A GATA-dependent right ventricular enhancer controls dHAND transcription in the developing heart

David G. McFadden1,*, Jeroen Charlé1,*,‡, James A. Richardson2, Deepak Srivastava1,3, Anthony B. Firulli1,4 and Eric N. Olson1,§

1Department of Molecular Biology, 2Department of Pathology, 3Department of Pediatrics, University of Texas Southwestern Medical Center at Dallas, 5323 Harry Hines Boulevard, Dallas, Texas 75390-9148, USA
4Department of Physiology, University of Texas Health Science Center, 7703 Floyd Curl Drive, San Antonio, Texas, 78284-7756, USA
*These authors contributed equally to this work
‡Present address: Department of Cell Biology, Erasmus University Rotterdam, Dr Molewaterplein 50, 3015GE Rotterdam, The Netherlands
§Author for correspondence (eolson@hamon.swmed.edu)

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SUMMARY

Heart formation in vertebrates is believed to occur in a segmental fashion, with discreet populations of cardiac progenitors giving rise to different chambers of the heart. However, the mechanisms involved in specification of different chamber lineages are unclear. The basic helix-loop-helix transcription factor dHAND is expressed in cardiac precursors throughout the cardiac crescent and the linear heart tube, before becoming restricted to the right ventricular chamber at the onset of looping morphogenesis. dHAND is also expressed in the branchial arch neural crest, which contributes to craniofacial structures and the aortic arch arteries. Using a series of dHAND-lacZ reporter genes in transgenic mice, we show that cardiac and neural crest expression of dHAND are controlled by separate upstream enhancers and we describe a composite cardiac-specific enhancer that directs lacZ expression in a pattern that mimics that of the endogenous dHAND gene throughout heart development. Deletion analysis reduced this enhancer to a 1.5 kb region and identified subregions responsible for expression in the right ventricle and cardiac outflow tract. Comparison of mouse regulatory elements required for right ventricular expression to the human dHAND upstream sequence revealed two conserved consensus sites for binding of GATA transcription factors. Mutation of these sites abolished transgene expression in the right ventricle, identifying dHAND as a direct transcriptional target of GATA factors during right ventricle development. Since GATA factors are not chamber-restricted, these findings suggest the existence of positive and/or negative coregulators that cooperate with GATA factors to control right ventricular-specific gene expression in the developing heart.

Key words: Heart formation, dHAND, GATA transcription factor, mouse

INTRODUCTION

Classical embryology and cell fate mapping experiments have defined the morphological events involved in formation of the vertebrate heart (reviewed by Olson and Srivastava, 1996; Fishman and Chien, 1997). Cardiac precursors in the anterior lateral plate mesoderm become committed to a cardiogenic fate in response to signals from the adjacent endoderm at embryonic day 7.5 (E7.5) in the mouse. These cells form the cardiac crescent and give rise to paired bilaterally symmetric cardiac primordia. As development continues and the embryo closes ventrally, the cardiac primordia fuse along the midline at E8.0 to form a single, linear, beating heart tube. Shortly thereafter, the linear heart tube loops to the right, signifying the first morphological manifestation of embryonic left-right asymmetry. Cardiac looping serves to juxtapose the future left and right ventricles, and to align the inflow and outflow tracts with the atrial and ventricular chambers. Following looping, septation of both ventricular and atrial chambers occurs, and populations of migrating neural crest cells contribute to the outflow tract and great vessels as the heart develops and grows to form the mature four-chambered organ (Jiang et al., 2000; Le Lievre and Le Douarin, 1975).

Although the morphologic events of cardiac development are well characterized, the underlying molecular mechanisms that specify different cardiac cell fates and regulate regional-specific patterns of gene expression in the developing heart are only beginning to be revealed. Recent analyses of several cardiac transcription factors and the genetic cascades in which they act have suggested that heart formation proceeds in a segmental fashion, with each cardiac chamber governed by an individual genetic program (reviewed by Fishman and Olson, 1997). Interestingly, atrial and ventricular cardiomyocytes, which exhibit differences in gene expression, contractility,
morphology and electrophysiology, appear to be specified well before chamber morphogenesis (Yutzey and Bader, 1995). There are also molecular distinctions between cardiomyocytes in the right and left ventricular chambers, but how these cells acquire their distinctive features is unknown.

Members of the basic helix-loop-helix (bHLH) family of transcriptional regulators play diverse roles in cell specification and differentiation in many tissues (reviewed in Massari and Murre, 2000). The related bHLH proteins, dHAND and eHAND, also known as Hand2/Thing2 and Hand1/Thing1, respectively, show dynamic and complementary expression patterns in the developing heart (Cross et al., 1995; Cserjesi et al., 1995; Hollenberg et al., 1995; Srivastava et al., 1995). During mouse embryogenesis, dHAND and eHAND are expressed in the cardiac crescent concomitant with cardiac differentiation. As the heart tube forms, dHAND is expressed throughout the ventral surface of the linear heart tube and, at the onset of cardiac looping, is downregulated in the future left ventricle (LV), with expression being maintained along the outer curvature of the right ventricle (RV) and in the outflow tract (OFT) (Thomas et al., 1998). In contrast, eHAND is downregulated in the region of the linear heart tube that contributes to the RV and, following looping, is expressed along the outer curvature of the LV and in portions of the OFT. The specific expression patterns of dHAND and eHAND exemplify the remarkable territoriality of gene expression in the developing heart and intimate the existence of spatially restricted transcriptional networks acting at the very earliest stages of cardiogenesis.

Consistent with their chamber-restricted expression patterns, the HAND genes appear to be essential for morphogenesis of their respective cardiac chambers. Mice homozygous for a null mutation in dHAND fail to form a RV and have severe abnormalities in the neural crest-derived aortic arch arteries, resulting in embryonic demise at E10.0 (Srivastava et al., 1997; Yamagishi et al., 2000). eHAND null embryos die from severe extraembryonic defects around E8.0, making a clear analysis of heart development difficult (Firulli et al., 1998; Riley et al., 1998). However, tetraploid rescue experiments, employed to circumvent the early embryonic lethality, have shown that rescued animals arrest at E10.5 with apparent defects in maturation of the left ventricular chamber (Riley et al., 1998). In the zebrafish, which has only a single ventricular chamber, only a single HAND gene, most closely related to dHAND, has been identified (Angelo et al., 2000; Yelon et al., 2000). Loss-of-function mutations in this gene, called hands off, result in ventricular ablation, suggesting that this single gene in the fish shares the combined functions of dHAND and eHAND in chamber morphogenesis in the mouse (Yelon et al., 2000).

Several other mouse mutations result in regionally restricted abnormalities in cardiac morphogenesis, further reinforcing the notion of chamber-specific transcriptional programs. Mice lacking the MADS-box transcription factor MEF2C, expressed throughout the heart, exhibit defects in cardiac looping and an absence of a future RV (Lin et al., 1997). This phenotype is highly reminiscent of the dHAND mutant phenotype. Whether the absence of a RV in MEF2C mutants, and the consequent absence of dHAND expression, reflects a role of MEF2C as a regulator of dHAND is unknown. Mice homozygous for a null mutation in the homeobox gene Nkx2.5 display defects in looping morphogenesis, an apparent absence of the left ventricular chamber (Lyons et al., 1995), and downregulation of eHAND expression, suggesting that eHAND is a key downstream target of Nkx2.5 that may contribute to cardiac defects in these animals (Biben and Harvey, 1997).

Analysis of the cis-regulatory elements of several cardiac genes in transgenic mice has also demonstrated the existence of anatomically restricted transcriptional programs that act through independent enhancers to control transcription in different regions of the heart (reviewed in Firulli and Olson, 1997; Kelly et al., 1999). In many cases, transcription factors that are expressed throughout the heart are required for regionally restricted activation of cardiac enhancers. How such factors act selectively in specific subsets of cardiomyocytes is unknown.

In the present study, we analyzed the dHAND upstream region for regulatory elements sufficient to recapitulate the chamber-restricted expression pattern of the endogenous gene. We describe independent enhancers that direct expression of a lacZ transgene in the heart and branchial arch neural crest in patterns that mimic dHAND expression throughout development. Deletion analysis of the cardiac-specific enhancer revealed that subregions regulate transcription in the OFT and RV and that two conserved binding sites for GATA transcription factors are required for enhancer activity in the RV. These results identify GATA factors as direct upstream activators of dHAND and demonstrate that the transcriptional activity of the GATA family is regulated in a chamber-specific manner during heart development.

### MATERIALS AND METHODS

#### Cloning and generation of reporter constructs

Two overlapping dHAND phage clones were isolated from a mouse 129SV genomic library using the dHAND cDNA as a probe (Srivastava et al., 1997). The longest clone contained 11 kb of upstream flanking sequence. Clones were characterized by endonuclease restriction mapping. To generate constructs 1-7, the indicated regions of upstream sequence were fused to the promoterless AUG-β-gal reporter.

One human dHAND genomic clone was isolated from a λ-phage library and characterized by restriction mapping and sequence analysis. Sequences were aligned with the mouse genomic flanking sequence using the Bestfit algorithm of GCG software.

To generate constructs 8-12, a 750 bp fragment containing the dHAND branchial arch enhancer (J. Charité and E. Olson, unpublished data) was blunt-cloned into the HindIII site of the hsp68lacZ vector (Kothy et al., 1989). The orientation of the branchial arch enhancer was confirmed by restriction mapping and DNA sequence analysis. The resulting vector (NC-hsplacZ) was digested with SmaI, DNA fragments were amplified from construct 2 by PCR using Pfu Turbo (Stratagene) DNA polymerase. The following PCR primer pairs were used: construct 8: Primer 1, 5' GATCTGTATTCCCTTTAAGAAA- GAGACTG-3' and Primer 2, 5'-GAGGGAGGGATCC-GATCCCTG- AATCAG-3'. Construct 9: Primer 3, 5'-GAGGGAGGGATCCGATC- TATCGGTTC-3' and Primer 2. Construct 11: Primer 4, 5'- CAGGTGCTTATCCTCCATA-GTCTCAGG-3' and Primer 5, 5'-TCTCGTAGAGCCTG-TTGGTGGGC-3'. Construct 12: Primer 1 and Primer 6, 5'-CTCTAGATCTTATGGGACTAAAC- CC-3'.

Construct 10 was generated by BglII digestion of construct 2, and ligation into NC(Rev)-hsplacZ, which is identical to NC-hsplacZ, except the branchial arch enhancer is in the reverse orientation. All
constructs were confirmed by restriction mapping and DNA sequence analysis.

**Generation of transgenic mice**

Reporter constructs were digested with 
Sall to remove vector sequences, and purified for injection using a QiaQuick spin column protocol (QIAGEN). Concentrated DNA was eluted into 10 mM Tris buffer, pH 7.4. Fertilized eggs from B6C3F1 female mice were collected for pronuclear injection as described (Lien et al., 1999). Foster mother ICR mice were sacrificed at E10.5, and embryos were collected and stained for β-galactosidase activity as described by Cheng et al. (1993). Following overnight staining, embryos were fixed for 12 hours in 4% paraformaldehyde in phosphate-buffered saline (PBS), pH 7.4. For sections, embryos were dehydrated in 2, 2-dimethoxypropane (DMP), cleared in light mineral oil, embedded in paraffin, sectioned at 10 μm, rehydrated and stained with Nuclear Fast Red (Moller and Moller, 1994).

**Mouse mutants**

Mice with mutations in dHAND (Srivastava et al., 1997), MEF2C (Lin et al., 1997), Nkh2.5 (Lyons et al., 1995), im (Yokoyama et al., 1993) and GATA4 (Molkentin et al., 1997) have been described previously. Inbred C57BL6 mice were used for intercrosses with dHAND-lacZ transgenic mice. Genotypes of embryos were determined by Southern blot analysis of yolk sac DNA.

**Electrophoretic mobility shift assays**

Oligonucleotides corresponding to the conserved GATA binding sites at –3039 and –3140 were synthesized (Integrated DNA Technologies) as follows:

<table>
<thead>
<tr>
<th>Primer Name</th>
<th>Sequence</th>
</tr>
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<tbody>
<tr>
<td>mut3039A</td>
<td>5'–TCGAGGGTGGATGCTATCTGGAGCT-3'</td>
</tr>
<tr>
<td>mut3039B</td>
<td>5'–TCGAGGTGTCAGTG-3'</td>
</tr>
<tr>
<td>mut3140A</td>
<td>5'–TCGAGGTGGATGGCGAGCTGCAGTG-3'</td>
</tr>
<tr>
<td>mut3140B</td>
<td>5'–TCGAGCTACATTGCAGGCATGGAGCT-3'</td>
</tr>
</tbody>
</table>

Mutant oligonucleotides were also synthesized as follows:

<table>
<thead>
<tr>
<th>Primer Name</th>
<th>Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>mut3140A</td>
<td>5'–TCGAGGGCACCATTGCAGGAGCTGCAGTG-3'</td>
</tr>
<tr>
<td>mut3140B</td>
<td>5'–TCGAGCCACGTATTGCAGGAGCTGCAGTG-3'</td>
</tr>
<tr>
<td>mut3039A</td>
<td>5'–TCGAGGCTACATTGCAGGAGCTGCAGTG-3'</td>
</tr>
<tr>
<td>mut3039B</td>
<td>5'–TCGAGGTGTCAGTG-3'</td>
</tr>
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Oligonucleotide pairs were resuspended, boiled for 10 minutes, and annealed by slowly cooling to room temperature. Annealed oligonucleotides were radiolabeled with [32P]dCTP using Klenow fragment of DNA polymerase and purified using G25 spin columns (Roche). COS-1 cells were transfected with pcDNA1-GATA4 (Lu et al., 1999) or empty vector. Whole cell extracts were isolated as previously described by Brockman et al. (1995). DNA binding assays were performed as described by Scott et al. (1994). Unlabeled wild-type and mutant competitor oligonucleotide was added to reactions at the indicated concentrations. DNA-protein complexes were resolved on a 5% nondenaturing polyacrylamide gel in 0.5× TBE.

**Site-directed mutagenesis**

Conserved GATA sites at –3039 and –3140 were mutated to Apal and BamH1 sites, respectively, as follows. DNA was amplified from construct 2 using Primer 1 and Primer 2 (see above), and subcloned into plasmid BK-pBSK for mutagenesis reactions. Two rounds of PCR-based mutagenesis on BK-pBSK were performed using

<table>
<thead>
<tr>
<th>Primer Name</th>
<th>Sequence</th>
</tr>
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<tbody>
<tr>
<td>mut3039A</td>
<td>5'–CCCCTGGAATTTGTAATTACCGGGATGCTATCTGGAGCT-3'</td>
</tr>
<tr>
<td>mut3140A</td>
<td>5'–CCCCTGGAATTTGTAATTACCGGGATGCTATCTGGAGCT-3'</td>
</tr>
<tr>
<td>mut3039B</td>
<td>5'–CCCCTGGAATTTGTAATTACCGGGATGCTATCTGGAGCT-3'</td>
</tr>
<tr>
<td>mut3140B</td>
<td>5'–CCCCTGGAATTTGTAATTACCGGGATGCTATCTGGAGCT-3'</td>
</tr>
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Restriction analysis confirmed the presence of the mutations, and the insert from GATAmutBK-pBSK was again amplified using Primer 1 and Primer 2. This fragment was cloned into the SmaI site of NC-hsplacZ. Integrity of the plasmid was confirmed by restriction mapping and sequence analysis.

**RESULTS**

**Identification of dHAND cardiac and branchial arch enhancers**

In order to define the cis-regulatory elements that control dHAND expression during cardiac development, two overlapping phage clones spanning approximately 11 kb of upstream genomic sequence were isolated. To determine if these sequences contained regions important for dHAND expression, a fragment from the 5' untranslated region (UTR) to –11 kb was fused to lacZ and tested for expression at E10.5 (Fig. 1, construct 1). Transgenic embryos showed X-gal staining in the heart as well as the first and second branchial arches. Expression in the heart at E10.5 was primarily localized to the outer curvature of the future RV and the OFT. Lower levels of expression were detected in the future LV (Fig. 1), a pattern that recapitulates that of endogenous dHAND transcripts (Thomas et al., 1998). Stable transgenic lines harboring construct 1 showed the same expression pattern of lacZ at E10.5 as that seen in F0 transgenics (data not shown). Of note, this 11 kb upstream region did not direct expression in lateral mesoderm, limb buds, or sympathetic ganglia, where dHAND is also expressed (Charité et al., 2000; Srivastava et al., 1995). This suggested that the regulatory elements responsible for expression within these tissues are located elsewhere.

To further localize the regulatory elements responsible for cardiac expression of dHAND, a fragment extending from the 5'UTR to –5.5 kb was fused to lacZ (Fig. 1, construct 2). This construct directed lacZ expression only in the developing heart, implying that the branchial arch enhancer lay between –5.5 and –11 kb, whereas the cardiac regulatory region was downstream of –5.5 kb. Subsequent analysis localized the branchial arch enhancer to the region between –8.0 and –7.75 kb (J. Charité and E. Olson, unpublished data). The level of cardiac expression from construct 2 was lower than from construct 1, although both showed preferential expression in the right ventricle. Since we found no cardiac regulatory sequences responsible for expression within these tissues are located elsewhere.

To facilitate a rapid analysis of the location of regulatory sequences responsible for cardiac expression of dHAND and to control for possible integration effects, we included the branchial arch enhancer in all subsequent deletion constructs. First, however, to rule out potential interference between the two regulatory regions, we tested the branchial arch enhancer fused to the 5’ end of construct 2 (Fig. 1, construct 3). This construct directed lacZ expression in the branchial arches and heart. Staining in the heart was identical to construct 2, leading us to conclude that the branchial arch enhancer did not interfere with the cardiac regulatory region when placed directly upstream (data not shown). Construct 4, which contained the branchial arch enhancer and deleted the region from –7.5 to –2.7 kb, abolished cardiac lacZ expression. In conjunction
with construct 2, this suggested that the cardiac regulatory region was located between –5.5 and –2.7 kb. Deletion of 3 kb from –7.5 to –4.5 kb from the entire 11 kb upstream region did not abolish cardiac expression (Fig. 1 construct 5), suggesting that a cardiac enhancer was between –4.5 kb and –2.7 kb. Construct 6, which contained a deletion from –4.7 to –3.2 kb, abolished all cardiac gene expression, except in a small number of cells always localized to the RV. Deletion of the region between –4.2 and –2.7 kb, in the context of 11 kb of upstream region, abolished all cardiac gene expression (Fig. 1, construct 7). This demonstrated that sequences in this region were required for cardiac dHAND expression. To conclude that the cardiac enhancer of dHAND lay between –4.2 and –2.7 kb.

**Expression of the dHAND cardiac enhancer during embryonic development**

We next sought to determine whether the dHAND cardiac enhancer was sufficient to recapitulate the complete spatiotemporal pattern of expression of endogenous dHAND. Therefore, we generated stable transgenic lines with construct 2, containing the 5.5 kb upstream region fused to lacZ. Nine transgenic lines were obtained, five of which showed comparable expression patterns during heart development. Line 165 showed robust expression of lacZ, and was therefore chosen for further characterization.

At E7.75, line 165 showed lacZ expression throughout the cardiac crescent, in a pattern identical to endogenous dHAND mRNA (Fig. 2A) (Thomas et al., 1998). At E8.0, lacZ was...
detected throughout the myocardial layer of the linear heart tube (Fig. 2B,J). At the onset of cardiac looping (E8.25), lacZ expression was downregulated in the future LV, mirroring the regulation of endogenous dHAND transcripts (data not shown). Following the completion of cardiac looping (after E8.5), lacZ expression was detected along the outer curvature of the future RV, OFT and pericardium, while lower levels were seen in the future LV (data not shown and Fig. 2C,D,K). Because the expression pattern of this enhancer replicates the dynamic pattern of endogenous dHAND mRNA expression during cardiac looping, we believe it responds to the signaling pathways that establish chamber-restricted expression of endogenous dHAND.

Following heart looping, the pattern of lacZ expression continued to mimic the pattern of endogenous dHAND mRNA. At E10.5, the graded right-left ventricular expression of lacZ was readily visible (Fig. 2D,L-O). Serial transverse sections of an E10.5 embryo revealed expression along the outer curvature of the right ventricle and portions of the outflow tract (oft); however, lacZ expression is not seen in the aorta or atrial chambers (Fig. 2D,L-O). Lower, patchy levels are again noted at the base of the left ventricle (lv; E-F). hf, head folds; ba, branchial arches; fra, future right atrium; fla, future left atrium; ra, right atrium.
expression detected at later time points were at the apex of the RV and IVS (Fig. 2G,H).

Anatomic reversal of dHAND enhancer activity in inv/inv mice

The right ventricular expression of dHAND is anatomically reversed in inv/inv mice, which display a reversal of left-right asymmetry, reflecting the orientation of the pulmonary ventricle to the left and the systemic ventricle to the right (Thomas et al., 1998). To test whether the dHAND cardiac enhancer also responded to the inv pathway in a manner analogous to the endogenous gene, we introduced transgene construct 2 into the inv/inv background by breeding. As shown in Fig. 3A, the enhancer was active on the left side of the heart in inv/inv embryos, corresponding to the position of the pulmonary ventricle. We conclude that the dHAND cardiac enhancer responds to transcriptional signals specific for the pulmonary ventricle, which normally is on the right, rather than signals for left-right asymmetry per se.

Activity of the dHAND cardiac enhancer in mouse mutants with altered ventricular development

We also introduced transgene construct 2 into several mouse mutants with altered ventricular development as a means of analyzing the fates of dHAND-expressing cells in hearts with various dysmorphologies. In MEF2C mutant embryos, the right ventricular region fails to develop (Lin et al., 1998). As shown in Fig. 3B, dHAND-lacZ expression was localized to the conotruncal region of MEF2C mutant hearts at E9.5, with almost no staining in the more posterior region of the heart, confirming that right ventricular cells that would normally express dHAND are absent in this mutant.

In dHAND mutant embryos, dHAND-lacZ expression was essentially identical to that in MEF2C mutants (Fig. 3C), consistent with the conclusion that the right ventricular chamber is missing in these embryos (Srivastava et al., 1997). Expression of lacZ was maintained in the conotruncal region, demonstrating that these cells do not require dHAND for specification or survival. The expression of dHAND-lacZ in these cells of the mutant also suggests that dHAND does not positively autoregulate its expression in these cells.

In Nkx2.5 mutant embryos, dHAND-lacZ expression extended from the conotruncus into the more posterior region of the heart tube (Fig. 3D). We interpret this to indicate that the right ventricular region is present in these embryos, but defects in looping and possibly in left ventricular development (Biben and Harvey, 1997) result in an altered distribution of β-gal-positive cells in the remainder of the heart.

Region-specific elements within the dHAND cardiac enhancer

To more precisely define the regulatory elements within the 1.5 kb enhancer, we created a series of deletions of this fragment, and analyzed their transcriptional activity in F0 embryos using the hsp68-lacZ reporter and the dHAND branchial arch enhancer as an internal control for integration effects. As mentioned above, the region from –4.2 to –2.7 kb (construct 8) was sufficient to direct expression of lacZ in the developing heart (Fig. 4B). Deletion of –4.2 to –3.7 kb completely abolished cardiac expression, suggesting that the enhancer was located in this region (Fig. 4A,C, construct 9). However, this 500 bp alone, or with an additional 1 kb of upstream sequence, was nearly inactive, directing only low level expression in a few cells of the distal OFT (data not shown and Fig. 4A,D, constructs 10 and 11).

Based on these data, it was possible that we split a critical element at –3.7 kb. To test this possibility, we fused the region from –4.2 to –3.2 kb to the hsp68-lacZ reporter (construct 12). Interestingly, this construct directed expression in the OFT, but not the right ventricle (Fig. 4E). This suggested that separable elements were present in the 1.5 kb enhancer, which controlled expression in different regions of the developing heart. In addition, because this deletion abolished RV expression, ventricular expression must require sequences in both the 5’ and 3’ regions of the 1.5 kb fragment. This is consistent with the expression pattern of construct 6 (Fig. 1), in which the region from –4.7 to –3.2 kb was deleted. In this context, most cardiac lacZ expression was abolished; however, a few cells, always located in the RV, stained with X-gal. This implies that elements downstream of –3.2 kb have some activity in cells of the RV.

Conservation of dHAND regulatory elements

To guide us in identifying potential regulatory elements within the dHAND cardiac enhancer, we isolated a human dHAND
GATA-dependent regulation of dHAND transcription

To determine if the conserved GATA sites were capable of binding GATA4 in vitro, we performed electrophoretic mobility shift assays (EMSA) using oligonucleotide probes. COS-1 cells were transfected with a GATA4 expression vector, and whole cell extracts were used in the assay. As shown in Fig. 6, GATA4 specifically shifted the wild-type probe containing the GATA site at –3140 bp, and DNA binding was effectively competed by an excess of unlabeled cognate competitor. However, the unlabeled mutant site was unable to compete for GATA4 binding. Similar results were seen with oligonucleotide probes containing both the –3039 and –3140 GATA sites.

To determine if these GATA sites were required for transgene expression in vivo, we mutated these sites in the context of the 1.5 kb fragment (–4.2 to –2.7 kb) and generated F0 embryos with this construct (Fig. 4A, construct 13; Fig. 7B). In 10 embryos expressing lacZ in the branchial arches at varying levels, cardiac expression was dramatically reduced, compared to the wild-type construct (Fig. 7, compare A (wild-type) and B (mutant)). As expected from our deletion analyses (Fig. 4, constructs 10 and 11), which showed OFT expression with constructs extending upstream of –3.7 kb and lacking the above GATA sites, residual expression was detected in the OFT with construct 13 (Fig. 7B).

To test whether GATA4 was uniquely required for enhancer activity in vivo, we crossed the 5.5 kb enhancer transgenic line (construct 2) into a GATA4 mutant background (Molkentin et al., 1997). Analysis of lacZ expression in GATA4 null embryos showed that transgene expression was maintained in the absence of GATA4 (Fig. 7C). GATA4 mutant embryos exhibit cardia bifida due to a defect in ventral morphogenesis of the embryo (Molkentin et al., 1997; Kuo et al., 1997). Intriguingly, dHAND-lacZ expression was much stronger in the right compared to the left cardiac tube in the mutant, suggesting that the mechanisms that restrict dHAND expression to the right ventricular chamber at the onset of cardiac looping are at least partially intact in these embryos. The finding that the GATA-dependent dHAND enhancer was active in GATA4 mutant embryos suggests that GATA5 or GATA6, which are expressed in an overlapping pattern with GATA4 during cardiac development, can substitute for GATA4 to activate the dHAND enhancer.
**DISCUSSION**

dHAND is an early marker of the future right ventricle and is required for normal development of this cardiac chamber (Srivastava et al., 1997; Thomas et al., 1998). Thus, identification of the factors acting upstream of dHAND should provide insight into the mechanisms for establishment of chamber-specific gene expression during cardiac development. Our results identify an enhancer responsible for early cardiac expression of dHAND and show that it is a direct target for activation by GATA transcription factors.

**Enhancer modules for distinct regions of the developing heart**

Cardiac expression of dHAND is controlled by a 1.5 kb enhancer (between −4.2 and −2.7 kb) that encompasses subregions responsible for transcription in the RV and OFT. Deletion of the 3’ 500 bp of the enhancer abolished ventricular expression and diminished, but did not eliminate, expression in the OFT. Although the region from −2.7 to −3.2 kb is necessary for transcription in the RV, it is not sufficient for expression in this cardiac segment, and relies on additional sequences within the OFT enhancer, demonstrating the requirement for overlapping, but distinct cis-regulatory regions for dHAND transcription in these cardiac segments. We have made numerous attempts to further delineate the boundaries of these enhancers, but all further deletions have abolished all expression, suggesting that essential elements within these enhancers are dispersed over a relatively large region. In contrast, the enhancer responsible for transcription of dHAND in the branchial arch neural crest is localized to a region of only about 200 bp, located between −8 and −7.8 kb (J. Charité and E. Olson, unpublished data).

The modular regulation of dHAND transcription in the developing heart is consistent with several recent studies of other cardiac genes and argues against the existence of a general cardiac gene regulatory program (reviewed by Firulli and Olson, 1997; Kelly et al., 1999). Instead, it appears more likely that cardiac transcription is controlled by unique combinations of cardiac-restricted and widely expressed transcription factors within each cardiac segment.

**Transcriptional regulation of dHAND by GATA factors**

The dHAND cardiac enhancer contains two conserved
high-affinity binding site for MEF2 in the activated. However, there does not appear to be a conserved dHAND-dependent pathway for RV morphogenesis is not expression in the future RV and that in the absence of MEF2C, raising the possibility that MEF2C is required for the possible regulation of cardiac enhancer is restricted to the conotruncus, and that overexpression of GATA4 enhances cardiogenesis (Greppin et al., 1997, 1995). GATA4 null embryos die around E8.5 from a defect in ventral closure, resulting in impaired fusion of the paired cardiac tubes (Kuo et al., 1997; Molkentin et al., 1997). Interestingly, GATA-6 is upregulated in GATA4 null embryos, suggesting that these factors may act redundantly. This may explain the finding that the dHAND cardiac enhancer was active in GATA4 null embryos.

The phenotype of dHAND and MEF2C mutant embryos is remarkably similar, with the absence of a right ventricular chamber and defects in looping morphogenesis (Srivastava et al., 1997; Lin et al., 1997). In MEF2C mutants, expression of the dHAND cardiac enhancer is restricted to the conotruncus, raising the possibility that MEF2C is required for dHAND expression in the future RV and that in the absence of MEF2C, the dHAND-dependent pathway for RV morphogenesis is not activated. However, there does not appear to be a conserved high-affinity binding site for MEF2 in the dHAND cardiac enhancer, which would require an indirect mechanism for possible regulation of dHAND by MEF2C. In this regard, recent studies showed that MEF2 factors can be recruited to cardiac genes lacking MEF2 sites, by association with GATA factors (Morin et al., 2000). Thus, it is conceivable that MEF2C might regulate cardiac expression of dHAND via the essential GATA sites in the dHAND cardiac enhancer.

GATA factors have also been shown to regulate Nkx2.5 transcription in the cardiac crescent and right ventricle through two independent upstream enhancers (Lien et al., 1999; Reecy et al., 1999; Searcy et al., 1998; Tanaka et al., 1999). Similarly, the CARP promoter contains a GATA binding site essential for transcription in a portion of the RV and OFT (Kuo et al., 1999). GATA-dependent transcriptional activation through this site is dependent on Nkx2.5 in vivo and in vitro. However, there are no apparent Nkx2.5 binding sites in the promoter, demonstrating how transcriptional synergy can occur between GATA factors and Nkx2.5 in the absence of cognate sites for both factors. Nkx2.5 also regulates transcription of GATA6 in the RV (Molkentin et al., 2000; Davis et al., 2000). Thus, Nkx2.5 and GATA transcription factors participate in mutually reinforcing regulatory networks in the developing heart in which each factor can activate and maintain the expression of the other.

**Potential mechanisms for chamber-restricted expression of dHAND**

Although GATA factors are required for dHAND enhancer activity in the right ventricular chamber, there is no apparent chamber-restriction of GATA factor expression in the developing heart. This suggests that dHAND expression requires additional factors, which cooperate with GATA factors to control right-ventricular transcription.

In principle, the highly restricted expression pattern of dHAND in the right ventricular chamber (and eHAND in the left) could be controlled by chamber-specific transactivators or by negative
regulators that suppress expression of the genes in the opposite chambers. While we cannot rule out the latter possibility, our deletion analyses failed to reveal evidence for negative regulatory elements that, when deleted, result in ectopic expression of dHAND in the left ventricle, leading us to favor a model in which chamber-restricted coregulators cooperate with GATA factors to confer right ventricular-restricted expression to dHAND.

As described above, GATA4 has been shown to cooperate with Nkx2.5 and MEF2 to activate cardiac target genes (Durocher et al., 1997; Sepulveda et al., 1998; Morin et al., 2000). Transcriptional activity of GATA factors has also been shown to be inhibited by the multitype zinc-finger protein FOG2, expressed predominantly in the heart (Tevosian et al., 1999; Sevensson et al., 1999; Lu et al., 1999). However, none of these factors show selective expression in one ventricle or the other. One possibility is that chamber-specific signals may be interpreted by cardiac transcription factors that themselves do not show chamber-specificity of expression, but which activate cardiac target genes only in the presence of specific signals. In this regard, the transcription factor NFAT3, which is activated by specific calcium-dependent signals, can cooperate with GATA factors to activate transcription (Molkentin et al., 1998), and repression of GATA-dependent transcription by FOG-2 can be relieved by certain signaling pathways (our unpublished results). Possible activation of such pathways in specific segments of the heart, either by regionally restricted ligands or in response to hemodynamic or contractile differences along the looping heart tube, could provide a signal for the highly specific expression patterns of cardiac genes.

Analysis of the cis-acting regulatory elements within cardiac enhancers is a powerful tool for decoding the combinatorial pathways in specific segments of the heart, either by regionally restricted ligands or in response to hemodynamic or contractile differences along the looping heart tube, could provide a signal for the highly specific expression patterns of cardiac genes. We gratefully acknowledge Chuanzhen Wu, Brian Mercer, Heather Lee, and John McAnally for generating transgenic embryos and Alisha Tizenor for assistance with graphics. J. C. was supported by an EMBO fellowship. D. G. M. was supported by a Medical Scientist Training Program grant from the NIH. A. B. F. is supported by NIH (ROI HL61677-01A1). D. S. is supported by grants from NIH and the March of Dimes. This work was supported by grants from the NIH and the D. W. Reynolds Foundation to E. N. O.

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GATA-dependent regulation of dHAND transcription


