Tangentially Migrating Transient Glutamatergic Neurons Control Neurogenesis and Maintenance of Cerebral Cortical Progenitor Pools

A. Teissier1, R. R. Waclaw2,3, A. Griveau1,4,5, K. Campbell2 and A. Pierani1

1CNRS-UMR 7592, Institut Jacques Monod, Université Paris Diderot, Sorbonne Paris Cité, 75205 Paris Cedex 13, France and 2Division of Developmental Biology, and 3Division of Experimental Hematology and Cancer Biology, Cincinnati Children’s Hospital Medical Center, University of Cincinnati College of Medicine, Cincinnati, OH 45229, USA, 4Department of Pediatrics, Division of Neonatology, University of California San Francisco, San Francisco, CA 94143-0525, USA and 5Howard Hughes Medical Institute and Eli and Edythe Broad Institute for Stem Cell Research and Regeneration Medicine, University of California San Francisco, San Francisco, CA 94143-0525, USA

R. R. Waclaw and A. Griveau have contributed equally to this work

Address correspondence to Dr Alessandra Pierani. Email: pierani.alessandra@ijm.univ-paris-diderot.fr.

The relative contribution of intrinsic and extrinsic cues in the regulation of cortical neurogenesis remains a crucial challenge in developmental neurobiology. We previously reported that a transient population of glutamatergic neurons, the cortical plate (CP) transient neurons, migrates from the ventral pallium (VP) over long distances and participate in neocortical development. Here, we show that the genetic ablation of this population leads to a reduction in the number of cortical neurons especially fated to superficial layers. These effects result from precocious neurogenesis followed by a depletion of the progenitor pools. Notably, these changes progress from caudolateral to rostromedial pallial territories between E12.5 and E14.5 along the expected trajectory of the ablated cells. Conversely, we describe enhanced proliferation resulting in an increase in the number of cortical neurons in the Gsx2 mutants which present an expansion of the VP and a higher number of CP transient neurons migrating into the pallium. Our findings indicate that these neurons act to maintain the proliferative state of neocortical progenitors and delay differentiation during their migration from extraneocortical regions and, thus, participate in the extrinsic control of cortical neuronal numbers.

Keywords: neocortical development, neurogenesis, neuronal numbers, progenitors, tangential migration, transient glutamatergic neurons

Introduction

The generation of an appropriate number of neurons in the central nervous system relies on a strict balance between onset of neurogenesis and maintenance of the progenitor pool (Caviness et al. 2003; Guillemot et al. 2006). At early stages of development, neuroepithelial and radial glia (RG) progenitors are restricted to the ventricular zone (VZ) and divide symmetrically at the apical side to expand the progenitor pool (Gotz and Barde 2005). At the onset of neurogenesis, VZ progenitors begin dividing asymmetrically to generate postmitotic neurons as well as intermediate progenitors (IPs or basal progenitors), which undergo a limited number of divisions in the basal VZ/subventricular zone (SVZ) and, thus, contribute to amplify the number of cortical neurons (Gotz and Huttner 2005; Pontious et al. 2008). Thereafter, newly born neurons migrate radially from the VZ/SVZ to organize in a laminated structure according to an "inside out" sequence whereby early-born neurons reside in deep layers and late-born neurons in more superficial layers (Berry et al. 1964; Bystrom et al. 2008). Although the progenitors in the VZ and SVZ undergo both proliferative and neurogenic divisions, their relative contribution to the final number of cortical neurons in deep and superficial layers is still controversial (Pontious et al. 2008; Kowalczyk et al. 2009; Puzzolo and Mallamaci 2010). Nevertheless, the control of their mode of divisions is crucial for the generation of an appropriate number of neuronal subtypes.

An increasing number of molecules regulating cell cycle properties, either the length of specific phases or the timing of cell cycle exit, have been shown to directly influence the mode of divisions of cortical progenitors (Dehay and Kennedy 2007; Glickstein et al. 2009; Holm et al. 2007; Faedo et al. 2008; O’Leary and Sahara 2008). In addition, recent evidence suggests that the secretion of growth factors and morphogens by postmitotic neurons, some of which reach the developing cortex by tangential migration, or by ingrowing thalamic axons provide an extrinsic control for cortical development (Dehay and Kennedy 2007; Komada et al. 2008; Seuntjens et al. 2009; Griveau et al. 2010). However, the mechanisms coordinating intrinsic versus extrinsic processes and their relative contribution to the final cortical cytoarchitecture remain elusive.

We have previously identified a novel population of transient glutamatergic neurons generated by Dbx1-expressing progenitors in the ventral pallium (VP) at the pallial/subpallial boundary (PSB) at E12.5 which progressively invade the pallium by tangential migration to distribute homogeneously in the neonatal cortex (Teissier et al. 2010). We showed that specific genetic ablation of these VP-derived cortical plate (CP) transient neurons, using E1-Ngn2/CRE;Dbx1DTA mutants, which exhibit an expanded VP (Yun et al. 2001; Stenman, Wang, et al. 2003), display an enhancement in progenitor proliferation as well as in the number of cortical neurons generated correlating with an increase in the number of the CP transient neurons. Our results show that these neurons contribute in a non-cell autonomous manner to maintain the neocortical progenitor pools and, thus, participate in the fine-tuning of cortical neuronal numbers.
Materials and Methods

Animals

All animals were kept in C57BL/6J background and use of mice in this study was approved by the Veterinary Services of Paris. The conditional ablation of Dbr1-derived cells was performed by crossing the Dbr1<sup>CagCat(CC)-EGFP</sup> mouse line (Bielle et al. 2005) with the E1-Ngn2/CRE (iresGFP) strain (Berger et al. 2004) expressing the CRE recombinase and the GFP under the control of the E1 enhancer element of the Ngn2 gene. The Dbr1<sup>IRE CreR</sup> mice, the Gsx2<sup>+/–</sup> mice, and the Catalog(CC)-EGFP mice were generated as previously described (Bielle et al. 2005; Nakamura et al. 2006; Waclaw et al. 2010). The Gsx2<sup>+/–</sup> animals were crossed with the Catalog(CC)-EGFP or Dbr1<sup>CRE iRES</sup> mice to generate Gsx2<sup>–/–</sup>:Catalog(CC)-EGFP and Gsx2<sup>+/+</sup>:Dbr1<sup>CRE iRES</sup> mice (Waclaw et al. 2010). Embryos and postnatal animals were genotyped by PCR using primers specific for the different alleles. For staging of animals, midday of vaginal plug was considered as embryonic day 0.5 (E0.5).

Tissue Preparation, Immunohistochemistry, and In Situ Hybridization

Embryos and postnatal animals collection and fixation were performed as previously described (Bielle et al. 2005). Embedded tissues were sectioned with a cryostat with a 12-14 µm step for embryonic and 18 µm for postnatal stages. Fluorescent immunohistochemistry, Nissl staining, and in situ hybridization were performed as previously described (Bielle et al. 2005). For whole-mount in situ hybridization, the following modifications were applied: brains were pretreated with 10 µg/mL proteinase K for 30 min, the prehybridization and hybridizations were done at 70 °C in the presence of 3 µg/mL digoxigenin-labeled probes. Primary antibodies produced in mice were anti-Pax6 (DSHB, 1:50), anti-Reelin (Calbiochem, G10, 1:500), and anti-Tuj1 (BAbCo, 1:1000); primary antibodies produced in rabbit were anti-BLBP (AbCys, 1:2000), anti-Cux1/2 (Santa Cruz, CDP M222, 1:600), anti-FoxP2 (Abcam, 1:5000), anti-Kis-<sup>5</sup> (AbCam, 1:1000), anti-Mer2c (ProteinTech Group, 1:2000), anti-PH3 (Millipore, Sc->10, 1:1000), anti-Tbr1 (Chemicon, 1:4000), and anti-Tbr2 (Chemicon, 1:8000). We also used rat anti-Ctip2 (AbCam, 1:600) and chick anti-GFP (AvesLab, 1:2000). For BrdU pulse experiments, embryos were obtained from females injected intraperitoneally with a single dose of BrdU (Sigma, 50 mg/kg) 1 h prior to collection. BrdU staining was performed using rat anti-BrdU (AbD Serotec, 1:400) after 5 min of 4 M HCl treatment and 10 min fixation in 4% paraformaldehyde (PFA). 0.1 M phosphate buffer (PB) pH 7.3. For IdU pulse experiments, embryos were obtained from females injected intraperitoneally with a single dose of IdU (Sigma, 60 mg/kg). For BrdU- and IdU double-labeling experiments, the slides were microwaved 6 min at 270 W in 0.1 M citric acid, phosphate-buffered saline (PBS) preheated 4 min at 740 W. Slides were subsequently cooled down for 30 min at room temperature (RT) and rinsed 3 times in PBS before being incubated with 2 M HCl in PBS for 30 min at RT. After several PBS washes, the slides were fixed for 10 min in 4% PFA, 0.1 M PB and rinsed again in PBS before incubation in PBS, 0.1% Triton, 1% horse serum. The BrdU signal was specifically detected using rat anti-BrdU specific (AbD Serotec, 1:100), whereas the IdU signal was detected using a mouse antibody recognizing both IdU and BrdU (BD Biosciences, 1:100). The sections were incubated overnight with the 2 primaries antibodies diluted in PBS, 0.1% Triton, 1% horse serum and revealed using the appropriate conjugated secondary antibodies (Alexa488-conjugated anti-mouse and Cy3-conjugated anti-rat, Jackson ImmunoResearch). This method identifies IdU-only cells (labeled only by the mouse primary antibody) and IdU/BrdU double-labeled cells (labeled by both the mouse and the rat antibodies). For triple staining with Tbr1, the primary and secondary antibodies' reactions to reveal Tbr1 were performed starting the preceding night and were fixed 10 min in 4% PFA, 0.1 M PB before starting the treatments for detection of the BrdU/IdU labeling. Nuclei staining was performed using Vectashield Mounting with 4',6-diamidino-2-phenylindole (DAPI) from Biovalley except for the BrdU and BrdU/IdU experiments which were incubated for 20 min at RT in his benzemide (Hoescht 33342, Coger). All fluorescent secondary antibodies were purchased from Jackson ImmunoResearch.

Data Collection

Counts of cells labeled by immunofluorescence and measures of the thickness of the deep and superficial layers were performed manually on calibrated pictures using ImageJ software.

1. rD and cl. levels determination: At embryonic stages, the rostro-dorsal (rD) level was identified as the most dorsal domain on coronal sections selected by the presence of the lateral ganglionic eminence (LGE) and septum but not the medial ganglionic eminence. The caudal lateral (cl) level was identified as the domain located just above the morphological hinge at the PSB on coronal sections selected by the presence of the caudal ganglionic eminence and the cortical hem. At E18.5 and P2 stages, the rD level was identified at the level of the prospective primary motor area on coronal sections, whereas the cl level was identified at the level of the prospective secondary sensory area, according to the Paxinos Mouse Atlases. For each experiment, the sections from the E1-Ngn2/CRE/Dbr1<sup>IRES</sup> or Gsx2<sup>–/–</sup> mutants were compared with sections from control littersmates and processed simultaneously.

2. Measurements of deep and superficial layers: The thickness of deep and superficial layers, in the P2 E1-Ngn2/CRE/Dbr1<sup>IRES</sup> mutant and control animals, was measured on sections stained by Nissl (Fig. 1A).

The layers of the CP were delineated based on the differential cell density. Since the Gsx2<sup>–/–</sup> animals do not survive at birth and Nissl staining is not precise enough to delineate cortical layers at E18.5, the thickness of the deep and superficial layers in the E18.5 Gsx2<sup>–/–</sup> mutant and control littersmates were measured based on coronal sections processed for in situ hybridization for Tbr1 mRNA (Fig. 8A). In all cases, the CP thickness of deep and superficial layers was measured in dorsal and lateral domains of 3 coronal sections for each specimen (only quantifications for rostro-dorsal and caudal domains are shown in Figs 1A and 8A).

3. PH3<sup>+</sup> cells quantifications: For quantifications of VZ and SVZ mitosis at E12.5, E14.5, and E16.5 (Figs 3 and 7), the number of PH3<sup>+</sup> cells was counted through the thickness of the pallium and normalized for 100-µm-wide strips at both rD and cl. levels on coronal sections. The number of PH3<sup>+</sup> cells in the VZ corresponds to labeled mitosis located at the border of the ventricle and that for the SVZ corresponds to the alveentricular ones.

4. Tbr2<sup>+</sup> cells quantifications: Tbr2<sup>+</sup> cells were counted through the thickness of the pallium and normalized for 100-µm-wide strips at both rD and cl. levels on coronal sections (Fig. 5).

5. VZ cell density: The cell density of the VZ was estimated on coronal sections on 14 µm thickness in E16.5 E1-Ngn2/CRE/Dbr1<sup>IRES</sup> mutant and control animals by counting the number of DAPI<sup>+</sup> cells in 100 x 100 µm boxes at dorsal and lateral levels. At least 5 boxes were counted for each level in 3 animals.

6. Quantification of the increase in CP transient neurons: The Dbr1<sup>CRE iRES</sup>:Catalog(CC)-EGFP mice in the Gsx2<sup>RA/RA</sup> mutant and Gsx2<sup>+/+</sup> control backgrounds were generated by crossing Gsx2<sup>RA/RA</sup> mice. The total number of GFP<sup>+</sup>Tbr1<sup>+</sup> and GFP<sup>+</sup>Mez<sup>+</sup> cells in the CP and MZ (corresponding to CR cells) of the neocortex were counted on coronal sections in 3 specimens for each background.

IdU, BrdU Injections, and Cell Cycle Analysis

Both IdU and BrdU are thymidine analogs which are incorporated during the S-phase of the cell cycle with a clearance in the brain of ~3 h. If we assume that progenitor cells in the telencephalic neuroepithelium 1) progress through the cell cycle asynchronously and 2) have similar cell cycle durations, we can conclude that in such a population of proliferating cells, the fraction of cells in a given phase of the cell cycle is directly proportional to the length of that phase relative to the total length of the cell cycle (Nowakowski et al. 1989). Therefore, upon one single IdU or BrdU injection, all the cells in S-phase at that time will be labeled, and therefore, their proportion among progenitors represents Ts/Tc. If we wait for a ΔT < 3 h for the mice to be sacrificed, the number of labeled cells will therefore represent the proportion of cells that have been in S-phase not only at the time of injections but also during the ΔT and therefore allow to estimate (Ts + ΔT)/Tc (Nowakowski et al. 1989).
**Figure 1.** Decrease in the number of cortical neurons is more pronounced in superficial layers upon Dbx1-derived CP transient neurons ablation. (A) Graphs show CP thickness in E1-Ngn2/Cre;Dbx1\textsuperscript{DTA} mutants relative to wild-type littermates at both rostroventral (rD) and caudolateral (cD) levels of P2 brains and for both deep (white columns) and superficial layers (gray columns) based on Nissl staining. The superficial layers are more affected than the deep layers at both cD and rD levels (rD deep layers: 17.38 ± 13.32%, P = 0.085; rD superficial layers: 38.96 ± 11.24%, P = 0.043; cD deep layers: 16.04 ± 9.01%, P = 0.084; cD superficial layers: 35.77 ± 14.58%, P = 0.010). Graphs represent means ± standard error of the mean (SEM). *P < 0.05. (B–E) Immunostaining for Tbr1 (B,C) and Cux1/2 (D,E) shows that both deep and superficial layers at rD levels are affected in E1-Ngn2/Cre;Dbx1\textsuperscript{DTA} mutants (C,E) compared with wild-type littermates (B,D), although the effect is more pronounced for the superficial layers. (F–G) Immunostaining for FoxP2 at E18.5 reveals a small increment in the number of neurons located in layer VI (white bars in F,G). (H–M) Immunostaining for Ctip2 (H,I) and in situ hybridization for Cdh8 (J,K) and Ror\textbeta (L,M) confirm a reduced neuronal numbers specifically affecting the superficial layers. Scale bars: B,F,J, 100 μm.

**Cell Cycle Length**

Pregnant mice were injected intraperitoneally with IdU (60 mg/kg), followed by a BrdU injection (50 mg/kg) 1.5 h later and were sacrificed 3 h after the IdU injection to collect the embryos at E12.5 or E14.5. Considering that some DAPI\textsuperscript{+} cells located in the VZ may be differentiated, we controlled that the proportion of TuJ1\textsuperscript{+} cells was small and that the differences between controls and mutants were negligible as compared with the total number of DAPI\textsuperscript{+} cells at all levels and stages studied (E12.5: rD = 5.05% in control vs. 5.8% in mutant animals; cD = 7.13% vs. 11.26%; E14.5: rD = 9.42% vs. 9.39%; cD = 9.73 vs. 12.25%; n = 2). In addition, previous studies have shown that a prolonged pulse of BrdU will label virtually all VZ cells at E12.5 (Estivill-Torrus et al. 2002), allowing us to assume that all the DAPI\textsuperscript{+} cells in the VZ were proliferating (P\textsubscript{cell}). Cells that have been labeled upon the IdU injection and that have exited the cell cycle at the time of the BrdU injection will be labeled by IdU and not by BrdU, and their number in the VZ is designated as the leaving fraction (L\textsubscript{cell}). The number of cells labeled with BrdU is designated as S\textsubscript{cell}. Therefore, the length of the S-phase is calculated using the formula: Ts/ΔT = S\textsubscript{cell}/L\textsubscript{cell} and the length of the cell cycle is estimated from the formula: Tc/Ts = P\textsubscript{cells}/S\textsubscript{cells} (Martynoga et al. 2005; Fukumitsu et al. 2006; Quinn et al. 2007).

**Q Fraction**

Pregnant mice were injected intraperitoneally once with IdU (60 mg/kg), then 7 times with BrdU (50 mg/kg) every 2 h and sacrificed 15 h after the initial IdU injection. Embryos were stained as described above. Since the normal duration of a cell cycle at E14.5 is ~17 h but Tc ~ Ts is ~14.5 h for cortical progenitors (Miyama et al. 1997; Calegari et al. 2005), all the proliferative cells have incorporated some IdU or BrdU. Cells located in the VZ/SVZ that have been labeled upon the IdU injection and that have exited the cell cycle at the time of the first BrdU injection will be labeled by IdU and not by BrdU. Therefore, they are considered as the cells that have exited the cell cycle during one cycle and their proportion among the total number of proliferative cells (IdU\textsuperscript{+} or BrdU\textsuperscript{+}) is designated as the Q fraction (Takahashi et al. 1996; Tarui et al. 2005).

**Statistical Analysis**

For all experiments, results have been obtained from at least 3 pairs of control and mutant littermates, and the number of counted cells is indicated in the Figure Captions. For all quantifications, normal distribution was confirmed and unpaired, 2-tailed t-test on group means was performed for statistical analysis, using Microsoft Excel software (*P < 0.05, **P < 0.005).

**Image Acquisition**

Brightfield images of brain sections were acquired using a color camera (Zeiss Axiocam HRc) coupled to a Zeiss Axiosvert 200 microscope and immunofluorescence images using an inverted confocal microscope (Leica TCS SP5 AOBS Tandem resonant scanner).
Results

Reduction of Cortical Neurons’ Numbers Especially in Superficial Layers upon CP Transient Neurons Ablation

We have previously shown that the specific ablation of the CP transient neurons derived from Dbx1-expressing progenitors at the VP/PSB in E1-Ngn2/CRE;iRES-GFP;Dbx1<sup>MUT</sup> animals leads to a ~20% reduction in CP thickness throughout the neocortex at E18.5, without affecting either cell density or death (Teissier et al. 2010). This population invades the preplate (PP) and the SVZ/intermediate zone (IZ) by tangential migration with a caudal-to-rostral gradient starting at E12.5 and is redistributed homogeneously in the CP along the rostrocaudal (RC) and mediolateral (ML) axes at birth.

In order to understand how the loss of Dbx1-derived CP transient neurons leads to a reduction of the CP thickness in E1-Ngn2/Cre<i>iresGFP</i>;Dbx1<sup>MUT</sup> animals, we analyzed the defects at caudalateral (cL) and rostrocaudal (rD) levels which represent cortical territories at short and long distances from their generation site, respectively (Teissier et al. 2010). Nissl staining analysis at P2 confirmed that the entire cortex showed a decrease in CP thickness, as previously described at E18.5, with respect to wild-type cortices (rD: 24.32% and cL: 23.87%) (Teissier et al. 2010 and data not shown) and also revealed that this reduction was clearly more pronounced for superficial layers (Fig. 1A, rD: 38.96%; cL: 35.77%) than for deep layers (rD: 17.38%; cL: 16.04%) at both rD and cL levels. No significant differences were observed in the extent of the defects between cL and rD levels. These results were confirmed by specifically labeling deep and superficial layers using Trh1 and Cux1/2 immunostaining, respectively. We observed in both cL and rD regions a small decrease in the thickness of Trh1<sup>+</sup> deep layers in addition to a severe reduction in that of Cux1/2<sup>+</sup> superficial layers in mutant brains (Fig. 1B–E). Laminar fate and positioning of cortical progenitors appeared to be preserved as observed by immunohistochemistry for Foxp2 (deep layers) and Ctip2 (prospective layer V subpopulations) (Fig. 1F–I) as well as in situ hybridization for <i>Cdh8</i> (prospective layers II–IV and subpopulation of layer V) and <i>Rorβ</i> (prospective layer IV) (Fig. 1J–M). In addition, an increase in the number of Foxp2<sup>+</sup> neurons was detected in deeper portions of layer VI (Fig. 1FG, white bars), whereas that of neurons fated to layer V, as identified by Ctip2 labeling (Fig. 1HI), was slightly decreased in mutant compared with control littersmates. A more pronounced decrement of <i>Cdh8</i> and <i>Rorβ</i> staining confirmed that superficial layers are more highly affected as revealed by Cux1/2 labeling (Fig. 1J–M). Finally, since another population of tangentially migrating cells, namely Cajal–Retzius (CR) cells, are also generated from Dbx1-expressing progenitors at the VP prior to the CP transient neurons and have been shown to influence cortical patterning (Griveau et al. 2010), we performed whole-mount in situ hybridization for <i>Lmo4</i> and <i>Cdh8</i> mRNAs on P0 animals (Supplementary Fig. S1). We observed no differences in area patterning between ablated and control littersmates cortices as expected from the absence of defects in CR cells distribution previously reported in the <i>E1-Ngn2/CRE;Dbx1<sup>MUT</sup></i> mutants (Teissier et al. 2010) and the late migration and homogeneous distribution of the CP transient neurons.

We conclude that the specific genetic ablation of the CP transient glutamatergic neurons generated from Dbx1-expressing progenitors in the VP leads to a homogeneous deficit in the total number of neurons, although this is more pronounced for the superficial layers, throughout the early postnatal neocortex.

Defects in Differentiation and Proliferation Progressively Affect the Entire Pallium along the Expected Trajectory of the Ablated CP Transient Neurons

Since the CP transient neurons progressively invade the pallium from caudalateral regions starting at E12.0 and reach the rostrodorsal territories by E14.5 (Teissier et al. 2010), we began by analyzing neuronal differentiation at E12.5 and E14.5 using immunostaining for TuJ1 and Trh1, markers of young postmitotic neurons (Memberg and Hall 1995) and early differentiated glutamatergic cortical neurons (Englund et al. 2005), respectively. We observed an increase in the number of both Trh1<sup>+</sup> and TuJ1<sup>+</sup> differentiating neurons in the CP (Fig. 2E–H, black bars) together with ectopically positioned labeled cells in the VP (arrowheads) in cl regions of E12.5 ablated telencephalons with respect to control littersmates. No defects in differentiation were observed in rD regions at this stage (Fig. 2A–D) correlating with the presence of numerous Dbx1-expressing CP transient neurons in cl but not in rD territories at E12.5 (Teissier et al. 2010). Interestingly, by E14.5, a similar increase in differentiation was observed in the rD region of mutant telencephalons (Fig. 2F–I and data not shown), whereas no differences were detected in the CP of the cl region, with the exception of ectopic Trh1<sup>+</sup> neurons in the VP (Fig. 2MN, arrowheads). Moreover, at E14.5 a slight thinning of the VP was apparent especially in mutant cl territories (Fig. 2MN, black bars).

In order to assess if the increase in differentiation was due to defects in proliferation occurring upon ablation, we quantified the number of mitotic cells, as labeled by PH3 staining, in the rD and cl regions of the developing pallium at E12.5, E14.5, and E16.5 (Fig. 3A–D). We detected an initial increase in the number of PH3<sup>+</sup> mitotic progenitors in the cl VP at E12.5 followed by a reduction clearly observed at E16.5 (Fig. 3C). At E14.5, corresponding to the time of arrival of the CP transient neurons in rD territories in control animals, enhanced VP proliferation was observed in rD regions of mutant cortices (Fig. 3AE,F), followed by a small decrease by E16.5 (Fig. 3A). Notably, the number of PH3<sup>+</sup> mitotic progenitors in the SVZ was strongly reduced at both cl and rD levels starting at E14.5 (Fig. 3BD,E–H).

Taken together, these results show that the loss of the CP transient neurons leads initially to an increment in the number of mitosis in the VP and of differentiating neurons (at E12.5 in cl and E14.5 in rD regions), followed by a decrement in the number of both VP and SVZ mitoses. Notably, changes in proliferation and differentiation appear to progress from the caudalateral to the rostrodorsal cortex and to correlate with the timing and trajectory of invasion of pallial regions by the CP transient neurons.

CP Transient Neurons Ablation Results in Precocious Neurogenesis

The defects observed in ablated animals could result from either a change in cell cycle length, an increase in the fraction of neurogenic divisions and/or a variation in the size of the progenitor pools. In order to discriminate between these possibilities, we started by measuring the length of the cell cycle using EdU and BrdU injections 3 and 1.5 h before collection of the embryos (see Materials and Methods) (Fig. 4A–C). At E12.5, we observed shortening of the cell cycle in progenitors located in the VP in cl (Tc = 13.31 h ±
2.91 in controls and Tc = 25.71 h ± 4.02 in mutants) but not in rD territories (Tc = 9.19 h ± 1.07 in controls and Tc = 11.96 h ± 1.09 in mutants). By E14.5, VZ progenitors at both cl and rD levels displayed a clear increase in Tc (rD: Tc = 11.74 h ± 0.54 in controls and Tc = 18.51 h ± 3.27 in mutants; cl: Tc = 17.81 h ± 2.80 in controls and Tc = 27.96 h ± 3.91 in mutants). Therefore, defects in proliferation and differentiation correlate with a lengthening of the cell cycle in E1-Ngn2/Cre;Dbx1DTA mutant embryos.

A lengthening of the cell cycle has been shown to characterize differentiative divisions (Miyama et al. 1997; Calegari et al. 2005). To address whether an increased fraction of cells exited the cell cycle (Q fraction) in E14.5 E1-Ngn2/Cre;Dbx1DTA animals, we performed a single injection of IdU followed by multiple injections of

Figure 2. Transient increase in differentiation progressively affects the entire pallium of E1-Ngn2/CRE;Dbx1DTA mutants. (A–H) Immunohistochemistry performed on E12.5 embryos shows no differences for Tbr1 (A,B) and TuJ1 (C,D) staining between control (A,C) and E1-Ngn2/CRE;Dbx1DTA (B,D) embryos at rD levels, whereas there is a strong increase for both in cl regions in mutants (F,H, black bars) compared with control littermates (E,G). Moreover, ectopic Tbr1⁺ and TuJ1⁺ cells are observed in the mutant VZ (arrowheads in F,H). (I–N) By E14.5, Tbr1 staining is increased at rD levels in mutants (J,L), whereas no differences are detected at cl levels (K,M) with respect to control littermates (I,K,M). Ectopic Tbr1⁺ neurons (arrowheads in L,N) are observed in the VZ of mutants at both levels as well as a thinning of the VZ at cl levels (black bars in M,N). K and L represent high magnifications of boxed areas in I and J, respectively. Scale bars: A,K, 20 μm; I, 100 μm.
BrdU (every 2 h) for a total of 15 h (Fig. 4D) and quantified the number of cells which failed to reentered the S-phase during the time of the experiment (IdU\textsuperscript{+}BrdU\textsuperscript{−}) among actively cycling cells (IdU\textsuperscript{+}BrdU\textsuperscript{+} or IdU\textsuperscript{−}BrdU\textsuperscript{+}) (see Materials and Methods). We observed that an increased proportion of cells exited the cell cycle in ablated cortices compared with controls at both cl and rD levels (Fig. 4E). Evaluation of the total number of postmitotic neurons generated during one cell cycle by counting the number of Tbr1\textsuperscript{−}BrdU\textsuperscript{−} cells relative to the size of the progenitor pool (IdU\textsuperscript{−}BrdU\textsuperscript{+} or IdU\textsuperscript{+}BrdU\textsuperscript{+}) also confirmed an enhanced fraction of neurogenic divisions in mutant compared with control littermates (Fig. 4F). Furthermore, we detected an increase in the expression of Ngn2, a proneural gene detected at high levels in neurogenic divisions (Shimjo et al. 2008; Ochiai et al. 2009), in the VZ and SVZ of mutant compared with control littermates (Fig. 4G,H). Together, these experiments suggested that there was an augmentation in the number of progenitors undergoing neurogenic instead of proliferative divisions in both the VZ and SVZ of ablated embryos.

To further analyze whether the cortical neuroepithelium was undergoing precocious neurogenesis, we performed communostaining for Tbr2, a gene expressed in both IP cells and early postmitotic neurons in the developing pallium (Englund et al. 2005) and TuJ1. We observed an increase in the number of Tuj1\textsuperscript{+} cells in the VZ of E14.5 E1-Ngn2/CRE;Dbx1\textsuperscript{DTA} mutant embryos and especially in that of Tuj1\textsuperscript{+}BrdU\textsuperscript{+} mutant embryos (green arrowheads in Fig. 4K-R). We also noticed that ectopic Tbr2\textsuperscript{+} cells were detected in the apical VZ almost at the ventricle in mutant animals (red arrowheads in Fig. 4P). Notably, a general increase in expression of the GFP, corresponding to the activity of the E1 enhancer element of the Ngn2 gene, was also detected in mutants particularly at the apical VZ (Fig. 4I-N) and correlated with the enhanced Ngn2 staining previously described. All GFP\textsuperscript{+} cells were Tbr2\textsuperscript{+} in the VZ, but not reciprocally, in both control and mutant E1-Ngn2/CRE;Dbx1\textsuperscript{DTA} cortices (Fig. 4K-P), suggesting that the GFP labels a specific subpopulation of the Tbr2\textsuperscript{+} cells. Moreover, the Tuj1\textsuperscript{+}BrdU\textsuperscript{−} cells in the apical VZ observed in control as well as the ectopic ones observed in mutant animals were almost always associated with GFP expression (green arrowheads in Fig. 4K-R), suggesting that the Tbr2\textsuperscript{+}GFP\textsuperscript{+} cells in the apical VZ are postmitotic neurons. Accordingly, we observed a higher proportion of Tbr2\textsuperscript{+}GFP\textsuperscript{+} cells among Tbr2\textsuperscript{+} cells at E12.5 in cl territories (cl: 20.62 ± 2.65% in controls compared with 51.42 ± 2.96% in mutants, the GFP is not expressed at rD level at this stage). A similar increase was detected in both cl and rD regions at E14.5 (cl: 31.85 ± 1.79% in controls compared with 52.76 ± 0.18% in mutants; rD: 29.39 ± 11.79% in controls compared with 63.19 ± 3.03% in mutants) and maintained at E16.5 (cl: 15.06 ± 1.40% in controls compared with 45.82 ± 9.68% in mutants; rD: 15.75 ± 0.78% in controls compared with 52.76 ± 0.18% in mutants; rD: 29.39 ± 11.79% in controls compared with 63.19 ± 3.03% in mutants). To conclude, we observed a higher proportion of Tbr2\textsuperscript{+}GFP\textsuperscript{+} cells among Tbr2\textsuperscript{+} cells at E12.5 in cl territories (cl: 20.62 ± 2.65% in controls compared with 51.42 ± 2.96% in mutants, the GFP is not expressed at rD level at this stage). A similar increase was detected in both cl and rD regions at E14.5 (cl: 31.85 ± 1.79% in controls compared with 52.76 ± 0.18% in mutants; rD: 29.39 ± 11.79% in controls compared with 63.19 ± 3.03% in mutants) and maintained at E16.5 (cl: 15.06 ± 1.40% in controls compared with 45.82 ± 9.68% in mutants; rD: 15.75 ± 0.78% in controls compared with 52.76 ± 0.18% in mutants; rD: 29.39 ± 11.79% in controls compared with 63.19 ± 3.03% in mutants).

Thus, together these experiments demonstrate that progenitors throughout the neocortical neuroepithelium undergo precocious neurogenic divisions in E1-Ngn2/CRE;Dbx1\textsuperscript{DTA} animals by midneurogenesis.
Depletion of Neocortical Progenitor Pools in Ablated Mutants

An increase in the neurogenic fraction of progenitor divisions and a decrease in that of proliferative divisions should lead to a progressive depletion of the progenitor pool. Indeed, the observed decrease in the number of mitosis in E14.5 and E16.5 in E1-Ngn2/Cre;Dbx1DTA embryos together with a reduction in Ki67 staining, a marker of proliferative cells, at caudal levels of E14.5 mutant pallium compared with control littermates (Fig. 5A–B') strongly suggested a global depletion of the progenitor pools. Since the decrease in the proliferation was most pronounced in the SVZ at E14.5, we first tested whether the pool of IPs was affected. We quantified the number of Tbr1+ among the double-labeled cells that have, thus, been generated during the 15 h of the experiment (rD: 15.37 ± 1.87% in controls with respect to 23.08 ± 2.64% in mutants, P = 0.030; cL: 20.83 ± 2.63% in controls with respect to 38.45 ± 3.08% in mutants, P = 0.007). In situ hybridization for Ngn2 mRNA suggests an increment in neurogenic division at both VZ and SVZ levels in E14.5 E1-Ngn2/CRE;Dbx1DTA mutants (H) compared with control littermates (G). Immunohistochemistry for GFP on coronal sections of E14.5 E1-Ngn2/CRE(iresGFP);Dbx1DTA mutants (L) compared with E1-Ngn2/CRE(iresGFP) control littermates (I) reveals a greater activation of the E1 enhancer of the Ngn2 gene in mutants. (K–R) Immunohistochemistry for GFP (K–N), Tbr2 (K,L,D,P), and TuJ1 (K,L,O,R) at rD levels on E14.5 control (K,M,O,D) and E1-Ngn2/CRE(iresGFP);Dbx1DTA (L,N,P,R) telencephalons. The Tbr2+;TuJ1+ cells located in the VZ often correspond to GFP+ cells (green arrowheads in K–R) and their number is more numerous in mutants. In addition, ectopic Tbr2+ cells are observed at the apical VZ in mutants (red arrowheads in P). Scale bars: G,J: 200 µm; blow up in G, 50 µm; K, 20 µm.
proliferation (Fig. 3B,D), these results show that the decrease in the total number of Tbr2+ cells corresponds to a depletion in the pool of IPs rather than of early postmitotic neurons (also Tbr2+).

In order to determine if the pool of RGs was also affected, we analyzed the expression of BLBP and Pax6 proteins, 2 specific markers of RG cells, at E16.5. We observed a decrease in their expression in mutant cL cortices (Fig. 5F–I) correlating with a ~25% reduction in cell density, as measured by DAPI staining, in the VZ (Fig. 5L). In addition, we observed at E16.5 a decrease in BrdU labeling (upon a 2 h pulse) in the VZ and SVZ of both rD and cl regions (Fig. 5J,K). We conclude that a depletion of both the IP and the RG progenitors’ pools occurs in the pallium of the E1-Ngn2/Cre;Dbx1DTA animals.

**Increased Number of Dbx1-Derived CP Transient Neurons in the Pallium of Gsx2 Mutants**

Since the E1-Ngn2/Cre;Dbx1DTA mutants represent a specific ablation of Dbx1-expressing progenitors at the VP, we sought to analyze Gsx2 null mice which have been reported to display opposite effects, namely an expansion of the Dbx1 expression domain in the VP (Yun et al. 2001; Carney et al. 2009). Notably, these mutants have recently been shown to present an increase...
in the number of Dbx1-derived glutamatergic neurons migrating into the lateral amygdala (Waclaw et al. 2010). The role of Gsx2 in dorsoventral patterning and neurogenesis of the subpallium has been analyzed in several studies (Corbin et al. 2000; Yun et al. 2001; Stenman, Toresson, et al. 2003; Yun et al. 2003; Carney et al. 2009). However, no major defects in pallial development had been reported so far.

In order to permanently trace Dbx1-derived CP transient neurons in the pallium of the Gsx2 mutants, we crossed DbxI^CRE;Gsx2^RA/RA animals with CagCat-EGFP;Gsx2^RA/RA animals (Waclaw et al. 2010). By immunostaining for Tbr1 on development had been reported so far. 2000; Yun et al. 2001; Stenman, Toresson, et al. 2003; Yun et al.

Gsx2 ing into the lateral amygdala (Waclaw et al. 2010). The role of addition, quantification of the number of GFP cells coexpressing Tbr1 and/or Mef2c, a gene which labels VP-derived neurons migrating into the amygdala (Waclaw et al. 2010), revealed a 124 ± 3.18% and 274.66 ± 5.72% increase in the CP of E18.5 Gsx2 mutants (Fig. 6F-I). Most supernumerary Dbx1-derived neurons were positioned in deep layers as expected from their early birthdate. No significant differences in the number or location of Dbx1-derived Reelin^+ CR cells was observed in E13.5 and E18.5 DbxI^CRE/+;CagCat-EGFP;Gsx2^RA/+ and DbxI^CRE+;CagCat-EGFP;Gsx2^RA/RA cortices (data not shown and Fig. 6I). We conclude that Gsx2 mutant animals display a specific increase in the number of CP transient neurons migrating into the pallium from early stages of development.

Enhanced Proliferation and Neurogenesis in the Pallium of Gsx2 Mutants

We started by analyzing the progression of differentiation using Tbr1 and TuJ1 immunostaining in E12.5 Gsx2 mutants and observed a global decline affecting both cl and rd regions, but this was more pronounced at cl levels (Supplementary Fig. S2). We also detected a concomitant enhanced proliferation in both the VZ and the SVZ, as revealed by Ki67 and BrdU staining (Supplementary Fig. S2). At E14.5, a strong increment in Ki67 and Ph3 immunostaining was detected in both the VZ and the SVZ of Gsx2 mutants at cl and rd levels (Fig. 7A-F and data not shown). Quantification of Ph3^+ cells at the apical VZ and the SVZ confirmed a higher number of ventricular and abventricular mitoses in these mutants (Fig. 7M,N). In addition, we observed more numerous Tbr2^+ cells in the SVZ (Fig. 7G,H) but not at the apical VZ (Fig. 7G,H,O), showing that both RG and IP progenitors display enhanced proliferation. Finally, we observed a reduction in Ngn2 staining in both the VZ and the SVZ of mutant animals (Fig. 7J) as well as a reproducible slight decrease in Tis21 expression, especially in the apical portion of the VZ (Fig. 7K,L), strongly arguing for a decrease in the fraction of neurogenic divisions. Notably, the number of Tbr1^+ neurons in the CP of E14.5 Gsx2 mutants was similar to that of control embryos (data not shown). Therefore, together these results suggest that an amplification of both RGs and IPs progenitor pools and a delayed neurogenesis occur in the pallium of Gsx2 mutants. These defects are opposite with respect to the precocious differentiation and depletion of the progenitor pools described in the E1-Ngn2/Cre;DbxI^Tet mutants at corresponding stages.

We then analyzed the phenotype at E18.5, the latest stage possible for Gsx2 mutants which die at birth and observed an increase in the thickness of the CP at both rd (25.49%) and cl (30.96%) levels. Tbr1 and Cux1/2 immunostaining showed that both deep and superficial layers were thicker (Fig. 8B-G) and appeared to be affected in a similar manner (Fig. 8A). Although the supernumerary CP transient neurons were positioned in deep layers. Finally, we observed a strong increase of neuronal numbers in layers V and II–IV upon immunostaining for FoxP2, Ctip2 and Mef2C, as well as by in situ hybridization for Cadb (Fig. 8H–I). In conclusion, we have shown that Gsx2 mutants present a surplus number of CP transient neurons and display opposite non-cell

Figure 6. Increased number of Dbx1-derived CP transient neurons migrating in the developing pallium of Gsx2 mutants. (A–D) Immunohistochemistry for GFP and Tbr1 shows an increase in the number of GFP^+ cells migrating tangentially into the pallium of E13.5 DbxI^CRE+;CagCat-EGFP;Gsx2^RA/RA mutant animals (B,D) compared with DbxI^CRE-;CagCat-EGFP;Gsx2^+/+ control littersmates (A,C). A higher number of Dbx1-derived GFP^+Tbr1^+ neurons is detected in the pallium of mutants compared with controls (C,D magnification of dashed boxes in A,B, respectively). (E–H) Immunohistochemistry for GFP and Mef2c on E18.5 DbxI^CRE+;CagCat-EGFP;Gsx2^RA/RA mutant animals (G,H) compared with DbxI^CRE+;CagCat-EGFP;Gsx2^+/+ control littersmates (E,F) confirms an increment in the number of GFP^+Mef2c^+ neurons in the CP at dorsolateral levels. (I) Graph represents the total number of GFP^+Tbr1^+ and GFP^+Mef2c^+ neurons in the CP of coronal sections of mutant and control cortices at E18.5, corresponding to the number of Dbx1-derived CP transient neurons, as well as the total number of GFP^+Tbr1^+ neurons in the MZ, corresponding to Dbx1-derived CR cells. These results confirm a strong increment in the number of Dbx1-derived glutamatergic neurons in mutants (GFP^+Tbr1^+: 23 ± 2.51 neurons per sections in controls vs. 51.66 ± 8.01 in mutants, P = 0.060). Graphs represent means ± SEM. *P < 0.05. Scale bars: A, 100 μm; E,F, 50 μm.
autonomous pallial defects to those observed upon their ablation in E1-Ngn2/CRE;Dbx1<sup>DTA</sup> animals, namely excessive proliferation of both VZ and SVZ progenitors and a consequent increased number of cortical neurons fated to both deep and superficial layers.

**Discussion**

We have shown that the specific ablation of CP transient neurons derived from Dbx1-expressing progenitors results in a decrement in the final number of cortical neurons as a consequence of the precocious differentiation of cortical progenitors. The kinetics of the defects observed in ablated mutants follow the expected trajectory of these cells, which migrate tangentially from the VP at the border of the developing pallium (Teissier et al. 2010). On the contrary, a gain of CP transient neurons, as observed in Gsx2 mutants, correlates with a delayed onset of neurogenesis in the pallium resulting in an increase in the size of the progenitor pools and in the total number of cortical neurons. Therefore, all together these results show that these transient glutamatergic neurons in the postmitotic compartment appear to control the mode of divisions of cortical progenitors in a non-cell autonomous manner over long distances from their generation site. Their dynamics of invasion of the CP together with their role in delaying differentiation might represent a novel mechanism to refine neurogenic gradients during cortical growth via cell migration.

**The Proliferation/Differentiation Transition of Cortical Progenitors Depends on the Number of CP Transient Neurons in Developing Pallial Territories**

The specific ablation of Dbx1-derived CP transient neurons results in an early increase in the leaving fraction and a lengthening of the cell cycle together with an enhanced expression of markers of neurogenic divisions. Correlating with the observed precocious neurogenesis, the generation of FoxP2<sup>+</sup> layer VI neurons is incremented in E1-Ngn2/CRE;Dbx1<sup>DTA</sup> animals. In addition, proliferation in the SVZ is reduced suggesting a defect in IPs generation from VZ progenitors. Thus, the early onset of differentiation leads to a progressive depletion of both VZ and SVZ progenitor pools and results in a general reduction of neuronal production although this is more pronounced for neurons fated to superficial layers. On the contrary, in Gsx2 mutants, which display an excessive generation of VP-derived CP transient neurons, the numbers of cycling VZ and SVZ progenitors and of cortical neurons are amplified. Thus, a delayed differentiation resulting in an enlarged progenitor pool occurs in Gsx2 mutants. However, unlike E1-Ngn2/CRE;Dbx1<sup>DTA</sup> mutants, Gsx2 mutants display a fairly homogeneous increase of both superficial and deep layer neurons. This is likely due to the fact that E1-Ngn2/CRE;Dbx1<sup>DTA</sup> mutants present only a partial (around 50%) ablation of the CP transient neurons (Teissier et al. 2010) because of a late onset of recombination starting after E11.5 whereas VP expansion is already well established at this stage in Gsx2 mutants (Yun et al. 2001). Nevertheless, our results show that E1-Ngn2/CRE;Dbx1<sup>DTA</sup> and Gsx2 mutants represent mouse models for studying loss and gain of function of Dbx1-derived CP transient neurons, respectively. In addition, this is the first time that a pallial phenotype is described for Gsx2 mutants. Indeed, previous studies have mostly focused on the
role of Gsx2 on dorsoventral patterning and have described a considerably smaller stratum resulting from patterning defects that lead to a specific decrease in proliferation in the LGE, notably affecting the SVZ at E12.5 (Corbin et al. 2000; Toresson et al. 2000; Toresson and Campbell 2001). This cell autonomous phenotype appears opposite to the one we describe in the pallium and supports an indirect function for Gsx2 in the development of the cortical primordium through the inhibition of expression of the Dbx1 gene (Yun et al. 2001; Winterbottom et al. 2010).

All together, our results strongly suggest that CP transient neurons have an active role in enhancing progenitor proliferative divisions and, thus, decreasing the probability of cell cycle exit. In addition, both E1-Ngn2/CRE;Dbx1DTA and Gsx2 mutants are strongly affected in SVZ proliferation, and present defects in both deep and superficial layers, supporting the hypothesis that IPs generate neurons fated to all layers and have a role in the amplification of RGs progeny rather than on neuronal fate (Pontious et al. 2008; Kowalczyk et al. 2009; Puzzolo and Mallamaci 2010). Accordingly, both CyclinD2 and Tbr2 mutants specifically affecting SVZ proliferation display a reduced number of neurons in both deep and superficial layers (Arnold et al. 2008; Sessa et al. 2008; Glickstein et al. 2009) although this is more pronounced in superficial layers. However, this appears to be in the absence of precocious differentiation of VZ progenitors. On the contrary, mutants that do result in premature differentiation, such as Pax6 and Tlx mutants, also display a depletion of the progenitor pool correlated with an increased leaving fraction and a consequent reduction in the thickness of superficial layers as described for E1-Ngn2/CRE;Dbx1DTA animals (Land and Monaghan 2003; Roy et al. 2004; Tuoc et al. 2009; Georgala et al. 2011). Interestingly, mutants for both Pax6 (Sey/Sey) and Tlx mutants present a loss of Dbx1 expression at the VP/PSB (Yun et al. 2001; Stenman, Yu, et al. 2003; Roy et al. 2004), and cell death has been reported to specifically occur at the PSB of Tlx mutants (Roy et al. 2004). Although both the Pax6 and the Tlx genes have been shown to control cell autonomously the mode of divisions of cortical progenitors (Quinn et al. 2007; Osumi et al. 2008; Zhang et al. 2008) it cannot be excluded that part of the phenotype in their respective mutants is dependent on alterations in the generation or specification of the CP transient neurons due to VP defects.

**CP Transient Neurons Migration and “Neurogenetic Gradients”**

Gradients of proliferation (rostrolateral^high^ to caudomedial^low^) and differentiation (lateral^high^ to medial^low^) have been suggested to regulate timing of early neurogenesis and, thus, neuronal numbers in distinct cortical territories (Bayer et al.
Neurogenesis has been shown to be initiated rostrolaterally at E10.5 and to expand caudomediaally but still maintaining a strong lateral to dorsal gradient between E12.5 and E14.5 (Miyama et al. 1997; Calegari et al. 2005). Accordingly, at midneurogenesis, the lateral regions of the pallium already start generating neurons fated to superficial layers while the rostromedial ones still generate exclusively neurons fated to deep layers (Polleux, Dehay, and Kennedy 1997; Polleux, Dehay, Moraillon, et al. 1997; Takahashi et al. 1999). We have shown that the CP transient neurons are generated with a peak at E12.5 and migrate tangentially to reach the rostromedial pallium by E14.5 along caudal to rostral and lateral to dorsal migratory pathways (Teissier et al. 2010). Therefore, CP transient neurons' migration parallels the neurogenic gradient occurring between E12.5 and E14.5. Strikingly, while the defects in proliferation follow the expected trajectory of ablated cells in E1-Ngn2/CRE;Dbx^{IPTA} animals (i.e., starting at the caudal PSB at E12.0–E12.5 and reaching the dorsal cortex by E14.5), the decrease in neuronal generation is homogeneous along the RC axis despite delayed onset of ablation effects in rostromedial regions, suggesting that the neurogenic gradients are unperturbed in ablated animals. Since the pattern of the E1/Ngn2 enhancer activity also correlates with gradients of differentiation (Berger et al. 2004) and the expression of Ngn2 increases in mutant animals, our data strongly suggest that ablation results in a switch to neurogenic divisions at the expense of proliferative divisions (lacoppeti et al. 1999; Kawaguchi et al. 2004). Dbx1-derived CP transient neurons might act by delaying differentiation possibly by maintaining low Ngn2 expression in progenitors. This occurs in the absence of defects in laminar fate and arealization, strongly suggesting that CP transient neurons do not affect the intrinsic sequence which leads progenitors to produce the whole set of layer-specific neurons once they have initiated neurogenesis (Shen et al. 2006; Gaspard et al. 2008). Most likely, they appear to time the exit from the cell cycle and, thus, to increase the total number of self-renewing cell cycle per progenitor.

**CP Transient Neurons Migration Provides an Extrinsic Mechanism to Control the Mode of Divisions of Cortical Progenitors**

We have shown that both RGs and IPs progenitors are affected upon modifications in the number of CP transient neurons. Our results indicate that the CP transient neurons might influence progenitors proliferation/differentiation transition while invading the pallium. Since these neurons migrate through both the IZ/SVZ and the developing PP at early stages of development (E12.5–E14.5) (Teissier et al. 2010), they could interact at this location by cell-cell-mediated contacts with the basal processes of RG cells or with IPs as well as by the secretion of signaling factors. Notably, the neurogenic gradient observed in the developing cortex has already been suggested to be initiated by signaling molecules secreted by the patterning centers and to progress by cell–cell contact through hemichannels propagating calcium waves. This process has been shown to be both necessary and sufficient to promote RGs proliferation (Bittman et al. 1997; Caviness et al. 2009; Liu et al. 2010). In addition, newly generated neurons and IPs are involved by presenting Delta ligands in maintenance of RGs proliferation through the activation of Notch signaling (Yoon et al. 2008). Lastly, an increasing number of evidence suggests that the secretion of diffusible molecules regulates the proliferation properties of cortical progenitors (Polleux et al. 1998; Dehay et al. 2001; Viti et al. 2003; Agasse et al. 2006; Dehay and Kennedy 2007; Scuettjes et al. 2009; Griveau et al. 2010). However, it is unlikely that Dbx1-derived CP transient neurons would use the same molecules expressed by all differentiating glutamatergic neurons to communicate with cortical progenitors, for example, Nt3/Fgf9 as in the case of Sip1 mutants (Scuettjes et al. 2009) or Notch ligands (Yoon et al. 2008). Indeed, they represent a small percentage of the neurons in the postmitotic compartment at any given stage and especially in rD at E14.5 when the effect upon ablation is already observed (Teissier et al. 2010) and their ablation would further be compensated by the precarious differentiation, initially generating more neurons.

Patterning, growth, and cell fate, by “mobile signaling cells/structures,” such as TCA axons and migrating cells (CR neurons, CP transient neurons, neural crests, meninges, and blood vessels) (Etchevers et al. 1999; Dehay et al. 2001; Schneider et al. 2001; Creuzet et al. 2004; Vasudevan et al. 2008; Javaherian and Kriegstein 2009; Siegenthaler et al. 2009; Stubbs et al. 2009; Griveau et al. 2010) depend critically on the timing of their generation, migration, and arrival in different cortical regions. Their early arrival (E10.5–E12.5) will affect regionalization and later arrival (E12.5–E13.5) the onset of neurogenesis in a tight interplay with intrinsic developmental programs of cortical progenitors. Therefore, it appears that multiple temporal, spatial, and qualitative levels of control underlie the role of these mobile “signaling” cells/structures in cortical development. The identification of this novel population and its crucial non-cell autonomous role in progenitor pool maintenance will now allow further studies aiming at the molecular characterization of how migrating CP transient neurons contributes to the extrinsic control of corticogenesis.

**Supplementary Material**

Supplementary material can be found at: http://www.cercor.oxfordjournals.org/

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References


Polleux F, Dehay C, Moraillon B, Kennedy H. 1997. Regulation of
Pilaz LJ, Patti D, Marcy G, Ollier E, Pfister S, Douglas RJ, Betizeau M,
O’Leary DD, Sahara S. 2008. Genetic regulation of arealization of the
Ochiai W, Nakashima S, Takahara T, Kainuma M, Masaoka M, Minobe S,
Siegenthaler JA, Ashique AM, Zarbalis K, Patterson KP, Hecht JH,
Shen Q, Wang Y, Dimos JT, Fasano CA, Phoenix TN, Lemischka IR,
Monaghan AP. 2004. The Tlx gene regulates the timing of neurogenesis
Hevner RF, West JD, Price DJ. 2007. Pax6 controls cerebral cortical
Neural Dev. 5:8.
Hevner RF, West JD, Price DJ. 2007. Pax6 controls cerebral cortical
epinephrine regulates exit from the cell cycle and specifies
Pilaz LJ, Patti D, Marcy G, Ollier E, Pfister S, Douglas RJ, Betizeau M,
O’Leary DD, Sahara S. 2008. Genetic regulation of arealization of the
Ochiai W, Nakashima S, Takahara T, Kainuma M, Masaoka M, Minobe S,
Siegenthaler JA, Ashique AM, Zarbalis K, Patterson KP, Hecht JH,
Shen Q, Wang Y, Dimos JT, Fasano CA, Phoenix TN, Lemischka IR,
Monaghan AP. 2004. The Tlx gene regulates the timing of neurogenesis
Hevner RF, West JD, Price DJ. 2007. Pax6 controls cerebral cortical
neocortex in the absence of a basal proliferative compartment.
Neural Dev. 5:8.
Quinn JC, Moliniek M, Martynoga BS, Zaki PA, Faedo A, Bullfone A,
Hevron RF, West JD, Price DJ. 2007. Pax6 controls cerebral cortical
neocortex in the absence of a basal proliferative compartment.
Neural Dev. 5:8.
Quinn JC, Moliniek M, Martynoga BS, Zaki PA, Faedo A, Bullfone A,
Hevron RF, West JD, Price DJ. 2007. Pax6 controls cerebral cortical
neocortex in the absence of a basal proliferative compartment.
Neural Dev. 5:8.
Quinn JC, Moliniek M, Martynoga BS, Zaki PA, Faedo A, Bullfone A,
Hevron RF, West JD, Price DJ. 2007. Pax6 controls cerebral cortical
neocortex in the absence of a basal proliferative compartment.
Neural Dev. 5:8.
Quinn JC, Moliniek M, Martynoga BS, Zaki PA, Faedo A, Bullfone A,
Hevron RF, West JD, Price DJ. 2007. Pax6 controls cerebral cortical
neocortex in the absence of a basal proliferative compartment.
Neural Dev. 5:8.
Quinn JC, Moliniek M, Martynoga BS, Zaki PA, Faedo A, Bullfone A,
Hevron RF, West JD, Price DJ. 2007. Pax6 controls cerebral cortical
neocortex in the absence of a basal proliferative compartment.
Neural Dev. 5:8.
Quinn JC, Moliniek M, Martynoga BS, Zaki PA, Faedo A, Bullfone A,
Hevron RF, West JD, Price DJ. 2007. Pax6 controls cerebral cortical
neocortex in the absence of a basal proliferative compartment.
Neural Dev. 5:8.
Quinn JC, Moliniek M, Martynoga BS, Zaki PA, Faedo A, Bullfone A,
Hevron RF, West JD, Price DJ. 2007. Pax6 controls cerebral cortical
neocortex in the absence of a basal proliferative compartment.
Neural Dev. 5:8.
Quinn JC, Moliniek M, Martynoga BS, Zaki PA, Faedo A, Bullfone A,
Hevron RF, West JD, Price DJ. 2007. Pax6 controls cerebral cortical
neocortex in the absence of a basal proliferative compartment.
Neural Dev. 5:8.
Quinn JC, Moliniek M, Martynoga BS, Zaki PA, Faedo A, Bullfone A,
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