Molecular Analysis of Patterning of Conduction Tissues in the Developing Human Heart

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Background—Recent studies in experimental animals have revealed some molecular mechanisms underlying the differentiation of the myocardium making up the conduction system. To date, lack of gene expression data for the developing human conduction system has precluded valid extrapolations from experimental studies to the human situation.

Methods and Results—We performed immunohistochemical analyses of the expression of key transcription factors, such as ISL1, TBX3, TBX18, and NKX2–5, ion channel HCN4, and connexins in the human embryonic heart. We supplemented our molecular analyses with 3-dimensional reconstructions of myocardial TBX3 expression. TBX3 is expressed in the developing conduction system and in the right venous valve, atrioventricular ring bundles, and retro-aortic nodal region. TBX3-positive myocardium, with exception of the top of the ventricular septum, is devoid of fast-conducting connexin40 and connexin43 and hence identifies slowly conducting pathways. In the early embryonic heart, we found wide expression of the pacemaker channel HCN4 at the venous pole, including the atrial chambers. HCN4 expression becomes confined during later developmental stages to the components of the conduction system. Patterns of expression of transcription factors, known from experimental studies to regulate the development of the sinus node and atrioventricular conduction system, are similar in the human and mouse developing hearts.

Conclusions—Our findings point to the comparability of mechanisms governing the development of the cardiac conduction patterning in human and mouse, which provide a molecular basis for understanding the functioning of the human developing heart before formation of a discrete conduction system. (Circ Arrhythm Electrophysiol. 2011;4:532-542.)

Key Words: heart development ■ human embryo ■ sinus node ■ atrioventricular axis

The initiation and propagation of the electric impulse in the mammalian heart is coordinated by the conduction system. The chamber-forming heart during early development, however, does not have a histologically distinct conduction system nor fibrous insulation between the atrial and ventricular myocardial masses, yet is still able to generate an adult-type ECG, including atrioventricular delay.1,2 The differential expression of fast-conducting gap junctional proteins in the different compartments of the embryonic heart provides the basis for the adult pattern of conduction.3 Recent studies in experimental animals have revealed some of the molecular mechanisms underlying the differentiation of atrial and ventricular working myocardium, along with the appearance of the different components of the conduction system.4 To date, however, lack of gene expression data for the developing human heart has precluded valid extrapolations from experimental studies to the situation in humans. Extant studies on the development of the conduction system in the human heart have been based on serial sections stained either nonspecifically5–10 or for neural tissue antigen GlN2/Leu7/ HNK-1,11,12 the function of which in the developing heart is unknown. Furthermore, although comparable methods have been used, conclusions from these studies have been far from consonant. To resolve these ongoing controversies, we have performed an immunohistochemical analysis, coupled with 3-dimensional reconstructions, in the developing human heart of the patterns of expression of several transcription factors and proteins known to affect the myocardial conduction properties. Although we have observed important differences in gene expression, our findings point to the comparability of the mechanisms governing the patterning and development of the cardiac conduction tissues in humans and mice.

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Materials and Methods

Human Embryos
Collection of human embryonic material and its preparation for histological studies was described previously.13 Additionally, we used 3 human embryos of about 8 weeks of development, one coming from the

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MRC–Wellcome Trust Human Developmental Biology Resource, managed by the Institute for Human Genetics of Newcastle University, United Kingdom, and the other 2 from the Center for anticonception, sexuality, and abortion, Leiden University Medical Center, The Netherlands. Embryos were examined under a stereomicroscope for gross anomalies and graded according to Carnegie criteria. In total, we used 3 embryos at stage 12, 5 embryos at stage 13 to 14, 6 embryos at stage 15 to 16, 4 embryos at stage 18, and 6 embryos at stages 21 to 23. We included only embryos considered normal. Because the blood was not removed from the embryos, immunohistochemical stainings with some fluorochromes resulted in erythrocyte autofluorescence. Collection and use of the human embryonic material for research were approved by the medical ethics committees of the Universities of Tartu, Estonia, Leiden, and Amsterdam, The Netherlands.

**Immunohistochemistry, In Situ Hybridization, and 3D Reconstructions**

Immunofluorescent staining, in situ hybridization, and 3D reconstructions were performed as described.13,14 Serial sections of the embryos collected at Leiden University Medical Center were processed by indirect immunohistochemistry. Detailed description of the protocols, antibodies, and riboprobe are given in the online-only Data Supplement.

**Limitations of Our Study**

Assessment of conduction requires direct measurements in the myocardium, which cannot be performed in human embryos. The assessment of expression patterns of fast-conducting gap-junctional proteins connexin40 and connexin43, which play an important role in the conduction of the myocardium of the mouse heart,18 including the transcription factor Tbx3.19 This factor represses the differentiation of chamber myocardium, permitting specific areas of the looping heart to develop into the conduction system.20 Using 3D reconstructions, we assessed the myocardial expression of TBX3 relative to the primordium of the sinus node. Tubx3 is expressed in the nodal primordium, in the right venous valve, and the myocardium of the atrioventricular canal, and, in late embryos, the atrioventricular junctions (Figure 2). At stages 14 through 16, at the stage of formation of the primary atrial septum, Tubx3 is expressed in the left venous valve, the leading edge of the atrial septal myocardium, and the floor of the right atrium, which, in turn, are contiguous with the atrioventricular canal (Figure 2A*). The expression of TBX3 outside the atrioventricular canal is weak (not shown) and disappears by the time of completion of atrial septation at stage 18 (Figure 2B**).

In stage 12 to 14 embryos, the entire wall of the systemic venous sinus and common atrium is positive for HCN4 (Figure 1A and 3A). At later stages, HCN4 expression gradually declines in the atrial walls and becomes confined to the myocardium surrounding the venous tributaries (Figure 1C, 1E, 3E, and 3I). In contrast to the broad expression of HCN4, only a small part of the walls of the systemic venous tributaries is positive for TBX3 (Figure 4A). This area, representing the sinus nodal primordium, increases in size at later stages (Figure 4E and 4I), and is from the outset virtually negative for expression of troponin I and α-smooth muscle actin (α-SMA) (Figure 3B and 3C). As with the definitive sinus node,13 the nodal primordium does not express connexin40 (Figure 3B, 3F, and 3J). No histological differences were found between the presumed nodal primordium and the right atrial wall (Figure 3D, 3H, and 3L).

Results

We first assessed the patterns of expression of the hyperpolarization-activated cyclic nucleotide–gated cation channel 4 (HCN4), known to be involved in the pacemaking mechanism of the sinus node.16 Mouse embryos, in which Hcn4 was knocked out, show extremely low heart rates and embryonic lethality.17 In the early period of development, spanning Carnegie stages 10 through 12, and corresponding to around 22 to 26 days of development, HCN4 is expressed throughout the looping heart tube, including the differentiating chamber myocardium, albeit with a decreasing gradient of expression from the venous to the arterial pole (Figure 1A and 1B). At the venous pole, HCN4 is initially expressed not only in the myocardial but also in the adjacent mesenchymal wall of the venous sinus (Figure 1A). At stage 16, equivalent to around 37 days of development, HCN4 is virtually absent from the ventricular chambers but remains highly expressed in the myocardium of atrioventricular canal and atrial walls, along with the myocardium at the developing veno-atrial junctions (Figure 1C through 1G). During late embryonic stages 18 through 23, which correspond to around 46 to 58 days of development, expression declines in the atrial chambers, but the strong expression seen in the sinus node primordium (see below) is also evident in the myocardium surrounding the atrioventricular junction and coronary sinus. Low expression remains in the myocardium surrounding the developing arterial valves at these late stages (Figure 1E through 1H).

Understanding the patterns of gene expression in the changing morphological context is facilitated by reading the results, described in the next paragraphs, along with the interactive 3D-PDF file from the online-only Data Supplement (accessible at http://circ.ahajournals.org).

Development of the Sinus Region

The definitive sinus node of the human heart is a comma-shaped structure located in the terminal groove at the junction of the superior caval vein and the right atrium. No such structure is seen in the early human embryos studied. The systemic venous sinus, or sinus venosus, representing the confluence of the systemic venous tributaries, is first recognizable at stage 12. Its walls are initially nonmuscular but already express HCN4 (Figure 1A). As the venous sinus shifts to the right, prominent venous valves form at its junction with the right atrium. The left superior caval vein acquires its position within the left atrioventricular groove, where it is recognizable as the precursor of the coronary sinus. The walls of the venous tributaries then muscularize, with the right lateral myocardial wall of the venous sinus becoming thickened and porous,13 remaining traceable along the right-sided sinoatrial junction in the oldest embryo analyzed (Figure 2 and Figure 3). We consider this structure to be the primordium of the sinus node.

Many molecular markers have been used to delineate the precursors of the definitive conduction axis in the embryonic mouse heart,15 including the transcription factor Tbx3.19 This factor represses the differentiation of chamber myocardium, permitting specific areas of the looping heart to develop into the conduction system.20 Using 3D reconstructions, we assessed the myocardial expression of TBX3 relative to the primordium of the sinus node. Tubx3 is expressed in the nodal primordium, in the right venous valve, and the myocardium of the atrioventricular canal, and, in late embryos, the atrioventricular junctions (Figure 2). At stages 14 through 16, at the stage of formation of the primary atrial septum, Tubx3 is expressed in the left venous valve, the leading edge of the atrial septal myocardium, and the floor of the right atrium, which, in turn, are contiguous with the atrioventricular canal (Figure 2A*). The expression of TBX3 outside the atrioventricular canal is weak (not shown) and disappears by the time of completion of atrial septation at stage 18 (Figure 2B**).
In addition to TBX3, the entirety of the systemic venous sinus was positive for ISL1, expression of this gene being complementary to that of NKX2–5 (Figure 4). Unlike the strong TBX18 expression in the epicardium, we observed different levels of TBX18 protein and mRNA expression in the sinus nodal primordium. Myocardial expression of TBX18 protein was weak (Figure 4B, 4F, and 4J), but expression of mRNA was robust and broader (Figure 4M). We found fundamental molecular differences between the nodal primordium within the venous sinus wall and the myocardial sleeve of the developing coronary sinus, suggested by some investigators to form a left-sided sinus node, albeit that they share the same developmental origin.23 The myocardium around the coronary sinus, unlike the developing sinus node, does not express TBX3, initiates early expression of connexin40, and is strongly positive for α-SMA. The developmental changes in gene expression at the venous pole of the heart are summarized in Figure 4N.

Figure 1. HCN4 expression in the developing human heart. Transverse sections were incubated with antibodies against HCN4 and troponin I (TnI) as myocardial marker. Note the HCN4 expression in part of the left ventricular wall (small arrows in B). Large arrows in B, D, F, and H point to weak HCN4 expression in the outflow tract myocardium; arrows in A point to the mesenchymal expression of HCN4 in the young embryonic heart. See text for further description. The autofluorescent signal within the cavities of the atria and ventricles (E, F, G, and H) is due to the massive presence of erythrocytes. At stage 16, HCN4 is expressed in the myocardium of the venous pole, but also in the atrioventricular canal musculature (C). AVC indicates atrioventricular canal; ao, ascending aorta; CS, coronary sinus; PA, pulmonary artery; pv(s), pulmonary vein(s); OFT, outflow tract; st, septum transversum; SV, sinus venosus; RA/LA, right/left atrium; RV/LV, right/left ventricle; rvv, right venous valve. Scale bars, 200 μm.

Development of the Atrioventricular Region at Intermediate Stages

Stages 13 through 16, equivalent to around 28 to 38 days of development, are marked by unmistakable growth of the chambers and formation of atrial and ventricular septal structures, along with a rightward shift of the atrioventricular canal.11 Previously we reported that in the early chamber-forming human heart, myocardial expression of TBX3 is first observed in the floor of the common atrium and the atrioventricular canal.14 By reconstructing the myocardial expression of TBX3 at later developmental stages, we have related the development of the atrioventricular conduction tissues to the changing cardiac morphology. At stage 16, TBX3 is expressed throughout the myocardium of the atrioventricular canal, contiguous with the TBX3 expression in the right venous valve, including the spurious septum, the leading edge of the atrial septum, and the right atrial wall located dorsal to the outflow tract (Figure 5A and 5A*). The TBX3-positive
atrioventricular canal myocardium does not express connexin40 and connexin43. In contrast, the ventricular trabeculations are positive for both connexin40 and connexin43, whereas the atrial walls and atrial septum express only for connexin40 (Figure 6D, 6E, 6J, and 6K). TBX3 is not only expressed in the atrioventricular canal dorsally and ventrally but also at the dorsal part of the base of the outflow tract and along the crest of the ventricular septum (Figure 5A*). The weakly TBX3-positive myocardium on top of the ventricular septum, corresponding to the presumptive bundle of His dorsally, and the so-called septal branch ventrally, is negative for connexin40. Unlike the situation in mouse, it does express connexin43 at this stage (Figure 6J and 6K).

Expression of the protein ID2, inhibitor of DNA binding, known to be important in the specification of the atrioventricular conduction axis in mouse, was not limited to the developing conduction tissues in humans. We observed weak expression in the atrioventricular canal musculature and ventricular trabeculations. Strong expression, however, was present in the epicardium and mesenchyme of the epicardial grooves (Figure 6C and 6I). As with the sinus nodal primordium, the myocardium of the atrioventricular canal and ventricular septum does not express α-SMA (Figure 6F and 6L), although the ventricular and atrial myocardial walls largely remain positive at these stages. In contrast to the sinus nodal primordium, the compact location of the cardiomyocytes at the top of ventricular septum, where also TBX3 expression is present, allows identification of the precursors of the atrioventricular conduction axis using routine histological staining (Figure 6A and 6G).

Establishment of the Atrioventricular Conduction Axis in the Late Embryonic Heart

At the end of the embryonic period, at stages 18 through 23, the atrioventricular junction undergoes major rearrangements, with septation being completed through fusion of several mesenchymal structures, and the atrial myocardium becoming insulated from the ventricular musculature by formation of epicardially derived fibrous tissue. With these changes, the expression of TBX3 in the atrioventricular canal becomes restricted to a figure-of-eight configuration in the lower rims of the atrial chambers (Figure 5B*, 5C*, and 5C**). These left and right atrioventricular ring bundles converge dorsally in the developing primordium of the atrioventricular node close to the orifice of the coronary sinus and ventrally behind the left ventricular outflow tract in the so-called retro-aortic “node” (Figure 5C, 5C*, and 5C**). By stage 23, the atrioventricular myocardial continuity is interrupted round the greater majority of the atrioventricular
junctions, albeit in incomplete fashion (Figure 7D and 7F). At the dorsal aspect of the atrioventricular junctions, in contrast, the developing atrioventricular conduction axis continues to provide muscular atrioventricular continuity (Figure 5B** and 5C**). By this stage, the primordium of the atrioventricular node, along with the lower rims of the atrial chambers, and the muscular strands that continue to cross the forming plane of atrioventricular insulation, are negative for connexin40 and connexin43 (Figure 7D, 7E, 7J, and 7K), representing slow-conducting tissues analogous to the atrioventricular canal musculature at earlier stages. The atrioventricular nodal precursors at this stage are directly contiguous with the TBX3-negative myocardium of the atrial and ventricular septa (Figure 7B). The base of the atrial septum, formed by myocardialization of the vestibular spine, shows a gradient of decreasing levels of connexin40 toward the site of the nodal primordium (asterisk in Figure 7D) derived from the atrioventricular canal myocardium. The ventricular septal myocytes, in contrast, express neither connexin40 nor connexin43 (Figure 7D and 7E), representing slow-conducting tissues analogous to the atrioventricular canal musculature at earlier stages. The atrioventricular nodal precursors at this stage are directly contiguous with the TBX3-negative myocardium of the atrial and ventricular septa (Figure 7B). The base of the atrial septum, formed by myocardialization of the vestibular spine, shows a gradient of decreasing levels of connexin40 toward the site of the nodal primordium (asterisk in Figure 7D) derived from the atrioventricular canal myocardium. The ventricular septal myocytes, in contrast, express neither connexin40 nor connexin43 (Figure 7D and 7E). The TBX3-positive area of the atrioventricular nodal primordium expresses HCN4 in relatively weak heterogeneous fashion, with the part adjacent to the atrial septum being more positive than the part contiguous with the ventricular septum (Figure 7C). The atrioventricular ring bundles and retro-aortic “node” are also weakly positive for HCN4 (Figure 7C and 7I), as has been reported for experimental animals. As with the primordium of the sinus node, the forming atrioventricular node shows a low level of troponin I (Figure 7D) and is recognizable as a lightly-stained mesh of cells by routine histology (Figure 7A), albeit that it was not yet possible at these stages to distinguish the transitional and compact portions characteristic of the definitive atrioventricular node.

When traced ventrocranially, the developing atrioventricular conduction axis enters the forming plane of fibrous insulation as the developing bundle of His, recognizable histologically on the crest of the ventricular septum (Figure 5C, 5C**, and 7G). The slightly darker stained cells of the developing conduction axis (Figure 7G) also express TBX3 and HCN4. After completion of ventricular septation, the developing bundle of His becomes negative for both connexin40 and connexin43 (Figure 7G through 7K). On both sides of the ventricular septum, the connexin40- and connexin43-positive trabeculations form the myocardial strands originating from the bundle of His (Figure 7G through 7K), corresponding to the future bundle branches. A higher expression of NKX2–5 was observed in the developing bundle (Figure 7L), as described previously for the early human fetal heart. In terms of expression of troponin I, the myocytes of the atrioventricular conduction axis did not differ much from the ventricular myocardium (Figure 7J) and were not yet insulated from the ventricular septal myocardium (Figure 7J).
Discussion

Although the early embryonic heart has no anatomically distinct conduction system and demonstrates widespread muscular atrioventricular continuity, it still achieves coordinated contractions of the atrial and ventricular chambers. The spatial distribution of connexins and ion channels play a crucial role in the electric patterning of the heart.\(^3\) During the last decades, numerous experimental studies have revealed the molecular mechanisms governing the early specification of the conduction system.\(^4\) The development of the conduction system in the human heart, however, has thus far been assessed only morphologically,\(^5–12\) with a lack of gene expression data preventing reliable extrapolation of experimental data to the human condition. Our previous studies showed that the expression patterns of some key cardiac genes in the developing human heart are similar to those reported for the developing mouse and chicken heart, but small differences in morphology were observed.\(^13,14\) Also, our current study on the molecular analysis of the patterning of the conduction tissues confirms the similarities in gene expression patterns between human and mouse.

Spatiotemporal Changes in Expression of Pacemaker Channel HCN4 Reflects Progressive Maturation of the Developing Myocardium

Working myocardium is characterized by its efficient contractile function and low automaticity, whereas the opposite is true for the conduction system. In the normal postnatal heart, spontaneous generation of the impulse is confined to the sinus node. In pathological situations, arrhythmogenic activity can originate from the atrioventricular conduction axis, along with diverse myocardial structures such as the pulmonary venous sleeves, the coronary sinus, the lower atrial rims, the right ventricular outflow tract, and even the atrial appendages.\(^31\) Despite their distinct developmental origins, all these structures share expression of the pacemaker channel HCN4 during development. At the intermediate stages, corresponding to around 6 to 7 weeks of development, we observed relatively high levels of HCN4 expression in these structures but very low levels, if any, in the ventricular chambers. Weak expression of HCN4 is also detectable initially in the myocardium of the developing cardiac outflow tract, increasingly

Figure 4. Expression of transcription factors in the developing sinus region. Serial sections at the same level as shown in Figure 3 were incubated with antibodies (A through L) or riboprobe (M) as indicated. At early stages, the left-sided wall of the venous sinus is positive for TBX3 (arrow in A), expression of which gradually confines to the right side only (E and I). Note the weak TBX18 expression in the venous sinus myocardium as compared with the epicardial expression (arrows in B, F, J, and M). Note also the almost strict complementarity between the expression domains of Nkx2–5 and Isll in the venous sinus. N summarizes the developmental changes in gene expression occurring at the venous pole of the heart (CS indicates Carnegie stage). lb indicates lung bud; for other abbreviations, see previous figures. Scale bars, 200 μm.

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recognized also as a source of arrhythmogenesis in the postnatal heart.\textsuperscript{32} During later stages, expression levels of HCN4 decline in the differentiating working myocardium at the venous pole of the heart, reflecting its ongoing maturation. In mouse, the transcription factor Nkx2–5 has been identified as an important factor in the formation of the sinoatrial boundary, suppressing Tbx3 and Hcn4 in the atrial working myocardium.\textsuperscript{33} In contrast, we observed HCN4 expression in NKX2–5-positive areas at the venous pole of the developing human heart, suggesting a difference in the regulation of HCN4 expression between mouse and human. Maintenance of HCN4 expression in these structures during maturation, along with dysregulation of the expression of fast-conducting connexins, may provide a mechanism of the initiation of certain tachyarrhythmias.

**Formation of the Sinus Node**

The definitive sinus node in humans has a distinct molecular architecture, which underlies its pacemaker function and differs significantly from that of adjacent atrial muscle.\textsuperscript{34,35} Several transcription factors, including Tbx3, Tbx18, and Nkx2–5, play a crucial role in the formation of the sinus node at the right-sided sinoatrial junction in the mouse heart.\textsuperscript{33,38} We observed similar expression patterns of these genes in the developing human heart, suggesting conservation of the molecular mechanisms governing its development. We observed almost strict complementarity between the expression domains of the transcription factors ISL1 and NKX2–5 at the venous pole (Figure 4). ISL1 is known to play a crucial role in the maintenance of the precursor state of the cardiac progenitor cells within the heart-forming regions. Its expression is switched off in the majority of the cardiomyocytes on their differentiation.\textsuperscript{34,37} As in the mouse,\textsuperscript{38} the myocytes of the systemic venous tributaries, including the primordium of the sinus node, continue to express ISL1, a finding deserving further investigation.

We have endorsed previous morphological studies\textsuperscript{5,6,9} showing that the thickening of the venous sinus wall is the first morphological evidence of the formation of the TBX3-positive nodal primordium in the embryonic human heart. However, the myocytes of the nodal primordium and the
atrial wall display no obvious histological differences. Published electrophysiological data also fail to support strict localization of the pacemaker within the developing sinus node during the early stages of development,39 which correlates well with our findings of extensive expression of HCN4 at the venous pole of the early human embryonic heart.

The specialized cardiomyocytes of the postnatal sinus node contain poorly developed myofibrils,40 resembling the phenotype of the primary myocardium. On the other hand, the initiation of expression of fast-conducting connexins and atrial natriuretic factor, along with the gradual disappearance of smooth muscle actin in the chamber myocardium, is a sign of progressive differentiation and maturation of the working myocardium.41 When first identified, the thickened right wall of the venous sinus in the developing human heart already contained a small subset of myocytes expressing very low levels of troponin I and α-SMA, both proteins being strongly expressed in the atrial and ventricular chamber myocardium at these stages (Figures 3 and 6). This troponin I– and α-SMA–negative area within the wall of the venous sinus does express TBX3, known to control the genetic programming of the sinus node development in mouse.36 This suggests that TBX3 also controls early specification of the myocytes of the systemic venous sinus into the pacemaker lineage in humans.

Human hearts with right atrial isomerism,42 as well as mouse hearts with complex malformations resembling right atrial isomerism caused by knockout of the left-right axis regulator Pitx2c,33 display bilateral sinus nodes. In normal human embryonic hearts, we did not observe in the myocardial wall of the coronary sinus the molecular phenotype characteristic of the developing sinus nodal primordium. Our observations, along with the absence of reports about bilateral sinus nodes in the setting of the normally arranged laterality, lend no support to the hypothesis of the presence of bilateral sinus nodal primordia22 in the normal developing heart.
Formation of the Atrioventricular Conduction Axis

To date, morphological studies on serial sections of human embryos have resulted in contradictory conclusions concerning the development of the atrioventricular conduction axis in humans.5–8,10–12 Thus, it has been suggested that the atrioventricular node develops through fusion of the ventral and dorsal parts of the atrioventricular ring of “histologically specialized” cardiomyocytes.8,12 We have found no evidence to support this hypothesis. At the intermediate stages of development, the entire atrioventricular canal is positive for the conduction system marker TBX3,19 with somewhat thicker portions dorsally and ventrally. The lumen of the canal, along with the atrioventricular endocardial cushions, separate these parts of the TBX3-positive atrioventricular canal myocardium. Subsequently, the mesenchymal tissues of the forming central fibrous body remain interposed between the developing atrioventricular node and the so-called retro-aortic “node,” the latter structure regressing in normal hearts but persisting in certain complex cardiac malformations.43

Recent lineage studies in mice have shown that, albeit atrioventricular canal musculature and the myocardializing vestibular spine both originate from a Tbx2-positive lineage, the compact part of the atrioventricular node develops in its entirety from the atrioventricular canal musculature,29 without contributions from the coronary sinus musculature, specifically expressing transcription factor Tbx18,24 or vestibular spine-derived myocardium, which is, unlike the atrioventricular node, marked by the MEF2c-AHF-Cre transgene.29 In the human embryonic heart, we failed to observe TBX18 expression in the TBX3-positive atrioventricular nodal primordium (data not shown).

In the developing mouse heart, the expression of the connexins, which ensure rapid myocardial conduction, is suppressed in the atrioventricular canal by the transcription factors Tbx3 and Tbx2.20 The cardiomyocytes on the crest of the ventricular septum, which form the atrioventricular conduction axis in mice, also express Tbx3 at early stages.19,24 The developing and maturing bundle of His in the mouse heart remains negative for connexin40 and connexin43.24 In the late embryonic human heart, we found a similar arrangement, where the cells of the
developing axis, after completion of ventricular septation, remained negative for both connexin40 and connexin43 (Figure 7J and 7K), corroborating that at these stages the developing bundle of His is a slow-conducting entity as in early fetal hearts. In contrast to the situation in mice, we found connexin43 expression on top of the ventricular septum (Figure 6E and 6K), the functional significance of which is unclear. Despite such differences in the timing of expression of connexin43 and in the intensity of ID2 expression, the similar patterns of expression of key regulatory and functional proteins in the developing human atrioventricular conduction system suggest evolutionary conservation of the general embryonic blueprint for the formation of atrioventricular conduction axis in humans and mice.

In the normal human postnatal heart, the atrioventricular conduction axis is the only muscular connection between the atrial and ventricular muscle masses. Defective formation of the plane of atrioventricular insulation in the mouse, particularly in the absence of transcription factor Tbx2, and Bmp-receptor 1a, has been shown to be associated with the persistence of accessory muscular bundles, which are capable of producing ventricular preexcitation. In humans, the connections, which are responsible for the Wolff-Parkinson-White syndrome, have fast-conducting properties and express connexin43. Even up to the neonatal period, when formation of the atrioventricular insulation plane is relatively complete, multiple accessory myocardial strands are still to be found crossing the fibrous plane of insulation. These remnants of the atrioventricular canal myocardium, however, are negative for connexins40 and connexin43 and would thus constitute slowly conducting pathways. The failure of disappearance of these strands, therefore, cannot be the sole mechanism for ventricular preexcitation. An additional requirement is the further differentiation of this primary myocardium into fast-conducting working myocardium.

In contrast to the postnatal situation, in which the atrioventricular node and the bundle of His are isolated from the myocardium of the ventricular septal crest by fibrous tissue, the TBX3-positive precursors of these structures seen at late embryonic stages are not yet isolated from the ventricular myocardium by fibrous tissue (Figure 7). In these stages, the cardiomyocytes making up the atrioventricular node and the penetrating atrioventricular bundle do not express fast-conducting connexins, thus producing an effective functional isolation in the setting of absent fibrous insulation. Persistence of the original muscular continuity between the myocytes of the atrioventricular conduction axis and the crest of the ventricular septum accounts for the so-called Mahaim connections, characterized by slow conduction.

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Disclosures
None.

References
Recent findings from studies in experimental animals have in part revealed the molecular mechanisms underlying the development and maturation of the conduction system and the myocardium of the atrial and ventricular chambers. Knowledge of the underlying molecular regulation of their formation is crucial for the understanding of the arrhythmogenic mechanisms. Recent findings from studies in experimental animals have in part revealed the molecular mechanisms underlying the differentiation toward either working myocardium or conduction system. Unfortunately, lack of gene expression data on human heart development does not allow validating extrapolations drawn from experimental studies to the human condition. We performed a molecular and 3-dimensional analysis of the development of the conduction system in the human embryonic heart. Our findings provide a molecular basis for the functioning of the human developing heart without a discrete conduction system, despite the absence of a discrete conduction system and atrioventricular insulation. Distinct expression patterns of ion channels and connexins in the different compartments of the embryonic heart are responsible for their differential conduction properties before the appearance of the anatomic components of the conduction system. Many cardiac arrhythmias are related to the development and maturation of the conduction system and the myocardium of the atrial and ventricular chambers. Knowledge of the underlying molecular regulation of their formation is crucial for the understanding of the arrhythmogenic mechanisms. Recent findings from studies in experimental animals have in part revealed the molecular mechanisms underlying the differentiation toward either working myocardium or conduction system. Unfortunately, lack of gene expression data on human heart development does not allow validating extrapolations drawn from experimental studies to the human condition. We performed a molecular and 3-dimensional analysis of the development of the conduction system in the human embryonic heart. Our findings provide a molecular basis for the functioning of the human developing heart without a discrete conduction system, and they point to the similarities in gene expression patterns between human and mouse, which is the widest used experimental model to study cardiac development. Additionally, we observed a gradual decrease of the expression of the pacemaker channel HCN4 in the venous pole myocardium during human development, failure of which may be the mechanism of initiation of supraventricular tachyarrhythmias.

**CLINICAL PERSPECTIVE**

At the onset of chamber formation, the early embryonic heart is able to produce coordinated atrial and ventricular contractions despite the absence of a discrete conduction system and atrioventricular insulation. Distinct expression patterns of ion channels and connexins in the different compartments of the embryonic heart are responsible for their differential conduction properties before the appearance of the anatomic components of the conduction system. Many cardiac arrhythmias are related to the development and maturation of the conduction system and the myocardium of the atrial and ventricular chambers. Knowledge of the underlying molecular regulation of their formation is crucial for the understanding of the arrhythmogenic mechanisms. Recent findings from studies in experimental animals have in part revealed the molecular mechanisms underlying the differentiation toward either working myocardium or conduction system. Unfortunately, lack of gene expression data on human heart development does not allow validating extrapolations drawn from experimental studies to the human condition. We performed a molecular and 3-dimensional analysis of the development of the conduction system in the human embryonic heart. Our findings provide a molecular basis for the functioning of the human developing heart without a discrete conduction system, and they point to the similarities in gene expression patterns between human and mouse, which is the widest used experimental model to study cardiac development. Additionally, we observed a gradual decrease of the expression of the pacemaker channel HCN4 in the venous pole myocardium during human development, failure of which may be the mechanism of initiation of supraventricular tachyarrhythmias.
Molecular Analysis of Patterning of Conduction Tissues in the Developing Human Heart
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Supplemental Methods

Immunofluorescence and Immunohistochemical Staining

Paraffin-embedded embryos were sectioned at 5 to 7 μm. Sections were mounted onto silane-coated slides, deparaffinized in xylene, rehydrated in graded ethanol series and washed in phosphate-buffered saline (PBS, pH 7.4).

Triple immunofluorescent staining was performed as described previously. Here we report the results of staining with the following primary antibodies: goat polyclonal for connexin40, rabbit polyclonal for NKX2-5, goat polyclonal for TBX3, goat polyclonal for TBX18, rabbit polyclonal for ID2 (all from Santa Cruz Biotechnology; diluted 1:250), mouse monoclonal for connexin43 (diluted 1:100), goat polyclonal for Islet-1 (1:250; Neuromics), rabbit polyclonal for HCN4 (1:250; Chemicon) and mouse monoclonal for α-smooth muscle actin (Sigma-Aldrich, 1:500). Every combination contained a mouse monoclonal antibody for troponin I (1:250; Chemicon) as myocardial marker. After washing in TNT (100 mM Tris, pH 7.4; 150 mM NaCl; 0.05% Tween-20, Sigma-Aldrich) sections were incubated at room temperature for 1.5-2 hr in the dark with a mix of fluorochrome-coupled secondary antibodies containing donkey-anti-goat Alexa568, chicken-anti-rabbit Alexa488 and donkey-anti-mouse Alexa680 (all diluted 1:250; Molecular Probes, Invitrogen). For TBX3 and TBX18 biotinylated anti-goat antibody (1:250; Jackson ImmunoResearch) and a Tyramide Signal Amplification kit (Perkins & Palmer) were used according to the manufacturer’s instructions.

For indirect immunohistochemical staining sections were pre-treated with PBS supplemented with 0.05% Tween-20 to reduce non-specific antibody binding. Then consecutive sections were incubated overnight at room temperature with different primary antibodies in repetition through the whole series. Here we report the results of staining with the goat polyclonal antibody for NKX2-5 (Santa Cruz Biotechnology; diluted 1:4000 in PBS with 1% bovine serum albumin). The next morning, after washing the sections for 3 times in PBS, they were incubated with appropriate biotin-coupled secondary antibodies for 1 hr at room temperature and washed again 3 times in PBS. For NKX2-5 binding visualization a horse-anti-goat antibody (Vectors Laboratories) was used at a dilution of 1:200 in PBS supplemented with 1.5% horse normal serum. Then the slides were incubated with the ABC reagent (Vector Laboratories) for 45 min, and washed again in PBS. Then 3-3'di-
aminobenzidin tetrahydrochloride (Sigma-Aldrich) diluted 400 μg/mL in Tris-maleate buffer (58 mM Tris; 50 mM maleic acid, pH 7.6; 50 mM NaOH) and supplemented with 5% H₂O₂ was added to the sections to develop the colour at the binding site of the primary antibody. Reaction was stopped by rinsing the sections in distilled water, after which they were counterstained in 0.1% hematoxylin (Merck) for 10 seconds, followed by rinsing in running tap water for 10 minutes. The slides were then dehydrated in graded ethanol series, washed in xylene and mounted with Entellan (Merck).

**Staining for general histology**

Subsequent to immunofluorescent staining and photography, sections were washed in PBS and stained with hematoxylin and azophloxin according to a standard protocol. Then sections were dehydrated in a graded ethanol series, washed in xylene and covered with Entellan (Merck).

**In situ Hybridization on Sections**

*In situ* hybridization was performed as described previously.² Here we report the results of staining with a TBX18 probe, transcribed from nucleotides 1039-1790 of the human TBX18 gene (GenBank reference nr NM_001080508). The template for the TBX18 probe was amplified using polymerase chain reaction from total cDNA synthesized using reverse transcription from RNA extracted from adult atrial myocardium and subcloned into pBluescript SK-II plasmid according to the standard protocols.

**Three-dimensional reconstructions**

Three-dimensional reconstructions from the fluorescently stained serial sections were performed essentially as described previously.¹² Some structures (e.g., dorsal mesenchyme, veins and arteries) were not labelled in their entirety for the sake of clarity. The myocardial expression domain of TBX3 from every third section of the series was projected upon the myocardium label without quantification. For technical reasons the areas containing scattered or graded patterns of expression were similarly labelled as the areas containing strong gene expression. The extent of the labels for other structures, which have not been specifically stained on the sections, was defined according to general embryology knowledge.³⁴ The 3D data from the Amira viewer were exported into Adobe Acrobat 9 Pro Extended (Adobe
Systems Inc., www.adobe.com) to generate the file in interactive 3D portable document format.5

Supplemental References


This PDF file is designed to interactively assess the morphology of the human embryonic heart and related structures in three dimensions. For the descriptions see the paper.

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**How to use this PDF file**

Every following page contains on the left the preset view buttons to enable the user to (re)set the 3D model into the orientation shown on the particular button.

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To further interact with the 3D model :

- **rotate**: click and hold the left mouse button and move the mouse
- **zoom**: click and hold the right mouse button and move the mouse
- **translate**: click and hold the left+right mouse buttons and move the mouse
human embryonic heart at stage 14 (31-35 days of development)
Page 3

Human embryonic heart at stage 16 (38-41 days of development)

views

structures

myocardium

TBX3-pos. myo.

mesenchyme

veins

great arteries

http://3d.hfrc.nl
Human embryonic heart at stage 18 (45-48 days of development)
Page 5 Human embryonic heart at stage 23 (56-58 days of development)

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TBX3-pos. myo.
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great arteries

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