In the developing central nervous system (CNS) of the vertebrate, various types of neurone are produced in precise positions along the dorsoventral (DV) and anteroposterior (AP) axes of the neural tube. Recent studies have drawn a scenario that gradient signals from the ventral and dorsal midline structures pattern the neural plate and neural tube (reviewed by Jessell, 2000). The diffusion of a secreted signalling factor Sonic hedgehog (Shh) from the notochord and the floor plate has been proposed to establish a ventral-to-dorsal gradient of Shh activity within the neural tube that directs subsequent patterns of neurogenesis (Roelink et al., 1994; Chiang et al., 1996; Ericson et al., 1996; Teleman et al., 2001). By contrast, several secreted molecules that belong to bone morphogenetic protein (BMP) family regulate the patterning of dorsal cell types (Liem et al., 1997; Lee and Jessell, 1999).

The role of Shh in the patterning of ventral neural tube has been well studied in the spinal cord. Several homeodomain (HD) proteins are expressed in specific domains of the ventricular zone of the developing spinal cord (Goulding et al., 1993; Ericson et al., 1997; Pierani et al., 1999). They are categorised into two classes: the genes whose expression is repressed by Shh (Pax6, Dbx2, Irx3, Dbx1 and Pax7) are known as class I, while those whose expression is induced by Shh (Nkx2.2 and Nkx6.1) are class II (Briscoe et al., 2000). Misexpression and loss of functions of the HD protein genes can cause alteration of the neuronal subtypes (Briscoe et al., 1999; Briscoe et al., 2000; Sander et al., 2000; Pierani et al., 2001). These data suggest that the progenitor cell identity and the neuronal subtypes are regulated via distinct regionalization of the ventricular zone in the neural tube represented by the combinatorial expression of the HD proteins, i.e., the HD code.

In the developing central nervous system (CNS) of the vetebrate, various types of neurone are produced in precise positions along the dorsoventral (DV) and anteroposterior (AP) axes of the neural tube. Recent studies have drawn a scenario that gradient signals from the ventral and dorsal midline structures pattern the neural plate and neural tube (reviewed by Jessell, 2000). The diffusion of a secreted signalling factor Sonic hedgehog (Shh) from the notochord and the floor plate has been proposed to establish a ventral-to-dorsal gradient of Shh activity within the neural tube that directs subsequent patterns of neurogenesis (Roelink et al., 1994; Chiang et al., 1996; Ericson et al., 1996; Teleman et al., 2001). By contrast, several secreted molecules that belong to bone morphogenetic protein (BMP) family regulate the patterning of dorsal cell types (Liem et al., 1997; Lee and Jessell, 1999).
Members of Pax family proteins are HD-containing transcription factors, and Pax6 is the most characterised member (reviewed by Gruss and Walther, 1992; Hill and Hanson, 1992; van Heyningen, 1998; Gehring and Ikeo, 1999). During development, Pax6 is expressed in the dorsal forebrain, including a region that gives rise to the cortex, dorsal thalamus and pretectum, and functions in patterning the brain (Walther and Gruss, 1991; Stoykova et al., 1997; Pratt et al., 2000; Osumi, 2001). In the hindbrain and spinal cord, Pax6 is expressed in the ventral region and plays crucial roles in generation of ventral neurones. Five types of neurones that are respectively marked with expressions of specific transcriptional factors differentiate in the ventral hindbrain. They are, from ventral to dorsal, branchiomotor (BM) and somatic (SM) motoneurones, and V2, V1 and V0 interneurones (Fig. 1A). In the hindbrain of Pax6 homozygous mutant mice and rats, the SM neurones and V1 interneurones are missing, while the BM neurones increased in number (Osumi et al., 1997; Ericson et al., 1997; Burill et al., 1997; Osumi and Nakafuku, 1998; Sun et al., 1998). However, in the Pax6 mutant spinal cord, SM neurones do develop and a small number of V1 interneurones appear at later stages. Therefore, how Pax6 functions in ventral neurone development is still enigmatic.

In the present study, we first performed detailed time-course analyses on expression of neuronal subtype markers in the hindbrain of the Pax6 homozygous rat embryo. We found that Isl1 and HB9/MNR2 (SM neurone markers) and En1 (V1 interneurone marker) were transiently expressed in a small number of cells, indicating that Pax6 expression is not an absolute requirement for the differentiation of these neurones. By comparing the expression of HD protein genes in the wild type and the mutant, we found that the domains of all other HD protein genes (i.e. Nkx2.2, Nkx6.1, Irx3, Dbx2 and Dbx1) were shifted dorsoventrally and their boundaries became fuzzy. Thus, Pax6 seems to be required for establishment of the progenitor domains for the ventral neurones. Moreover, Pax6 overexpression in the wild type altered the expressions of other HD protein genes, and Pax6 electroporation into the Pax6 mutant hindbrain rescued the expression of Isl1 and En1, but only in the normal positions. To know reasons for perturbed progenitor domain formation in Pax6 mutant, we further examined patterns of Shh signalling and cell kinetics. The expression of Ptc1, Gli1 and Gli2 was slightly altered in the mutant, although Shh itself was similarly expressed in the floor plate, suggesting that Pax6 may modify the Shh signalling in the progenitor domains for the motoneurones. The position and number of TUNEL-positive cells were unchanged in the Pax6 mutant. Although the proportion of cells that were BrdU-positive increased in the mutant, there was no relationship with progenitor domains. These findings suggest that Pax6 regulates the specification of the ventral neurones by establishing the correct progenitor domains.

**MATERIALS AND METHODS**

**Animals**
Pax6 homozygous rat embryos were obtained by inter-crossing male and female heterozygotes of Small eye rats (rSey2) (Osumi et al., 1997). Wild-type Sprague-Dawley (SD) rats were purchased from Charles River Japan. The midday of the vaginal plug was designated as 0.5 day. E10.5-13.5 embryos were used for analyses. In this study, 24- and 36-somite stages were defined as E11.5 and E12.5, respectively. The following experimental procedures were approved by The Committee for Animal Experiment of Tohoku University Graduate School of Medicine.

**Immunohistochemistry**
Immunohistochemistry on frozen sections was performed as described previously (Osumi et al., 1997). Anti-Pax6 rabbit polyclonal antibody (Inoue et al., 2000) was used at 1:1000 dilution. 40.2D6 anti-Isl1/2 (1:100) (Ericson et al., 1992), 74.5A5 anti-Nkx2.2 (1:50) (Ericson et al., 1997) and 81.5C10 anti-MNR2 (1:25) (Tanabe et al., 1998) mouse monoclonal antibodies were obtained from the Developmental Studies Hybridoma Bank (University of Iowa), and used at the specified dilution. Although rat HB9 homologue has not been identified, the staining pattern with the anti-chick MNR2 monoclonal antibody was similar to previous reports for HB9 expression in the mouse embryo (Arber et al., 1999; Thaler et al., 1999). As amino acid sequence of MNR2 is very similar to that of HB9, it is possible that anti-chick MNR2 antibody recognised HB9 and/or HB9 related protein on the rat tissue. Anti-Lim3 rabbit polyclonal antibody was kindly provided by S. L. Pfaff and used at 1:5000 (Sharma et al., 1998). Anti-GFP mouse monoclonal antibody was purchased from Clontech and used at 1:1,000. Antigen enhancement was performed according to the method described previously (Osumi et al., 1997). As secondary antibodies, Cy3-conjugated affinity-purified donkey anti-rabbit IgG (1:600) and anti-mouse IgG (1:400) solutions, FITC-conjugated affinity-purified donkey anti-mouse IgG (1:200) and anti-rabbit IgG (1:200) solutions, and biotin-conjugated affinity-purified donkey anti-rabbit IgG (1:200) and anti-mouse IgG (1:200) solutions (Jackson Immunoresearch Laboratories, Chemicon International, respectively) were used. ABC kit (Vector Laboratories) and Metal enhanced DAB kit (Pierce) were used for detection with horseradish peroxidase.

**In situ hybridisation**
RT-PCR was performed to obtain rat cDNA clones for templates. Total RNA taken from the head of E13.5 SD rat embryos was purified by RNeasy column (Qiagen) and cDNA was synthesised using reverse transcriptase and oligo dT primer (Superscript preamplification system; Gibco BRL). Oligonucleotides used to amplify cDNAs were as follows: Chx10, 5'-AGCGCTGAGCAAGCCAAATT-3' and 5'-CTAAGGCATCTCTCCAGCT-3'; Dbx1, 5'-TCTAGAATGATGTTCCCAGG-3' and 5'-CTAGGACGTTGTATTTCTCT-3', according to previously described mouse sequences (Liu et al., 1994; Lu et al., 1994). Amplification was performed with a thermal cycler (Mastercycler Gradient; Eppendorf) using Taq DNA polymerase (Promega) using the following protocol: denaturation for 5 minutes at 96°C, annealing for 1 minute at 62.4°C (Chx10) or 63.4°C (Dbx1), extension for 1 minute at 72°C, 35 cycles. These cDNA fragments, including the open reading frames, were cloned into pBluescript II SK (-) (Stratagene) and sequenced to confirm they were rat counterparts. Rat En1, Nkx2.2, Shh and Pax6 cDNAs were used previously (Matsuo et al., 1993; Osumi and Nakafuku, 1998), and rat Isl2 cDNA was a kind gift from S. Pfaff (Tsuchida et al., 1994). Rat Smoothened cDNA (Stone et al., 1996) was kindly provided by A. Rosenthal. To synthesise other probes, mouse cDNA clones were used. Evt1 cDNA (Bastian and Gruss, 1990) was provided by M. Goulding, Nkx6.1 cDNA (Qiu et al., 1998) by J. Rubenstein, Irx3 cDNA (Bosse et al., 1997) by P. Gruss, Dbx2 cDNA (Shoji et al., 1996) by N. Takahashi, Gli1 and Gli2 cDNAs (Ding et al., 1999) by H. Sasaki, and Patched1 cDNA (Goodrich et al., 1996) by M. Scott. Digoxigenin-labelled antisense riboprobes were generated with T3 or T7 RNA polymerase (Promega). In situ hybridisation on frozen sections was performed as described previously (Ishii et al., 2000). In some cases,
immunohistochemistry was performed on the same sections after in situ hybridisation.

**Electroporation into cultured rat embryos**

The method used for electroporation into cultured mammalian embryos was described previously (Osumi and Inoue, 2001). Chamber-type electrodes (8×20 mm electrodes and 20 mm distance between electrodes) were used in this study. To construct pCAX expression plasmid, blunted Spl-KpnI fragment of mouse Pax6 cDNA (a kind gift from P. Gruss) (Walther and Gruss, 1991) was inserted into blunt HindIII-KpnI site of pCAX expression plasmid containing the cytomegalovirus enhancer and chicken β-actin promoter (pCAX and pCAX-GFP plasmids were kindly provided by the late K. Umesono). At E10.75 stage, the uterus was dissected out from anaesthetised rSeY2 heterozygous females, and littermate embryos were dissected out with their placenta and yolk sac intact. After a 2 hour preculture, the embryos were transferred into the chamber-type electrodes and DNA solution of pCAX-mPax6 and pCAX-GFP (9:1) dissolved in PBS at 5 mg/ml was injected into the hindbrain. Immediately, square pulses (50 microseconds, 70 V, five times) were sent using an electroporator (CUTY21; NEPPA GENE), and the embryos were further cultured. At this point, we could not distinguish homozygous embryos from external features. Twelve hours later when the cultured embryos developed to the stage corresponding to E11.5, the yolk sac was opened and homozygous embryos were identified based on morphological defects in the brain and eyes. In electroporation of the Pax6 mutant at early E11.5 (22-somite stage), littermate embryos were dissected with the yolk sac opened, and homozygous embryos that were identified from the external features were used for electroporation. Both the wild-type and homozygous embryos were precultured for 2 hours, and electroporated with square pulses (50 milliseconds, 70-90 V, five times). The cultured embryos were fixed with 4% paraformaldehyde (PFA) in phosphate-buffered saline (PBS) overnight at 4°C. Selected embryos in which GFP fluorescence was seen only in one side of the neural tube were processed for further analyses as described above. In total, 10 wild-type and eight homozygous mutant embryos at early E11.5, and three mutant embryos at E10.75 were used for analysis.

**Assay for cell death and cell proliferation**

Cell death was assayed quantitatively by terminal deoxynucleotidyl transferase-mediated biotinylated UTP nick end labelling (TUNEL) as described previously (Wakamatsu et al., 1998) with minor modification. The embryos were fixed with 4% PFA in PBS overnight at 4°C. Frozen sections were treated with 1 mg/ml proteinase K/PBS for 5 minutes at 37°C, and refixed with 4% PFA in PBS for 10 minutes. Sections were incubated with TdT buffer containing bovine-14-ATP (Gibco BRL) and terminal transferase (Roche Molecular Systems) for 1 hour at 37°C. Labelled cells were detected with avidin-Cy3 (1:200, Jackson). Immunohistochemistry was performed on the same sections after in situ hybridisation.

**RESULTS**

**V1 interneurones and SM neurones transiently emerge in the hindbrain of the Pax6 mutant**

Previous studies have shown the lack of V1 interneurones expressing Enl in both the hindbrain and spinal cord in Pax6 homozygous mutants at E10.5 in mice and at E12.5 in rats (Ericson et al., 1997; Burill et al., 1997; Osumi and Nakafuku, 1998). However, Enl transcripts are detected in the spinal cord of Pax6 homozygous mice at E12.5 (Burill et al., 1997). Therefore, we carefully re-explored whether Enl transcripts were detected in the Pax6 homozygous rat hindbrain from E10.5 to E13.5. In the wild type, Enl-positive cells were firstly observed at E12.0, and more Enl-positive cells were observed at E13.0 (Fig. 1E). In the Pax6 homozygous embryos at E12.0-12.75, Enl expression was undetectable throughout the hindbrain and spinal cord, but at E13.0 a few Enl-positive cells were found at r3-6 level of the Pax6 homozygous embryos (Fig. 1I). At r7 level, transient expression of Enl was not seen throughout stages analysed (Fig. 1B). At E13.5, Enl expression at r3-6 diminished in the mutant (Fig. 1B). These results indicate that differentiation of V1 interneurones is not entirely dependent on Pax6 function in the hindbrain.

Next, we investigated differentiation of other interneurones, including V2 (Chx10-positive) and V0 (Evx1-positive) populations, in the Pax6 homozygous embryos. Chx10 transcripts were detected from E12.0 in the hindbrain of wild-type and Pax6 homozygous embryos (Fig. 1A,B,D,H). It has previously been reported that cells expressing Chx10 protein are reduced at r7 in the mouse Pax6 homozygous embryo (Ericson et al., 1997). In the rat Pax6 homozygous embryo, however, we did observe Chx10-positive cells at E12.0-13.5, and the domain of Chx10 expression expanded somewhat dorsally (bracket in Fig. 1H). The onset of Evx1 expression was later than that of Enl and Chx10; Evx1-positive cells emerged from E12.5 and afterwards in the hindbrain of the wild type (Fig. 1A,F). In the Pax6 mutant, Evx1-positive cells were not observed until E13.5 at r7 level, while they were found to expand somewhat ventrally at r3-6 levels on E12.75-E13.0 (Fig. 1B,J). Thus, differentiation of the ventral interneurones was impaired in the Pax6 mutant hindbrain.

We have previously demonstrated that mutation in Pax6 gene results in loss of SM and increase of BM neurones in the rat hindbrain (Osumi et al., 1997). The same defect is seen in the homozygote of small eye mouse mutant (Ericson et al., 1997; Burill et al., 1997). However, the SM neurone defect is less severe at the cervical level of the spinal cord. Thus, we re-examined the expression of Islet2 with special reference to embryonic stages and AP levels. At r5 and r7 levels in the wild-type rat hindbrain, Islet2 expression was first detected at E11.5 and maintained at E13.5 (Fig. 1A). In the Pax6 homozygous embryos, Islet2 transcripts were not detected until E12.5, as reported previously (Fig. 1B) (Osumi et al., 1997). However, we found a few cells expressing Islet2 at r7 level during E12.75-13.0 in the Pax6 mutant embryos (Fig. 1Q). We further checked whether the expression of HB9/MNR2, another marker for SM neurones, transiently emerged in the Pax6 homozygous embryos. In the wild-type rat embryo, HB9/MNR2 immunoreactivity was observed from E11.5 (Fig. 1A). In the Pax6 mutant, cells expressing HB9/MNR2 were not seen in the E12.5 mutant hindbrain, but a few cells expressing...
HB9/MNR2 were observed at r7 level of E12.75-13.0 (Fig. 1R). Such Islet2 and HB9/MNR2-positive cells were no longer detected at E13.5 in the mutant (Fig. 1B). As for another marker of SM neurones, Lim3, it was expressed in most of Islet2-positive cells of E11.5-13.0 wild-type hindbrain (data not shown) (Varela-Echavarria et al., 1996). However, Islet2-positive cells transiently observed in E12.75-13.0 mutant did not express Lim3 (data not shown).

In summary, emergence of SM neurones and V1 interneurones in the hindbrain, although transiently, suggests that Pax6 is not directly required for induction of these cell types.

**Progenitor domain formation is perturbed in the Pax6 mutant**

Transient emergence of small number of SM neurones and V1 interneurones prompted us to assume that neuronal progenitor domains for these populations become narrower in the Pax6 mutant.
183.6±7.7 cells/section were positive for the expression of the HD protein genes in the hindbrain at E11.5-12.5 between the wild type and Pax6 mutant. We found that the expression patterns of Nkx2.2, Nkx6.1, Irx3, Dbx2, and Dbx1 (Fig. 2A-E) in the wild-type rat embryos were the same as reported in the mouse (Lu et al., 1992; Shoji et al., 1996; Bosse et al., 1997; Ericson et al., 1997), while all those in the Pax6 mutant rat were markedly different (Fig. 2F-J). The Nkx2.2 domain, which faces the Pax6 domain, expanded dorsally (white arrowhead in Fig. 2F) as previously reported (Ericson et al., 1997; Osumi and Nakafuku, 1998). The dorsal boundary of Nkx6.1 expression was slightly ‘blurred’ (double green arrowhead in 2G). Irx3 expression markedly expanded ventrally into Nkx2.2 domain (red arrowhead in Fig. 2H). The ventral boundary of Dbx2 expression was also ‘blurred’ (double green arrowhead in Fig. 2I). Cells expressing Dbx1 were scattered ventrally (red arrowhead in Fig. 2I) and decreased in number when stained cells were counted in five sections from three embryos for both the wild type and mutant; 183.6±7.7 cells/section were positive for Dbx1 in the wild-type hindbrain, while 101.8±7.9 cells/section were positive in the mutant (t-test; P<0.001).

Fig. 2K,L illustrates schematically the expression patterns of the HD protein genes in the hindbrain of the wild-type and Pax6 homozygous embryos. Expression domains of Irx3 and Dbx1 (class I HD code genes) extended ventrally. The ventral expression boundary of Dbx2, another class I HD code gene, became blurred. Expression of Class II HD code genes also changed in the mutant; Nkx2.2 domain expanded dorsally, and the boundary between Dbx2 and Nkx6.1 was indistinct. As a result, formation of the progenitor domains was severely perturbed in the Pax6 mutant. The progenitor domains for V1 interneurones and SM neurones, which are defined by expression boundaries of Dbx1/Nkx2.2, respectively, became narrower. This explains very well why a very small number of V1 interneurones and SM neurones were produced in the Pax6 mutant. By contrast, progenitor domains for BM neurones, V2 interneurones and V0 interneurones became expanded. This is consistent with the observation that the number of V2 interneurones increased in the mutant rat.
Repressed *Nkx2.2* expression (bracket in Fig. 4B). By contrast, expression of *Irx3*, *Dbx2* and *Dbx1* were ectopically induced on the transfected side (arrowheads in Fig. 4D-F). These effects of *Pax6* overexpression were similarly observed in the *Pax6* mutant background (Fig. 4G-L). In the region where exogenous *Pax6* is expressed (Fig. 4G), *Nkx2.2* expression was downregulated (bracket in Fig. 4H), but *Nkx6.1* expression did not seem different (Fig. 4I). Ectopic induction of *Dbx2* and *Dbx1* expression was also observed (arrowheads in Fig. 4K,L). Induction of *Irx3* could not be detected in the *Pax6* mutant hindbrain, as *Irx3* expression had already shifted ventrally (Fig. 4J). Taken together, these results indicate that *Pax6* represses the expression of class II HD code genes such as *Nkx2.2*, while it induces the expression of class I HD code genes such as *Irx3*, *Dbx2* and *Dbx1*.

**Rescue of En1 and Islet2 in the Pax6 mutant by Pax6 misexpression**

We further investigated the effects of *Pax6* transfection on the expression of subtype specific markers of ventral neurones. As described above, *En1*-positive and *Islet2*-positive cells were mostly missing in the *Pax6* mutant (Fig. 1I,Q). We thus asked whether *Pax6* transfection could rescue this defect. First, we transfected *Pax6* expression vector into the hindbrain of wild-type embryos at 22-somite stage (early E11.5) when expression of *Islet2*, HB9/MNR2 and *En1* was undetectable (see Fig. 1A). The electroporated embryos were cultured for 26-30 hours up to the stage corresponding to E12.5. In the electroporated side at r7 level (Fig. 5A), ectopic expression of *Evx1* (Fig. 5E), but not of *Chx10* and *En1* (Fig. 5C,D), was observed. Ectopic expression of *Evx1* could be explained by the induction of *Dbx1* (see Fig. 4F), as *Dbx1* transfection induced *Evx1* expression (Pierani et al., 2001). We also noticed fewer cells expressing *Islet2* (Fig. 5B) and HB9/MNR2 (data not shown) in response to *Pax6* overexpression. Thus, *Pax6* overexpression did alter the specification of neuronal subtypes.

Then we analysed the effects of exogenous *Pax6* in the mutant background. *Pax6* electroporation (Fig. 5F) at early E11.5 did not induce *Islet2* expression (Fig. 5G). However, we did observe expression of *En1* in the *Pax6* mutant hindbrain electroporated with exogenous *Pax6* (arrowheads in Fig. 5I), although *En1* expression was not observed at the r7 level in E12.5 mutant hindbrain (left side in Fig. 5I; also see Fig. 1B). The number of *En1*-positive cells was far less than the number in wild type, but similar to that in the *Pax6* mutant at E13.0 (see Fig. 1I). Importantly, these *En1*-positive cells were never seen in ectopic positions, suggesting that *Pax6* is not sufficient for promoting development of V1 interneurones. *Chx10* expression was upregulated in the *Pax6* mutant (left side in Fig. 5H; also see Fig. 1H), but decreased in the electroporated area (right side in Fig. 5H). We sometimes observed *Chx10*-positive cells in ectopic positions (arrowhead in Fig. 5H). We also found a small number of cells expressing *Evx1* in normal and ectopic positions (arrow and arrowheads in Fig. 5J, respectively). As mentioned above, *Evx1*-positive cells never appeared at r7 level by E13.5 in our analysis (see Fig. 1B). Therefore, exogenous *Pax6* electroporated at early E11.5 induced *Evx1* expression, but the number of *Evx1*-positive cells was far less than that in normal development.

As differentiation to SM neurones started in the wild-type

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**Altered expression of HD code genes by misexpression of exogenous Pax6**

As HD code gene expressions were altered in the loss-of-function condition of *Pax6*, we next examined the effects of *Pax6* gain-of-function on the expression of the HD code genes. *Pax6* expression vector (*pCAX-mPax6*) and *GFP* expression vector (*pCAX-GFP*) were co-transfected into the hindbrain of wild-type and *Pax6* mutant embryos by electroporation at 22-somite stage (early E11.5) in the rat embryos. These electroporated embryos were cultured for 26-30 hours up to the stage corresponding to 35- to 36-somite stage (E12.5; see Fig. 3A). We analysed embryos transfected on the right side of the hindbrain excluding the floor plate (Fig. 3C-H). In this electroporation, the expression of *Shh* was not affected (Fig. 3E,H).

In the wild-type hindbrain, *Pax6* overexpression (Fig. 4A)
hindbrain at E11.5 (Fig. 1A), electroporation at early E11.5 might be too late to rescue Islet2 and HB9/MNR2 expression. Therefore, we next electroporated exogenous Pax6 into the hindbrain of E10.75 Pax6 mutant embryo, and analysed the results after 42 hours culture (corresponding to E12.5). Although the efficiency of gene transfer at E10.75 was very low (Fig. 5K), in the area where Pax6 was electroporated (Fig. 5K, L) a small number of Islet2-positive and HB9/MNR2-positive cells were detected at the ventral hindbrain (Fig. 5M-P). It was at E12.75-E13.0 that small populations of cells expressing Islet2 and HB9/MNR2 were observed at r7 in the Pax6 homozygous embryos (Fig. 1Q,R). Thus, the induction of Islet2 and HB9/MNR2 expression was likely to be caused by exogenous Pax6 expression. The induction of Islet2 and HB9/MNR2 was only seen in a small number of cells (compare Fig. 5N, P with Fig. 1Q, R). Importantly, expression of these markers were never observed ectopically out of the positions where SM neurones normally exist, again suggesting that Pax6 function is not sufficient to induce these neurones.

In summary, these results of the overexpression experiments together with the loss-of-function data suggest that Pax6 plays a crucial role in establishing V1 and SM progenitor domains and in subsequent differentiation of V1 and SM neurones.

Expression of Shh signalling molecules in the Pax6 mutant hindbrain

What kind of mechanism is involved in progenitor domain formation? Expression of HD proteins in the spinal cord is influenced by graded action of Shh (Briscoe et al., 2000). Moreover, in the telencephalon of Pax6 mutant mice, the domain expressing Shh expanded dorsally compared to that of the wild type (Stoykova et al., 2000). However, the expression patterns of Shh were not altered in the hindbrain and spinal cord of Pax6 mutant mice and rats (Fig. 6A,G) (Ericson et al., 1997; Osumi and Nakafuku, 1998). To explore whether altered expression of HD code genes in the Pax6 mutant hindbrain is due to changes in Shh signalling, we examined the expression of Shh receptor patched1 (Ptc1) and Gli family genes, both of which are direct targets of Shh signal (Goodrich et al., 1996; Hynes et al., 1997; Lee et al., 1997; Sasaki et al., 1999).

In the wild-type rat hindbrain at E12.5, Ptc1 expression was seen in the region that included all the progenitor cells of the ventral neurones mostly in a ventral-to-dorsal gradient, with the highest expression in SM progenitor domain (bracket in Fig. 6C). This reflects the gradient distribution of Shh protein because Ptc1 is induced in response to Shh activity (Goodrich et al., 1996). In the Pax6 mutant, the overall expression pattern of Ptc1 was not drastically changed, but the strong expression in the ventral region was not seen (Fig. 6I).

Expressions of Gli1 and Gli2 were detected at high level in the SM progenitor domain (bracket in Fig. 6D,E), and the ventral limits of the domains are adjacent to the dorsal limit of Nkx2.2 domain (black arrowhead in Fig. 6B,D,E). The dorsal limit of Gli1 and Gli2 domains corresponded to that of Dbx1 domain (red arrowhead in Fig. 6D-F). In the hindbrain of Pax6 mutant, Gli1 and Gli2 were similarly expressed in the region between dorsal limits of Nkx2.2 and Dbx1 (green and red arrowheads, respectively, in Fig. 6H,J-L), but the high levels of Gli1 and Gli2 expression in the ventral region decreased. We also examined the expression patterns of a co-receptor of Shh, Smootherned (Smo) (Stone et al., 1996). In the hindbrain, Smo was expressed in the entire ventricular zone within the hindbrain, and the expression pattern was not altered in the Pax6 mutant (data not shown). Thus, altered expressions of Shh signalling molecules were restricted to the progenitor domain of SM neurones in the Pax6 mutant hindbrain, while expression
patterns of these molecules were unchanged in the dorsal regions, including the progenitor domains for V2, V1 and V0 interneurones.

**Cell death and cell proliferation in the Pax6 mutant hindbrain**

The impaired progenitor domain formation could be due to altered cell kinetics in the Pax6 mutant. That is, the unstable narrow V1 and SM progenitor domains in Pax6 mutant may be resulted from the change in cell death/proliferation in these and flanking domains. Thus, we investigated the relationship between cell death/proliferation and individual progenitor domains.

To detect apoptotic cells, we performed TUNEL staining at E12.5 stage (Fig. 7A,C) and counted the number of TUNEL-positive cells per section within the ventral region, including Dbx1 domain. The mean number of TUNEL-positive cells in the wild-type hindbrain (9.4±1.1/section, ±s.e.m., n=10) was not significantly different from that in the Pax6 mutant (12.3±1.3/section, n=10, t-test; P>0.1, Fig. 7E). Moreover, apoptotic cells were observed in random regardless of the progenitor domains.

Next, we performed BrdU pulse labelling, which detected cells in S-phase. The labelling index (percentage of BrdU+/DAPI+ cells per section) of the wild-type hindbrain was 27.0±0.32% (n=10, means±s.e.m.), and 31.1±0.57% (n=10) in the Pax6 mutant (Fig. 7F). Although the ratio of S-phase cells was slightly higher in the Pax6 mutant (t-test; P<0.001), there were no increase or decrease of BrdU-positive cells in particular progenitor domains (Fig. 7B,D).

These results indicate that the disturbance of the progenitor domains in the Pax6 mutant hindbrain is not attributed to change of cell death or proliferation in the specific progenitor domains.
Pax6 and the progenitor domains

**DISCUSSION**

**Pax6 regulates formation of correct progenitor domains**

The Pax6 mutant hindbrain has been characterised by the loss of SM neurones and V1 interneurones (Ericson et al., 1997; Osumi et al., 1997). However, in the present study, we found the emergence of a small number of SM neurones and V1 interneurones, although transiently, in the mutant hindbrain. Previous studies also reported that SM neurones indeed differentiate in the mutant spinal cord. Thus, Pax6 does not appear to be required for specification of SM neurones. This implies that the function of Pax6 may differ from other HD code genes.

The most important finding in this study is that loss of Pax6 function leads to failure in formation of the correct progenitor domains within the ventricular zone. As illustrated in Fig. 2L, the expression boundaries of all HD protein genes are blurred and shifted in the Pax6 mutant. Expression of Nkx2.2 and Dbx2 expands dorsally, while that of Nkx6.1, Irx3 and Dbx1 shifts ventrally. The altered expression patterns of the HD code genes in the Pax6 mutant explain very well why a small number of V1 interneurones and SM neurones emerge; the progenitor domains for V1 interneurones and SM neurones, which are defined by the expression boundaries of Dbx1/Dbx2 and Irx3/Nkx2.2, respectively, are formed as extremely narrow domains in the Pax6 mutant. Emergence of these V1 and SM neurones was not seen in the Pax6 mutant hindbrain.

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**Fig. 6.** Expression patterns of Shh signalling molecules in the Pax6 mutant hindbrain. Adjacent sections of E12.5 wild-type (A-F) and Pax6 mutant (G-L) hindbrains at r7 level. In the Pax6 mutant hindbrain, Shh expression in the floor plate is no different from the wild-type (A,G). (B-F) In the wild type, Ptc1 is expressed in all ventral progenitor cells with a ventral-to-dorsal gradient, and is especially strong in the SM progenitor domain (bracket in C). Ventralt limits of Gli1 and Gli2 expression domains are adjacent to the dorsal limit of Nkx2.2 domain (black arrowhead in B,D,E). The expression is missing in the BM progenitor cells expressing Nkx2.2, while it is detected at a high level in the SM progenitor cells (bracket in D,E). The dorsal limits of Gli1 and Gli2 expression domains correspond to that of Dbx1 domain (red arrowhead in D-F). (H-L) In the Pax6 mutant, strong Ptc1 expression in the ventral region was not seen. Gli1 and Gli2 was expressed in the region between dorsal limits of Nkx2.2 and Dbx1 (green and red arrowheads, respectively, in Fig. 6H,J-L).

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**Fig. 7.** Cell death and cell proliferation in the Pax6 mutant hindbrain. Sections at r7 level of E12.5 wild-type (A) and Pax6 mutant (C), and cultured wild-type (B) and Pax6 mutant (D) embryos. (E,F) Comparison of TUNEL- (E) and BrdU- (F) positive cells per section within the ventral region, including the Dbx1 domain using 10 sections from three embryos. (E) There is no significant difference in the number of apoptotic cells between the two groups. (B,D) Pulse labelling of BrdU was performed for embryos cultured for 20 minutes and BrdU labelled cells were detected with anti-BrdU antibody. The ratio of BrdU labelled cells is slightly increased in the Pax6 mutant (t-test; *P<0.001).
neurones may be transient (only for about ~10 hours) because these expression boundaries are not firmly maintained and such neurones will be diminished soon after. By contrast, progenitor domains for BM neurones, V2 interneurones and V0 interneurones became expanded. This is consistent with the observation that the number of V2 interneurones increased in the mutant rat, which differs from the results in the Pax6 mutant mice reported by Ericson et al. (Ericson et al., 1997).

If Pax6 is required for establishment of the progenitor domains in a correct manner, is it sufficient for progenitor domain formation? To answer this question, we performed overexpression of Pax6 by electroporation into cultured rat embryos, and indeed rescued development of SM neurones and V1 interneurones in correct positions. The numbers of these rescued neurones were less than in normal development. The reason for this partial rescue may be that exogenous Pax6 cannot fully re-establish the progenitor domains for SM neurones and V1 interneurones at the stage of electroporation. Irx3, the gene reported to repress SM fate in the chick spinal cord (Briscoe et al., 2000), was already expanded ventrally at the time of electroporation. Alternatively, exogenous Pax6 could not cause a complete repression of the expanded expression of Nkx2.2. Taking these loss-of-function and gain-of-function studies together, we conclude that Pax6 seems to regulate formation of the precursor domains in the hindbrain, thereby specify the fates of ventral neurones (Fig. 8).

**Possible mechanisms for progenitor domain formation**

The expression of Nkx2.2 expands dorsally in the Pax6 mutant, while overexpression of Pax6 downregulated Nkx2.2 expression (Ericson et al., 1997) (our present data). In the chick spinal cord, Pax6 and Nkx2.2 are reported to repress expression of each other (Briscoe et al., 2000; Muhr et al., 2001). Such mutual repression of Pax6 and other transcription factors is commonly observed in other regions of the developing brain (e.g. forebrain/midbrain boundary and cortex/LGE boundary), and is considered to be one of the mechanisms that defines brain territories (Matsunaga et al., 2000; Stoykova et al., 2000; Toresson et al., 2000; Yun et al., 2001). However, Pax6 also influences formation of the progenitor domains dorsal to SM progenitor domain within the hindbrain. Expression boundaries of Nkx6.1, Irx3, Dbx2 and Dbx1 are included within Pax6 domain, and the boundaries of all these genes within Pax6 domain were very blurred in the Pax6 mutant. What kind of other mechanism is therefore involved in setting the progenitor domains properly?

The expression of HD code proteins is regulated by graded action of Shh released from the floor plate (Ericson et al., 1997; Briscoe et al., 2000). Therefore, we examined the expression patterns of the genes that are known to be direct targets of Shh signalling. We found that in the Pax6 mutant, strong expression of Ptci1, Gli1 and Gli2 was eliminated in the ventral region corresponding to the SM precursor domain. Altered expression of Shh signalling molecules in the ventral region may suggest that establishment of SM progenitor domain may require Pax6 function to respond properly to Shh signal. However, this might conversely be resulted from the perturbed progenitor domain formation.

The next possibility is different cell kinetics in individual progenitor domains. Previous studies have demonstrated that Pax6 regulates cell proliferation in development of the diencephalon, telencephalon and retina (Caric et al., 1997; Warren and Price, 1997; Götz et al., 1998; Marquardt et al., 2001). The frequency and positions of dead cells were not different in the hindbrains of wild type and Pax6 mutants. Although BrdU incorporation was slightly higher in the mutant, there was no relationship with specific progenitor domains. Therefore, it seems that overall disruption of progenitor domain boundaries in the mutant hindbrain is not explained by the alteration of cell death and proliferation.

Another possibility is that cell motility is accelerated in the neuroepithelium of the Pax6 mutant. Notably, cell tracing analyses in chick embryos have revealed a widespread dispersal of neuroepithelial cells in the early stages, but such cell mixing becomes less obvious in later development when progenitor domains are established (Clarke et al., 1998; Erskine et al., 1998). There are accumulating data to suggest that Wnt signal regulates cell motility (Heisenberg et al., 2000; Jönsson and Anderson, 2001), and expression of Wnt7b is actually diminished in the Pax6 mutant hindbrain (Osumi et al., 1997). It has also been reported that Pax6 controls R-cadherin expression in the developing neocortex (Stoykova et al., 1997) (T. Inoue and N. O., unpublished). We have also found that the motility of neuroepithelial cells in the ventral telencephalon, where cadherin-6 is normally expressed, seems to be increased in cadherin-6 deficient mice (Inoue et al., 2001). Pax6 also controls granule cell migration in the cerebellum by modulating cytoskeletal components (Yamasaki et al., 2001). Collectively, Pax6 may regulate, directly or indirectly, certain cell adhesion molecule(s) and/or cytoskeletal molecule(s) expressed in the neuroepithelium, thereby functioning in the establishment of the rigid precursor domains in the hindbrain.

**Dose-dependent effect of Pax6 in specification of ventral neurones**

The progenitor domain for SM neurones corresponds to the region where Pax6 expression is low (Ericson et al., 1997) (Fig. 2A). Overexpression of Pax6 in the Pax6low SM progenitor domain in the early E11.5 wild-type hindbrain repressed the production of Islet2-positive SM neurones. By contrast, exogenous Pax6 in the E10.75 mutant embryos induced Islet2- and HB9/MNR2-positive cells. In the E10.75 hindbrain, Pax6 protein distribution is not seen in a gradient pattern (data not shown). Therefore, it is likely that differentiation of SM neurones is dependent on temporary different doses of Pax6.

![Fig. 8. The proposed model of Pax6 function in neuronal specification. The model indicates that Pax6 functions in establishment of progenitor domains in a correct manner, thereby regulating specification of neuronal subtypes. Shh, Sonic hedgehog.](image-url)
In fact, it has been reported that Pax6 influences eye formation and development of the diencephalic dorsal midline secretory radial glia in a dose-dependent manner (Schedl et al., 1996; Estivill-Torrús et al., 2001). Therefore, another interesting issue to investigate would be how much Pax6 is required for precise specification of SM neurons and perhaps other types of neurons.

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