basal progenitor [also known as an intermediate progenitor (Noctor et al. 2004) or nonsurface dividing cell (Miyata et al. 2004)] lacks obvious processes and undergoes mostly symmetric, neurogenic division at the basal end of the VZ and subventricular zone (SVZ) (Fig. 1A, orange). An OSVZ progenitor [also known as an outer radial glial (oRG) cell (Hansen et al. 2010)] undergoes asymmetric, neurogenic division at the OSVZ, the inner region of brain parenchyma that is partitioned from the SVZ in primate cortex (Smart et al. 2002) (Fig. 1A, magenta). Notably, time-lapse lineage analyses have showed that apical progenitors can produce all three types of



Figure 1 Major lineage of neural progenitors in mammalian cerebral cortex and interkinetic nuclear migration (INM) of apical progenitor. (A) Three kinds of neural progenitors identified in developing mammalian cortex (1-3) and postmitotic neuron (4) are illustrated. 1: Apical progenitor (green). 2: Basal progenitor (orange). 3: OSVZ progenitor (magenta). 4: Postmitotic neuron (light blue). Reported representative lineages from each progenitor (Fietz & Huttner 2011; Lui et al. 2011) are indicated in the square box. Cell cycle phases (G1, S, G2 and M) and the nuclear movement in each phase (arrow) of apical progenitor are described. VZ, ventricular zone; SVZ, subventricular zone; and OSVZ, outer subventricular zone. See text for details. (B) Schematics of mode of nuclear movements and proposed driving forces for INM. Arrows show directions of nuclear movements in each cell cycle phase (red: G1 phase, blue: G2 phase). Proposed driving forces for each direction of nuclear movement are indicated as (a) two opposing driving forces, (b) uni-directed driving force and displacement effect for the other direction from surrounded nuclei. See text for detail. The centrosome (yellow) may play an important role in INM because the functions of many centrosomal proteins are involved in INM. Tpx2 protein (magenta) is required for INM (basal-to-apical movement) and only observed in the apical process at G2 phase during interphase, suggesting that Tpx2 links cell cycle machinery with INM. See text for detail.

progenitor cells, but other types of progenitors do not produce the apical progenitors (Miyata *et al.* 2001, 2004; Noctor *et al.* 2001, 2004; Haubensak *et al.* 2004; Shitamukai *et al.* 2011; Wang *et al.* 2011) (Fig. 1A). Thus, apical progenitors can be considered as the stem of all neural progenitor subtypes.

Interkinetic nuclear migration

What is INM?

During the progression of cell cycle phases, the nucleus of an apical progenitor conducts a unique mode of movement, named as 'INM' or 'elevator movement' (Fig. 1). INM is initially proposed by Sauer in 1935 in the embryonic vertebrate neural tube (Sauer 1935). Sauer postulated that the translocation of nuclear position occurs in accordance with the cell cycle progression; the cell division (M phase) of the neural progenitor cells takes place at the apical (ventricular) surface, followed by the nuclear movement from apical to basal during G1 phase. S phase occurs at the most basal end of the VZ and then the nucleus comes back to the apical position in G2 phase for the next cell division. A couple of decades after the first report, an experimental proof of the concept was demonstrated by labeling S-phase nuclei with ³H-thymidine, resulting in the appearance of radioactive label-incorporated chromatids in M-phase cells at the apical surface (Sauer & Walker 1959; Sidman et al. 1959; Fujita 1962). Recent advances in both light microscopy and tissue culturing methods (Miyata et al. 2001; Noctor et al. 2001) allow direct time-lapse imaging of INM.

INM has been identified not only in the embryonic neural tube of vertebrates, but also in other pseudostratified epithelial systems including invertebrates. For instance, retina in the developmental stage is a good model to analyze INM because of its relatively simple structure and accessibility for various experimental approaches, especially live-imaging to track nuclear migrations (Baye & Link 2007; Agathocleous & Harris 2009). Although much knowledge about INM has been derived from studies in the central nervous system (ectodermal origin), it has been demonstrated that INM also occurs in endoderm-originated digestive organs such as epithelia emanating from the liver bud (Bort et al. 2006) or intestin (Grosse et al. 2011) during development. Considering the evolutional aspect, it is important to compare vertebrate and invertebrate systems to clarify the types of molecules originally used for INM.

Recent studies demonstrating the existence of INM in the *Drosophila* wing disc (Meyer *et al.* 2011) and *Nematostella* ectoderm (Meyer *et al.* 2011; Nakanishi *et al.* 2012) showed that both microtubule and actomyosin motor systems (see below) are required in more phylogenetically primitive organisms, suggesting that it is difficult to presume which motor system was primarily acquired during the nervous system evolution (Kosodo 2012).

Molecular mechanisms of INM

It has been a fascinating trial to uncover the mechanism of INM; how does the direction of nuclear migration correlate to each phase of cell cycle? Using drug treatments to disrupt cellular cytoskeletons, the importance of actin (Messier & Auclair 1974; Murciano et al. 2002) and microtubule (Langman et al. 1966; Karfunkel 1972) organization for INM was determined. Moreover, the molecular machineries controlling several steps of INM were recently revealed by advanced genetic manipulations. For the basal-to-apical nuclear migration, the association of the dynein motor proteins with Lis1 to the microtubule cytoskeleton plays a major role (Gambello et al. 2003; Tsai et al. 2005). Dynactin-1 and NudC, proteins forming a complex with dynein/ Lis1, are also required for the basal-to-apical nuclear migration (Del Bene et al. 2008; Cappello et al. 2011). Centrosomes, which localize at the apical surface during interphase (Chenn et al. 1998), act as a microtubule-organizing center. The disruption of centrosomal protein functions, such as TACC, Cep120, Hook3, PCM1, and Dock7, have been found to perturb INM progression (Xie et al. 2007; Ge et al. 2010; Yang et al. 2012) (Fig. 1B). KASH proteins and SUN proteins form a physical link between the nuclear envelope and the dynein complex (Del Bene et al. 2008; Zhang et al. 2009; Yu et al. 2011). In spite of accumulated evidence that the microtubule motor system is important for the basal-to-apical nuclear migration, this is not always the case in INM of all epithelial tissue. It has been reported that in the zebrafish retina (Norden et al. 2009; Leung et al. 2011) and Drosophila wing disc (Meyer et al. 2011), not the dynein/microtubule motor system but the nonmuscle myosin with actin cytoskeleton is the main driver for the basal-toapical nuclear migration. Interestingly, Rac1, a Rho family small GTPase involved in both microtubule and actin cytoskeletal regulation (Kawauchi 2011), is reported to control the basal-to-apical nuclear

migration of neural progenitors (Minobe *et al.* 2009).

In contrast to what is known basal-to-apical nuclear migration, little information is available for apical-to-basal migration. Recent studies propose significant roles for kinesin, microtubule-associated motor, or actomyosin systems in nuclear apical-tobasal movement (Schenk et al. 2009; Tsai et al. 2010) (Fig. 1Ba). Notably, a critical role for physical displacement as a nonautonomous driving force of INM has been independently demonstrated in two systems (Fig. 1Bb). In developing zebrafish retina, it has been implicated that the trajectories of nuclear movements are largely stochastic, as mathematically postulated to fit nuclear positions (Norden et al. 2009). Subsequently, development of time-lapse quantitative analysis of nuclear movement in retina and hindbrain of zebrafish led to the conclusion that stochastic nuclear movement during phases other than the G2 phases arises passively in response to apical migration in neighboring cells (Leung et al. 2011). In developing mouse cortex, it was demonstrated that apical-to-basal migration is driven by a crowding effect in the epithelial tissue that results from continuous accumulation of nuclei due to the basal-to-apical active nuclear migration. This conclusion is achieved by nonautonomous movement of fluorescent beads from apical to basal, perturbation of basally oriented movement by disruption of basal-to-apical movement of surrounding cells, and simulation analysis (Kosodo et al. 2011). For active basal-to-apical movement, the actomyosin (Norden et al. 2009) or dynein/microtubule (Kosodo et al. 2011) motor system is used (Fig. 1Bb). The uni-directed active movement in INM would help to minimize the imbalance of nuclear density in the apical and basal regions of pseudostratified epithelia so as to preserve the homeostasis of tissue architecture during these developmental stages (Kosodo et al. 2011).

Cell cycle regulations associated with INM

Relationship between cell cycle regulation and INM

As discussed in the previous section, the nuclear movement in INM is tightly coupled to the cell cycle progression. From this standpoint, it arises the following questions: whether cell cycle progression can be a driver of INM or whether the nuclear positions can control the cell cycle progression? Inhibition of INM by the chemical inhibitor-mediated disruption of microtubule or actomyosin has been shown to have essentially no effect on cell cycle progression (Karfunkel 1972; Messier & Auclair 1974; Messier 1978; Gambello et al. 2003). However, treatment with drugs that interfere with several cell cycle steps result in the ectopic accumulation of nuclei in the neuroepithelia of developing mouse and zebrafish (Ueno et al. 2006; Kosodo et al. 2011; Leung et al. 2011). At a molecular resolution, G1 phase arrest, achieved by overexpressing p18^{Ink4c}, an inhibitor protein of cyclin-dependent kinase (CDK) 4 and/or CDK6 (Sherr & Roberts 1999; Thullberg et al. 2000), leads to the accumulation of nuclei at a basal position in the VZ of developing mouse brains (Kosodo et al. 2011). Taken together, these results indicate that cell cycle progression likely regulates the activity of migration machineries.

How then, does the cell cycle progression correlate to the driving force of INM? It has been demonstrated that the function of Tpx2 protein connects cell cycle phases to the organization of the microtubule cytoskeleton required for INM. Tpx2, a microtubule-associated protein, is not observed in G1 phase, but appears during S phase and accumulates during G2 phase and then strongly associates to the mitotic spindle in M phase in HeLa cells (Gruss et al. 2002). In the apical progenitors in mouse brains, Tpx2 localizes on the microtubule in the apical process (but not in the basal process) of G2-phase cells, but not in G1 phase (Kosodo et al. 2011). Microtubule bundles in the apical processes of G2 phase are loosened by knockdown of Tpx2, resulting in a perturbation of basal-to-apical nuclear migration (Kosodo et al. 2011). Another study reported cell cycle control of actomyosin motor systems in zebrafish retina. Visualization of myosin regulatory light chain tagged with fluorescent protein showed its G2 specific recruitment to the basal side of nuclei. This is required for the basal-to-apical nuclear migration, likely by squeezing nuclei toward the apical side of the neuroepithelium (Leung et al. 2011).

Possible involvement of INM in fate determination

As described above, our understanding of INM has greatly expanded, especially with regard to the molecular machineries that generate the forces of nuclear migrations. What remains to be uncovered in the next stage of research is clarification as to whether INM is linked to cell fate determination, particularly in the developing central nervous system (Kosodo 2012). Interestingly, certain correlations between the S-phase positions and the cell fate of neural stem cell exist. In the retina of zebrafish, proliferative cells can be distinguished from neurogenic cells as different populations by the distance of S-phase positions from the apical surface (Baye & Link 2007). One possible scenario to generate this difference in cell fate is the concentration gradient of morphogen or signaling molecule along the axis of apico-basal polarity within the tissue, with nuclei receiving different amounts of neurogenic factor at specific cell cycle phases during INM (Latasa et al. 2009). In support of this hypothesis, Notch signaling-related proteins, whose activity can promote proliferation and cell cycle re-entry of neural stem cells (Pierfelice et al. 2011), show heterogenous apico-basal distributions. INM defects caused by a dynactin mutation result in altered exposure to Notch signals and impair neurogenesis in zebrafish retina (Del Bene et al. 2008).

Provided that S-phase positioning is one of the regulating factors of cell fate in apical progenitors, it is important to consider where nuclei enter into S phase. Using an elegant time-lapse study in the developing zebrafish nervous system, nuclear movement in each stage of cell cycle has been described (Leung *et al.* 2011); there is a basal drift at the beginning of G1 phase, strong basal-to-apical movement in G2 phase, and complete stochastic movement during S phase. This result essentially matches the nuclear movements observed in the developing mouse cortex (Kosodo *et al.* 2011).

Given that S-phase nuclei have no underlying directionality, how are the positions of S phase determined? Here, we need to consider the length of G1 phase and the mechanism of apical-to-basal nuclear migration during G1 phase (see previous section). If apical-to-basal nuclear movement is driven by an active motor system, it is likely that the position at the end of G1 phase (just before S-phase entry) from the apical surface toward the basal region changes in proportion to the length of G1 phase. However, if G1 nuclear movement is driven by a passive displacement factor, the position of the S-phase cell is likely to be dependent on both the length of G1 phase and the proportion of G2-phase length to the entire cell cycle. A recent report on accelerating the G1 phase of neural progenitors in the developing mouse brain may answer this question.

Co-over-expression of Cdk4 and cyclinD1 using *in utero* electroporation in the developing mouse cortex results in a shortened G1 phase, which evokes delayed neurogenesis (Lange *et al.* 2009). In this

study, INM progression with over-expression or down-regulation of Cdk4/cyclinD1, which causes shortening or lengthening of G1 phase, respectively, is examined. Surprisingly, the positions of S-phase entry and exit are essentially the same between untransfected cells and electroporated cells in both shortened and lengthened G1 phase without affecting the number of apical progenitors (Lange et al. 2009). The experimental results show that the length of G1 phase was shortened to 65% by the over-expression of Cdk4 and cyclinD1 (from 9.0 to 5.9 h). As the position of S-phase entry is same in the overexpressed situation, this data do not appear to fit the active migration model unless the velocity of G1-phase nuclei was increased due to a side effect of Cdk4 and cvclinD1 over-expression on the motor system for the apical-to-basal nuclear migration. Next, it was demonstrated that the proportion of G2 phase (including M phase) to the entire cell cycle length increases by 1.36 times (from 14% to 19%) in the Cdk4 and cyclinD1 over-expressed condition. An increased proportion in the G2 phase raises the number of descending nuclei in a unit of time, which results in the higher density of nuclei in the apical region. According to the displacement model (see previous section), increased density of the apical region would raise the pressure to translocate nuclei in G1 phase from apical to basal. This might increase the velocity of apical-to-basal nuclear migration and compensate for a shortened G1-phase length, which would result in no obvious change for the nuclear position of S-phase entry. Perhaps, such a robust mechanism of INM might minimize effects of local disturbances of cell cycle progression on the architecture of the developing brain.

Neuronal migration

Multistep mode of neuronal migration

Newly generated immature neurons begin the pial surface-directed migration from the ventricular (apical) side, which is essential for the formation of architectural and functional cerebral cortex with a six-layered structure (Rakic 2006; Ayala *et al.* 2007; Kawauchi & Hoshino 2008; Marin *et al.* 2010; Govek *et al.* 2011; Kwan *et al.* 2012). A number of previous studies have indicated that migrating neurons exhibit multistep migration with various morphological changes (Kawauchi & Hoshino 2008) (Fig. 2). Migrating neurons first exhibit multipolar morphologies and subsequently form a leading process and an axon



Figure 2 Multistep mode of neuronal migration. Postmitotic excitatory neurons are generated at the ventricular zone (VZ) or subventricular zone (SVZ) (See the enlarged drawing of the VZ and SVZ in Fig. 1) and migrate radially toward the pial surface (Blue cells). Neurons first display multipolar morphology at the lower part of the intermediate zone (IZ) and transform into locomoting neurons. Locomoting neurons possess a leading process and migrate over a long distance along radial glial fibers with elongation of an axon in a reverse direction. The migration mode switches from the locomotion mode into a radial glial fiber-independent terminal translocation mode during the final phase of migration. CP, cortical plate; IZ, intermediate zone; MZ, marginal zone; SVZ, subventricular zone; and VZ, ventricular zone.

while retracting other neurites (Stensaas 1967; Shoukimas & Hinds 1978; Tamamaki et al. 2001; Tabata & Nakajima 2003; Noctor et al. 2004). The resulting bipolar-shaped neurons, called locomoting neurons, migrate over long distances along radial glial fibers, apical progenitor-derived long processes, with backward elongation of their axons (locomotion mode) (Rakic 1972, 2006; Nadarajah et al. 2001; Hatanaka & Murakami 2002; Noctor et al. 2004). At the final phase of migration, neurons switch from the migration mode into a radial glial fiber-independent terminal translocation mode (Nadarajah et al. 2001; Sekine et al. 2011). During the terminal translocation, dendrite maturation begins. Thus, neuronal migration is required for not only finding the final position but also neuronal maturation (Fig. 2). Defects in neuronal migration cause several neurological disorders, such as periventricular heterotopia and lissencephaly (Gleeson & Walsh 2000; Kawauchi & Hoshino 2008).

c-jun N-terminal kinase pathway and microtubule-associated proteins

The first molecules identified to be involved in the morphological changes of migrating immature neurons were a Rho family small GTPase, Rac1, and its downstream kinase, c-jun N-terminal kinase (JNK) (Kawauchi et al. 2003) (Fig. 3). JNK regulates the transition from multipolar cells into locomoting neurons. JNK phosphorylates several microtubule-associated proteins, such as microtubule-associated protein 1B (MAP1B) and DCX (also known as doublecortin) (Chang et al. 2003; Kawauchi et al. 2003, 2005; Gdalvahu et al. 2004) (Fig. 3). Mutations in DCX gene cause X-linked lissencephaly in males and subcortical band heterotopia (also known as double cortex syndrome) in females (Gleeson et al. 1998; des Portes et al. 1998). Although both MAP1B and DCX promote microtubule stability (Francis et al. 1999; Gleeson et al. 1999; Goold et al. 1999; Horesh et al. 1999; Gordon-Weeks & Fischer 2000; Kawauchi et al. 2005; Trivedi et al. 2005), JNK-mediated phosphorylation diminishes their microtubule-binding affinities, resulting in decreased the microtubule stability (that is, increases the microtubule dynamics) (Chang et al. 2003; Kawauchi et al. 2003, 2005; Gdalyahu et al. 2004). Consistent with the fact that microtubule stability is kept at low levels at the tips of neurites (Shea 1999), phosphorylated MAP1B is strongly observed at the tips of axons (Goold et al.



Figure 3 c-jun N-terminal kinase (JNK) pathway in postmitotic migrating neurons. JNK is required for the formation of a leading process (a surface-directed thick neurite of a locomoting neuron, see Fig. 2) and neuronal migration through the regulation of microtubule dynamics. MAP1B and DCX stabilize microtubules, but the phosphorylation by JNK enhances their dissociation from microtubules, resulting in an increase in microtubule dynamics.

1999; Gordon-Weeks & Fischer 2000). It has been reported that suppression of JNK or MAP1B disturbs neurite elongation (Takei *et al.* 2000; Kawauchi *et al.* 2003; Oliva *et al.* 2006; Eto *et al.* 2010). *In vivo* suppression of JNK disturbs the leading process morphology of migrating neurons and the pial surface-directed neuronal migration (Kawauchi *et al.* 2003).

As JNK belongs to a MAP kinase family, its activity is controlled by MAPKKs and MAPKKKs (Huang et al. 2004) (Fig. 3). Gene disruption of MKK4 or MKK7, MAPKKs for JNK, delays neuronal migration and disturbs axon formation (Wang et al. 2007; Yamasaki et al. 2011). Although the phosphorylation of MAP1B, but not DCX, is decreased in MKK4deficient mice, the phosphorylation of both is suppressed in the MKK7 knockout mice. In addition, inhibition of DLK/MUK, a MAPKKK for JNK, results in similar phenotypes (Hirai et al. 2006). Interestingly, gene targeting for MEKK4, another MAP-KKK for JNK, shows severe migration defects, resembling periventricular heterotopia (Sarkisian et al. 2006). Filamin A, a causative gene product of periventricular heterotopia (Fox et al. 1998), has also been reported to mediate the JNK signaling pathway

in non-neuronal cells (Nomachi *et al.* 2008; Nakagawa *et al.* 2010) as well as the morphological changes and migration of cortical neurons (Nagano *et al.* 2004). Thus, the JNK-mediated pathway has important roles in neuronal migration and axon formation, and its defects may be associated with several cortical malformations.

Cdk5 and cell adhesion

DCX is also phosphorylated by cyclin-dependent kinase 5 (Cdk5) and MAP/microtubule affinity-regulating kinase 2 (MARK2, also known as Par-1) (Schaar et al. 2004; Tanaka et al. 2004) (Fig. 4A). Cdk5 is an unconventional CDK because its activity is mainly observed in postmitotic neurons (Tsai et al. 1993). Cdk5 is activated by p35, p39, and cyclin I, but not cyclin D, E, and A (Lee et al. 1996; Hisanaga & Saito 2003; Brinkkoetter et al. 2009; Su & Tsai 2011). In vivo suppression of Cdk5 activity by gene targeting, in vivo RNA interference and dominant negative experiments, has been shown to lead to severe neuronal migration defects (Ohshima et al. 1996; Gilmore et al. 1998; Kawauchi et al. 2003, 2006) (Fig. 4B). Similar to JNK, Cdk5 is required for the formation of leading process of migrating immature neurons (Kawauchi et al. 2006). However, Cdk5 also regulates multipolar cell morphologies, compared to the lesser effect of JNK on this aspect (Hirai et al. 2006; Kawauchi et al. 2006). A recent study showed that Cdk5 activity is required for the locomotion mode of neuronal migration (Nishimura et al. 2010), indicating that Cdk5 is a central regulator for multistep migration of immature neurons (Fig. 4B).

Cdk5 phosphorylates many substrate molecules, including p27^{kip1} (Kawauchi et al. 2006), Dixdc1 (Singh et al. 2010), Ndel1 (also known as Nudel) (Niethammer et al. 2000), focal adhesion kinase (FAK) (Xie et al. 2003), p21-activated kinase 1 (PAK1) (Rashid et al. 2001), neurabin I (Causeret et al. 2007), as well as DCX (Tanaka et al. 2004) (Fig. 4A). Ndel1 binds to Lis1, a causative gene product for lissencephaly (Reiner et al. 1993), and Ndel1 and Lis1 cooperatively control cytoplasmic dynein functions (Niethammer et al. 2000; Sasaki et al. 2000; Yamada et al. 2008). The Ndel1 phosphorylated by Cdk5 interacts with 14-3-3 ϵ , which regulates the localization of Ndel1 and Lis1 (Toyooka et al. 2003). FAK is phosphorylated on Ser732 by Cdk5, and this phosphorylation is required for perinuclear microtubule organization (Xie et al. 2003). However, Cdk5 phosphorylates a neuron-specific



Figure 4 Roles of Cdk5 and cell adhesion molecules in multistep mode of neuronal migration. (A) Cdk5 phosphorylates many substrate molecules, including microtubule- and actin cytoskeleton-regulatory proteins (purple and green arrows, respectively). (B) Cdk5 is required for multiple steps of neuronal migration. Cdk5 (blue) regulates multipolar morphology of migrating neurons in a p27^{kip1}-dependent manner, but its function in the transition into locomoting neurons is independent of p27^{kip1} as suppression of p27^{kip1} does not affect this step. Several small GTPases (green) also play important roles in the multistep mode of neuronal migration. Their functions are partly mediated by the regulation of cell adhesion molecules, N-cadherin and α 5 β 1-integrin (red).

F-actin-binding protein, neurabin I (Causeret *et al.* 2007). Furthermore, Cdk5-mediated phosphorylation of p27^{kip1} promotes actin reorganization, as described below. *In vivo* suppression of these Cdk5 substrates, p27^{kip1}, Ndel1, FAK, and Neurabin I, disturbs neuronal migration mainly due to cytoskeletal defects.

In addition to cytoskeletal proteins, Cdk5 is known to regulate cell adhesion. Cell adhesion can

be classified into cell-to-cell adhesion and cell-toextracellular matrix (ECM) adhesion (Kawauchi 2012). Recent studies indicate that N-cadherin-mediated cell-to-cell adhesion plays essential roles in the multipolar and locomotion modes of neuronal migration (Kawauchi et al. 2010; Shikanai et al. 2011), whereas \$\alpha 5\beta 1-integrin, a cell-to-ECM adhesion molecule that binds to fibronectin (Kawauchi 2012), is required for the terminal translocation (Sekine et al. 2012) (Fig. 4B). Rab family small GTPases, Rab5 and Rab11, regulate the intracellular trafficking of N-cadherin, which is required for the locomotion mode of neuronal migration (Kawauchi et al. 2010; Kawauchi 2011). A ras family small GTPase, Rap1, promotes the activities of N-cadherin and integrin at the early and final phases of neuronal migration, respectively (Franco et al. 2011; Jossin & Cooper 2011; Sekine et al. 2012) (Fig. 4B). Interestingly, Cdk5 can control both N-cadherin and integrin in a small GTPase-independent manner in vitro (Kwon et al. 2000; Huang et al. 2009), although it is still unclear whether Cdk5-mediated regulation of cell adhesion is involved in neuronal migration in vivo.

Linking mechanisms of cell cycle exit and neuronal migration

Cdk5 and p27^{kip1} in cell cycle exit, neuronal differentiation and migration

The cell cycle exit, neuronal differentiation, and migration occur concurrently, along with suppression in the activities of cyclin-CDKs. However, as described above, Cdk5 is strongly activated in postmitotic neurons. Although many studies indicate that Cdk5 is a regulator for cytoskeletal organization and signal transduction, rather than cell cycle, some notable facts remain. One is that Cdk5 directly phosphorylates p27kip1, a CDK inhibitor protein (Kawauchi et al. 2006). In addition, some mature neurons in the cortical plate abnormally re-enter the cell cycle in Cdk5-deficient mice (Cicero & Herrup 2005), similar to what is observed in the brains of $p27^{kip1}/p19^{Ink4d}$ double knockout mice (Zindy et al. 1999), suggesting a functional relationship between Cdk5 and other cell cycle proteins.

It is known that p27^{kip1} regulates G1 length and cell cycle exit in the ventricular zone of the developing cerebral cortex via suppression of conventional CDK activities (Sherr & Roberts 1999; Mitsuhashi *et al.* 2001; Tarui *et al.* 2005). In contrast, Ser10 of p27^{kip1} is phosphorylated by Cdk5 in postmitotic neurons and this phosphorylation promotes its protein stability through the protection of p27^{kip1} from proteasome-dependent protein degradation (Ishida et al. 2000; Kotake et al. 2005; Kawauchi et al. 2006), suggesting that Cdk5 is an upstream positive regulator for p27^{kip1}, a CDK inhibitor protein, in G0-arrested neurons, although p27^{kip1} acts as a negative regulator for conventional CDKs (Fig. 5). Furthermore, the increased protein levels of p27kip1 have essential roles in cortical neuronal migration and the formation of multipolar cell morphologies (Kawauchi et al. 2006). Cdk5-p27^{kip1} pathway enhances actin reorganization via the suppression of RhoA activity and thereby activation of an actin-binding protein, cofilin (Kawauchi et al. 2006). It has been reported that p27kip1 is also involved in the regulation of microtubule organization (Baldassarre et al. 2005; Godin et al. 2012). Interestingly, a recent study indicates that connexin 43, a component of gap junction involved in both neural progenitor proliferation and neuronal migration (Elias & Kriegstein 2008), acts upstream of p27^{kip1} to regulate the multipolar morphology of



Figure 5 A possible link in mechanisms between cell cycle exit, neuronal differentiation, and neuronal migration. In the developing cerebral cortex, cell cycle exit, neuronal differentiation, and initiation of neuronal migration occur concurrently. A cyclin-dependent kinase (CDK) inhibitor protein, p27^{kip1}, controls the G1 length and cell cycle exit in neural progenitors via the suppression of Cyclin-CDK activities. In addition to these cell cycle regulatory functions, p27^{kip1} promotes neuronal differentiation via the up-regulation of Ngn2 protein level and neuronal migration through the suppression of RhoA activity and thereby activation of an actin-binding protein, Cofilin. Ngn2 activates the transcription of p35 as well as neuronal differentiation-related genes. In postmitotic neurons, p35 binds to and activates Cdk5, which directly phosphorylates and stabilizes p27kip1 protein and is required for the maintenance of growth arrest. A proposed feedback loop of Cdk5/ p35-p27^{kip1}-Ngn2-p35-Cdk5 is shown (red circle).

migrating neurons (Liu *et al.* 2012). Taken together, these findings suggest that $p27^{kip1}$ acquires additional functions in cytoskeletal regulation and neuronal migration during growth arrest and that this functional switch is mediated at least in part by Cdk5 (Fig. 5).

Cdk5-mediated phosphorylation of Dixdc1 also functions as a molecular switch between neural progenitor proliferation and neuronal migration (Singh *et al.* 2010). Nonphosphorylated Dixdc1 binds to Disrupted in Schizophrenia-1 (DISC1) and controls neural progenitor proliferation. In contrast, Cdk5 phosphorylates Dixdc1 in postmitotic neurons, resulting in increased interaction between Ndel1 and DISC1 and promotion of neuronal migration.

In addition to the dual functions in neural progenitors and migrating neurons, p27kip1 is involved in neuronal differentiation. A previous report showed that p27^{kip1} increases the protein levels of Neurogenin 2 (Ngn2), a basic helix-loop-helix-type transcription factor required for neuronal differentiation, and promotes neuronal differentiation (Nguyen et al. 2006). Furthermore, Cdk5 deficiency partially disturbs neuronal differentiation (Cicero & Herrup 2005; Zheng et al. 2010) as well as neuronal migration, and Cdk5-mediated phosphorylation of p27kip1 at Ser10 and Thr187 is involved in the regulation of neuronal differentiation (Zheng et al. 2010). Interestingly, p35, an activator for Cdk5, was identified as a target molecule of Ngn2 (Ge et al. 2006), and it has been reported that Ngn2 is also required for neuronal migration (Hand et al. 2005; Ge et al. 2006; Heng et al. 2008). These findings implicate a positive feedback loop of Cdk5/p35-p27kip1-Ngn2-p35 that has important roles in the growth arrest-associated neuronal differentiation and initiation of migration (Kawauchi & Hoshino 2008) (Fig. 5). The identity of the molecule(s) that turn on the positive feedback loop for the synchronized cellular events of cell cycle exit, neuronal differentiation, and initiation of neuronal migration is still unclear, but there is evidence to indicate that Notch signaling suppresses p27kip1 mRNA and/or protein levels (Sarmento et al. 2005; Vernon et al. 2006; Murata et al. 2009), suggesting that weakened Notch signal may enhance p27^{kip1} expression and thereby the positive feedback loop.

Other CDK inhibitor proteins and Rb-E2F

Other cell cycle-related proteins have also been reported to have dual functions in proliferating and arrested cells. CDK inhibitor proteins include members of Cip/Kip (p21^{cip1}, p27^{kip1}, and p57^{kip2}) and Ink4 (p16^{Ink4a}, p15^{Ink4b}, p18^{Ink4c}, and p19^{Ink4d}) families (Sherr & Roberts 1999) (Fig. 6A). Although p57^{kip2} mainly controls the cell cycle exit of earlyborn neurons (deep layer neurons), p27^{kip1} preferentially regulates the growth arrest of late-born neurons (upper layer neurons) (Mairet-Coello *et al.* 2012) (Fig. 6B). In the postmitotic neurons, it has been reported that not only p27^{kip1} but also p57^{kip2} is involved in neuronal migration (Itoh *et al.* 2007). Consistently, both proteins are localized at the leading process and cell soma as well as nucleus in migrating neurons (Kawauchi *et al.* 2006).

Furthermore, retinoblastoma (Rb) protein and E2F family transcription factors are reported to regulate both cell cycle in neural progenitors and migration in postmitotic neurons. Rb protein binds to and represses the E2F functions, whereas Cdk-dependent phosphorylation of Rb dissociates E2Fs from the Rb protein, allowing E2Fs to interact with target DNA sequences (Giacinti & Giordano 2006) (Fig. 6A). Knockout of the Rb gene perturbs the neuronal positioning in cerebral cortex, and the phenotypes are rescued by double knockout of Rb and E2F3, but not E2F1 (Ferguson et al. 2005; McClellan et al. 2007). Although the switching mechanism of Rb-E2F functions is unclear, a recent study shows that Cdk5 has the ability to phosphorylate Rb protein (Futatsugi et al. 2012). In addition to the regulators for G1/S transition, Aurora A and anaphase-promoting complex/cyclosome (APC/C), both of which mainly function at M phase, are reported to regulate neuronal migration and axon/dendrite formation (Konishi et al. 2004; Kim et al. 2009; Mori et al. 2009; Takitoh et al. 2012). Therefore, growth arrest signals may provide additional functions beyond cell cycle regulation for some cell cycle-related proteins.

Growth arrest and developmental neurological disorders

Disruption of the balance between progenitor selfrenewal and cell cycle exit (neuronal differentiation) leads to several neurological disorders. For example, abnormally enhanced cell cycle exit of neural progenitors leads to premature differentiation and thereby exhaustion of neural progenitors, resulting in microcephaly (small brain) (Mochida & Walsh 2004; Bond & Woods 2006; Lizarraga *et al.* 2010; Miyata *et al.* 2010; Buchman *et al.* 2011; Gruber *et al.* 2011). Interestingly, microcephaly is sometimes accompanied by neuronal migration disorders. Mutation in *AtfGEF2* causes



Figure 6 Cyclin-dependent kinase (CDK) inhibitor proteins regulate cell cycle progression, growth arrest, and postmitotic neuronal migration. (A) Molecular mechanisms for G1/S transition. The transition from G1 to S phase is dependent on CyclinD-Cdk4/6 and CyclinE-Cdk2 activities, which phosphorylate Rb protein. The phosphorylated Rb protein dissociates E2F family transcription factors. Both E2F1 and E2F3 promote G1/S transition in neural progenitors, whereas E2F3, but not E2F1, regulates neuronal positioning. The activities of Cyclin-CDK complexes are suppressed by CDK inhibitor proteins, which are composed of a Cip/Kip family $(p21^{cip1}, p27^{kip1}, and p57^{kip2})$ and Ink4 family $(p16^{Ink4a}, p15^{Ink4b}, p18^{Ink4c}, and p19^{Ink4d})$. (B) Roles of CDK inhibitor proteins, $p27^{kip1}$ and $p57^{kip2}$, in cell cycle exit and subsequent neuronal migration. p57kip2 and p27kip1 preferentially control the cell cycle exit of neural progenitors for early-born (deep layer) and late-born (upper layer) neurons, respectively. p27kip1 mainly functions in basal progenitors (orange cells) rather than apical progenitors (green cells). Both p27^{kip1} and p57^{kip2} have been shown to regulate the migration of postmitotic neurons as well as the cell cycle exit.

microcephaly and periventricular heterotopia (Sheen et al. 2004). ArfGEF2 encodes Big2/ArfGEF2 protein, which regulates membrane trafficking from Golgi apparatus via the activation of Arf family small GTPases. Furthermore, it is reported that Big2 is also localized at recycling endosomes (Shin et al. 2004). Consistent with this, endocytosis and recycling of a cell-cell adhesion molecule, N-cadherin, are known to play essential roles in the locomotion mode of neuronal migration (Kawauchi et al. 2010; Shikanai et al. 2011). Interestingly, N-cadherin is also required for the maintenance of neuroepithelial (ventricular zone) structures (Kadowaki et al. 2007), whose disruption is observed in the brains with periventricular heterotopia (Ferland et al. 2009). Therefore, the regulation of membrane trafficking may be another mechanism that links neural progenitor proliferation and neuronal migration.

Human mutations in the Nde1 gene result in microcephaly with lissencephaly (referred to as 'microlissencephaly') (Feng & Walsh 2004; Alkuraya et al. 2011). Furthermore, knockdown of abnormal spindle microcephaly (ASPM), a causative gene for autosomal recessive primary microcephaly (MCPH, for microcephaly primary hereditary), disturbs neuronal migration as well as neural progenitor proliferation in mice (Fish et al. 2006; Buchman et al. 2011). In addition to human neurological disorder-related genes, many molecules, including Lis1, dynein, SUN proteins, and Rac1, are required for both INM and neuronal migration (Hirotsune et al. 1998; Gambello et al. 2003; Kawauchi et al. 2003; Tsai et al. 2005, 2007; Yoshizawa et al. 2005; Minobe et al. 2009; Zhang et al. 2009; Kawauchi 2011; Yu et al. 2011). Because most of these proteins function in both neural progenitors and postmitotic neurons, neural progenitor proliferation and neuronal migration share several common intracellular pathways in centrosome and/or microtubule regulation. Considering that Cdk5 acts upstream of Lis1, dynein, and Rac1 (Niethammer et al. 2000; Xin et al. 2004; Govek et al. 2011) and that $p27^{kip1}$ is involved in the regulation of microtubules as well as actin cytoskeleton (Baldassarre et al. 2005; Kawauchi et al. 2006; Godin et al. 2012), the growth arrest-mediated Cdk5 activation by the upregulation of p35 protein may alter the function of several cell cycle-related proteins, which exert different cellular events in part using common machineries.

Growth arrest in postmitotic mature cells

In adulthood, many cells, including mature neurons, maintain a quiescent state throughout life. It has been reported that cyclin E binds to and suppresses the activity of Cdk5, resulting in the enhancement of synapse formation (Odajima *et al.* 2011). This suggests that some cell cycle-related proteins also function in mature neurons. Thus, alternative functions for cell cycle-related proteins are important for growth-arrested cells. However, several studies have indicated that cell cycle re-entry by perturbing growth arrest is a trigger for cell death.

Mammalian auditory epithelium, composed of hair cells and supporting cells, has limited capability for regeneration, which remains an obstacle for the development of therapeutics for sensorineural hearing loss (Roberson & Rubel 1994; Forge et al. 1998; White et al. 2006). In contrast, in the avian auditory epithelium, the loss of hair cells leads to re-entry of supporting cells into the cell cycle, giving rise to both hair cells and supporting cells (Corwin & Cotanche 1988; Ryals & Rubel 1988). For the purpose of promoting regeneration of the cochlea in mammals, knockdown of p27^{kip1} in the postmitotic supporting cells of mouse auditory epithelia was performed (Ono et al. 2009). That study reported the successful re-activation of the proliferative capacities of the auditory supporting cells, but induction of the apoptotic pathway occurred several days later (Fig. 7A).

Re-activation of cell cycle machinery in mature neurons is also associated with cell death. In the brains of Alzheimer's disease mouse models, re-expression of cell cycle proteins, such as cyclin A and PCNA, and DNA replication are observed before neuronal cell death (Yang et al. 2001, 2003; Varvel et al. 2008). These 'cell cycle events' themselves do not seem to directly induce neuronal cell death, but are thought to be important priming phenomena for neurodegenerative diseases (Yang & Herrup 2007). Furthermore, it has been reported that the abnormal activation of Cdk5 is involved in neurodegeneration. Inhibition of Cdk5 induces cell cycle events, suggesting that Cdk5 suppresses the cell cycle in mature neurons (Cicero & Herrup 2005; Zhang et al. 2008). The activator for Cdk5 is changed from p35 into a more stable isoform, p25, through a calpain-mediated cleavage in brains with neurodegenerative diseases (Patrick et al. 1999; Kusakawa et al. 2000; Lee et al. 2000). It is known that Cdk5/p35 and Cdk5/p25 exhibit different substrate specificities. Unlike Cdk5/ p35, Cdk5/p25 strongly phosphorylates tau and MAP1B (Patrick et al. 1999; Kawauchi et al. 2005), and their hyperphosphorylation is observed in Alzheimer's diseased brains (Hasegawa et al. 1990; Ulloa et al. 1994; Cruz et al. 2003; Hisanaga & Saito 2003;



Figure 7 Alternative functions of cell cycle-related proteins in the construction and maintenance of brains throughout life. (A) Cell cycle-related proteins function in not only the proliferation of neural progenitors but also various aspects of brain construction and its maintenance throughout life. Cell cycle machinery controls interkinetic nuclear migration (INM) in neural progenitors, and after growth arrest, several cell cyclerelated proteins change their functions to control the migration and morphology of postmitotic neurons. However, cell cycle re-entry by disturbance of growth arrest is thought to trigger cell death. (B) Cdk5 functions in brain development and neurodegenerative diseases. Cdk5, binding to its activator, p35, phosphorylates many substrate molecules and controls the multistep mode of neuronal migration in developing brains (see Fig. 4). In contrast, p35 is cleaved into the more stable p25 in pathogenic conditions, including Alzheimer's disease. Cdk5/p25, but not Cdk5/p35, strongly phosphorylates tau and MAP1B, which may be associated with the formation of neurofibrillary tangles in neurodegenerative diseased brains.

Tsai *et al.* 2004; Su & Tsai 2011). Cdk5/p25 interacts with and inhibits the activity of histone deacetylase 1 (HDAC1), and suppression of HDAC1 induces double-stranded DNA breaks and cell cycle activity

in neurons (Kim *et al.* 2008). These results indicate that the re-activation of cell cycle machinery, including DNA replication, in mature postmitotic cells induces cell death and further suggest that the growth arrest of mature neurons plays essential roles in neuronal survival and normal brain functions.

Conclusion remarks

The tight regulation of cell cycle proteins is essential for the proliferation and cell cycle exit of neural progenitors during brain development. Recent studies also indicate that cell cycle-related proteins contribute to much broader events beyond the cell cycle regulation in the developing and adult brains (Fig. 7A). In neural progenitors, the cell cycle machinery is closely associated with and actively controls INM at least in part through Tpx2-mediated organization of microtubules. Even after growth arrest, cell cycle-related proteins, such as p27^{kip1} and Rb, exhibit alternative functions that affect the migration and changes in morphology of postmitotic neurons. Interestingly, although these alternative functions are essential for brain development, disruption of growth arrest in mature neurons or other postmitotic cells is closely associated with cell death, suggesting that re-activation of cell cycle progression itself may be harmful to postmitotic neurons. As a large proportion of cells in adulthood are in a postmitotic state, it is possible that growth arrest contributes to the maintenance of cellular homeostasis in the whole body.

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