HCN4 Dynamically Marks the First Heart Field and Conduction System Precursors

Xingqun Liang,* Gang Wang,* Lizhu Lin, Jennifer Lowe, Qingquan Zhang, Lei Bu, Yihan Chen, Ju Chen, Yunfu Sun, Sylvia M. Evans

Rationale: To date, there has been no specific marker of the first heart field to facilitate understanding of contributions of the first heart field to cardiac lineages. Cardiac arrhythmia is a leading cause of death, often resulting from abnormalities in the cardiac conduction system (CCS). Understanding origins and identifying markers of CCS lineages are essential steps toward modeling diseases of the CCS and for development of biological pacemakers.

Objective: To investigate HCN4 as a marker for the first heart field and for precursors of distinct components of the CCS, and to gain insight into contributions of first and second heart lineages to the CCS.

Methods and Results: HCN4CreERT2, -nuclear LacZ, and -H2BGFP mouse lines were generated. HCN4 expression was examined by means of immunostaining with HCN4 antibody and reporter gene expression. Lineage studies were performed using HCN4CreERT2, Isl1Cre, Nkx2.5Cre, and Tbx18Cre, coupled to immunostaining with CCS markers. Results demonstrated that, at cardiac crescent stages, HCN4 marks the first heart field, with HCN4CreERT2 allowing assessment of cell fates adopted by first heart field myocytes. Throughout embryonic development, HCN4 expression marked distinct CCS precursors at distinct stages, marking the entire CCS by late fetal stages. We also noted expression of HCN4 in distinct subsets of endothelium at specific developmental stages.

Conclusions: This study provides insight into contributions of first and second heart lineages to the CCS and highlights the potential use of HCN4 in conjunction with other markers for optimization of protocols for generation and isolation of specific conduction system precursors. (Circ Res. 2013;113:399-407.)

Key Words: arrhythmias, cardiac ■ cardiac biomarkers ■ cardiac conduction system ■ cardiac development ■ cardiac lineage ■ HCN4 ■ heart field ■ transgenic model

Cardiac arrhythmias are a leading cause of death and are often a result of abnormalities in the specialized cardiac conduction system (CCS). Understanding origins of CCS lineages and identifying markers that can be used for their isolation from human embryonic stem cells or induced pluripotent stem cells are essential steps toward modeling diseases of the CCS, to study drug responses of specific CCS lineages, or to develop biological pacemakers.

The CCS consists of sinoatrial node (SAN), atrioventricular node (AVN), and peripheral components of the fast conducting His-Purkinje fibers. CCS formation is a complex process that involves multiple cell types. During mouse development, the first heartbeat is recorded in the inflow tract as early as E8.01,2 and, later, the sinus venosus of the forming heart tube functions as a primitive pacemaker region. The first morphologically discernable SAN is formed at E11.5, which becomes further mature and fully functional at E13.5,3,4 A subset of atrioventricular canal tissue gives rise to atrioventricular conduction system.5 Early retroviral labeling studies demonstrated that CCS and working myocyte lineages shared a common progenitor,6,7 and that the Purkinje fibers are derived from differentiated ventricular cardiomyocytes.8-11 However, questions remain as to lineage origins and the dynamic formation of each component of the CCS during development.

In the past decade, a new paradigm for heart development has emerged from lineage studies, which demonstrated distinct populations giving rise to the heart, the first and the second heart lineages, based on dye labeling studies in chick and...
retrospective clonal analysis in mouse embryos.\textsuperscript{12–14} These lineages are thought to diverge around the onset of gastrulation.\textsuperscript{15}

The first lineage gives rise to the first heart field, which is defined as the first cells to differentiate in the cardiac crescent.\textsuperscript{12,16} Thus, the first heart field comprises differentiated myocytes that are precursors of distinct myocyte populations within the developing heart. Myocytes of the first heart field give rise to the early heart tube and later give rise to most myocytes of the left ventricle and a subset of myocytes within both atria.

The second lineage gives rise to the second heart field that, in contrast to the first heart field, comprises undifferentiated progenitors. At cardiac crescent stages, second heart field progenitors are localized medial and posterior to the first heart field. Growth of the heart after early heart tube stages occurs by successive addition of differentiating second heart field cells to both poles of the heart. The second heart field will give rise to the right ventricle, outflow tract, and a majority of cells within the left and right atria. Studies of the second heart field have been greatly facilitated by discovery of the transcription factor Is1 as a marker for progenitors of the second heart field.\textsuperscript{17} In contrast, studies of the first heart field have been constrained by lack of a comparable marker.

It has been shown that a posteriormost subset of the second heart field, the posterior heart field, marked by Tbx18Cre contributes to SAN formation.\textsuperscript{18,19} However, contributions of first or second heart fields to each component of the developing CCS have not yet been addressed.

The hyperpolarization-activated nucleotide-gated cation channel HCN4 is a pacemaker channel that is highly expressed in the SAN during development and in the adult.\textsuperscript{20–22} In study–channel HCN4 is a pacemaker channel that is highly expressed in the SAN during development and in the adult.\textsuperscript{20–22} In study or second heart fields to each component of the developing CCS have not yet been addressed.

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RNA in situ analyses and expression of the HCN4nLacZ reporter (Figure 1A). Wholemount Xgal staining and coinmunostaining at E7.5 with antibody to Isl1, a marker of the second heart field, revealed that HCN4nLacZ expression was adjacent and lateral to Isl1-expressing second heart field cells (Figure 1D, arrowhead), suggesting that earliest HCN4 expression marks the first heart field.

At E10.5 to E12.5, HCN4lacZ was highly expressed in some components of the CCS, including SAN, AVN, and left bundle branches; Figure 1E, 1E′, 1G, and 1G′. Interestingly, expression of HCN4lacZ at these stages was also prominent in left ventricular myocardium and atria, with some expression in a small subset of right ventricular myocardium (Figure 1H, inset). Consistent with expression in the CCS, a portion of HCN4H2BGFP cells express pecam (Figure 2D, inset). A few HCN4H2BGFP cells were also observed in right ventricular trabeculae around the ventricular septum (vs). Few if any HCN4H2BGFP cells were observed in the free wall of the right ventricle (Figure 2A, inset 1).

By E9.5, few if any HCN4H2BGFP cells in the heart express endothelium/endocardial marker pecam (Figure 2C, inset). Majority of HCN4H2BGFP cells in the left ventricle coexpress mf20 (Figure 2G, inset) or but not pecam (Figure 2H, inset). HCN4CreERT2 lineage–labeled cells (tdTomato) coexpressed mf20 (G, inset), consistent with HCN4 expression in some endothelial populations.

HCN4 Is Expressed in Cardiomyocytes and in Some Endothelial Populations

Expression of HCN4H2BGFP during development was consistent with that of HCN4lacZ (Online Figure II). To
examine the cell identity of HCN4-expressing cells within the heart, we performed immunostaining with antibodies to cardiomyocytes (MF20, Troponin T, and Nkx2.5) and endothelial cells (PECAM) and colocalized these markers with HCN4H2BGFP at E9.5 to E12.5 (Figure 2A–2F and not shown). At E9.5, HCN4H2BGFP cells were observed prominently in the left ventricle and atria, with a few GFP cells in right ventricular trabeculae, but not right ventricular wall (Figure 2A, inset 1 and 2). These HCN4H2BGFP cells coexpressed cardiomyocyte markers MF20 (Figure 2A, inset 2), Nkx2.5, and Troponin T (not shown). However, expression of HCN4H2BGFP at this stage did not colocalize with the endothelial marker PECAM (Figure 2B, inset). At E12.5, HCN4H2BGFP was expressed in endothelial cells of the aorta and pulmonary artery, coexpressed with PECAM (Figure 2D, inset), but not with MF20 (Figure 2C, inset). The majority of HCN4H2BGFP cells in left ventricle at E12.5 coexpressed MF20 (Figure 2E, inset), and a subset of HCN4H2BGFP cells also expressed PECAM (Figure 2F, inset).

To examine the fate of HCN4-expressing cells, we generated an HCN4 tamoxifen-inducible Cre by knocking CreERT2 into the endogenous HCN4 locus (Online Figure I). To examine whether the earliest HCN4 lineages contributed to myocardium and endothelium/endocardium, HCN4CreERT2 mice were crossed with Rosa-tELoTomato indicator mice.25 Pregnant females were fed with tamoxifen at E7.5, and hearts were analyzed at E12.5 by direct visualization of tdTomato and coimmunostained with MF20 or PECAM antibodies. HCN4CreERT2 lineage-labeled cells (red) were observed in the left ventricle, which coexpressed MF20 (Figure 2G, inset), but not PECAM (Figure 2H, inset).

Together, these studies suggested that earliest HCN4 lineages do not contribute to endocardium, and that HCN4 is de novo expressed in endothelial/endocardial cells at later developmental stages. At later stages of development (E16.5) and adult, we also observed expression of HCN4nLacZ in a subset of endothelial cells of the aorta, pulmonary artery, and coronary arteries, but not in superior vena cava (Online Figure III, data not shown).

Contribution of HCN4 Lineages to First Heart Lineages and the CCS During Development Revealed by HCN4CreERT2 Fate Mapping

To examine further the fate of HCN4-expressing cells during development, HCN4CreERT2 mice were bred into an R26RLacZ reporter background.24 Tamoxifen inductions were performed at distinct stages of embryonic development, harvesting at E16.5 when the CCS is well defined29,30 (Figure 3).

To analyze the fate of HCN4-expressing myocytes of the first heart field, HCN4CreERT2;R26RLacZ mice were fed with tamoxifen at distinct developmental stages as indicated, hearts were harvested at E16.5 and stained with Xgal. A–F, Ventral and dorsal view; (A–F) serial section; A and A', A few HCN4 lineage-labeled cells (Xgal+) were found in coronary sinus (cs) and atrioventricular region (arrow) when tamoxifen induction was performed at E6.5. B and B', Inductions at E7.5 resulted in labeling of cells in left ventricle and trabeculae/Purkinje fibers (pf), left bundle branch (lbb), both atria, coronary sinus (cs), venous valves (vv), and a small number of cells in atrioventricular node (avn). A few labeled cells were also observed in the Crista terminalis (Ct), and distal tail of san. C and C', Inductions at E8.5 resulted in a similar labeling pattern to that observed at E7.5, except that labeling of cells in san, avn, and His-bundle was markedly increased. D–F, Inductions at E9.5 (D and D'), E11.5 (E and E'), and E12.5 (F and F') resulted in selective labeling of cells in san, avn, and coronary sinus. At E9.5, there was some labeling of Purkinje fibers and ventricular and atrial myocytes, which disappeared with later inductions. No significant labeling was observed in His-bundle or bundle branches with inductions at these stages.
with tamoxifen at E6.5 and E7.5. When harvested at E16.5, a few Xgal-labeled cells were observed in the coronary sinus after inductions at E6.5 (Figure 3A and 3A'). Inductions at E7.5 (Figure 3B and 3B') resulted in selective labeling of cells within the coronary sinus, SAN tail, venous valves, left bundle branch, Purkinje fibers, left ventricle, ventricular septum, and both atria. Infrequent labeling was also observed of Purkinje fibers within right ventricle, consistent with low levels of HCN4nLacZ/H2BGFP observed at E10.5 and E12.5 within the right ventricular trabeculae. Inductions at E8.5 (Figure 3C and 3C') labeled the foregoing populations and, in addition, the SAN head, AVN, His-bundle, and atrial septum. Inductions at E9.5 (Figure 3D and 3D') resulted in labeling of more restricted cell populations than at E8.5, with reduced labeling of Purkinje fibers, left ventricle, and atria, and strong labeling of the SAN, AVN, atrial septum, left superior vena cava, and the coronary sinus. Inductions at E11.5 to E12.5 resulted in labeling of SAN, AVN, left superior vena cava, and the coronary sinus, with few or no cells labeled in left ventricle (Figure 3E, 3E', 3F, and 3F').

**Contribution of HCN4 Lineages to Components of the Forming CCS**

To confirm that HCN4CreERT2 lineages were giving rise to cells of the CCS, inductions were also performed in an HCN4CreERT2;Rosa mT/mG indicator background to facilitate communostaining with markers of the CCS. HCN4 was used to label SAN, AVN, and His-bundle, and Cx40 was used to label bundle branches and Purkinje fibers (Figure 4).

Inductions were performed at multiple stages, harvesting at E16.5, as previously, and gave results consistent with those with the R26RLacZ reporter.

Tamoxifen induction at E7.5 resulted in labeling of cells (mGFP) in a subset of cells in SAN, venous valves, and AVN as seen by colocalization with endogenous HCN4 (Figure 4A–4B'). HCN4CreERT2 lineage–labeled cells were also found in left bundle branch and Purkinje fibers as seen by colocalization with Cx40 (Figure 4C–4D'). A subset of myocytes in atria (Figure 4A) and left ventricle (Figure 4D) that do not actively express HCN4 at E16.5 were also labeled.

Induction at E9.5 resulted in increased labeling of cells in SAN and AVN as marked by HCN4 (Figure 4E–4F'), and labeling of left bundle branch and Purkinje fibers marked by Cx40 (Figure 4G–4H'). Similar to inductions at E7.5, no HCN4CreERT2 lineage–labeled cells were found in right bundle branch and His-bundle (Figure 4F, not shown).

Inductions at E12.5 resulted in labeling of cells in SAN, AVN, venous valves, and a few cells in His-bundle (Figure 4I–4J'), but no labeled cells were observed in left bundle branch or Purkinje fibers (Figure 4K–4L'). However, inductions performed at E16.5, harvesting at postnatal day

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**Figure 4.** HCN4CreERT2;Rosa mR/mG fate mapping and communostaining with markers of CCS during heart development. Tamoxifen was given to HCN4CreERT2;Rosa mT/mG pregnant females at distinct developmental stages as indicated. Hearts were harvested at stages indicated, and sections coimmunostained with antibody to HCN4 as a marker for sinoatrial node (san), atrioventricular node (avn), and His-bundle (hb); and Cx40 as marker for His-bundle and Purkinje fibers (pf). **A,** HCN4; **B,** Cre; **C,** Cx40; **D,** HCN4CreERT2;Rosa mT/mG indicator background. **A′–D′,** no cells labeled in left ventricle. **E,** HCN4; **F,** Cre; **G,** Cx40; **H,** HCN4CreERT2;Rosa mT/mG indicator background. **E′–H′,** strong labeling of the SAN, AVN, and His-bundle, as marked by HCN4 (E′ and E′), and Purkinje fibers as seen by colocalization with Cx40 (G′ and H′). **I,** HCN4; **J,** Cre; **K,** Cx40; **L,** HCN4CreERT2;Rosa mT/mG indicator background. **I′–L′,** no labeled cells were observed in left bundle branch or Purkinje fibers (L′), as seen by colocalization with Cx40 (K′ and L′). **M,** HCN4; **N,** Cre; **O,** Cx40; **P,** HCN4CreERT2;Rosa mT/mG indicator background. **M′–P′,** strong labeling of the SAN, AVN, and His-bundle, as marked by HCN4 (M′–N′), left bundle branch (N′–O′), and Purkinje fibers as marked by Cx40 (P′ and P′).
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Figure 5. Nkx2.5Cre, Isl1Cre, and Tbx18Cre fate mapping to investigate lineage origins of the CCS. Lineage tracing experiments were performed at E16.5 using Cre and Rosa-mT/mG mouse lines, including Nkx2.5Cre, Isl1Cre, and Tbx18Cre. Commonstaining was performed with antibodies to Tbx3 (A′–4′) to mark sinoatrial node (san), atrioventricular node (avn), and His-bundle (hb); and Cx40 (J′–M′) to mark bundle branches (bb) and Purkinje fibers (pf). A–C, A majority of san cells (marked by Tbx3) were derived from Isl1Cre (B) and Tbx18Cre (C) lineages (mGFP), whereas only a small subset of peripheral san cells directly adjacent to atrial myocardium was labeled by Nkx2.5Cre (mGFP; A). D–F, A majority of avn cells (marked by Tbx3) were derived from Nkx2.5Cre (D) lineage (mGFP), whereas only a small subset of avn cells was labeled by Isl1Cre (E), but no significant contribution of Tbx18Cre to avn was observed (F). G–I, Contribution of Nkx2.5Cre (G), Isl1Cre (H), and Tbx18Cre (I) to His-bundle. J–K, Contribution of Nkx2.5Cre (J) and Isl1Cre (K) to left bundle branch (lbb; arrow) and Purkinje fibers (arrowhead) of left ventricle. L–M, Right bundle branch (rbb) and Purkinje fibers were derived from Isl1Cre (M) and Nkx2.5Cre (L) lineages. Tbx18Cre lineages did not contribute to His-bundle, bundle branches, or Purkinje fibers (data not shown). N, Model for lineage derivation and timing of differentiation of CCS precursors in developing heart: the earliest HCN4 expression marks first heart field, contributing to left bundle branches, Purkinje fibers, and a small subset of right Purkinje fibers (N, blue), and slightly later His-bundle, avn, and a small subset of san tail (N, purple and pink). In contrast, a majority of the san and right Purkinje fibers were derived from Isl1 second heart field lineages (N, pink and orange).

1 (P1; Figure 4M–4P′), resulted in labeling of all components of the CCS, including those not labeled by inductions at E12.5, the His-bundle, bundle branch, and Purkinje fibers (Figure 4N–4P′), demonstrating re-expression or de novo expression of HCN4 in distinct components of the CCS at later stages.

Contribution of the First and Second Heart Fields to Components of the CCS

These data suggested that the earliest expression of HCN4 in the cardiac crescent and early heart tube labeled the first heart field because HCN4 lineages were largely excluded from second heart field–derived outflow tract and right ventricle. To investigate further the contribution of first and second heart lineages to the CCS, we performed lineage tracing experiments using several Cre mouse lines. Nkx2.5Cre labels the first and second heart fields, Isl1Cre labels the second heart field,17 and Tbx18Cre labels a posteriori most subset of the second heart field, which will contribute to the SAN.18,19,32 Each of these Cre was bred into the Rosa-mT/mG indicator background,26 and commonstaining were performed at E16.5 using Tbx3 to label SAN, AVN, and His-bundle (Figure 5A′–5I′), and Cx40 to label bundle branches and Purkinje fibers (Figure 5J′–5M′).

A majority of cells in AVN, His-bundle, left bundle branch, and Purkinje fibers were labeled by Nkx2.5Cre (Figure 5D, 5G, 5J, and 5L), whereas only a small subset of Nkx2.5Cre-labeled cells were found at the boundary of the SAN and right atria (Figure 5A′). In contrast, a majority of SAN cells were found to be Isl1Cre and Tbx18Cre labeled (Figure 5B and 5C), whereas only a small subset of AVN cells was labeled by Isl1Cre, but no significant contribution of Tbx18Cre to AVN was observed (Figure 5E, 5H, 5K, and 5M). A majority of cells in right bundle branches, and a substantial number of Purkinje fibers in the right ventricle were also labeled by Isl1Cre (Figure 5K and 5M).

Quantitative assessment of the contribution of each lineage to distinct components of the CCS was performed (Table). Results of these analyses were consistent with lineage data generated by early inductions (E6.5–E8.5) of HCN4CreERT2 (Figure 3A–3C). Consistent with their derivation from the first heart field, a majority of cells within the AVN (98±1.1%), His-bundle (91.4±3.5%), left bundle branch (89.8±2.5%), and Purkinje fibers were selectively labeled by Nkx2.5Cre (Table; Figure 5D, 5G, 5J, and 5L), but not Isl1Cre (Figure 5E, 5H, 5K, and 5M).

Nkx2.5Cre lineages contributed to a small subset of cells within the SAN tail (9.4±3.2%; Figure 5A), consistent with...
Table. Lineage Contribution of the First and Second Heart Fields to Components of the Cardiac Conduction System

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<th>Is1Cre, %</th>
<th>Nkx2.5Cre, %</th>
<th>Tbx18Cre, %</th>
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<tr>
<td>SAN head</td>
<td>99.3±1.4</td>
<td>11.3±1.4</td>
<td>89.4±3.5</td>
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<tr>
<td>SAN tail</td>
<td>99.3±1.4</td>
<td>17.6±3.2</td>
<td>54.3±5.3</td>
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<tr>
<td>AVN</td>
<td>9.4±3.2</td>
<td>98±1.1</td>
<td>NS</td>
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<tr>
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<td>NS</td>
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<td>89.8±2.5</td>
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<td>92±1.8</td>
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<td>RPF</td>
<td>59±1.9</td>
<td>88±2.2</td>
<td>NS</td>
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Percentages of Cre-lineage labeled cells at E16.5 in the SAN, AVN, and HB were expressed as total Cre-lineage positive cells (mGFP) per area (≥10 sections per heart with significant labeling, 3–5 hearts) among total HCN4-expressing cells in the same areas. Percentages of Cre-lineage labeled cells in the LBB, RBB, LPF, and RPF were expressed as total Cre-lineage positive cells (mGFP) per area (≥10 sections per sample, 3–5 samples) among total Cx40-expressing cells in the same areas. AVN indicates atrioventricular node; HB, His-bundle; LBB, left bundle branch; NS, not significant; RBB, right bundle branch; and SAN, sinoatrial node.

Altogether, our data suggest a model for lineage derivation and timing of differentiation of CCS precursors in developing heart, as summarized in Figure 5N. Precursors to left Purkinje fibers, left bundle branch, and a subset of right Purkinje fibers were among first heart field myocytes marked by HCN4CreERT2 inductions at E7.5 (cardiac crescent; blue). The foregoing CCS lineages and precursors to the His-bundle and AVN were marked by slightly later inductions of HCN4CreERT2 at E8.5 (Figure 3C), suggesting that, in addition to marking the first heart lineage selectively at earliest stages, by E8.5 HCN4 is also expressed in the posterior second heart field, overlapping with Isl1 in SAN precursors.

A majority of cells in the right bundle branch (90.5±3.8%) was labeled by Is1Cre (Table; Figure 5M), but was not labeled by HCN4CreERT2 at early stages (Figure 3), confirming derivation from the second heart field. Purkinje fibers within the right ventricle arise both from second heart field and first heart field, as indicated by labeling of a subset of these cells by Is1Cre (59±1.9%) and a subset by Nkx2.5Cre (88±2.2%), respectively (Table; Figure 5L and 5M).

Our data have given new insights into lineage origins of the CCS, and the order in which distinct precursors for each component express HCN4 and are allocated to the CCS (Figure 5N). The earliest HCN4-expressing cells of the first heart field contribute a few cells to the SAN, but later HCN4-expressing cells from the posterior second heart field contribute a majority of cells to the SAN (Figure 5N, pink). HCN4 is expressed very early in precursors of the left and a subset of right Purkinje fibers and left bundle branch (Figure 5N, blue), and slightly later also marks precursors of the His-bundle (Figure 5N, purple), but expression within these cell populations themselves is downregulated by E11.5, with HCN4 expression remaining on only in components of the central CCS, SAN, and AVN. Previous studies using a Tbx2Cre allele, which demonstrated that atrioventricular canal myocardium participates in formation of the AVN, but not of the His-bundle and bundle branches, indicate that AVN and His-bundle do not develop from a common progenitor population, but segregate early in development.3 Our data suggest that left bundle branch precursors differentiate before precursors of the AVN and His-bundle (Figure 5N, blue and purple). The lineage relationship between trabecular myocardium and the Purkinje fiber network has been reaffirmed using an inducible Cx40Cre, which demonstrated that early trabeculae will give rise to both Purkinje fibers and working myocytes,6,33 consistent with our observations of HCN4CreERT2 labeling both lineages. By E16.5 through adult stages, HCN4
is expressed throughout the CCS, suggesting reactivation in most components of the ventricular conduction system, and de novo activation in right bundle branch, which was not significantly marked by earlier inductions of HCN4CreERT2 (Figure 5N, orange and blue).

Our data highlight the use of HCN4 as a marker for precursors of the CCS and emphasize that HCN4 expression marks distinct precursors or components of the CCS at distinct times during development. Our data suggest the use of HCN4 in conjunction with other markers to optimize protocols for the generation of specific conduction system precursors. In this context, it is also important to note that we have also observed HCN4 expression in several endothelial populations at distinct stages of development, including endothelium of the aorta and pulmonary artery, some coronary vessel endothelium, and a subset of endocardial cells (Figure 2; Online Figure III).

The HCN4-knockin mouse lines that we have generated should be of use for future studies on HCN4 lineages. Although we have not observed any baseline electrophysiological phenotypes in mice that are heterozygous for HCN4, in keeping with the published literature, heterozygosity of HCN4 should be kept in mind as a potential complicating factor when using these mice, particularly in the case of ablation of other genes important for conduction system function, in light of potential genetic interactions. In experiments with HCN4CreERT2, our controls included mice both with and without tamoxifen treatment, and we did not observe leaky activity of the Cre. However, this must be kept in mind as a possibility when using these mice.

Conclusion
In summary, these studies have demonstrated that earliest expression of HCN4 specifically marks the first heart field, permitting early inductions of HCN4CreERT2 to shed light on cell fates adopted by the first heart field. Dynamic expression of HCN4, in concert with other lineage specific Cres, has allowed us to examine the temporal recruitment of CCS lineages, and their lineage origins, giving new insight into formation of the CCS. Additionally, our data highlight the potential of HCN4 in concert with other markers in identifying distinct CCS precursor populations, both in mouse embryos and potentially in embryonic stem cells or other pluripotent stem cells.

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Disclosures
None.

References
What Is Known?

- Cardiac arrhythmias, often consequent to abnormalities of cardiac conduction system (CCS), are a leading cause of death.
- Understanding lineage origins of CCS and defining markers to identify and isolate conduction system precursors are of clinical relevance.
- HCN4 is a marker of the developing cardiac pacemaker and is expressed in early differentiating cells of the cardiac crescent.

What New Information Does This Article Contribute?

- Earliest expression of HCN4 marks the first heart field.
- Distinct components of the CCS derive from the first and second heart fields.
- Distinct components of the CCS express HCN4 in a temporally defined sequence, suggesting a model for progressive differentiation of distinct CCS components.

Novelty and Significance

Comprehensive studies that define contributions of first and second heart fields to each component of the CCS have been lacking, hampered in part by lack of a suitable marker for the first heart field. Here, we addressed the contribution of first and second heart fields to each component of the CCS, by using HCN4CreERT2, in conjunction with other Cre lines, which mark the second, or first and second heart fields. Our studies identify first and second heart field contributions to each component of the CCS, and provide a new model for progressive differentiation of distinct CCS components throughout development. These studies have also highlighted the use of HCN4, in conjunction with other markers, as a marker for precursors of each component of the CCS. The findings should greatly facilitate isolation of these cells for both basic and translational research purposes.
HCN4 Dynamically Marks the First Heart Field and Conduction System Precursors
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Supplemental Methods

Animals and tamoxifen induction
To generate HCN4CreERT2 knockin mouse lines,129/SV ES cell genomic DNA was used to
PCR amplify a 4.9-kb 5′ homologous arm containing HCN4 untranslated region of exon 1 and a
5-kb 3′ homologous arm containing exon 1. A short coding sequence in exon 1 including ATG
would be deleted upon homologous recombination. To construct HCN4-CreERT2 knock-in
targeting vector, a Sall DNA cassette containing Cre-ERT2 followed by FRT-floxed neomycin
resistant gene (FRT-mclNeo) was inserted between 5′ and 3′ homologous arms at the Sall site.
An AatII-linearized vector was electroporated into mouse embryonic stem (ES) cells. DNA from
neomycin resistant ES cell clones was digested with EcoRV and screened for recombinant
clones by Southern bot analysis using a 5′ probe. Wild-type allele gave rise to a 14.8 kb band
and targeted allele gave rise to a 9.3 kb band. Two recombinant clones were used for blastocyst
injections and chimeric mice were crossed to C57BL/6J females to generate heterozygous
HCN4CreERT2 knock-in mice (Figure S1A). A similar strategy was used to generate
HCN4H2BGFP and HCN4nLacZ knock-in allele (Figure S1B, C). FRT-mcl-neomycin was
removed by crossing knockin mice with Flpase mice.

For lineage tracing analysis, Cre mice (Isl1Cre, Nkx2.5Cre, Tbx18Cre, HCN4CreERT2) were
crossed with RosaLacZ1, Rosa-tdTomato 2 or Rosa mT/mG3 reporter mice and female mice with
vaginal plugs were considered to be at embryonic day (E) 0.5. Embryos were harvested at
desired time points and fixed in 4% paraformaldehyde and processed for further analyses. To
induce Cre activity of HCN4-CreERT2, pregnant mice were fed 150 µl (≤E11.5) to 250 µl
(≥E12.5) of tamoxifen (10mg/ml, Sigma-Aldrich, St. Louis, MO) by oral gavage. Samples were
harvested at E16.5 or desired time points.

All the experiments involving mice were carried out in accordance with protocols approved by
the Institutional Animal Care and Use Committee of USCD, USA (A3033-01) and by the Animal
Committee of Tongji University School of Medicine, China (TJmed-010-10).

Immunohistochemistry and X-gal staining
Samples were fixed on ice for 1-2 hours in 4% paraformaldehyde (PFA), dehydrated in sucrose
solution series, embedded in OCT and sectioned to 10-µm. For Cre-lineage samples from
Cre;Rosa mt/mG embryos, sections were immunostained with antibodies as listed below and
visualized directly under confocal microscope (Olympus FV1000). The following antibodies were
used: rat anti-HCN4 (Abcam), rabbit anti-Cx40 (Santa Cruz Biotechnology), goat anti-Tbx3
(Santa Cruz Biotechnology), mouse anti-NKX2.5 (Santa Cruz Biotechnology), rat anti-PECAM-1
(BD Pharmingen, cat# 553708), mouse anti-MF-20 (DSHB) and mouse anti-Troponin T
(NeoMarkers, MSZ-295-P). The secondary antibody was Alexa Fluor 488, 594 and 647
conjugated (Invitrogen).

For wholemount immunostaining, samples were fixed in 4% PFA at 4°C overnight, washed and
derehydrated in gradients of methanol (100, 70 and 50%) for 1 hour each. Samples were fixed in
methanol/DMSO (4:1) overnight, then transferred to methanol/DMSO /H2O2 (4:1:1) at room
temperature for 6 hours to block endogenous peroxidase activity. Samples were then
rehydrated in gradients of methanol (100, 70 and 50%) for 1 hour each, and PBS with 0.5%
Triton-100 (PBST), 30 minutes X2, and stained at 4°C with antibody to Isl1 (DSHB) in PBST
with 5% milk (PBSMT) for 48 hours.Samples were washed in PBSMT X 4, 1 hour each, and
stained with secondary antibody in PBSMT for 24 hours at 4°C, then washed in PBST for 1 hour
X 3 at room temperature, incubated in DAB solution (Vector) for 30 minutes, and post-fixed in 4% PFA.

For whole-mount X-gal staining, samples were fixed in 4% paraformaldehyde for 15–60 min, permeabilized (10% Nadeoxycholate, 10% NP40 in PBS), and stained in X-gal solution (50mM K-ferricyanide, 50mM K-ferrocyanide, 200mM MgCl2, 100 mg ml21 X-gal in PBS) for 4–12 h. For section X-gal staining, samples were cryosectioned to 6–8-µ, post-fixed in 4% paraformaldehyde for 6–8 min and stained in X-gal solution.

For quantitative assessment, sections of appropriate developmental stages were cut at 10µm, every fourth to six section was stained and cells positive for lineage marker (mGFP+) within each defined area of the CCS were counted. Relative contribution of each lineage was expressed as a percentage of total number of Tbx3 or Cx40 expressing cells within the same CCS area.

**Statistical Analyses**
Data are presented as mean±SEM and student t-test was used for 2-group comparisons. Differences were considered statistically significant at a value of P<0.05.

**References**

Online Figure I. HCN4 Targeting Constructs

Shown are HCN4 wild-type locus and targeting construct for HCN4CreERT2 (A), HCN4-nuclear (n) LacZ (B) and HCN4H2BGFP (nGFP) (C). Southern blot screening of recombinant ES cell colonies. DNA from neomycin resistant ES cell clones was digested with EcoRV and screened with a 5’ probe. The wild-type allele gave rise to a 14.8 kb band and the targeted allele gave rise to a band of 9.8 kb (CreERT2) (A’), or 10.3 kb (nLacZ) (B’) or 10.5 kb (H2BGFP) (C’).
Online Figure II. Expression of HCN4H2BGFP in the heart during development

A, B) HCN4H2BGFP was expressed in cardiac crescent and heart tube at E7.5 to E8.75, similar to expression of HCN4nLacZ. C) At E9.5, HCN4H2BGFP was highly expressed in the sinus venosus (sv), and at lower levels in common atrium (a) and ventricle (v). D) At E12.5, HCN4H2BGFP was expressed in left ventricle (lv), coronary sinus (cs), some cells within the atria and a small number of cells in right ventricle (rv). Expression was also observed in sinoatrial node (san), atrioventricular node (avn) and left bundle branch (lbb). At E16.5 (E) and adult heart (F), expression of HCN4H2BGFP specifically marked the cardiac conduction system.
(CCS), including SAN, AVN, His bundle (hb), bundle branches (bb) and Purkinje fibers (pf), as well as in venous valves (vv).
Online Figure III. Expression of HCN4nLacZ in subset of cardiac endothelium

At E16.5, HCN4nLacZ was expressed in endothelial cells of proximal ascending aorta (ao) (A, A'), proximal coronary artery (ca) (A, A', B, B', arrow), ventricular side of tricuspid valve (t) (B, arrow head), proximal pulmonary artery (pa) (C, C', arrow). However, HCN4nLacZ was not expressed in endothelial cells of right superior vena cava (rsvc) (D, E, arrowhead), left superior vena cava (lsvc) and coronary sinus (cs) (F, arrowhead).