Distinct phases of cardiomyocyte differentiation regulate growth of the zebrafish heart

Emma de Pater1, Linda Clijsters1, Sara R. Marques2,3, Yi-Fan Lin2, Zayra V. Garavito-Aguilar2, Deborah Yelon2,* and Jeroen Bakkers1,4,*

Amongst animal species, there is enormous variation in the size and complexity of the heart, ranging from the simple one-chambered heart of Ciona intestinalis to the complex four-chambered heart of lunged animals. To address possible mechanisms for the evolutionary adaptation of heart size, we studied how growth of the simple two-chambered heart in zebrafish is regulated. Our data show that the embryonic zebrafish heart tube grows by a substantial increase in cardiomyocyte number. Augmented cardiomyocyte differentiation, as opposed to proliferation, is responsible for the observed growth. By using transgenic assays to monitor developmental timing, we visualized for the first time the dynamics of cardiomyocyte differentiation in a vertebrate embryo. Our data identify two previously unrecognized phases of cardiomyocyte differentiation separated in time, space and regulation. During the initial phase, a continuous wave of cardiomyocyte differentiation begins in the ventricle, ends in the atrium, and requires Islet1 for its completion. In the later phase, new cardiomyocytes are added to the arterial pole, and this process requires Fgf signaling. Thus, two separate processes of cardiomyocyte differentiation independently regulate growth of the zebrafish heart. Together, our data support a model in which modified regulation of these distinct phases of cardiomyocyte differentiation has been responsible for the changes in heart size and morphology among vertebrate species.

KEY WORDS: Fgf, Differentiation, Heart, Islet1, Zebrafish

INTRODUCTION

The vertebrate heart acquires its three-dimensional (3D) structure during embryonic development. In all vertebrates, the heart starts out as a simple linear tube. Expansion of the linear heart tube is followed by valve formation and septation to form a two-, three- or four-chambered heart. The regulation of heart size and its relationship to the evolution of the cardiac chambers remain longstanding mysteries.

Growth of the heart tube could be mediated either through cell proliferation or by recruitment of new cardiomyocytes into the organ. Although cardiac cells do proliferate, it is rare in the linear heart tube. In the chick heart, myocardial proliferation only starts at stage 12, when the heart tube has already looped and chambers start to emerge (Soufan et al., 2006). The early work of de la Cruz in the chick embryo demonstrated that the heart lengths by the addition of cells to the arterial (outflow) pole of the heart (de la Cruz et al., 1977). Later studies in mouse and chick confirmed that, in these organisms, the embryonic primitive heart tube grows and becomes structurally elaborate owing to the significant addition of cells to the right ventricle and the outflow tract (OFT) from the pharyngeal mesoderm, which is also referred to as the secondary or anterior heart field (Kelly et al., 2001; Mjaatvedt et al., 2001; Waldo et al., 2001). Later studies revealed an extension of this population of progenitor cells, more posteriorly, that also contribute to the venous pole of the heart (atria) (Cai et al., 2003). The progenitor cells located within the pharyngeal mesoderm that contribute cardiomyocytes to both the arterial pole and the venous pole are referred to as the second heart field (SHF), as opposed to the first heart field, which gives rise to the cells of the early cardiac tube (Buckingham et al., 2005). A lack of markers that are specific for the primary heart field has made it difficult to determine its location. The recent observation that Islet1 protein, previously used as a marker for the SHF, is present in all cardiomyocytes has initiated a discussion about significance of the different heart fields (Prall et al., 2007). This discussion has led to the alternative suggestion that the heart tube grows by a continuous differentiation process (Moorman et al., 2007). However, the inability to visualize cardiomyocyte differentiation has made it difficult to resolve these issues.

Here, we investigate the dynamics of cardiomyocyte differentiation during cardiac development, and by taking advantage of opportunities for high-resolution and live imaging of the zebrafish heart, we visualize this process for the first time. By using a developmental timing assay and a photoconvertible marker, we identify two phases of cardiomyocyte differentiation. These previously unrecognized phases of cardiomyocyte differentiation are separated in time, space and the molecular mechanisms by which they are controlled.

MATERIALS AND METHODS

Zebrafish lines

All transgenic strains were analyzed as heterozygotes in our studies, and all embryos were grown at 28.5°C. To identify cardiomyocytes and for the developmental timing assay we used Tg(myl7:EGFP)twu26 (Huang et al., 2003) and Tg(−5.3myl7:nDsRed2)j2 (Mably et al., 2003) lines. Founder fish with germline integration of Tg(cmlc2:kaede) were generated by Tol2 transposase-mediated transgenesis (Fisher et al., 2006) and were outcrossed to produce embryos for photoconversion. The islet1 mutant K88X (isl1EX0026) was isolated from an ENU-mutagenized library, using target-selected mutagenesis, as described before (Wienholds et al., 2002).
Cell counts and developmental timing assay

To count cardiomyocytes at various stages, we used the Tg(cmlc2:dsred2-nuc) line stained using an α-DsRed antibody (Clontech). The embryos were grown under normal culture conditions (Westerfield, 1995) up to the desired stage and subsequently fixed (overnight at 4°C) in 2% paraformaldehyde containing glycerol and washed with PBS containing 0.1% Tween (PBST) the following day. The embryos were counterstained with DAPI [15 minutes at room temperature, 1:5000 DAPI (Boehringer Mannheim) in PBST]. The embryos were flat-mounted and imaged ventrally in Vectashield containing DAPI (Vector Laboratories).

Mounted embryos were imaged using a Leica TCS SPE confocal microscope with a 20× oil immersion lens. The images were zoomed in to 1.96× with the LAS-AF TCS SPE software and sequential confocal images were taken using the laser channels 405, 488 and 532 nm with a standardized step size of 0.642 μm in the z-direction. The pinhole was set to 1 airy unit and the scanning speed was 600 Hz.

3D reconstructions of confocal stacks were made using Velocity version 4.1 software (Improvision). Quantification of the GFPposDsRedpos and step size of 0.642 μm in the z-direction. The pinhole was set to 1 airy unit and the scanning speed was 600 Hz.

Photoconversion of Kaede

Photoconversion of Kaede fluorescence from green to red was achieved by exposing transgenic embryos to UV light on a Zeiss Axioplan microscope equipped with a DAPI filter set, as previously described (Hatta et al., 2006). Confocal z-stacks were obtained using a Zeiss LSM 510 laser-scanning microscope and analyzed with Zeiss LSM and Velocity software.

Histological methods

BrdU labeling was performed by soaking the embryos in embryo medium containing 5 mg/ml BrdU (Roche) for 24 hours. α-BrdU (Roche) and α-phospho-His (Upstate) antibody labeling was performed on 6- and 10-μm thick paraffin sections, respectively, which were then stained with 3,3’-Diaminobenzidine (DAB). Other antibodies used in this study were: α-DsRed (Clontech), α-eGFP (Chemokine) and α-Isl (Hybridoma bank clone 39.405). Immunofluorescence was performed according to Smith et al. (Smith et al., 2008).

**SU5402 treatment**

Embryos were treated with either DMSO or SU5402 at a concentration of 12.5 μM in embryo medium from 24 hpf until 48 hpf in glass vials at the dark at normal culture temperatures.

**Morpholinos**

Antisense morpholinos targeting fgf8 (Draper et al., 2001) or isl1 (Hutchinson and Eisen, 2006) were injected at the one-cell stage. Uninjected and control MO (Gene Tools) injected embryos from the same egg lay were used as controls for all experiments.

**RESULTS**

**Cardiomyocyte cell number in the zebrafish heart tube increases during looping**

Growth of the two-chambered zebrafish heart has not been studied systematically. To determine the number of cells in the zebrafish heart, we counted the differentiated cardiomyocytes present in the linear heart tube and the looped chambers. We used Tg(cmlc2:dsred2-nuc) embryos that express nuclear DsRed from the cardiac myosin light chain 2 (cmlc2; myl7 – Zebrafish Information Network) promoter in all differentiated cardiomyocytes (Mably et al., 2003). To identify all cardiomyocytes expressing DsRed, Tg(cmlc2:dsred2-nuc) embryos were fixed for immunofluorescence staining using an α-DsRed antibody (Fig. IA-F). At 24 hours post-fertilization (hpf), the heart tube has formed from the cardiac disk and was found to contain 151±12 (mean±s.e.m., n=5) cardiomyocytes. Over the next 24 hours, a
significant increase in the number of cardiomyocytes was observed (to 311±10, n=5, at 48 hpf; Fig. 1E; see also Table S1 in the supplementary material). One explanation for the marked increase in cardiomyocyte number could be cell proliferation. To test this hypothesis, serial sections were stained with an antibody recognizing phosphorylated histone (phospho-His). Only a minimal amount of phospho-His staining was present in the myocardium at 30, 36 and 48 hpf, whereas in the surrounding tissues, such as the lateral plate mesoderm, many phospho-His-positive cells were observed (Fig. 1G,H).

To quantify the total number of cardiomyocytes that had undergone at least one round of DNA replication during heart looping, embryos were soaked in a solution containing BrdU from 24 hpf until 48 hpf. When sectioned and stained by an α-BrdU antibody, only 16±2 (n=6) BrdU-positive cardiomyocytes per embryo were observed (Fig. 1J; see also Figs S1, S2 in the supplementary material). Surprisingly, 54% of the BrdU-positive cells found in the myocardium were located near the two cardiac poles (within four tiers of cells at the end the myocardial tube), adjacent to the highly proliferating mesenchyme (Fig. 1J). From the BrdU incorporation analysis and the phospho-His staining, we conclude that the low rate of proliferation within the myocardium cannot account for the substantial increase in cardiomyocyte number that we observed in the heart between 24 and 48 hpf.

Distinct phases of cardiomyocyte differentiation at the venous and arterial poles

Our finding that a large fraction of BrdU-positive cells was located near the poles suggested either a local zone of proliferation or the addition and differentiation of cells that originate from the adjacent proliferating mesenchyme to the poles of the heart tube. To investigate cardiomyocyte differentiation, we used a developmental timing assay by examining double transgenic animals expressing both eGFP and DsRed in differentiating cardiomyocytes from the cardiac myosin light chain 2 (cmlc2) promoter.
and the arterial poles (Fig. 2G-I). In a single expressing material). By contrast, newly differentiating cells that begin produce additional green Kaede (see Fig. S5 in the supplementary material). The DsRed fluorescence was detectable by confocal microscopy only from 36 hpf onwards. Intriguingly, we found two pools of cardiomyocytes, eGFPposDsRedpos and eGFPposDsRedneg cells (Fig. 2D-F), suggesting that cardiomyocyte differentiation had indeed occurred in different phases. The eGFPposDsRedpos cells, which had initiated differentiation early, were located in the ventricle and in a specific region of the atrium (the inner curvature). The eGFPposDsRedneg cells, which had initiated differentiation at a later time point, were consistently found in the atrium (mainly in the outer curvature) and at the arterial pole (Fig. 2D-F). This is consistent with our observation that the number of cmlc2-expressing cells in the lateral plate mesoderm increases gradually over time, with expression in ventricular precursors preceding expression in atrial precursors (see Fig. S4 in the supplementary material). At 48-55 hpf we still observed eGFPposDsRedneg cells located at both the venous and the arterial poles (Fig. 2G-I). In a single z-scan, at the level of the ventricle/outflow region, the different intensities of the eGFP versus the DsRed signal could be appreciated, and is suggestive of the addition of newly differentiating cardiomyocytes at the arterial pole (Fig. 2J-L).

To examine the timing of cardiomyocyte addition in more detail, we employed a transgene [Tg(cmlc2:eGFP)/Tg(cmlc2:dsred2-nuc)]. At 24 hpf, the heart tube has formed, and strong eGFP fluorescence was detected in the cardiomyocytes (Fig. 2A). The DsRed fluorescence was still not detectable (Fig. 2B,C), even though antibody staining demonstrated that the DsRed protein was abundantly present at that time (see Fig. S3 in the supplementary material). The DsRed fluorescence was detectable by confocal microscopy only from 36 hpf onwards. Intriguingly, we found two pools of cardiomyocytes, eGFPposDsRedpos and eGFPposDsRedneg cells (Fig. 2D-F), suggesting that cardiomyocyte differentiation had indeed occurred in different phases. The eGFPposDsRedpos cells, which had initiated differentiation early, were located in the ventricle and in a specific region of the atrium (the inner curvature). The eGFPposDsRedneg cells, which had initiated differentiation at a later time point, were consistently found in the atrium (mainly in the outer curvature) and at the arterial pole (Fig. 2D-F). This is consistent with our observation that the number of cmlc2-expressing cells in the lateral plate mesoderm increases gradually over time, with expression in ventricular precursors preceding expression in atrial precursors (see Fig. S4 in the supplementary material). At 48-55 hpf we still observed eGFPposDsRedneg cells located at both the venous and the arterial poles (Fig. 2G-I). In a single z-scan, at the level of the ventricle/outflow region, the different intensities of the eGFP versus the DsRed signal could be appreciated, and is suggestive of the addition of newly differentiating cardiomyocytes at the arterial pole (Fig. 2J-L).

To examine the timing of cardiomyocyte addition in more detail, we employed a transgene [Tg(cmlc2:kaede)] in which expression of the red-to-green photoconvertible fluorescent protein Kaede (Ando et al., 2002) is driven by the cmlc2 promoter. In Tg(cmlc2:kaede) embryos, photoconversion of Kaede can mark the differentiated cardiomyocytes present at a specific timepoint: the green form of Kaede in all cmlc2-expressing cells converts into the red form, labeling these cells with red fluorescence even as they continue to produce additional green Kaede (see Fig. S5 in the supplementary material). By contrast, newly differentiating cells that begin expressing cmlc2 after the time of photoconversion will fluoresce green, but not red (Fig. S5 in the supplementary material).

Photoconversion at 34 hpf, followed by examination of fluorescence at 48 hpf, revealed a population of green, but not red, cardiomyocytes at the distal portion of the arterial pole, indicating the addition of these cells between 34 and 48 hpf (n=8/8; Fig. 2P-R; see also Fig. S5 in the supplementary material). However, we did not observe the addition of cardiomyocytes to the venous pole during the same timeframe (n=8/8; see Fig. S5 in the supplementary material). Instead, the addition of atrial cells seems to occur at earlier stages. Photoconversion at 19 hpf, followed by examination at 26 hpf, demonstrated that cardiomyocytes are added to a portion of the atrium (its future outer curvature) following the initial differentiation of the ventricle and the future atrial inner curvature (n=4/4; Fig. 2M-O). In these embryos, we did not observe any cells being added to the arterial pole. Synchronizing these data with the results of our developmental timing assays, we find a defined sequence for cardiomyocyte differentiation in zebrafish. An initial wave of differentiation begins with the formation of the ventricle and continues to gradually create the atrium; subsequently, additional cardiomyocytes are appended to the arterial pole.

Isole1 mutants have reduced cardiomyocyte differentiation at the venous pole

Next we wanted to identify the signals that regulate these two waves of cardiomyocyte differentiation. Isole1 ( Isl1 ) deficient mouse embryos lack part of the atria and most of the outflow tract and right ventricle, suggesting that Isl1-expressing cells contribute to both the venous and the arterial poles of the mouse heart (Cai et al., 2003). More recent studies demonstrated that Isl1 is expressed throughout the heart (Prall et al., 2007), and is also required for heart morphogenesis and early cardiomyocyte specification in Drosophila and Xenopus, respectively (Brade et al., 2007; Tao et al., 2007). To identify a possible Isl1-positive cardiac progenitor cell population in the zebrafish, we analyzed expression at various stages. Using an antibody recognizing both Isl1 and Isl2 proteins (Hutchinson and Eisen, 2006; Wan et al., 2006), we observed a strong nuclear signal in the trigeminal sensory ganglia, the vascular endothelium, and the endoderm, which lays dorsal to the cardiac field (Trinh Le and Stainier, 2004) (Fig. 3B,C). We also observed a nuclear signal in cells located at the periphery of the cardiac field where future atrial cells are located (Fig. 3A-F; see Fig. S6 in the supplementary material). Frequently the Isl-positive cells are located (Fig. S6 in the supplementary material). At 24 hpf, the isl1 mutant embryos look morphologically normal but are immotile, which can be explained by the function of the Isl-positive cells.

To address whether zebrafish Isl1 is required for normal heart development, we screened for mutant alleles in an ENU-mutagenized library (Wienholds et al., 2002). We identified one allele that results in a premature stop codon in the third exon, removing part of the LIM-domain and the entire homeobox (Fig. 4A,B). At 24 hpf, the isl1 mutant embryos look morphologically normal but are immotile, which can be explained by the function of the Isl-positive cells.

![Fig. 3. Isl localization in cardiomyocytes of the future atrium.](image-url)
Isil described in primary motoneurons (Hutchinson and Eisen, 2006) (see Fig. S7A-D in the supplementary material; data not shown). In addition to the motility defect, the heart of isil mutant embryos contracts irregularly and with a reduced frequency (bradycardia; Fig. 4C). Whereas the heart frequency in wild-type siblings will rise from 80±1 beats/minute at 24 hpf to 163±4 beats/minute at 48 hpf, the heart frequency of isil mutant siblings will rise from 80±1 beats/minute at 24 hpf to 163±4 (bradycardia; Fig. 4C). Whereas the heart frequency in wild-type siblings will rise from 80±1 beats/minute at 24 hpf to 163±4 beats/minute at 48 hpf, the heart frequency of isil mutant embryos contracts irregularly and with a reduced frequency (bradycardia; Fig. 4C). Whereas the heart frequency in wild-type siblings will rise from 80±1 beats/minute at 24 hpf to 163±4 beats/minute at 48 hpf, the heart frequency of isil mutant siblings will rise from 80±1 beats/minute at 24 hpf to 163±4 beats/minute at 48 hpf, the heart frequency of isil mutant (E) embryos. Black arrow (D) indicates bmp4 expression in the sinus venosus of a wild-type embryo; red arrow (E) indicates the inflow area of a representative isil mutant embryo lacking bmp4 expression. Embryos are shown as frontal-ventral views (OFT to the top).

To identify a possible cause for the cardiac defects observed in isil mutant embryos, we performed in situ hybridizations with several cardiac marker genes. Although nks2.5 and cmlc2 were normally expressed, bmp4 expression was clearly affected in isil mutants (Fig. 4D,E; data not shown). In wild-type siblings, bmp4 was expressed in the OFT, the atrioventricular canal (AVC) and the sinus venosus (SV). Surprisingly, although bmp4 expression in the OFT and the AVC was unaffected in isil mutants, bmp4 expression in the SV was completely abolished.

To address whether the observed cardiovascular defects in isil mutant embryos could result from a defect in cardiomyocyte differentiation, we used the above-described developmental timing assay. To do so, we crossed the isil mutation into Tg(cmlc2:eGFP)/Tg(cmlc2:dsred2-nuc) double transgenic embryos and quantified the number of eGFPposDsRedneg cardiomyocytes and eGFPposDsRedneg cardiomyocytes in confocal images after 3D reconstruction (Fig. 5A-F). We observed no significant difference in the number of eGFPposDsRedneg cells (siblings, 200±6; mutants, 203±7) nor in the number of eGFPposDsRedneg cells at the arterial pole (sibs, 28±1; mutants, 32±2; Fig. 5G-K; see also Table S3 in the supplementary material), demonstrating that cardiomyocyte differentiation still occurs. We did, however, observe a significant reduction in the number of eGFPposDsRedneg cells at the venous pole of isil mutants (25±3 in sibling hearts and 10±3 in mutant hearts, P<0.01; Fig. 5D-F,K). To confirm that the observed defects in cardiomyocyte differentiation resulted from the loss of Isl1 function, we used antisense morpholinos (MO) against isil, which affect splicing of the isil mRNA and thereby prevent Isl1 protein production (Hutchinson and Eisen, 2006) (see Fig. S8 in the supplementary material). Using the developmental timing assay, we again observed a significant reduction in the number of eGFPposDsRedneg cells at the venous pole, while the number of eGFPposDsRedneg cells at the arterial pole remained unaffected. The stronger effects on cardiac morphology and the number of eGFPposDsRedneg cells observed after isil MO injection were probably due to an additional toxic effect of the MO injection.

Because isil mutant embryos display cardiac dysfunction, we addressed whether cardiac dysfunction by itself can affect cardiomyocyte addition. To interfere with cardiac function, we injected tnnt2 MOs (Sehnert et al., 2002). Although cardiac contraction was abolished in tnnt2 Mo-injected embryos, the addition of new cardiomyocytes to both poles of the heart tube was not significantly altered (see Fig. S9 in the supplementary material).

In conclusion, the loss of bmp4 expression in the SV combined with the reduced number of eGFPposDsRedneg cardiomyocytes at the venous pole demonstrate that, in zebrafish, Isl1 is specifically required to complete cardiomyocyte differentiation at the venous pole and not at the arterial pole. This suggests that other, Isl1-independent pathways regulate the addition of cardiomyocytes to the arterial pole (see Discussion).

**Fgf signaling is required for cardiomyocyte addition at the arterial pole**

Two previous studies using conditional and hypomorphic Fgf8 alleles in mouse have demonstrated that Fgf signaling is crucial for the recruitment of SHF cells to the arterial pole of the heart (Illan et al., 2006; Park et al., 2006). Consistent with the suggested role for fgf8 in arterial pole formation, the zebrafish fgf8 mutation acerebellar (ace) is known to diminish the size of the ventricle (Reifers et al., 2000). Furthermore, inhibition of Fgf signaling between 24 and 48 hpf reduces the number of ventricular cardiomyocytes in the zebrafish heart, but the cellular mechanism responsible for this deficiency has not yet been elucidated (Marques et al., 2008). To address whether Fgf signaling is activated at the arterial pole, we analyzed sprouty4 (spry4) expression at stages between 24 and 48 hpf, because Sprouty proteins are Fgf antagonists that are induced by Fgf signaling (Furthauer et al., 2001; Hacohen et al., 1998). At 24 hpf, we observed very strong spry4 expression at the midbrain-hindbrain boundary and much weaker expression near the arterial pole of the linear heart tube (Fig. 6A,B). At 36 hpf, spry4 expression was observed in the heart tube and at the position where the arterial pole connects to the head mesoderm (Fig. 6C). Speculating that Fgf8 might regulate the addition of cells to the arterial pole of the zebrafish heart tube, we injected the eGFP/DsRed double transgenic embryos with an antisense MO targeting fgf8 and...
reproducing the ace/fgf8 mutant phenotypes (see Fig. S10 in the supplementary material) (Draper et al., 2001). In agreement with the reported role of Fgf signaling in cardiomyocyte specification, the hearts of fgf8 MO-injected embryos were much smaller than those of wild type, and we found that the total number of myocardial cells was significantly decreased (control, 305±23, n=3; fgf8 MO, 196±6, n=4; P<0.05; Fig. 6E-G,N). In addition, a significant reduction in the number of eGFPposDsRedneg cells at the arterial pole was observed (control, 29±1, n=3; fgf8 MO, 17±4, n=4; P<0.05), while the number of eGFPposDsRedneg cells at the venous pole did not change significantly (control, 32±4, n=3; fgf8 MO, 26±2, n=4; Fig. 6N,O; see also Table S3 in the supplementary material).

Next, we used the Fgfr inhibitor SU5402 to address the temporal requirement for Fgf signaling during the addition of cells to the arterial pole. SU5402 efficiently blocked Fgf signaling (Fig. 6C,D). Double eGFP/DsRed transgenic embryos were treated from 24 hpf until 48 hpf with SU5402, and eGFPposDsRedpos and eGFPposDsRedneg cells were quantified. In SU5402-treated embryos, the number of eGFPposDsRedpos cells was unchanged, indicating normal cardiomyocyte specification (Fig. 6H-J,N; see also Table S3 in the supplementary material). Furthermore, the number of eGFPposDsRedneg cells at the venous pole of the SU5402-treated embryos was equal to the number of eGFPposDsRedneg cells in DMSO-treated embryos (DMSO, 30±1, n=3; SU5402, 31±3, n=5; Fig. 6O). By contrast, the number of eGFPposDsRedneg cells at the arterial pole of SU5402-treated embryos was significantly reduced (DMSO, 30±4, n=3; SU5402, 6±2, n=5; P<0.01; Fig. 6K-M,O). Together, these results demonstrate that Fgf signaling between 24 and 48 hpf is required for the addition of new cardiomyocytes to the arterial pole of the zebrafish heart.

**DISCUSSION**

By using live imaging in the zebrafish model, we have been able to visualize the dynamics of cardiomyocyte differentiation in a vertebrate embryo, revealing distinct phases of cardiomyocyte differentiation. Both the GFP/DsRed developmental timing assay and the Kaede photoconversion experiments demonstrated that the cardiomyocytes of the future ventricle are the first to differentiate. New cardiomyocytes are added to the heart by two distinct phases of cardiomyocyte differentiation. First, a cardiomyocyte differentiation program starting in the ventricle and progressing along the atrium allows the continuous addition of new cardiomyocytes to the venous pole of the heart tube. At the arterial pole, a second phase of cardiomyocyte differentiation that is temporally distinct from the initiation of atrial differentiation was observed. This population of cells forming from the second phase of differentiation will contribute to the outflow tract. In addition to this separation in time and space (venous versus arterial pole, respectively), we also demonstrated differences in the regulation of the two phases of cardiomyocyte differentiation.

**Cardiomyocyte differentiation at the venous pole**

By using two different assays, developmental timing and Kaede photoconversion, we demonstrated that cardiomyocyte differentiation is initiated in the ventricle. Subsequently, atrial cells are added at the venous pole by a continuation of cardiomyocyte differentiation. These results are in agreement with the previous findings in both chick and zebrafish that the induction of atrium-specific myosin gene expression occurs after the induction of ventricle-specific myosin expression (Berdougo et al., 2003; Yutzey et al., 1994). Our Kaede photoconversion experiments demonstrate that the differentiation at the venous pole is completed by 34 hpf at the latest. Finally, our results demonstrate that Isl1 is required to complete the cardiomyocyte differentiation process at the venous pole. Interestingly, we observed bradycardia and frequent pauses in cardiac contraction in the zebrafish isl1 mutant embryos. This was not reported for the mouse isl1 mutants, which could have been because of the severe heart failure observed in these embryos (Cai et al., 2003). Earlier experiments in chick demonstrated that intrinsic heart beat frequency increases over the anteroposterior axis and that a single pacemaker area becomes established at the venous pole (Moorman et al., 1998). Problems in pacemaker activity result in a so-called sick sinus syndrome, which is characterized by arrhythmias, such as sinus bradycardia and sinus pauses, or arrests...
Therefore, the reduced heart frequency and the pauses in contraction that we observed in isl1 mutant embryos could be explained by a failure of cardiomyocyte differentiation at the venous pole. Indeed, we observed a specific loss of bmp4 expression and a significant reduction in the number of eGFPposDsRedneg cells at the venous pole, which demonstrated reduced cardiomyocyte differentiation at the venous pole. One explanation for this residual cardiomyocyte differentiation observed in isl1 mutant embryos could be that Isl1 is redundant with other Islet factors, which, from the arguments described above, we do not believe to be likely. An alternative and more likely explanation would be that these differences reflect evolutionary differences between teleosts and amniotes, differences that are responsible for the recruitment of the extra cardiomyocytes required to form additional chambers (see also below).

**Cardiomyocyte differentiation at the arterial pole**

The Kaede photoconversion experiments demonstrate that there is discontinuity between the initial phase of differentiation, which gives rise to cardiomyocytes that form the ventricle and atrium, and the later addition of cells to the arterial pole. At 19-26 hpf, when cardiomyocytes are still added to the venous pole, addition of new cardiomyocytes to the arterial pole was hardly observed. Addition of new cardiomyocytes at the arterial pole was apparent only at later stages of cardiac development (34-48 hpf). Interestingly, BrdU labeling in chick has revealed a population of labeled cardiomyocytes at the venous pole at stage 10, when no such cells...
were evident at the arterial pole (Soufan et al., 2006). It was suggested that these venous pole cells had incorporated BrdU in the splanchnic mesoderm before being added to the venous pole. Together with the observation that cells are not added to the arterial pole until after stage 12 (de la Cruz et al., 1977; Mjaatvedt et al., 2001), this would suggest that cardiomyocyte differentiation at the venous pole is occurring much earlier than differentiation at the arterial pole in chick embryos. However, the visualization of cardiomyocyte differentiation in mouse or chick embryos would be required to allow a direct comparison of the dynamics.

Our data demonstrate that cardiomyocyte differentiation at the arterial pole is independent of Isl1 but requires Fgf8 signaling. The small ventricle previously observed in ace/fgf8 mutant fish and the small ventricle generated by blocking Fgf signaling at the linear heart tube stage (Marques et al., 2008; Reifers et al., 2000) can now be explained by diminished cardiomyocyte differentiation at the arterial pole. The differences that we observe after fgf8-MO injection or SU5402 treatment can be explained by a difference in timing when Fgf signaling is blocked by these different treatments (Marques et al., 2008). In the case in which Fgf8 signaling is inhibited by the MO injection, Fgf8 signaling is inhibited already at very early stages during cardiomyocyte specification, which provides an explanation for the reduction in the number of eGFPposDsRedpos cells we observed. In the case of SU5402 treatment, we added the inhibitor only at the tube stage (24 hpf), and therefore this treatment affects only later cardiomyocyte addition. Whether these two phases of Fgf requirement during cardiomyocyte differentiation also exist in other vertebrates has been difficult to address owing to the early lethality of mouse mutants with reduced Fgf signaling during gastrulation (Dono et al., 1998; Feldman et al., 1995; Meyers et al., 1998). However, by using different conditional Fgf8 mutant alleles, Park et al. showed that the early loss of Fgf8 affects both ventricle and atrium formation, whereas the late and specific deletion of Fgf8 in the anterior heart field specifically affects the OFT (Park et al., 2006).

Surprisingly, cardiomyocyte differentiation in zebrafish at the arterial pole does not require Isl1 (also discussed above). This demonstrates that not only is the temporal regulation of cardiomyocyte differentiation at both poles different, but also the mechanism and signals involved in regulating cardiomyocyte differentiation are different at each pole of the zebrafish heart.

Evolutionary adaptation

Our observation that cardiomyocyte differentiation at the arterial pole is temporally separated from and regulated differently to the continuous wave of differentiation in the rest of the heart tube may also help to explain the different phenotypes (broad heart defects versus OFT defects) observed in several mouse mutants. Mice deficient for Isl1 display broad cardiac defects that affect the formation of ventricles as well as atria (Cai et al., 2003). We now suggest that the role for Isl1, which is required to complete the continuous differentiation process in zebrafish, has been expanded in amniotes to increase the relative size of the heart. Interestingly, during growth of the heart tube in amniotes, both the venous and the arterial pole remain connected to the dorsal mesocardium, where Isl1 is expressed. In zebrafish, however, the Isl1-positive cells located laterally in the cardiac field are physically separated from the future ventricle cells that are located medially in the cardiac field.

Taken together, our results demonstrate that two distinct phases of cardiomyocyte differentiation contribute to the observed growth of the embryonic heart. This is the first time that the temporal regulation of cardiomyocyte differentiation has been visualized in any vertebrate organism. We believe that this new concept of two separate phases of cardiomyocyte differentiation that require different molecular mechanisms for their completion provides new insight into how the vertebrate heart grows and could have expanded during vertebrate evolution.

We thank Dr Cuppen (Hubrecht Laboratory) and Dr Stemple (Welcome Trust Sanger Institute) for providing the isl1k88x zebrafish mutant, which was generated as part of the ZF-MODELS Integrated Project in the 6th Framework Programme (Contract No. LSHG-CT-2003-503496) funded by the European Commission. We also thank R. Kelly for discussions and suggestions when this work was in progress, K. Poss for providing the Tg(cmlc2:dset2-nuc) Hsh, A. Moorman and K. Smith for critical reading of the manuscript and members of the Bakker laboratory for stimulating discussions. Work in J.B.’s laboratory was supported by the Royal Dutch Academy of Arts and Sciences. Work in D.Y.’s laboratory was supported by the National Institutes of Health. E.d.P. was supported by EU FP6 grant LSHM-CT-2005-018833, EUGeneHeart. S.M. was supported by the GABBA program and the Portuguese Foundation for Science and Technology (POCI 2010-033). Deposited in PMC for release after 12 months.

Supplementary material

Supplementary material for this article is available at http://dev.biologists.org/cgi/content/full/136/10/1633/DC1

References


Sec. 4.1: Phases of cardiomyocyte differentiation


Table S1. Cardiomyocyte number at various stages

<table>
<thead>
<tr>
<th>Stage</th>
<th>Cardiomyocytes*</th>
<th>n</th>
</tr>
</thead>
<tbody>
<tr>
<td>24 hpf</td>
<td>150.6±11.5</td>
<td>5</td>
</tr>
<tr>
<td>36 hpf</td>
<td>213.2±11.7</td>
<td>5</td>
</tr>
<tr>
<td>48 hpf</td>
<td>310.6±9.7</td>
<td>5</td>
</tr>
</tbody>
</table>

*As determined by α-DsRed antibody staining in Tg(cmlc2:DsRed) embryos. Values are mean±s.e.m.

Table S2. Heartbeats per minute

<table>
<thead>
<tr>
<th>Stage</th>
<th>24 hpf</th>
<th>48 hpf</th>
<th>72 hpf</th>
<th>n</th>
</tr>
</thead>
<tbody>
<tr>
<td>isl1K88X siblings</td>
<td>80±1.3</td>
<td>135.5±1.8</td>
<td>163±4.4</td>
<td>5</td>
</tr>
<tr>
<td>isl1K88X mutants</td>
<td>80±1.3</td>
<td>94.6±3.2*</td>
<td>57.5±2.9*</td>
<td>10</td>
</tr>
</tbody>
</table>

*P<0.01. Values are mean±s.e.m.

Table S3. Cell count of GFPpos/DsRedpos and GFPpos/DsRedneg myocardial cells

<table>
<thead>
<tr>
<th>Treatment</th>
<th>GFPpos/DsRedpos</th>
<th>Arterial pole</th>
<th>Venous pole</th>
<th>Total</th>
<th>n</th>
</tr>
</thead>
<tbody>
<tr>
<td>isl1K88X siblings</td>
<td>199.7±6.2</td>
<td>28.4±1.5</td>
<td>24.9±3.1</td>
<td>253±9.2</td>
<td>7</td>
</tr>
<tr>
<td>isl1K88X mutants</td>
<td>203.3±7.1</td>
<td>32±2.1</td>
<td>10.1±2.6**</td>
<td>245.4±7.2</td>
<td>7</td>
</tr>
<tr>
<td>Uninjected control†</td>
<td>249.8±12.6</td>
<td>23.5±3.3</td>
<td>26.5±1.8</td>
<td>299.8±9.1</td>
<td>4</td>
</tr>
<tr>
<td>isl1 MO</td>
<td>214±13.4*</td>
<td>20.2±2.2</td>
<td>8.2±2.2**</td>
<td>242.4±14.0**</td>
<td>5</td>
</tr>
<tr>
<td>Control MO‡</td>
<td>170±4.6</td>
<td>16.3±2.0</td>
<td>22±2.0</td>
<td>208.3±6.6</td>
<td>4</td>
</tr>
<tr>
<td>sih MO</td>
<td>173±7.0</td>
<td>17.7±5.8</td>
<td>26.3±2.8</td>
<td>217±15.6</td>
<td>3</td>
</tr>
<tr>
<td>Uninjected control¶</td>
<td>243.7±28.6</td>
<td>28.7±1.3</td>
<td>32.3±4.1</td>
<td>304.7±22.6</td>
<td>3</td>
</tr>
<tr>
<td>fgf8 MO</td>
<td>153±5.5*</td>
<td>16.8±3.8*</td>
<td>25.8±2.3</td>
<td>195.5±5.9*</td>
<td>4</td>
</tr>
<tr>
<td>DMSO§</td>
<td>247±9.1</td>
<td>29.7±4.3</td>
<td>29.7±0.7</td>
<td>306.3±5.0</td>
<td>3</td>
</tr>
<tr>
<td>SUS402</td>
<td>246±10.8</td>
<td>6.2±2.0**</td>
<td>31±2.6</td>
<td>283.6±13.4</td>
<td>5</td>
</tr>
</tbody>
</table>

*Significant difference with control P<0.05.
**Significant difference with control P<0.01.
†Control for Isl1 MO experiment.
‡Control for sih MO experiment.
¶Control for fgf8 MO experiment.
§Control for DMSO experiment.
Control for SUS402 experiment.