Pax6 regulates regional development and neuronal migration in the cerebral cortex

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Pax6 regulates regional development and neuronal migration in the cerebral cortex


Abstract

Mutations in the Pax6 gene disrupt telencephalic development, resulting in a thin cortical plate, expansion of proliferative layers, and the absence of the olfactory bulb. The primary defect in the neuronal cell population of the developing cerebral cortex was analysed by using mouse chimeras containing a mixture of wild-type and Pax6-deficient cells. The chimeric analysis shows that Pax6 influences cellular activity throughout corticogenesis. At early stages, Pax6-deficient and wildtype cells segregate into exclusive patches, indicating an inability of different cell genotypes to interact. At later stages, cells are sorted further based on telencephalic domains. Pax6-deficient cells are specifically reduced in the mediocaudal domain of the dorsal telencephalon, indicating a role in regionalization. In addition, Pax6 regulates the process of radial migration of neuronal precursors. Loss of Pax6 particularly affects movement of neuronal precursors at the subventricular zone/intermediate zone boundary at a transitional migratory phase essential for entry into the intermediate zone. We suggest that the primary role of Pax6 is the continual regulation of cell surface properties responsible for both cellular identity and radial migration, defects of which cause regional cell sorting and abnormalities of migration in chimeras.

Keywords: Pax6; Small eye; Cerebral cortex; Neuronal migration; Cell autonomous

Introduction

During development of the cerebral cortex, neurons are generated in the ventricular zone (VZ), a pseudostratified columnar epithelium that lies adjacent to the lateral ventricles. After the final cell division, newly postmitotic cells leave the VZ and migrate through the subventricular zone (SVZ) and the intermediate zone (IZ) to the cortical plate, the precursor of the cerebral cortex. Neurons generated later bypass the older ones and form the more superficial layers of the cortex in an inside-first outside-last sequence ( Angevine and Sidman, 1961; Bayer and Altman, 1991; Rakic, 1974). Neuroblasts in their route to the cortical plate migrate along the surface of radial glia (Rakic, 1978).

Alleles of mouse small eye (Pax6<sup>Sey</sup>) result from mutations in the Pax6 gene (Hill et al., 1991). Studies of the developing telencephalon in homozygous Pax6<sup>Sey/Sey</sup> mice show several abnormalities in the cerebral cortex, such as...
expansion of the germinal epithelium, heterotopic germinal cells, and a thinner than normal cortical plate (Caric et al., 1997; Schmahl et al., 1993). Recent evidence suggests that cortical areas are established by homeodomain protein gradients in the VZ. One of these proteins is PAX6, which at early stages of cortical development, is expressed at high levels at the anterior and lateral domains of the ventricular zone, reducing to lower levels at the mediocaudal region (Bishop et al., 2000; Walther and Gruss, 1991). Two studies have proposed that both Pax6 and Emx2, expressed in a complementary gradient pattern in cortical progenitor cells, specify area identities in the neocortex (Bishop et al., 2000; Mallamaci et al., 2000). In addition, Pax6 has a role in dorsoventral patterning of the telencephalon (Stoykova et al., 2000; Toresson et al., 2000; Yun et al., 2001).

A difficulty in analysing telencephalon development in Pax6-deficient mice is that the telencephalon develops in an abnormal environment; thus, it is difficult to establish which are the primary telencephalic defects and which are secondary to the failure of other tissues or cell types. For example, Pax6<sup>Sey/Sey</sup> mice have no olfactory placodes, which are required for induction of the olfactory bulbs and, overall, for forebrain growth (Graziadei and Monti-Graziadei, 1992). Other telencephalic signaling centres are affected in the Pax6<sup>Sey/Sey</sup> mutation. WNT signalling at both the cortical hem (caudal–medial edge of the cortical field) (Muzio et al., 2002a) and the lateral edge at the pallial and subpallial boundary is impaired (Kim et al., 2001). Thus, it is likely that forebrain defects are a result of both an intrinsic Pax6 deficiency and a lack of induction by the olfactory placodes and cortical signalling centres. In addition, radial glia cells, that are required for migration of the neuronal precursors, are defective (Caric et al., 1997; Gotz et al., 1998). To overcome these problems, we have analysed fetal mouse aggregation chimeras containing a mixture of wildtype and Pax6<sup>Sey/Sey</sup> mutant cells. In aggregation chimeras, the facial primordia, including the olfactory placodes, develop normally (Quinn et al., 1996), and mutant cells develop alongside wildtype cells in a more normal environment. Previously, chimeric analysis has been successfully used in defining the role of Pax6 in the eye (Collinson et al., 2000, 2001; Quinn et al., 1996).

Here, the mouse chimera approach enabled analysis of neuronal precursors in the developing forebrain and showed that Pax6 regulates forebrain development from the earliest stages affecting fundamental cell surface properties during corticogenesis. Analyses of later stages suggested that Pax6 regulates a specific step in the radial migratory process. In
addition, neuronal precursors in the process of lateral migration are affected by the loss of Pax6. Both cell–cell recognition and neuronal migration are dependent on the composition of the cell surface; thus, we suggest that the primary role of Pax6 in forebrain development is the regulation of fundamental cell surface properties.

Materials and methods

Mice and production of chimeras

Mice stocks, maintenance, and production of chimeras have been described previously (Quinn et al., 1996). Chimeras were made by aggregating eight-cell-stage embryos obtained from two different crosses. Two different small eye mutant alleles, Pax6Sey and Pax6Sey-Neu, were used. Both small eye strains were pigmented and homozygous for Gpi1b. Pax6Sey/– males were also homozygous for the reiterated silent β-globin transgene marker TgN(Hbb-bs83Clo (Quinn et al., 1996). Heterozygous Pax6Sey-Neu/+ females were crossed to Pax6Sey/– males to produce embryos that were pigmented, homozygous for the glucose phosphate isomerase Gpi1b allele, hemizygous for the β-globin transgene (Tg +/–, referred to as Tg +), and differing at the small eye locus. These embryos were aggregated to (BALB/c × A/J) F2 embryos (nonpigmented, homozygous for Gpi1b allele, noncarriers of the β-globin transgene, and wild type at the Pax6 locus) and cultured overnight before transfer into recipient pseudopregnant albino (homozygous for Gpi1b allele) females. Pregnancies were timed according to the pseudopregnant female, with the day of vaginal plug designated 0.5 day postcoitum (E0.5). Embryos were allowed to develop in utero to E10.5, E12.5, E14.5, E16.5, and E18.5.

Analysis of chimeras

Fetuses were dissected into cold phosphate-buffered saline (PBS). To determine proportion of cell contribution within chimeric fetuses, tissue samples from the tail and forelimbs were dissected into H2O/glycerol 50:50 for GPI1 electrophoresis and scanning densitometry (West and Flockhart, 1994). The average percentage of GPI1B in the fetal tail and forelimb was 6–7%, ranging from 5.6–7.0% as described in Quinn et al. (1996).

DNA–DNA in situ hybridisation

Fixed brains embedded in wax were sectioned sagittally at 10 μm and mounted on slides coated with 3-aminopropyltriethoxysilane (Sigma). In situ hybridisation using a digoxigenin-labeled DNA probe was performed for visualisation of the β-globin transgenic cell marker (Keighren and West, 1993). The DNA probe was detected by diaminobenzidine (DAB) staining for peroxidase-labeled antibody (nonradioactive DNA labeling and detection kit; Boehringer Mannheim). Slides were counterstained with hematoxylin and eosin and examined by bright-field and phase-contrast light microscopy. From each E16.5 chimeric brain, two nonconsecutive sagittal sections corresponding to the lateral brain and two nonconsecutive sagittal sections corresponding to the medial brain were analysed. In the medial neocortex, two fields were analysed: one in the rostral portion (not including the RMS) and one in the caudal neocortex. In the lateral brain, the DNA in situ analysis showed no differences between rostral and caudal domains; thus, only one field was quantified in the rostral portion. The percentage of transgene-positive cells (Tg + cells) throughout the depth of the telencephalic wall was estimated by counting numbers of nuclei vs numbers of hybridisation signals in 160 × 160 μm2 squares using an eyepiece grid (Graticules Ltd). The percentage of Tg + cells within each of the three embryonic layers (cortical plate, intermediate zone, and proliferative layers) was calculated.

Immunohistochemistry

Sections were blocked in Tris-buffered saline (TBS) containing 1% normal serum, 1% bovine serum albumin and incubated overnight at 4°C with the following primary antibodies: anti-β tubulin isotype III (Sigma, 1:400), MAP2 (ICN, 1:300), NeuN (Chemicon, 1:100), and anti-polysialylated N-CAM (Pharmingen, 1:200). After rinsing in TBS, sections were incubated with the appropriate biotinylated secondary antibodies (Dako, 1:400) followed by avidin–biotin–HRP complex (Vector) and visualised with diaminobenzidine (Vector).

Results

The mutant embryos used for chimera production arose from matings in a Pax6Sey-Neu+/– × Pax6Sey+/– cross. Four possible chimeric genotypes were produced: the fetuses of interest containing a mixture of Pax6−/− cells and wild-type cells designated mutant chimeras, Pax6Sey-Neu/Sey ↔ Pax6−/–, and three classes of control chimeras: Pax6Sey+/+ ↔ Pax6−/+; Pax6Sey-Neu+/ ↔ Pax6−/+; and Pax6Sey−/ ↔ Pax6−/+. The global percentage of cells derived from the different aggregated embryos in the chimera was estimated by quantitative analysis of GPII isozyme composition of the limbs, with the percentage of the GPI1B isozyme representing the contribution
of cells in the chimera derived from the Pax6\textsuperscript{Sey-Neu/+} × Pax6\textsuperscript{Sey/+} cross. To identify the distribution of cells derived from this cross, DNA in situ hybridisation to the \(\beta\)-globin transgene, carried homozygously by the Pax6\textsuperscript{Sey/+} male mice, was performed (labelled cells are referred to as \(Tg^+\) cells). Thus, in the mutant chimeras, the Pax6\textsuperscript{Sey-Neu/Sey\textsuperscript{Sey+}} mutant cells (referred to as \(Pax6^{-/-}\)) were distinguished from the wild-type by the presence of a brown spot in the nucleus.

**Accumulation of Pax6\textsuperscript{-/-} cells in subdomains of the SVZ in E16.5 chimeras**

We examined the forebrain of chimeras at embryonic day 16.5 (E16.5) to establish the distribution of cortical cells in the chimera. We produced 21 E16.5 chimeras of different day 16.5 (E16.5) to establish the distribution of cortical cells in E16.5 chimeras. Sections through the caudal neocortex contained Pax6\textsuperscript{-} cells in the SVZ. In the rostral SVZ, \(Tg^+\) cells were significantly reduced in thickness (data not shown). In these chimeras, the mutant cells accumulate in the SVZ, giving rise to an abnormal proliferative region (Fig. 1A; 15% GPI1B). Analysis of a number of cell clusters showed stripes of mutant cells that extended radially both from the clusters to an abnormal proliferative region (Fig. 1A; 15% GPI1B). The medial telencephalon at E16.5 showed a rostral to caudal gradient (Fig. 1B). Within the same medial sections, the caudal neocortex contained Pax6\textsuperscript{-/-} cells that were not distributed in apparent clusters in the SVZ or showed smaller clusters (Fig. 1C). In contrast, in the lateral chimeric forebrain, Pax6\textsuperscript{-/-} cells were distributed throughout the SVZ, showing very little difference between rostral and caudal domains (Fig. 1A). This phenotype was found in all of the mutant chimeras independent of the percentage of Pax6\textsuperscript{-/-} cells in the chimera. In control chimeras, the \(Tg^+\) cells were distributed throughout the VZ to the pial surface in lateral neocortex and rostral (Fig. 1E) and caudal (Fig. 1F) medial neocortex with no detectable clustering as seen in the mutant chimeras.

The differential accumulation of Pax6\textsuperscript{-/-} cells at E16.5 was quantified based on the percentage of \(Tg^+\) cells throughout the width of the telencephalic wall in sagittal sections through the medial and lateral (L) neocortex. The medial sections were further analysed in both rostral (R) and caudal (C) regions of the neocortex (Fig. 2A). The telencephalic wall was subdivided into three embryonic zones (proliferative layers: VZ and SVZ, the IZ, and the cortical plate), and the contribution of \(Tg^+\) cells to each layer was determined (Fig. 2B–J). We compared control and mutant chimeras over a range of GPI1B percentages [Fig. 2B–E, and G represent the lower-percentage (<50%) embryos; Fig. 2F, and H–J representing the higher-percentage embryos]. In the control chimeras (Fig. 2B, D, F, and H), there were no significant differences in the percentages of overall \(Tg^+\) cells between the rostral (R) and caudal (C) fields as compared with control chimeras. Furthermore, in the control chimeras (Fig. 2B, D, F, and H), in the three areas analysed (L, R, and C), the \(Tg^+\) cells contributed similarly to the cortical plate and proliferative regions. In all of the mutant chimeras (Fig. 2C, E, G, I, and J), the majority of the \(Tg^+\) cells in the rostral–medial forebrain (R) and lateral forebrain (L) were localised in the proliferative region, while in the cortical plate and intermediate zone, the \(Tg^+\) cells were underrepresented. The mutant cells that accumulated in the proliferative region represented between 70 and 90% of the total \(Tg^+\) in the telencephalic wall. Although in the quantitative analysis, the VZ and SVZ were both included as components of the proliferative region, most \(Tg^+\) cells in the mutant chimeras resided in the SVZ near the IZ boundary at a distance from the ventricular cavity (Fig. 1A and B). Thus, this analysis in the mutant chimeras confirmed that there is underrepresentation of Pax6\textsuperscript{-/-} cells in the caudal neocortex and an area-

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**Fig. 2.** Quantitative analysis of the distribution of \(Tg^+\) cells in E16.5 chimeras. (A) Representation of sagittal views of the telencephalon showing the lateral (L), medial–rostral (R), and medial–caudal (C) areas analysed and a representation of the neocortex with the embryonic regions analysed in the quantification: cortical plate (CP), intermediate zone (IZ), and proliferative zone (SVZ + VZ). The histograms show the average percentages (±S.E.M.) of \(Tg^+\) cells through the width of the telencephalic wall in control chimeras (B, D, F, H) and mutant chimeras (C, E, G, I, J) with different percentages of chimerism (B–E, G contain less than 50% mutant cells by GPI1 analysis) (F, H–J contain greater than 50% mutant cells by GPI1 analysis). In all histograms, the y-axis depicts the percentage of \(Tg^+\) cells. Each bar (total percentage of \(Tg^+\) cells in the telencephalic wall) is divided, showing the percentage of \(Tg^+\) cells in the cortical plate (white), intermediate zone (pattern), and proliferative zone (black) that contribute to the total. In control chimeras, the \(Tg^+\) cells contributed to L, R, and C domains and were distributed between the three different embryonic layers. In mutant chimeras, \(Tg^+\) cells contributed to the L and R domains but were localised mainly in the proliferative region; this accumulation correlated with a diminution of \(Tg^+\) cells in CP and IZ. In all the mutant chimeras, the total percentage of \(Tg^+\) cells in the medial–caudal neocortex was reduced.
specific accumulation of Pax6<sup>−/−</sup> cells in the proliferative zone in rostral and lateral cortex.

**Neuronal precursors are affected in the mutant chimeras**

To determine which cell type was affected in the chimeras, we used markers that distinguish neuronal precursors. We used the neuron-specific class III β-tubulin isotype. At E16.5 in the control chimeras, there is immunoreactivity throughout the CP, subplate, and IZ with an intensely stained band of cells at the border between the SVZ and the IZ (Fig. 3A). In both stages of mutant chimeras analysed (E16.5 and E18.5; see below), the clustered Pax6<sup>−/−</sup> cells expressed this early neuronal marker (Fig. 3B). In order to determine the stage of differentiation of Pax6<sup>−/−</sup> cells, we used MAP2, a cytoskeletal component important in maintaining a differentiated neuronal cellular structure. In all the E16.5 chimeras, strong immunoreaction for MAP2 was shown in cell bodies and dendrites through the neocortex, subplate neurons, and cells in the IZ and SVZ (Fig. 3D and E). In the mutant chimeras, the clusters of Pax6<sup>−/−</sup> cells were additionally immunoreactive for this neuronal marker (Fig. 3E). In contrast, NeuN (Mullen et al., 1992) is expressed in older neurons and is found throughout the cortical plate, in particular the early formed superficial layer and subplate, and intermediate zone, with low expression in the proliferative regions (Fig. 3G). In the mutant chimeras, the expression in the cortical plate was similar to the controls. Interestingly, Pax6<sup>−/−</sup> cells that accumulated in the SVZ were negative for NeuN immunostaining (Fig. 3H). The
Fig. 4. Analysis of cell distribution at early stages of corticogenesis. Sections of E10.5 (A, B) and E12.5 (C, D) dorsal telencephalon comparing distribution of Tg cells in +/+×+/+ wildtype (A, C) and Pax6−/− × +/+ mutant (B, D) chimeras. In (B) and (D), Tg cells are segregated into exclusive cell patches. Histogram (E) of the analysis of the regional distribution of Tg cells at E12.5 in +/+×+/+ wildtype and Pax6−/− × +/+ mutant chimeras. Medial sections were taken, and the Tg cell distribution was analysed in rostral and caudal regions.
identification of the Pax6\(^{-/-}\) cell clusters was clear; however, adjacent sections were used for the DNA in situ hybridisation to confirm their identity (data not shown). These results suggest that the clustered mutant cells are neuronal, although they do not express the late neuronal marker (NeuN) apparent in cells that leave the proliferative zone.

We have used the same neuronal markers in the Sey mutants (Pax6\(^{Sey/Pax6^{Sey}}\)) (Fig. 3C, F, and I). Cells of the abnormal SVZ were immunopositive for class III \(\beta\)-tubulin (Fig. 3C) and MAP2 (Fig. 3F), but negative for NeuN (Fig. 3I), suggesting that the clusters seen in the chimeras are equivalent to those reported in the mutant. Furthermore, cells that did leave the proliferative region expressed NeuN, suggesting that the Pax6 mutation does not completely block cell differentiation, but that Pax6 is required for efficient migration.

**Distribution of wild-type and Pax6\(^{-/-}\) mutant cells at other stages in development**

Neurogenesis begins at around E12.5 in the mouse telencephalon, and this stage was examined for an early Pax6 role in the corticogenic precursors. At this stage, we detected no difference in the rostral to caudal distribution of Pax6\(^{-/-}\) cells in the Pax6\(^{Sey-Neu/Sey} \leftrightarrow Pax6^{+/-}\) chimeras (Fig. 4C-E). Analysis of cell number suggested that there is no difference in the percentage of Pax6\(^{-/-}\) cells comparing rostral and caudal regions (Fig. 4E). However, the Pax6\(^{-/-}\) cells are segregated into patches both rostrally and caudally with very little intermixing of the Pax6\(^{-/-}\) and wildtype cells (Fig. 4C and D).

The stage that segregation of Pax6\(^{-/-}\) and wildtype cells occurs was traced further back to E10.5 well before neurogenesis. At these early stages of corticogenesis, the mutant and wildtype cells reside in well-segregated patches (Fig. 4A and B). Thus, Pax6 has an influence on cortical cells during development of the telencephalon at these initial stages. Such segregation of cells suggests that cell–cell recognition is affected, indicating a fundamental cell surface difference in mutant and wildtype cells at these stages.

A later stage of development (E18.5) was examined to define the culmination of the phenotype at E16.5. Cell distribution analysis in sagittal sections throughout the brain showed that the irregular clusters of cells (Fig. 5B) were, as at E16.5, entirely composed of Pax6\(^{-/-}\) mutant cells (Fig. 5D). Serial sections showed that these aggregates, however, were found throughout the SVZ of the telencephalon. Accumulation of mutant cells in the SVZ (Fig. 5D) was associated with a reduction of mutant cells in the cortical plate (Fig. 5B). In the control chimeras, the telencephalon had a normal appearance (Fig. 5A and C). In these chimeras, Tg\(^{+}\) cells were distributed throughout the width of the telencephalon from the VZ to the cortical plate. Thus, the analysis of cell distribution in the E18.5 mutant chimeras showed both a reduction of mutant cells in the cortex and accumulation in clusters throughout the SVZ.

**Pax6\(^{-/-}\) cells in lateral migratory pathways**

During development, neuroblast migration also occurs tangentially to the brain surface (Fishell et al., 1993; O’Rourke et al., 1992, 1995; Walsh and Cepko, 1992). Pax6 is expressed in the lateral portion of the proliferative region that gives rise to tangentially oriented migratory pathways in the chimeras. The distribution of the Pax6\(^{-/-}\) cells in these pathways was examined. Pax6\(^{-/-}\) cells were found through the entire rostral migratory stream (RMS) (Fig. 6B). However, the Pax6\(^{-/-}\) cells formed abnormal clusters through all the RMS continuous with the neocortical SVZ (Fig. 6B). To confirm that Pax6\(^{-/-}\) cells were found in other tangential streams, the lateral cortical stream (LCS) (Bayer et al., 1991) was also examined. This stream, found at the junction of the neocortex and the basal ganglia, contained Pax6\(^{-/-}\) cells in the mutant chimeras (Fig. 6D). Together, these results show that Pax6\(^{-/-}\) cells are localised throughout the lateral pathways, presumably migrating from the anterior lateral ventricle; however, the Pax6\(^{-/-}\) cells remain segregated within these streams of migrating cells.

**Discussion**

**Pax6 required for neocortical regionalisation**

During development of the cerebral cortex, migration along radial glia cells is considered the primary guidance system (Rakic, 1972). In homozygous Pax6\(^{Sey/Sey}\) mutant mice, previous studies showed that radial glial cells are present in the neocortex (Caric et al., 1997; Gotz et al., 1998), but exhibit altered morphology, tenascin expression, and cell cycle characteristics (Gotz et al., 1998; Heins et al., 2002). The morphological defects are cell-autonomous and may contribute to the failure of migration in the homozygous mutant cerebral cortex (Gotz et al., 1998; Heins et al., 2002). Previously, we concluded in analysis of homozygous Pax6\(^{Sey/Sey}\) mutants that Pax6 had nonautonomous effects on neuronal migration (Caric et al., 1997). Here, the nature of the Pax6 defect on neuronal migration in mouse chimeras is addressed. Based on the hypothesis that mutant cortical cells in the presence of wildtype cells would display their full developmental potential, we have been able to focus on Pax6 functions in corticogenesis predicted to be cell-autonomous.

These chimera studies showed that, initially, Pax6 activity could be traced to a stage prior to neurogenesis. At E10.5, at least a day before neurogenesis begins, Pax6\(^{-/-}\) and wildtype cells have fully segregated into distinct patches in the telencephalon. This cell-segregation phenomenon is typically associated with cell surface differences
Neocortical regionalisation was proposed to be controlled by both intrinsic (Rakic, 1988; Miyashita-Lin et al., 1999) and extrinsic mechanisms (O’Leary, 1989), with recent evidence suggesting an important role for molecular determinants intrinsic to the proliferative zone of the neocortex. Several molecular gradients have been described (Donoghue and Rakic, 1999), and it has been proposed that the Pax6 gradient in combination with the complementary Emx2 expression gradient (high caudomedially, low rostro-laterally) are responsible for neocortical arealization (Bishop et al., 2000; Mallamaci et al., 2000). The graded expression may control local identity, proliferation, and/or radial migration from the proliferative region to the neocortex, and in that way may control the cortical regionalization.

The proposed role for Pax6 in telencephalic regionalization is based on the Pax6 expression gradient and on studies of gross morphological defects in the homozygous Pax6Sey/Sey mutant embryo (Bishop et al., 2000). Using chimeras and focusing on those that have a low contribution of mutant cells (i.e., less than 40%) has enabled analysis of the role of Pax6 in regionalization in an environment that more nearly reflects wildtype. We found that the differential accumulation of Pax6−/− cells inversely correlates with the Pax6 gradient of expression (Bishop et al., 2000; Walther and Gruss, 1991). In the mediocaudal region, which shows the lowest expression of Pax6, Pax6−/− cells are preferentially lost or sorted out. Conversely, in the mediorstral and the lateral regions, areas of highest Pax6 expression, Pax6−/− cell numbers are appreciably higher.

Since in the rostral and lateral domains (regions of highest Pax6 expression) there is no wholesale exclusion of cells, it appears that Pax6 is not required for regionalisation in these neocortical domains. In contrast, loss of Pax6−/− cells in the mediocaudal region suggests a regional dependence on Pax6 expression. We suggest therefore that this dependence on Pax6 requires coexpression of other areal determinants. For example, Pax6 may be required in the caudal region but in combination with high concentrations of Emx2. Clearly, during corticogenesis, Pax6 and Emx2 operate in combination, as evidenced by the Pax6/Emx2 double mutant (Muzio et al., 2002b). Thus, Pax6 is necessary but only in combination with other factors for normal caudal development at these stages. The apparent reduction in the size of the rostral cortex previously reported in the Sey mutants (Bishop et al., 2000) may result from the loss of olfactory bulbs and placodes which are rescued in the chimeras.

**Cell-autonomous requirement for Pax6 in neuronal migration**

Cells deficient for Pax6 accumulate at the SVZ/IZ boundary. These clusters of mutant cells are committed to a neuronal lineage as shown by expression of class III β-tubulin and MAP-2; however, these cells were not immunoreactive for NeuN. These three neuronal markers provide graded indices of neuronal differentiation, NeuN antibody marking cells that have moved into the IZ. Although committed to a neuronal lineage, the Pax6−/− cells found in the clusters lack later neuronal markers characteristic of cells that have moved from the proliferative regions.

The lack of NeuN expression is likely to be due to the position of the cells clustered at the SVZ/IZ boundary. Based on observations in the (nonchimeric) Pax6Sey/Sey mutant forebrain, cells in the IZ and cortical plate express NeuN, suggesting that mutant cells have the capacity for expression and arguing that expression is dependent on position of the cell along the migratory route. Transplantation experiments (Caric et al., 1997) further suggest that Pax6 mutant cells possess the capacity to terminally differentiate to at least some cell types, having occupied a position in the cortical plate. Thus, the mutant cells appear to express markers relevant to their position, and upon reaching the cortical plate, express the repertoire of genes required for differentiation. We suggest that the neuronal property disrupted by the Pax6 mutation is the efficient migration of neuroblasts, and in the absence of Pax6, neuroblast migration is impeded in the SVZ at the point of entry to the IZ.

Two modes of radial migration were proposed for development of the cerebral cortex (Nadarajah et al., 1999): radial glia-mediated locomotion and soma translocation. Clearly, in the chimera, Pax6−/− neuroblasts migrate away from the ventricular edge to the SVZ/IZ boundary. It is not clear which mode of cellular translocation, if defective, would abandon cells at the SVZ/IZ boundary. Interestingly, Altman and Bayer (1990) suggested that some (or perhaps all) neurons interrupt their radial migration for a significant time period within the SVZ, indicating a transitional phase at this boundary. We suggest that radial migration requires additional genetic input at the point of the SVZ/IZ transition.
and that Pax6 plays a role in this process. In the absence of Pax6, the period and number of migrating cells that are impeded at the boundary increase significantly, leading to accumulation into large clusters.

**Pax6 role in radial vs tangential migration**

Our experiments further suggest that Pax6 affects both radial and tangential migration of neuronal precursors. Segregation of wild type and Pax6\(^{-/-}\) cells was found in both long tangential migratory streams that were analysed, the LCS and the RMS. Previous time-course studies suggest abnormalities in the LCS in homozygous Pax6\(^{Sey/Sey}\) mutants (Brunjes et al., 1998). Although there is no conclusive information concerning the origin of the migrating cells through this pathway, i.e., the VZ of the LGE, the neocortical VZ, or both (Bayer and Altman, 1991; De Carlos et al., 1996), Pax6 is expressed in this corticostriatal boundary domain extending to the VZ of the LGE (Stoykova et al., 1997; own data). The substrate used by these migrating neurons from the corticostriatal sulcus is not clear, even though curved radial glial fibers have been shown throughout this pathway in Golgi preparations (De Carlos et al., 1996; Smart and Sturrock, 1979) and by RC2 colocalisation (Edwards et al., 1990). Alternately, tangential migration might occur along axonal pathways as in other brain regions. The RMS originates from the rostrolateral part of the lateral ventricle. Neurons migrating through this stream reach the olfactory bulb, where they differentiate into interneurons (Luskin, 1993). Neurons migrate in a neurophilic mode, moving along one another in chain formations (Lois et al., 1996; Wichterle et al., 1997). There were phenotypic differences between the mutant and wildtype cells found in the LCS and RMS. In the RMS, the aggregates of mutant cells were continuous with and had the same appearance as the clusters found through the SVZ of the neocortex. These

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**Fig. 5.** Cell distribution in the chimera at E18.5. Comparative analysis of cell distribution between control (A, C) and mutant (B, D) chimeras with similar GPI1B percentage. (A) DNA in situ analysis in a 36% GPI1B control chimera shows distribution of Tg\(^+\) cells throughout the cortical plate, (C) IZ, and proliferative layers. (D) DNA in situ analysis in a 32% GPI1B mutant chimera, showing that the abnormal clusters of cells in the SVZ are constituted of Pax6\(^{-/-}\) cells. Accumulation of Pax6\(^{-/-}\) cells in the proliferative region is associated with a diminution of Pax6\(^{-/-}\) cells in the cortical plate (B). Broken lines in (C) and (D) mark the upper edge of the subventricular zone. Scale bars, 25 \(\mu m\) (A, C, D); 10 \(\mu m\) in (B). CP, cortical plate; IZ, intermediate zone; SVZ, subventricular zone; VZ, ventricular zone.
observations indicate that Pax6 affects cellular interactions required for neurons to migrate both tangentially and radially.

Cell surface changes in the neuronal precursors

We suggest that the primary role for Pax6 during brain development is in the control of cell surface properties, and this is the basis for cell segregation found in the early stage chimeras. Furthermore, Pax6 regulates components of the surface which are required for normal migration and are critical for movements of cells into the intermediate zone. Previous in vitro studies have suggested changes in the adhesive properties of the Pax6−/− cortical cells as they segregated from the wildtype in short-term segregation assays (Stoykova et al., 1997). Chimeric analysis of the function of Pax6 in the developing eye has shown segregation of wild-type and Pax6−/− cells, supporting the role of Pax6 in controlling cell surface properties (Collinson et al., 2000; Quinn et al., 1996). These cell surface properties are important for cell–cell interactions, which we suggest play a part in the migration process.

Appropriate radial guided neuronal migration to the cortical plate involves several processes, such as neuron–glial recognition, neuron–glial adhesion, active migration, as well as arrest of migration once the neuron arrives to the correct location. Cell adhesion molecules (CAMs) such as the immunoglobulin (Ig) and cadherin families, as well as integrins, mediate recognition and adhesion. Previous studies have demonstrated that several CAMs are regulated by Pax proteins (Edelman and Jones, 1998); in particular, in vitro experiments have shown that Pax6 activates L1 expression in neural cells (Meech et al., 1999). Additional evidence for a link between Pax6 and CAMs comes from the altered expression of R-cadherin in the developing cortex of the small eye mutant (Stoykova et al., 1997).

The chimeras provide the opportunity to examine mutant cell behaviour in the presence of wildtype cells and determine the earliest stages at which there is a clear requirement for Pax6. In the presence of wildtype cells undergoing the presumed normal migratory process, mutant neuronal precursors were identified and found to be deficient at distinct stages of this process. The effects attributed to the lack of Pax6 in the chimeras appear to have a basis in abnormal cell–cell interactions. We suggest a fundamental role for Pax6 during neurogenesis is the continued regulation of components at the cell surface.

Fig. 6. Segregation between wild type and Pax6−/− cells in lateral migratory pathways. (A, C) Distribution of Tg+/− cells in a control chimera through (A) the rostral migratory stream (RMS) and (C) through the lateral cortical stream (LCS). (B, D) Distribution of Pax6−/− cells in mutant chimeras in both the (B) RMS and (D) LCS. Note that the distribution of Pax6−/− cells through the RMS is similar to the aggregates found in the neocortical SVZ. Segregation between wild type and Pax6−/− cells was found in both pathways. Scale bar, 25 μm.
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