Six1 controls patterning of the mouse otic vesicle

Hidenori Ozaki1, Kazuaki Nakamura1, Jun-ichi Funahashi2, Keiko Ikeda1, Gen Yamada3, Hisashi Tokano4, Hiro-oki Okamura4, Ken Kitamura4, Shigeaki Muto5, Hayato Kotaki6, Katsuko Sudo6, Reiko Horai6, Yoichiro Ikawara6 and Kiyoshi Kawakami1,*

1Division of Biology, Center for Molecular Medicine, Jichi Medical School, Tochigi 329-0498, Japan
2Department of Molecular Neurobiology, Institute of Development, Aging and Cancer, Tohoku University, Sendai 980-8575, Japan
3Division of Transgenic Technology, Center for Animal Resources and Development, Kumamoto University, Kumamoto 860-0811, Japan
4Department of Otolaryngology, Tokyo Medical and Dental University, Tokyo 113-8519, Japan
5Division of Nephrology, Department of Internal Medicine, Jichi Medical School, Tochigi 329-0498, Japan
6Division of Cell Biology, Center for Experimental Medicine, Institute of Medical Science, University of Tokyo, Tokyo 108-8639, Japan

*Author for correspondence (e-mail: kkawakami@jichi.ac.jp)

Summary

Six1 is a member of the Six family homeobox genes, which function as components of the Pax-Six-Eya-Dach gene network to control organ development. Six1 is expressed in otic vesicles, nasal epithelia, branchial arches/pouches, nephrogenic cords, somites, and a limited set of ganglia. In this study, we established Six1-deficient mice and found that development of the inner ear, nose, thymus, kidney and skeletal muscle was severely affected. Six1-deficient embryos were devoid of inner ear structures, including cochlea and vestibule, while their endolympathic sac was enlarged. The inner ear anomaly began at around E10.5 and Six1 was expressed in the ventral region of the otic vesicle in the wild-type embryos at this stage. In the otic vesicle of Six1-deficient embryos, expressions of Otx1, Otx2, Lfng and Fgf3, which were expressed ventrally in the wild-type otic vesicles, were abolished, while the expression domains of Dlx5, Hmx3, Dach1 and Dach2, which were expressed dorsally in the wild-type otic vesicles, expanded ventrally. Our results indicate that Six1 functions as a key regulator of otic vesicle patterning at early embryogenesis and controls the expression domains of downstream otic genes responsible for respective inner ear structures. In addition, cell proliferation was reduced and apoptotic cell death was enhanced in the ventral region of the otic vesicle, suggesting the involvement of Six1 in cell proliferation and survival. In spite of the similarity of otic phenotypes of Six1- and Shh-deficient mice, expressions of Six1 and Shh were mutually independent.

Key words: Six1, Otic vesicle, Inner ear, Pattern formation, Cell proliferation, Shh, Mouse

Introduction

The Six gene family was identified as a homologue of the Drosophila sine oculis (so) and is conserved in various species (Seo et al., 1999; Kawakami et al., 2000). Six gene products are characterized by the Six domain and Six-type homeodomain, which are required for specific DNA binding activity and function as transcription factors (Kawakami et al., 1996; Spitz et al., 1998; Ohto et al., 1999; Li et al., 2002; Lagutin et al., 2003). At present, six members of the family have been identified in mammals, and all members show a spatiotemporal pattern of expression during embryogenesis, suggesting their involvement in embryonic development (Seo et al., 1999; Kawakami et al., 2000). The Six gene family is known to function as a component of the Pax-Six-Eya-Dach gene network. This property was originally identified in genetic studies using Drosophila. Compound eye formation has been extensively examined as a model system of organ development, and the important eye-forming genes, eyeless (ey, a Pax6 homologue), twin of eyeless (toy, another Pax6 homologue), sine oculis (so, a Six homologue), eyes absent (eya, an Eya homologue) and dachshund (dac, a Dach homologue), have been identified. Genetic and biochemical studies have revealed the hierarchy, cooperative relationships and physical interactions among these genes and their encoded proteins; toy activates ey (Czerny et al., 1999), and ey and/or toy activate so and eya (Halder et al., 1998; Niimi et al., 1999; Zimmerman et al., 2000), then so and eya cooperate to activate dac (Pignoni et al., 1997; Chen et al., 1997). In addition to such a hierarchy, reciprocal feedback loops operate to form complex regulatory gene networks (Chen et al., 1997; Pignoni et al., 1997). Of note is that the vertebrate homologues of these Drosophila genes, Pax6 (Walther and Gruss, 1991), Six3/Six6 (Oliver et al., 1995a; Toy et al., 1998), Eya1/Eya2/Eya3 (Xu et al., 1997) and Dach1/Dach2 (Caubit et al., 1999; Davis et al., 2001), are expressed in the developing eyes, and some of them were shown to be involved in eye development (Hill et al., 1991; Ton et al., 1991; Glaser et al., 1992; Oliver et al., 1996; Kobayashi et al., 1998; Loosli et al., 1999; Lagutin et al., 2001; Carl et al., 2002; Li et al., 2002; Lagutin et al., 2003). A similar gene network was found to control chick myogenesis, in which Six1, Eya2 and Dach2 synergistically regulate the expression of myogenic genes such as myogenin and MyoD (Heanue et
al., 1999). In addition, Pax3 induces the expression of Six1 and Eya2 before induction of MyoD and myogenin expression (Ridgway and Skerjanc, 2001). Pax3 is involved in myogenesis also by activating Dach2 expression and is reciprocally activated by Dach2 (Heanue et al., 1999; Kardon et al., 2002). Furthermore, homologues of these gene families are expressed in various developing organs in a spatially and temporally overlapping manner during embryogenesis, suggesting that similar gene networks regulate the development of various organs in addition to the eye and skeletal muscles. In fact, an increasing number of loss-of-function mutations in Pax, Eya and Six genes have been reported to cause defects in various organs. Pax2-deficient mice show defects in eyes, ears and the urogenital system (Favor et al., 1996; Torres et al., 1996). Loss of Eya1 in mice results in the absence or anomalies in the ear, thymus, parathyroid gland, kidney, thyroid and skeleton (Xu et al., 1999; Xu et al., 2002). For Six genes, inactivation of mouse Six6 is associated with hypogenesis of the pituitary gland and retina (Li et al., 2002). SIX3 mutations in humans cause holoprosencephaly, and Six3 inactivation in mice results in a lack of anterior head structures, including eyes and nose (Wallis et al., 1999; Lagutin et al., 2003).

Six1 is expressed in otic vesicles, nasal epithelia, branchial arches/pouches, nephrogenic cords, somites and a limited set of ganglia (Oliver et al., 1995b). However, it is unknown whether or how Six1 is involved in the development of the inner ear, nose, branchial arch/pouch-derived organs, kidney, ganglia and skeletal muscles. To address this question, we generated and analyzed the organ development of Six1-deficient mice. The inner ear, nose, thymus, kidney and skeletal muscles are severely affected in Six1-deficient mice, suggesting crucial roles for Six1 in the development of these organs. Among these phenotypes, the defects in inner ear development in the mutant mice are intriguing because inner ears develop elaborate structures with precise disposition and orientation in normal embryogenesis. They are derived from the otic vesicle by successive transformation and compartmentalization, but it is poorly understood how the patterning of the otic vesicle is established and what are the key factors for such complex processes. Thus, this paper focused on the analysis of inner ear development and identified the essential roles of Six1 in otic vesicle patterning.

Materials and methods

Construction of the Six1 targeting vector

The entire coding region of the murine Six1 gene was isolated from a 129/SvJ mouse genomic library (Stratagene, La Jolla, California) using a Six1 cDNA (Oliver et al., 1995b) as a probe, and the exon-intron organization was determined. An Ncol site was generated at the initiation codon by PCR mutagenesis to allow the insertion of an in-frame enhanced green fluorescent protein (EGFP) gene. The targeting vector was constructed in pBluescript KS(+) (Stratagene, La Jolla, California), and the organization is shown in Fig. 1A. In this construct the entire coding region, including exons 1 and 2, the intervening intron and the short stretch of the 3′ untranslated region of exon 2 were replaced with an EGFP fragment (Ncol-Splt, 1.0 kb) from pEGFP-N3 (Clontech, Palo Alto, California) and an hph cassette (EcoRV-PvuII, 2 kb) from pPGK-hph-bpA (Horai et al., 1998). The diphtheria toxin A cassette (dt) (XhoI-NorI, 1.4 kb) from pMC1DTpA (Yagi et al., 1993) was added at the 3′ terminus for the negative selection. The resulting plasmid was linearized with SalI at the 5′ end of the insert.

ES cell screening and chimeric mouse production

The linearized targeting vector (80 µg) was electroporated (250 V, 500 µF) into 1 × 10^7 E14.1 ES cells (Kuhn et al., 1991) and transformants were selected with hygromycin B (230 µg/ml; Invitrogen Japan K.K., Tokyo) for 5–9 days. Homologous recombinants were screened by Southern blot hybridization. Genomic DNA from each resistant clone was digested with NcoI, analyzed by Southern blotting using the probes Ncol-SacI, 1.2 kb fragment upstream of 5′ homology (5′ probe), and XbaI-EcoRI, 2.0 kb fragment downstream of 3′ homology (3′ probe), to confirm the correct homologous recombination at 5′ and 3′ sides, respectively (Fig. 1A). Chimeric mice were produced by the aggregation method (Horai et al., 1998). Male chimeras were bred with C57BL/6 female mice to check germline transmission. Heterozygous mice were intercrossed to produce Six1-deficient mice. Genotyping was carried out by Southern blot analysis (Fig. 1B) or PCR (data not shown) in combination with morphological analyses. In the PCR analysis, the targeted allele was detected with primers WtmSix1F (GCC CCC CCC GCC GTC CGC CCC) and KOmSix1R (TGC CCC CCC ATG TTG CCG TTC), and the wild-type allele with primers WtmSix1F and WtmSix1R (GCT TTC AGC CAC AGC TGC CAC AGC AGC TGG TGC). In this study, Shh mutant mice with a targeted deletion of exon 2 of the gene were also used (Chiang et al., 1996) (kindly supplied by C. Chiang and C. C. Hui).

Mice were kept under specific pathogen-free conditions in environmentally controlled clean rooms at the Center for Experimental Medicine, Jichi Medical School, and at the Laboratory Animal Research Center, Institute of Medical Science, University of Tokyo. All mice used in this study were sacrificed by cervical translocation or anesthesia with diethyl ether. The experiments were conducted according to the institutional ethical guidelines for animal experiments and safety guidelines for gene manipulation experiments.

Histological examinations

Embryos and neonates were fixed in 10% formalin or 4% PFA in PBS, embedded in paraffin wax and then cut into 5-µm thick serial sections. De-waxed sections were stained with hematoxylin and eosin as described previously (Ozaki et al., 2001). Alcian Blue/Alizarin Red staining of neonatal skeletons was performed as described previously (Wallin et al., 1994).

RNA in situ hybridization

In situ hybridization was performed using digoxigenin (DIG)-labeled antisense riboprobes as described previously (Xu and Wilkinson, 1998). Eya1 riboprobe was synthesized from a 528 bp HindIII fragment of pHM6Eya1 (Ohito et al., 1999) subcloned into pBluescript KS(+). Six4 riboprobe was synthesized from a 630 bp PstI fragment (nt 1545-2175 of Six4 SM type cDNA) subcloned into pBluescript KS(+). The following cDNAs were also used for in situ hybridization probes: Six1 (Olive et al., 1995b), Otx1 and Otx2 (Matsuoka et al., 1995), Fgf3 (Wilkinson et al., 1988), Lfng (Morsli et al., 1998), Dlx5 (Miyama et al., 1999), Dach1 (Caubit et al., 1999), Dach2 (Davis et al., 2001), Pax2 (Nishinakamura et al., 2001), Bmp4 (a kind gift from N. Ueno), Hmx3 (Wang et al., 1998), Shh (Urabe et al., 1996), Pch (Goodrich et al., 1996), Git1 (Hui et al., 1994), Wnt2b (Riccomagno et al., 2002).

TUNEL analysis

For terminal deoxynucleotidyl transferase-mediated dUTP nick-end labeling (TUNEL), embryos were fixed in 4% PFA in PBS, embedded in OCT compound, and frozen and sectioned into serial cryosections. Apoptotic cells were detected with the In Situ Cell Death Detection Kit, POD (Roche Diagnostics Mannheim, Germany). Briefly,
followed by incubation in 0.6% H2O2 in PBS for 30 minutes at room temperature and rinsed with 0.1 M borate buffer (pH 8.5), treated with 2 N HCl/0.5% Triton X-100 in PBS for 30 minutes at room temperature. Subsequently, the sections were incubated overnight in peroxidase-labeled anti-BrdU (Roche) at 4°C. After washing, sections were stained in 0.4 mg/ml diaminobenzidine, 0.68 mg/ml imidazole, 0.01% H2O2, and 50 mM Tris-HCl (pH 7.4).

Paint-fill analysis
Paint-fill was performed as described previously (Bissonnette and Fekete, 1996). In brief, embryos were fixed in Bodian’s fixative, dehydrated through graded ethanol solutions, then cleared in methyl salicylate and injected into the lumen of the membranous labyrinth with white paint diluted 1 to 100 in methyl salicylate.

ABR threshold measurements
The auditory evoked response was recorded with stainless steel needle electrodes inserted subcutaneously into the vertex (active), left and right of the retro-auricular regions (inactive) and the opposite thigh (ground). The stimulus sound in peak equivalent sound pressure level (peSPL) of a tone pips of 0.1 millisecond slopes, 1 millisecond duration, 70 millisecond repeat interval with 5.6, 8.0, 12.0, 18.0, 24.0, 32.0 kHz frequencies was given by free field in an electrically shielded room. A tweeter (PT-RIII, Pioneer) was placed 10 cm in front of the external acoustic foramen. The stimulus sound pressure was corrected by a Bruel & Kjaer-type 2636 noise meter. A microcomputer (ER-2104, GE Marquet) was used to analyze the response. Auditory thresholds were obtained for each stimulus by varying at 10 dB steps up and down to identify the lowest level at which an auditory brain response (ABR) pattern could be recognized. These experiments were conducted in five wild-type and six heterozygous mice at 5 to 6 weeks of age.

Results
Generation of Six1-deficient mice
To explore the developmental roles of Six1, we inactivated Six1 in ES cells by replacing the entire coding region with EGFP gene (Fig. 1A). Two independent ES clones were confirmed as homologous recombinants (data not shown), and both of them gave germline chimeric mice. These chimeric mice were crossed with C57BL/6 to obtain F1 heterozygous mutant mice. Heterozygotes appeared normal in appearance and grew up to adulthood as wild type (data not shown). The concentrations of Na+, K+, Cl−, Ca2+, Mg2+, inorganic phosphate, urea nitrogen, creatinine, albumin and uric acid in serum and urine were measured with an auto-analyzer, and we observed no significant difference in the concentrations of all these parameters between the wild-type and heterozygous mutant mice (data not shown). We also performed ABR testing for hearing impairment in the heterozygous mutant mice. The ABR thresholds were 25.0±5.3, 14.0±5.2, 14.0±5.2, 11.0±3.2, 10.0±0.0 and 14.0±5.2 dBpeSPL for the wild-type mice and 23.3±4.9, 15.0±5.2, 10.8±2.9, 10.0±0.0, 10.8±2.9 and 14.2±5.1 dBpeSPL for the heterozygotes at frequencies of 5.6, 8.0, 12.0, 18.0, 24.0 and 32.0 kHz, respectively, and there were no significant differences in these values between the wild-type and heterozygous mutant mice.

Homozygous mutants were born at Mendelian frequency and showed few body movements but were apnoeic and died immediately after birth. They had micrognathia, and the eyelids were sometimes open (data not shown). No Six1 mRNA was detected in homozygotes (Fig. 1C), confirming that the entire coding region of Six1 was replaced by EGFP gene in this mutant. In the following analyses, we used neonates and embryos from F1 heterozygous matings.

Defects in ears, nose, thymus, kidneys and skeletal muscles of Six1-deficient neonates
Dissection analyses and hematoxylin and eosin (H-E) staining of sections of the neonates revealed defects in the ears, nose, thymus, kidneys and skeletal muscles in Six1-deficient neonates.
the Six1-deficient mice. In the inner ear, the dorsalmost parts of semicircular canals and the endolymphatic sac remained as a common fused space. The endolymphatic sac was present but was irregularly larger in size than that of wild-type littermates (Fig. 2A,B). The enlargement was confirmed by comparing the diameter of the paint-filled endolymphatic sacs of the Six1-deficient and the wild-type embryos (data not shown). The expansion of the expression domain of Wnt2b, an expression marker for the endolymphatic sac and duct, also supports the enlargement of the endolymphatic sac (Fig. 2C,E). Other parts of the inner ear were completely absent, including the cochlea, vestibule and accompanying vestibulo-acoustic ganglia (Fig. 2G,H, data not shown). These structural defects were also demonstrated by paint-fill analyses (Fig. 2Q,R,R'). Because Six1
expression was evident in the branchial arch and periopic mesenchymes (Fig. 1C, Fig. 4C), we examined the middle ear defects in the Six1-deficient neonates and found malformations of the malleus and the incus and the absence of the stapes (Fig. 2L,J). In the nose, Six1-deficient mice manifested a hollowed nasal region with traces of nasal bleeding (data not shown). A pair of mere simple, rounded nostrils was present with no nasal epithelium, by contrast to the well-branched cavities with thick layers of nasal epithelia in the wild-type littermates (Fig. 3A,B).

Both nasal cavities did not connect with the oral cavity or the nasal region with traces of nasal bleeding (data not shown). A pair of mere simple, rounded nostrils was present with no nasal epithelia in the wild type (A), and a pair of simple round cavities with no nasal epithelia is seen in the Six1-deficient mice (data not shown). The surrounding ossified region was abnormally enlarged (Fig. 3B), as observed in the inner ear (Fig. 2B,H). Six1-deficient mice also lacked a thymus (Fig. 3C,D). Kidneys were severely affected to variable degrees (Fig. 3E,F). Small kidneys with normal structure were found in mild cases (data not shown), while both kidneys were absent in extreme cases, although the ureters were always formed but were occasionally shorter (Fig. 3F). We also found markedly reduced skeletal muscle mass of the trunk, limbs, diaphragm and tongue (Fig. 3G,H, data not shown). The thymus, kidney, ear, nose and skeletal muscle defects are consistent with the Six1-deficient mice with different targeting strategy (Laclef et al., 2003a; Laclef et al., 2003b; Xu et al., 2003). These affected organs correlated well with the expression sites of Six1 during development, such as otic vesicles, nasal pits, branchial arches/pouches, nephrogenic cords and somites (Oliver et al., 1995b). These results indicate that Six1 is required for the formation of the ear, nose, thymus, kidneys and skeletal muscles.

Defects in inner ear appear at mid-gestation in Six1-deficient embryos

To determine the developmental stages at which the inner ear defects start to appear, Six1-deficient mice of several embryonic stages were sectioned and analyzed by H-E staining. At E9.5, otic vesicles were morphologically normal in Six1-deficient embryos, but the vestibulo-acoustic ganglia were missing (data not shown). At E10.5 and E11.5, the otic vesicles began to compartmentalize into saccular and utricular regions. The saccular region extended to the ventral side as a thin bulge in the wild type (Fig. 2K). By contrast, the extension of the saccular region to the ventral side did not occur in Six1-deficient embryos (Fig. 2L). The endolymphatic duct was observed as a thin outpocketing from the medial side of the otic vesicle in wild-type embryos, while the endolymphatic duct was observed as a large swelling in Six1-deficient embryos (Fig. 2K,L). The thin outpocketing and the large swelling region coincided with the expression domain of Wnt2b (Fig. 2D,F). We also used paint-fill analyses to compare otic vesicle structures at E10.5 with those of the wild type and confirmed the absence of the thin outpocketing and the dilatation of the endolymphatic duct in Six1-deficient otic vesicles (Fig. 2S,T, data not shown). At E12.5, the main structures of the inner ear (cochlea, saccule, utricle, endolymphatic duct and canal plates, from which three semicircular canals and common crus are formed) were distinguishable in the wild type (Fig. 2M,O, data not shown). By contrast, the dorsal extremity of the semicircular canals and common crus was observed as a fused cavity, and abnormally large endolymphatic duct was present (Fig. 2N), while other parts were completely absent in Six1-deficient embryos (Fig. 2P, data not shown).

In summary, the development of the inner ear was defective at mid-gestation around E10.5-12.5.

Expression of Six1 in the developing inner ear

To gain insight into the function of Six1 during inner ear development, we first examined the expression pattern of Six1 by in situ hybridization in the wild type (Fig. 4A-F) and GFP fluorescence in heterozygous embryos (Fig. 4G-I). Six1 mRNA was first detected in the otic placode and the surrounding surface ectoderm at E8.5 (Fig. 4A). Six1 expression became prominent at the invaginating otic pit and the nascent otic vesicle at E9.5 (Fig. 4B,C), consistent with previous observations (Oliver et al., 1995b). Notably, the expression level was considerably lower in the dorsalmost region than in the other region of the otic vesicle (Fig. 4C). At E10.5, Six1 development, such as otic vesicles, nasal pits, branchial arches/pouches, nephrogenic cords and somites (Oliver et al., 1995b). These results indicate that Six1 is required for the formation of the ear, nose, thymus, kidneys and skeletal muscles.

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expression was limited to the ventral half of the otic vesicle (Fig. 4D,G). Subsequently, the expression domain of Six1 became gradually restricted to the cochlear region at E11.5 (Fig. 4E) and E12.5 (Fig. 4F,H). At later stages, Six1 transcripts were detected exclusively in the cochlea at E14.5 (Fig. 4I), and the expression of Six1 in the cochlear duct persisted in the neonate (data not shown).

**Six1 is required for correct patterning of the otic vesicle**

The morphological defects in Six1-deficient mice were not restricted to the cochlea but extended to all regions of the inner ear except the dorsal extremity of the semicircular canals (Fig. 2). The missing ventral structures of the mutant mouse inner ear appeared to be related to the expression domain of Six1 in the ventral otic vesicle at E9.5-10.5 (Fig. 4C,D). The absence of cochlea and vestibule and the enlargement of the endolymphatic sac prompted us to examine the following three possibilities: that the specification along the dorsoventral axis within the otic vesicle is altered in Six1-deficient embryos, that the cells within the ventral region of the Six1-deficient otic vesicle undergo enhanced apoptotic cell death, and that the cells within the ventral region of the Six1-deficient otic vesicle proliferate at a lower rate than those of the wild type. We assessed the first possibility by comparing the expression pattern of genes differentially expressed within the otic vesicle at E9.5-10.5. The ventralmost cells of the otic vesicle are marked by the co-expression of Otx1 and Otx2 (Morsli et al., 1999). Otx1 and Otx2 were not expressed in the Six1-deficient otic vesicle, by contrast to the wild type, although an ectopic expression domain was expanded ventrally along the lateral sides almost down to the ventral half of the otic vesicle. (E) At E11.5 and (F,H) E12.5, Six1 is expressed exclusively in the cochlea. (I) Expression of Six1 in the cochlea is maintained at E14.5 embryos. (J) A bright field image of the section in (I) stained with hematoxylin and eosin. More than three embryos at each stage were analyzed and virtually the same results obtained. d, dorsal; la, lateral. Scale bars: 100 μm.

early marker for the superior, lateral and posterior cristae. It was expressed in the restricted regions of the otic vesicle in the wild type (Fig. 5I), but no such expression was noted in Six1-deficient mice (Fig. 5I).

The dorsal side of the otic vesicle gives rise to the semicircular canals and endolymphatic duct/sac and is well marked by the expression of Dlx5, which is required for the normal development of the semicircular canals and endolymphatic duct/sac (Fig. 5K) (Acampora et al., 1999; Depew et al., 1999). In Six1-deficient embryos, the expression domain of Dlx5 expanded to the entire otic vesicle (Fig. 5L). The expression domains of Hmx2 and Hmx3, both of which are required for the formation of the vestibular structures (Wang et al., 1998; Wang et al., 2001), expanded ventrally from the dorsolateral side in the Six1-deficient otic vesicle (Fig. 5M,N, data not shown). Dach1 is a member of the Dach family genes, which constitute the Pax-Six-Eya-Dach gene network. It was also expressed at the dorsal edge of the otic vesicle in the wild-type embryos (Fig. 5O). Dach1 expression expanded ventrally along the medial and lateral sides almost down to the ventral end in Six1-deficient embryos (Fig. 5P). Dach2, another member of Dach family genes, was expressed mainly in the dorsal end of the otic vesicle in wild-type embryos, but Dach2 expression domain was expanded ventrally along the lateral side of the otic vesicles (Fig. 5Q,R).

We also examined the expression pattern of Pax2, Eya1 and Six4 to clarify whether the expression of these genes is dependent on Six1. These genes are components of the Pax-Six-Eya-Dach gene network and are co-expressed in the otic vesicle. Pax2 was expressed in the medial side of the otic vesicle of the wild-type and Six1-deficient embryos (Fig. 5S,T). Eya1 expression in the ventral side of the wild-type otic vesicle was maintained in the Six1-deficient otic vesicle (Fig. 5U,V). Six4 was expressed in the ventral side of the otic vesicle in wild-type embryos, and this expression pattern was almost the same in the Six1-deficient embryo (Fig. 5W,X). However, the most abundantly expressed regions of Eya1 and Six4 appeared slightly shifted from the ventromedial (wild-type) to the ventrolateral (Six1-deficient) side of the otic vesicle. These results suggest that the expression of Pax2, Eya1 and Six4 in the otic vesicle is not dependent on Six1.
In conclusion, loss of Six1 expression leads to marked changes in the expression domains of many genes in the otic vesicle, suggesting that the first possibility listed above is the case: i.e. the specification along the dorsoventral axis within the otic vesicle is altered in Six1-deficient embryos. Next, we assessed the second and third possibilities by TUNEL method and BrdU incorporation.

Enhanced apoptosis and reduced cell proliferation in the ventral otic vesicle
We examined whether enhanced apoptotic cell death or reduced cell proliferation within the ventral region of the otic vesicle contributes to the inner ear phenotype. TUNEL method was used to detect apoptotic cells in the otic vesicle at E10.5 and E11.5, just before the extensive morphological changes. Several apoptotic cells were detected in the wild-type, while enhanced apoptotic cell death was observed in the ventral and medial sides of the otic vesicles of Six1-deficient embryos at E11.5 (Fig. 6A,B). Statistical analysis revealed significant augmentation of apoptosis at E10.5 and E11.5 (Fig. 6C). We also examined BrdU incorporation in the otic vesicle at the same developmental stages. In the wild type and in the Six1-deficient embryos at E11.5, BrdU incorporation was abundant in the ventral region of the otic vesicle (Fig. 6D). By contrast,
the incorporation was profoundly reduced in the ventral side of the otic vesicles of Six1-deficient embryos at E11.5 (Fig. 6E). A significant decrease in the number of BrdU-incorporated cells was observed at E11.5 but not at E10.5 (Fig. 6F). The reduced cell proliferation observed in Six1-deficient otic vesicles may be in line with the roles of Six1 in cell cycle control (Ford et al., 1998). These results suggest that the lack of ventral structures of the inner ear in the Six1-deficient mice is partly due to enhanced apoptosis and reduced cell proliferation, as well as altered patterning of the otic vesicle.

**Sonic hedgehog (Shh) signaling pathway is independent of Six1**

We noticed that the inner ear phenotype of Six1-deficient mice is similar to that of Shh-deficient mice, which is characterized by the absence of the cochlear duct and vestibulocochlear ganglia, ventral expansion of the expression domains of Dlx5, loss of the expression domain of Otx2, and ventral restriction of Otx1 expression (Ricomagno et al., 2002). The similarity of the phenotypes could be explained by the assumption that the Shh signaling pathway is dependent on Six1 expression or vice versa. To test this possibility, we first examined the expression of Shh and the Shh-inducible genes, Ptc1 and Gli1 in Six1-deficient embryos. Shh was expressed in the notochord and the floor plate near the otic vesicles in the wild type (Fig. 7A), and this expression pattern was virtually unchanged in Six1-deficient embryos (Fig. 7B). Ptc1 and Gli1 were expressed in the otic vesicle and periosteal mesenchyme in the wild-type embryo, and these expression patterns were similar in Six1-deficient embryos (Fig. 7C-F). Next, we examined Six1 expression in Shh-deficient embryos (Chiang et al., 1996). Six1 expression was abundant in the ventral region of the otic vesicles in Shh-deficient embryos, as observed in the wild type (Fig. 7G,H). These results indicate that the Shh signaling pathway is independent of Six1 and that the expression of Six1 in the otic vesicle is also independent of the Shh signaling pathway.

![Fig. 6. Apoptosis and cell proliferation in the otic vesicle.](image1)

![Fig. 7. Expression patterns of Shh, Gli1, Ptc1 and Six1.](image2)
Although it is unknown whether these genes are regulated, Dlx5 and Dach1, Hmx3, Lfng, Otx1, and Otx2 are expressed in the ventral half of the otic vesicle. In the otic vesicle of Six1–/–, the expression domains of Dlx5, Hmx3, Dach1 and Dach2 are expanded ventrally, and the expressions of the ventral marker genes (Otx1, Otx2, Fgf3 and Lfng) are lacking due to the absence of Six1. (B) Regulation of gene expression by Six1 in the ventral otic vesicle. Six1 activates the expression of ventral marker genes, Otx1, Otx2, Lfng and Fgf3, but represses dorsal marker genes, Dlx5, Hmx3, Dach1 and Dach2, and contributes to the patterning of the otic vesicle. D, dorsal; L, lateral; M, medial; V, ventral.

Fig. 8. (A) Schematic representation of expression of genes in otic vesicles of the wild-type (left) and Six1–/– mice (right) at E10.5. In the otic vesicle of the wild-type, otic genes are expressed in the specified regions represented in different colors. In the wild-type otic vesicle, Six1 is expressed directly by Six1, it is concluded that Six1 plays a key role in establishing otic vesicle patterning.

In addition to the patterning of the otic vesicle along the dorsoventral axis, Six1 may play roles in the otic vesicle patterning along the anteroposterior and/or mediolateral axes, because anteroposteriorly and/or mediolaterally asymmetrical expression patterns of Otx1, Otx2, Lfng, Fgf3 and Bmp4 were also affected (Fig. 5). For these issues, further histological examinations and analyses of molecular marker expression will be required.

Furthermore, our results showed a marked reduction of cell proliferation and enhanced apoptosis in the ventral otic vesicle in Six1-deficient embryos (Fig. 6). This may contribute to the inner ear phenotype lacking most of the ventral structures. Thus, Six1 controls inner ear development by regulating cell death and proliferation as well as by establishing otic vesicle patterning.

Phenotypic similarity of the inner ear compared with Shh-deficient mice

Previous and present studies indicated that specification of the cochlea is dependent on Shh signaling and that perturbation of otic vesicle patterning in Shh-deficient mice (Riccomagno et al., 2002) is similar to that of Six1-deficient mice. Considering these phenotypic similarities of inner ear formation between Six1- and Shh-deficient mice, we assumed a genetic interaction between Six1 and Shh. However, the expression patterns of Shh, Gli1 and Ptc1 in Six1-deficient mice and that of Six1 in Shh-deficient mice (Chiang et al., 1996) indicate that the expressions of Shh, Gli1 and Ptc1 are not dependent on Six1, and that the expression of Six1 is not dependent on the Shh signaling pathway in and around the otic vesicle at E10.5 (Fig. 7). Another possible mode of genetic interaction is through functional cooperation between Six1 and the components of Shh signaling cascades. Shh protein is emanated from the notochord and/or the floor plate, probably giving a gradient of Shh across the otic vesicle with a high concentration in the ventral side and a low concentration in the dorsal side. This Shh gradient would enhance putative collaborative interaction between downstream components of Shh signaling cascades and Six1 in the ventral otic vesicle. Modulation of the transactivating function of Six1 by Shh signaling would be one of the plausible mechanisms. However, we cannot exclude
Six genes function as components of the Pax-Six-Eya-Dach gene network in organ development. In the ventral otic vesicle, Six1 is co-expressed with Pax2, Pax8, Six4 and Eya1 to control inner ear development. Outside the otic vesicles, various combinations of Pax, Six, Eya and Dach genes are co-expressed in the primordia of the organs affected in Six1-deficient mice: the olfactory placode (Pax6, Six1, Six2, Six3, Six4, Six6, Eya1, Eya2, Eya4); the thymus (Pax9, Six1, Six4, Eya1); the metanephros (Pax2, Pax8, Six1, Six2, Six4, Eya1); and the somite/myotome (Pax3, Six1, Six4, Eya1, Eya2, Eya4, Dach1). Six1 plays important roles in the development of these organs, probably through the control of patterning and/or cell proliferation, as observed in the otic vesicle. Notably, Dach genes are not co-expressed with Six and Eya genes in the ventral otic vesicle, nose or kidney (Figs 4, 5, data not shown). Furthermore, Dach expression domains were expanded ventrally in the Six1-deficient otic vesicle, indicating that Six1 represses the expression of Dach genes in the ventral otic vesicle. Likewise, augmentation of Dach expression was observed in the nasal pit of Six1-deficient embryos (data not shown), indicating that expression of the Dach gene is repressed by Six1 also in the nasal pit. These findings are in contrast to Drosophila compound eye formation and chick myogenesis. In both those cases, Pax, Six and Eya are co-expressed with Dach, cooperatively to execute the developmental programs. Thus, the Pax-Six-Eya-Dach gene network lacking Dach may demarcate the two placode-derived sensory organs, the inner ear and the nose, and the kidney from other organs such as the eye and the skeletal muscles. In addition, hierarchy among Pax, Six, Eya and Dach genes in the otic vesicle has been revealed in this study. That is, the expression patterns and levels of Eya1 and Pax2 were not affected but expression domains of Dach1 and Dach2 were expanded ventrally in the Six1-deficient otic vesicle (Fig. 5). Conversely, Six1 expression is lost but Pax2 expression is not disturbed in the Eya1-deficient otic vesicle (Xu et al., 1999). Thus, in the otic vesicle, expression of Eya1 and Pax2 is independent of Six1, expression of Six1 depends on Eya1, and Six1 controls Dach1 and Dach2 expression. In the myotome, Six4 expression is not dependent on Six1, as observed in the otic vesicle (Laclef et al., 2003a), but Pax2 expression is dependent on Six1 in metanephric mesenchyme (Xu et al., 2003). The similarities among these organ primordia in the context of the Pax-Six-Eya-(Dach) network and the diversity in selecting members from respective gene hierarchies among them raise interesting issues regarding the ontogeny of these organs during evolution.

In conclusion, our study identified the essential role of Six1 in the regulation of otic vesicle patterning. Together with mice homozygous for other Pax, Six, Eya and Dach genes, Six1-deficient mice should allow a comprehensive understanding of the roles of the Pax-Six-Eya-Dach gene network in various organogeneses.

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