Endothelin receptor type A expression defines a distinct cardiac subdomain within the heart field and is later implicated in chamber myocardium formation

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SUMMARY

The avian and mammalian heart originates from two distinct embryonic regions: an early differentiating first heart field and a dorsomedially located second heart field. It remains largely unknown when and how these subdivisions of the heart field divide into regions with different fates. Here, we identify in the mouse a subpopulation of the first (crescent-forming) field marked by endothelin receptor type A (Ednra) gene expression, which contributes to chamber myocardium through a unique type of cell behavior. Ednra-lacZ/EGFP-expressing cells arise in the ventrocaudal inflow region of the early linear heart tube, converge to the midline, move anteriorly along the outer curvature and give rise to chamber myocardium mainly of the left ventricle and both atria. This movement was confirmed by fluorescent dye-labeling and transplantation experiments. The Ednra-lacZ/EGFP-expressing subpopulation is characterized by the presence of Tbx5-expressing cells. Ednra-null embryonic hearts often demonstrate hypoplasia of the ventricular wall, low mitotic activity and decreased Tbx5 expression with reciprocal expansion of Tbx2 expression. Conversely, endothelin 1 stimulates ERK phosphorylation and Tbx5 expression in the early embryonic heart. These results indicate that early Ednra expression defines a subdomain of the first heart field contributing to chamber formation, in which endothelin 1/Ednra signaling is involved. The present finding provides an insight into how subpopulations within the crescent-forming (first) heart field contribute to the coordination of heart morphogenesis through spatiotemporally defined cell movements.

KEY WORDS: Cardiac development, Heart fields, Endothelin, Mouse

INTRODUCTION

The heart is the first functioning organ to develop during embryogenesis. Different sources of cell populations from the cardiogenic mesoderm and the cardiac neural crest coordinately contribute to the formation of elaborate cardiac structures, including the four specialized chambers, the valves and supporting tissues, and the conduction system (Buckingham et al., 2005; Cai et al., 2008; Kirby, 2007; Zhou et al., 2008). Myocardial progenitor cells first appear bilaterally in the anterior splanchnic mesoderm and then the primary heart tube. Through subsequent growth by accretion of cells at the poles from a newly identified progenitor population called the second heart field (Cai et al., 2003; Galli et al., 2008; Kelly et al., 2001; Mjaatvedt et al., 2001; Waldo et al., 2001), the heart tube loops and in subsequent steps is sculpted into a four-chambered heart in mammals and birds (Abu-Issa and Kirby, 2007; Buckingham et al., 2005; Laugwitz et al., 2008).

The distinction between these two heart fields is further supported by retrospective clonal analysis using recombinant lacZ labeling (Meilhac et al., 2004). This analysis, in embryonic day (E) 8.5 mouse embryos, revealed two distinct cell lineages with different patterns of regionalization in the heart tube. The first lineage contributed to all left ventricular myocardium, some of the right ventricular myocardium, the atrioventricular canal and both atria. The second lineage contributed to the outflow tract and all other myocardial regions except for the left ventricle. Notably, the second lineage appears to correspond roughly to the second heart field marked by Islet1 (Isl1 – Mouse Genome Informatics) expression in terms of regional contribution (Cai et al., 2003; Galli et al., 2008). The clonal analysis also revealed that the two cell lineages segregate from a common progenitor around the time of gastrulation (Meilhac et al., 2004). Based on these findings, the first lineage is postulated to segregate first from the common progenitor pool to form the heart tube (Buckingham et al., 2005).

Following their segregation, the heart fields are probably further regionalized and diversified into various cell types. However, it remains largely unknown when and how different subpopulations arise within these heart-forming fields and how they interact with each other to coordinate heart morphogenesis.

Endothelin 1 (Edn1)/endothelin receptor type A (Ednra) signaling is known to be involved in cardiovascular and craniofacial development (Clouthier et al., 1998; Kurihara et al., 1994; Ozeki et al., 2004; Sato et al., 2008a; Sato et al., 2008b). Mice deficient in Edn1/Ednra signaling exhibit aortic arch malformation and outflow anomalies, which are attributed to cardiac neural crest defects (Kurihara et al., 1995; Yanagisawa et al., 1998). Correspondingly, Ednra is expressed in cranial and...
cardiac neural crest-derived mesenchymal cells (Clouthier et al., 1998; Kurihara et al., 1995; Maemura et al., 1996; Yanagisawa et al., 1998).

Recently, we established mice in which lacZ (which encodes β-galactosidase) and EGFP (which encodes enhanced green fluorescent protein) were introduced into the Ednra locus to recapitulate its endogenous expression (Sato et al., 2008a). Consequently, lacZ/EGFP expression emerged in the developing heart with a characteristic pattern. We then focused on this expression, expecting that it might lead to the identification of a novel myocardial subpopulation. Here, we demonstrate that early Ednra-lacZ/EGFP expression marks a subpopulation of the heart field with distinct regional identity. Ednra-lacZ/EGFP-positive cells are first localized in the ventral inflow region, move anteriorly along the outer curvature following the formation of the heart tube, and give rise to chamber myocardium. Dye-labeling and transplantation experiments confirmed this movement and contribution to chamber formation. We also observed developmental abnormalities in Ednra-null embryonic hearts, indicating the involvement of Edn1 as a mitotic factor in early cardiac development.

MATERIALS AND METHODS

Mice

Ednra<sup>lacZ<sup>-</sup>/lacZ (lacZ knock-in) mice have been described previously (Sato et al., 2008a). To generate mice carrying the Ednra<sup>EGFP</sup> (EGFP knock-in) allele, we performed Cre recombinase-mediated cassette exchange (RMCE) on Ednra<sup>loxP</sup> embryonic stem (ES) cells in which an exchangeable floxed site was introduced into the Ednra locus as described previously (Sato et al., 2008a) (see Fig. S1 in the supplementary material). Briefly, the EGFP cassette excised from the pEGFP-N3 expression vector (Clontech) was introduced into the knock-in vector p66-2272 containing multiple cloning sites between loxP66 and lox2272 (Araki et al., 2002). The resultant plasmids were transfected into Ednra<sup>loxP</sup> ES cells with AxCANCre recombinant adenovirus expressing the recombinase Cre tagged with a nuclear localization signal under the control of the CAG promoter (Kanegae et al., 1995). Targeted ES clones were injected into ICR blastocysts to generate germline chimeras that were then crossed with ICR females. Mice were housed in an environmentally controlled room at 23±2°C, with a relative humidity of 50-60% and under a 12-hour light:12-hour dark cycle. Genotypes were determined by PCR on tail-tip or amnion DNA using primers specific for RMCE-mediated recombination.

Fluorescent dye labeling

Embryos from 6- or 7-somite stages were collected, transferred to DMEM/F12 containing 10% FCS, and injected with PKH67 (green) or PKH26 (red) fluorescent dyes (Sigma) using a needle drawn from glass capillary tubing in order to label cells in the lacZ- or EGFP-expressing or adjacent regions. Embryos were then placed in a 15-ml culture bottle containing 2 ml culture medium (50% rat serum plus 50% DMEM/F12) and rotated at 20 rpm at 37°C while being continuously supplied with a suitable concentration of O<sub>2</sub> (5 or 20%) and CO<sub>2</sub> (5%) balanced with N<sub>2</sub> for 30 hours. Labeled embryos were observed using a Leica MZFLIII stereomicroscope equipped with a Hamamatsu C4742-95 digital camera. Some embryos were fixed for X-gal staining. For whole-heart labeling, E8.25 (6- to 7-somite stage) embryos were incubated in DMEM/F12 with 1 μM SYTO16 (Molecular Probes), which stains the nuclei of live cells, at 37°C in 5% CO<sub>2</sub> for 30 minutes, and the heart tubes were excised.

Transplantation and explant culture experiment

Cardiac inflow tissues corresponding to the Ednra-lacZ/EGFP-positive region were excised from E8.25 (5- to 7-somite stage) embryos and transplanted into the same regions of recipient embryos (without removing their own inflow regions) using fine glass and tungsten needles. The Ednra-EGFP-positive tail regions were also transplanted as a control experiment. For transplantation of SYTO16-labeled cells, heart tubes were cut into three parts (outflow, ventricular and inflow regions) and were transplanted into the inflow regions of recipient embryos. Embryos were then placed in a collagen-coated 3.5-cm dish containing 500 μl α-MEM with 10% horse serum at 37°C in 5% CO<sub>2</sub> balanced with N<sub>2</sub> for 24 hours. Following culture, embryos were observed under a fluorescence microscope or fixed in 4% paraformaldehyde and subjected to immunostaining. For explant culture, dissected SYTO16-labeled tissues were placed onto collagen-coated dishes and were incubated in α-MEM with 10% horse serum at 37°C in 5% CO<sub>2</sub> for 24 hours.

BrdU labeling

Pregnant female mice at E9.5 were injected intraperitoneally with bromodeoxyuridine (BrdU; 0.2 mg/g body weight; Sigma). After 1 hour of BrdU exposure, embryos were harvested on ice-cold PBS to stop BrdU incorporation and were fixed in 4% paraformaldehyde for 1 hour. Cryosections were treated with 2 M HCl and subjected to immunostaining with anti-BrdU antibody. For each sample, two sequential transverse sections through the widest region of the left and right ventricles were taken and BrdU-positive nuclei were counted in the compact, trabecular and endocardial layers of the ventricular wall. The sections were then counterstained with Hematoxylin to visualize nuclei and the total
number nuclei was counted in order to calculate the ratio of BrdU-positive to total nuclei. Statistical significance (P<0.05) was determined using the paired t-test. Data are presented as mean±s.e.m.

### Phosphorylation of ERK

Hearts were collected from E9.5 wild-type, **Ednra**/EGFP and **EdnralacZ/EGFP** embryos and lysed with lysis buffer [50 mM Tris-HCl (pH 8.0), 150 mM NaCl, 1 mM EDTA, 1% Triton X-100, 0.1% SDS, 0.1% sodium deoxycholate, protease inhibitor cocktail (Roche), 1 mM sodium orthovanadate and 1 mM sodium fluoride]. The lysates were subjected to SDS-PAGE and immunoblotted using a mouse monoclonal antibody to phosphorylated ERK1/2 and a rabbit polyclonal antibody to total ERK1/2 (both Cell Signaling Technology). To evaluate the effect of Edn1, E9.5 wild-type hearts were incubated in serum-free DMEM with or without 10 μM BQ123 (a cyclic peptide) for 3 hours then stimulated with 100 nM Edn1 for 5 minutes at 37°C. To evaluate the effect of BQ123 on basal ERK phosphorylation, E9.5 wild-type hearts were incubated in DMEM containing 10% fetal calf serum with or without 10 μM BQ123 for 3 hours. Signal intensity was quantified with ImageJ software (NIH). One-way analysis of variance (ANOVA) with Tukey’s test was applied for comparisons of phosphorylated ERK levels among genotypes.

### Conventional RT-PCR

Hearts were collected from E8.25 and E9.5 embryos and sorted into EGFP-positive and EGFP-negative cells using a FACS Vantage SE (BD Biosciences). Total RNA was extracted from sorted fractions with the use of Isogen (Nippon Gene, Tokyo, Japan) and 1 μg samples were then reverse-transcribed using ReverTra Ace (Toyobo, Osaka, Japan) with oligod(T) primer (Takara Bio, Shiga, Japan). The resulting cDNAs were amplified with Taq polymerase (Takara Bio) in a thermocycler. The sequences of the forward and reverse primers as well as the amplicon lengths are listed in Table S1 in the supplementary material. Custom primers were designed using Primer-BLAST online software (http://www.ncbi.nlm.nih.gov/tools/primer-blast/). Thermal cycling was performed for 25-30 cycles to maintain PCR conditions within the linear range of amplification before saturation was reached. Each cycle consisted of 30 seconds of denaturation at 94°C, 30 seconds of annealing at each annealing temperature (see Table S1 in the supplementary material) and 30 seconds of extension at 72°C. Glyceraldehyde-3-phosphate dehydrogenase (*Gapdh*) was used as an internal control.

### RESULTS

**Ednra-lacZ/EGFP expression defines a distinct subdomain within the cardiac crescent**

We characterized marker gene expression in the embryonic heart of **Ednra**/EGFP and **EdnralacZ/EGFP** mice. **Ednra-lacZ/EGFP**-positive cells were first detected in the crescent-forming cardiogenic mesoderm around the 1-somite stage (~E7.8) (Fig. 1A-A’). At the 1- to 3/4-somite stages (E7.8–E8.0), **Ednra-lacZ** signals coincided with detection of endogenous expression of **Ednra** (Fig. 1B,C) and were colocalized with **Ncx2.5** and **Mlc2a** (Fig. 1A’-C). Double immunostaining on sections revealed that **Ednra-lacZ/EGFP** expression overlapped with **Ncx2.5** expression in the ventral region of the heart tube (Fig. 1F-F’). In the caudal region, **Ednra-lacZ/EGFP** expression extended to the **Ncx2.5**-negative lateral plate mesoderm (Fig. 1B,G-G’) and to the extra-embryonic mesoderm of the amnion along the border with the embryonic pericardial coelom; pm, pharyngeal mesoderm.

Quantitative real-time RT-PCR

Left ventricles were isolated from E9.5 embryos. To evaluate the effect of Edn1, isolated ventricles were cultured in DMEM plus 5% fetal calf serum with or without 100 nM Edn1 for 24 hours. Total RNA was extracted from a pool of seven samples for each genotype or culture condition. Quantification of the amount of each mRNA was performed by real-time RT-PCR analyses using a LightCycler (Roche) and Real-Time PCR Premix with SYBR Green (RBC Bioscience) following the manufacturer’s protocol. The primers and reaction conditions are shown in Table S1 in the supplementary material. Thermal cycling was performed for 47 cycles after incubation at 96°C for 10 minutes in at least three separate runs. Each cycle consisted of 10 seconds of denaturation at 95°C, 10 seconds of annealing at each annealing temperature (see Table S1 in the supplementary material) and 11 seconds of extension at 72°C. The second-derivative maximum method was adopted to determine the crossing points automatically for individual samples, and relative amounts of mRNA were calculated based on the control. The Mann-Whitney U-test was applied for comparisons of relative mRNA levels between genotypes or culture conditions.
fig. 2. β-galactosidase staining and in situ hybridization for Nkx2.5 on Ednra-lacZ hearts. (A-D) Hearts at 6/7- (A,B; ventral views) and 9/10- (C,D; left lateral views) somite stages, stained for β-galactosidase activity (A,C) or Nkx2.5 expression (B,D). β-Galactosidase activity is most intense in the inflow region (arrowheads in A) and then extends towards the atrioventricular canal and left ventricle (arrowheads in C). (E-H) Dissected hearts at the 10- (E,F) and 13- (G,H) somite stages, stained for β-galactosidase activity and viewed from the inferior (E), ventral (F,G) and left-dorsal (H) sides. White arrowheads indicate boundaries of β-galactosidase expression. (I-K) Transverse sections of E9.5 Ednra-lacZ hearts stained for β-galactosidase activity. Sections are counterstained with Orange G. β-Galactosidase-positive cells contribute to the first heart field. Arrowheads indicate expression boundaries along the inner curvature. Dorsal mesocardium and proepicardium were also negative for β-galactosidase activity. (L,M) Ventral (L) and dorsal (M) views of an E10.5 heart stained for β-galactosidase activity. Sections are counterstained with Orange G. β-Galactosidase-positive cells contribute to the first heart field. Arrowheads indicate expression boundaries along the inner curvature. Dorsal mesocardium and proepicardium were also negative for β-galactosidase activity. (A-D) Co-immunostaining for EGFP and cardiac markers in early Ednra-EGFP hearts. Transverse sections of E8.25 (7-somite stage; A-A'), E9.5 (B-D') Ednra-EGFP embryos immunostained for EGFP (A-D,D') and myosin heavy chain (MHC; A',B'), desmin (C') or CD31 (D',D') with TOPRO-3 staining (A',B',C'). ht, heart tube; lv, left ventricle; l/r(c)a, left/right (common) atrium; l/rv, left/right ventricle; oft, outflow tract; pe, proepicardium.

Ednra-lacZ/EGFP-positive cells contribute to the chamber-forming myocardium

During linear tube formation at the 6/7-somite stage (~E8.25), Ednra-lacZ expression was largely confined to the caudal inflow region corresponding to the venous pole (Fig. 2A,B). Subsequently, Ednra-lacZ expression was extended to the left lateral wall of the loop heart, forming an apparent trajectory along the outer curvature (Fig. 2C,D). At the 10- to 13-somite stage (~E8.5), β-galactosidase-positive cells were distributed from the venous pole to the left ventricle through a narrow region within the left lateral wall of the atrioventricular canal and atria (Fig. 2E-H). By contrast, the dorsal side of the heart, along the inner curvature and the outflow tract, lacked β-galactosidase expression (Fig. 2E-H). In the right ventricle, only the caudal (posterior) region was populated by β-galactosidase-positive cells (Fig. 2F,G). These patterns were almost identical to the endogenous Ednra expression revealed by in situ hybridization (see Fig. S2 in the supplementary material). At E9.5, β-galactosidase-positive cells were distributed in the common atrium, left ventricle and a posterior part of the right ventricle (Fig. 2I-K). By contrast, the trabeculation-free region in the inner curvature, dorsal mesocardium and proepicardium lacked β-galactosidase expression (Fig. 2I-K). At E10.5, β-galactosidase was widely expressed in the four chambers, whereas the atrioventricular canal and outflow tract were mostly negative (Fig. 2L,M).

To confirm that Ednra-lacZ/EGFP expression marked the myocardial cell lineage, we examined myocardial marker expression. In the E8.25 heart tube and the E9.5 left ventricle, EGFP expression overlapped with myosin heavy chain expression (Fig. 3A,B). At E9.5, EGFP-expressing cells also expressed desmin (Fig. 3C), a marker for chamber-forming myocardium (Schaart et al., 1989). By contrast, EGFP expression did not overlap with CD31 expression, which marks endothelial cells (Fig. 3D). EGFP-expressing cells were further characterized by fluorescence-activated cell sorting (FACS) and RT-PCR. At E8.25 and E9.5, only EGFP-positive fractions expressed Ednra and EGFP. Remarkably, expression of Tbx5, a T-box transcription factor gene crucial for early heart development (Bruneau et al., 2001; Takeuchi et al.,
Dye injected into the ventral inflow region follows the subsequent distribution of the Ednra-lacZ/EGFP-positive subdomain

Extension of Ednra-lacZ/EGFP expression along the outer curvature raises the possibility that Ednra-lacZ/EGFP-expressing cells in the ventral inflow region move into the linear heart tube to give rise to chamber-forming cardiomyocytes, including Tbx5-positive cells arising in the inflow region.

When transplanted, the Ednra-lacZ/EGFP-positive inflow region contributes to left ventricular and atrial myocardium

To confirm the movement from the ventral inflow region to the developing left ventricle and atrium, we transplanted, at E8.25 (5- to 7-somite stage), the Ednra-lacZ/EGFP-positive inflow region into the same region of wild-type embryos (Fig. 5A). After 24 hours, Ednra-EGFP-positive cells were detected in the left ventricle in five out of eight recipient embryos transplanted with the EdnraEGFP/+ inflow region (Fig. 5B-B’). By contrast, no EGFP signals were detected when Ednra-EGFP-positive tails from EdnraEGFP/+ embryos were transplanted (n=7; Fig. 5C-C’). No fluorescent signals were observed in the left ventricle of wild-type recipients transplanted with a wild-type inflow region (n=7; Fig. 5D-D’). EdnraEGFP/+ recipients transplanted with the EdnraEGFP/+ inflow region exhibited strong endogenous EGFP signals in the ventricle, as expected (n=6; Fig. 5E-E’).

To verify further the regional specificity with respect to movement, we transplanted different regions of the E8.25 heart tube, labeled with SYTO16 fluorescent dye, into the inflow region of the heart at the same developmental stage (Fig. 5F). When SYTO16-labeled cells were transplanted into the outflow or ventricular region, no upward movement was detected after 24 hours (n=5 for each; Fig. 5G-G’,H-H’). By contrast, SYTO16-labeled cells were found to distribute along the outer curvature towards the left ventricle after 24 hours in all five embryos transplanted with cells in the inflow region (Fig. 5I-I’). These results strongly support the movement and contribution of Ednra-lacZ/EGFP-positive inflow cells to the developing left ventricle.

As indicated by β-galactosidase staining, Ednra-lacZ/EGFP was widely expressed in the four chambers after E9.5, raising the possibility that many Ednra-negative cells in the early heart tube might become Ednra-positive at later stages. To test this idea, we performed explant culture of the ventricular and inflow regions of the E8.25 heart tube separately. At the start of culture, EGFP signals were clearly detectable in the inflow region, but were very low in the ventricle (see Fig. S3 in the supplementary material). After 24 hours, ventricular and inflow regions both demonstrated
intense EGFP signals (see Fig. S3 in the supplementary material). These results suggest that tube-forming cells that are Ednra negative at early stages might start to express Ednra later.

**Defects in ventricular chamber formation in Ednra-null mice**

In addition to outflow abnormalities as a result of cardiac neural crest defects, some Edn1-null embryos from Edn antagonist-treated pregnant mice exhibited ventricular hypoplasia (Kurihara et al., 1995), indicating involvement of Edn signaling in cardiac chamber development. To investigate this further, we revisited the Ednra-null phenotype.

At E9.5, when cardiac neural crest cells are not yet seen in the conus arteriosus (Jiang et al., 2000), Ednra<sup>lacZ/EGFP</sup> (Ednra-null) embryos were obtained at the expected Mendelian ratio (49:102:56 wild-type:heterozygous:null). Of the 43 Ednra<sup>lacZ/EGFP</sup> embryos examined, 26 (60%) showed normally developed hearts (Fig. 6A,B). By contrast, 17 (40%) showed a gourd-shaped heart with disproportionate chamber sizes (Fig. 6C). These morphological changes indicate that Ednra-mediated signals might be involved in normal growth during chamber formation. To further characterize the Ednra-null phenotype, we compared the distribution of β-galactosidase-positive cells in the hearts of Ednra<sup>lacZ/EGFP</sup> and Ednra<sup>lacZ/EGFP</sup> embryos at E9.5. β-galactosidase expression in the caudal (posterior) ventricular wall tended to distribute from left to right to a lesser extent in Ednra<sup>lacZ/EGFP</sup> embryos than in Ednra<sup>lacZ/EGFP</sup> littermates (see Fig. S4 in the supplementary material). Histological examination revealed that Ednra<sup>lacZ/EGFP</sup> embryos often had a poorly developed ventricular wall with a low distribution of β-galactosidase-positive cells (Fig. 6D-G).

Next, we performed BrdU labeling to examine whether the Ednra-null phenotype was associated with changes in proliferation. The number of proliferative cells incorporating BrdU was significantly decreased in the compact and trabecular layers of the ventricular wall of Ednra-null embryos compared with those of heterozygous Ednra<sup>lacZ/EGFP</sup> embryos (Fig. 6H-M). Decreased BrdU uptake in the right ventricle could possibly be explained by low proliferation rates of β-galactosidase-positive cells populated in the caudal (posterior) region (Fig. 2F,G). Indeed, in the right ventricular region, the number of BrdU-labeled cells with a low β-galactosidase-positive population was similar in Ednra-null and heterozygous embryos (data not shown). To confirm this, we double stained serial ventricular sections for β-galactosidase activity and phosphohistone H3 (pHH3), a marker of mitosis (Cimini et al., 2003), and counted pHH3-positive cells separately in populations positive and negative for β-galactosidase. The mitotic frequency of β-galactosidase-positive, but not β-galactosidase-negative, cells was decreased in the left and right ventricles of the Ednra-null heart (Fig. 6N). Decreased BrdU incorporation in the endocardium of the Ednra<sup>lacZ/EGFP</sup> right ventricle is likely to be an indirect effect because the endocardial layer does not express Ednra-lacZ. We did not observe differences in the proportion of apoptotic cells between Ednra-null and heterozygous or wild-type embryos (data not shown).

Edn1 has been reported to act as a mitogen on cardiomyocytes by stimulating ERK phosphorylation (Sugden, 2003). We therefore examined ERK phosphorylation in E9.5 wild-type, Ednra<sup>lacZ/EGFP</sup> and Ednra<sup>lacZ/EGFP</sup> hearts. ERK phosphorylation levels were decreased in proportion to the number of Ednra-null alleles (Fig. 7A,B). In E9.5 hearts in vitro, stimulation of ERK phosphorylation by Edn1 was abolished by the Ednra antagonist BQ123 (Fig. 7C). Basal ERK phosphorylation was also decreased by BQ123 (Fig. 7D). Taken together, these results suggest that the Ednra signal is involved in myocardial development as a mitogenic factor at early stages. By contrast, no differences in ERK phosphorylation were observed at E10.5 (data not shown), indicating that the negative effect of the Ednra-null mutation on myocardial proliferation might be overcome by other factors at later stages.
Changes in T-box transcription factor gene expression in Ednra-null hearts

To examine whether the Ednra-null mutation affected gene expression in the early developing heart, we performed in situ hybridization for several marker genes on E9.5 Ednra+/EGFP and EdnralacZ/EGFP hearts. EdnralacZ/EGFP left ventricles showed decreased expression of Tbx5 and its downstream gene Cx40 (Fig. 8A,B), whereas the expression of other chamber myocardium markers such as ANF, Hand1, Cited1 and Mlc2a was not affected (Fig. 8C-F). Decreased mRNA levels of Tbx5 and Cx40, but not Hand1, were also confirmed by quantitative RT-PCR (Fig. 8G). Furthermore, Tbx5 mRNA levels were increased by Edn1 in excised E9.5 heart explants (Fig. 8H).

The effect of the Ednra-null mutation on gene expression patterns was examined further by whole-mount in situ hybridization. In E8.25 Ednra+/EGFP and EdnralacZ/EGFP hearts, Tbx5 expression in the inflow region had a similar pattern to that of Ednra (Fig. 9A). At E9.5, Tbx5 expression was expanded anteriorly towards the left ventricle in Ednra+/EGFP embryos (Fig. 9B), as described previously (Bruneau et al., 1999). This anterior expansion of Tbx5 expression was decreased in EdnralacZ/EGFP hearts, whereas Tbx5 expression in the posterior (inflow) region was similar to that of Ednra+/EGFP embryos (Fig. 9C). By contrast, the Tbx2-expressing region, which normally corresponds to the atrioventricular canal (Aanhaanen et al., 2009), was reciprocally expanded in EdnralacZ/EGFP hearts (Fig. 9D,E). Bmp2 expression in the atrioventricular canal was similar in Ednra+/EGFP and EdnralacZ/EGFP hearts (Fig. 9F,G), indicating that the expansion of Tbx2 expression was independent of Bmp2, an inducer of Tbx2 in the atrioventricular canal (Kokubo et al., 2007; Yamada et al., 2000). These results indicate that Edn1/Ednra signaling might be involved in the regulation of T-box transcription factor gene expression in early developing hearts.
DISCUSSION

Regionalization of the first heart field and contribution to chamber formation

Here, we identified an Ednra-lacZ/EGFP-expressing cell population that is first detected in the cardiac crescent. At the early heart tube-forming stage, these cells are present in the ventral inflow region. Subsequently, dye-labeling experiments indicate that they move upward along the outer curvature between the 6/7-somite and 9/10-somite stages. This timing corresponds to the start of looping just after the formation of the linear heart tube (Abu-Issa and Kirby, 2007), indicating that the linear heart tube is mainly composed of Ednra-negative cells and that the Ednra-positive cells are recruited into the looping heart tube. This upward cell movement was confirmed and was shown to be specific for cells in the inflow region by dye-labeling and transplantation experiments. These findings suggest that Ednra-positive cells arising from the crescent-forming first heart field are a distinct subpopulation and contribute to chamber formation in a manner different from that of the early tube-forming cells.

de la Cruz and colleagues have performed extensive in vivo labeling experiments in the chick and showed that the inflow region between the interventricular grooves and the caudal end of the linear heart tube contributes to the trabeculated portion of the left ventricle (de la Cruz et al., 1989). The present study identified cells in the ventral wall within this inflow region as a subpopulation with a distinct gene expression signature and cell movement; cells at both sides converge to the midline and move upward along the outer curvature. In the chick embryo, the outer curvature is formed by the ventral seam after fusion of the bilateral cardiogenic fields (Abu-Issa and Kirby, 2008). Although in the chick embryo, unlike in the mouse, the bilateral heart fields remain separate until the tube-forming stage without forming the cardiac crescent, the mode of outer curvature formation by midline convergence of bilateral cells might be common to chick and mouse embryos.

The Ednra-lacZ/EGFP-expressing cell population is characterized by the presence of cells that express Tbx5, which is expressed in a posterior-to-anterior gradient in the inflow region and is important for left ventricular identity (Hoogaars et al., 2007). The Ednra-expressing region is distinct from the second heart field, marked by Isl1 expression. However, Isl1 expression was detected in both Ednra-EGFP-positive and -negative cells at E8.25 in our FACS and RT-PCR experiment. Recently, van den Berg et al. reported that, in chick, an Isl1-positive proliferating center caudal to the inflow tract provides cells to the venous and arterial poles of the elongating heart tube (van den Berg et al., 2009). Apparently, Ednra-lacZ/EGFP-positive cells are distinct from this population because they are localized to the ventral region of the inflow and are Isl1-negative at the crescent/tube-forming stages. However, Ednra-lacZ/EGFP-positive cells might also be derived from the Isl1-positive pool as Isl1 is initially expressed in all cardiogenic mesoderm and is downregulated on differentiation (Prall et al., 2007; Yuan and Schoenwolf, 2000). At later stages, many atrial cells express Ednra-lacZ/EGFP, suggesting that the second heart field-derived cells may also start to express this gene.

Fig. 7. Analysis of ERK phosphorylation. (A) Western blot of individual hearts excised from E9.5 wild-type, EdnraEGFP and EdnraEGFP/EGFP embryos using antibodies to phosphorylated (pERK) and total ERK1/2 (ERK). (B) Quantification of the ratio of phosphorylated to total ERK protein levels in A, normalized to control (wild-type) samples (n=5 per group). Data are presented as means±s.e.m. *P<0.05. (C) Edn1 stimulates ERK phosphorylation in isolated E9.5 hearts. Edn1-induced ERK phosphorylation is completely abolished by the Ednra antagonist BQ123. (D) BQ123 downregulates basal ERK phosphorylation in isolated E9.5 hearts.

Fig. 8. Gene expression analysis of E9.5 Ednra-null hearts. (A-F) In situ hybridization of EdnraEGFP(a,a’) and EdnraEGFP(b,b’) hearts for Tbx5(A), Cx40(B), ANF(C), Hand1(D), Cited1(E) and Mlc2a(F). a’ and b’ are magnifications of the regions indicated in a and b, respectively. lv, left ventricle; rv, right ventricle. (G,H) Real-time RT-PCR analysis. (G) Tbx5 and Cx40, but not Hand1, expression levels are lower in EdnraEGFP hearts than in EdnraEGFP hearts (n=5 per group). (H) In E9.5 wild-type ventricles, Tbx5 expression is upregulated by stimulation with 100 nM Edn1 for 24 hours (n=4 per group). Data are presented as mean±s.e.m. *P<0.05, **P<0.01.
at a later time than do first heart field-derived cells. Thus, Isll-positive cells may eventually express Ednra, but the timing might be different between cardiac regions. Indeed, explant culture experiments revealed that Ednra-negative cells in the early heart tube might become Ednra-positive at later stages, indicating that later Ednra-positive cardiomyocytes are derived both from early Ednra-positive inflow cells and from tube-forming cells that are Ednra-negative at early stages.

According to the ballooning model for chamber formation, which is now widely accepted, the ventricular chambers bulge from the outer curvature of the looped heart (Christoffels et al., 2000). The developing chambers show high proliferative activity and are characterized by the upregulation of chamber-specific myocardial genes. A two-step model has been proposed for this process: the first step is the formation of a primary heart tube and the second step is characterized by the upregulation of chamber-specific myocardial genes. The present study characterizes further the Ednra-null phenotype in other tissues, decreased mitotic frequency in β-galactosidase-positive cells, but not in β-galactosidase-negative cells, of the Ednra-null heart supports the possibility that the phenotype is the result of a direct effect on early cardiomyocytes through the Ednra signaling pathway.

The Edn1/Ednra signal is known to induce hypertrophic growth of cardiac myocytes through G_{i}α_{11}-mediated activation of the ERK pathway (Sugden, 2003). Consistently, ERK phosphorylation tended to decrease in E9.5 Ednra-null hearts and was stimulated by Edn1 treatment. G_{i}α_{11}-deficient embryos have severe myocardial hypoplasia in both the compact and trabecular layers, which might account for the mid-gestation lethality of these embryos (Oppermann et al., 1998). These findings lead us to speculate that Edn1/Ednra might be involved in the activation of a G_{i}α_{11}-mediated mitotic pathway crucial for early myocardial development.

In addition, Tbx5 and Cx40 expression was downregulated in Ednra-null hearts and upregulated by stimulation with Edn1. Recent studies have implicated Tbx5 in the regulation of myocardial growth and proliferation (Georges et al., 2008; Goetz et al., 2006) and expression of Tbx5 is affected by growth factors (Georges et al., 2008). Given these findings, it would be interesting to investigate further the relationship between Edn1/Ednra signaling and Tbx5-dependent myocardial growth/proliferation and chamber specification. Conversely, Tbx2 expression was expanded towards the left ventricle without changes in Bmp2 expression in Ednra-null hearts. Recently, Aanhaanen et al. reported that Tbx2-expressing cells arising in the bilateral limbs of the crescent contribute to the atrioventricular canal and, subsequently, to the Tbx2-negative left ventricle, particularly to the basal free wall where Tbx2 expression is lost (Aanhaanen et al., 2009). In Tbx2-null hearts, the atrioventricular canal differentiates prematurely to chamber myocardium and proliferates at increased rates similar to that of chamber myocardium, indicating that Tbx2 might regulate the timing of chamber myocardial differentiation of Tbx2-expressing cells allocated to the left ventricular free wall (Aanhaanen et al., 2009). Considering that the Ednra-lacZ/EGFP-
positive cell population of the E8.25 heart expresses both Tbx5 and Tbx2, these results raise the possibility that Edn1/Ednra signaling might be involved in chamber formation through the regulation of T-box transcription factor gene expression.

**Relationship between cell populations expressing Ednra at early and late stages in cardiac development**

The present study has revealed that Ednra-lacZ/EGFP-expressing cells represent a distinct subset of the first heart field and of the inflow region of the heart, contributing to chamber myofarcion. Identification of this population has revealed novel aspects of early cell behavior contributing to heart morphogenesis. It has also shown an expansion of Ednra expression within chamber-forming cardiomyocytes and implicates the Ednra signal as a mitotic factor and potential regulator of T-box transcription factor gene expression in early cardiac development. The present experiments, investigating cellular distribution/movement and gene expression profiles, indicate that the early Ednra-expressing cells contribute partly to the late Ednra-expressing population together with cardiomyocytes, which start to express Ednra around E9.5 or later. These findings might provide new insight into the understanding of normal cardiac development, which is relevant to the pathogenesis of congenital heart diseases involving abnormalities of chamber morphogenesis.

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**Competing interests statement**

The authors declare no competing financial interests.

**Supplementary material**

Supplementary material for this article is available at Development.

**References**


Fig. S1

Ednra⁺

Exon1  Exon2

Targeting construct

Neo  pA

lox71  lox2272

Ednraneo

Exon1  Exon2

Neo  pA

+ Cre recombinase

EdnraEGFP

Exon1  Exon2

EGFP  Puro  pA

lox66  FRT  FRT  lox2272

Lox71/66  FRT  FRT  lox2272
Fig. S2

A

B

C

D

E

EGFP

Tbx5

a

a'

b

c

E8.25

heart tube

sinus venosus
Fig. S3

Heart tube

Inflow

Ventricle

0h  24h
A  B
C  D
C  D
E  F
G  H
Fig. S4

A  Ednra<sup>lacZ/+</sup>  

B  Ednra<sup>lacZ/EGFP</sup>
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**Real time PCR**

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