FGF signaling enforces cardiac chamber identity in the developing ventricle

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SUMMARY STATEMENT

The FGF signaling pathway suppresses plasticity in the developing ventricle by promoting ventricular chamber characteristics in both early-differentiating and late-differentiating cardiomyocytes.
ABSTRACT

Atrial and ventricular cardiac chambers behave as distinct subunits with unique morphological, electrophysiological, and contractile properties. Despite the importance of chamber-specific features, chamber fate assignments remain relatively plastic, even after differentiation is underway. In zebrafish, Nkx transcription factors are essential for the maintenance of ventricular characteristics, but the signaling pathways that operate upstream of Nkx factors in this context are not well understood. Here, we show that FGF signaling plays an essential part in enforcing ventricular identity. Loss of FGF signaling results in a gradual accumulation of atrial cells, a corresponding loss of ventricular cells, and the appearance of ectopic atrial gene expression within the ventricle. These phenotypes reflect important roles for FGF signaling in promoting ventricular traits, both in early-differentiating cells that form the initial ventricle and in late-differentiating cells that append to its arterial pole. Moreover, we find that FGF signaling functions upstream of nkh genes to inhibit ectopic atrial gene expression. Together, our data suggest a model in which sustained FGF signaling acts to suppress cardiomyocyte plasticity and to preserve the integrity of the ventricular chamber.
INTRODUCTION

The vertebrate heart is divided into atrial and ventricular chambers that work together to drive circulation, yet have unique morphological, electrophysiological, and contractile attributes (Barth et al., 2005; McGrath and de Bold, 2009). These chamber-specific characteristics reflect the distinct molecular traits of atrial and ventricular cardiomyocytes: for example, each chamber expresses particular transcription factors (Bao et al., 1999; Bruneau et al., 2001; Wu et al., 2013; Xin et al., 2007), utilizes specific myosin isoforms (Berdougo et al., 2003; Bisaha and Bader, 1991; Yelon et al., 1999; Yutzey et al., 1994), and possess discrete ion channel components (Flagg et al., 2008). Despite the well-established differences between atria and ventricles, our understanding of the mechanisms that regulate these features remains incomplete.

Fate mapping studies in chick and zebrafish have demonstrated that atrial and ventricular lineages are separate and spatially organized in the early embryo (Garcia-Martinez and Schoenwolf, 1993; Keegan et al., 2004; Redkar et al., 2001; Stainier et al., 1993). The early diversification of these lineages is indicated by distinct gene expression programs that are evident even before the heart tube assembles (Berdougo et al., 2003; Yelon et al., 1999; Yutzey et al., 1994). For example, in zebrafish, the expression patterns of *atrial myosin heavy chain (amhc)* and *ventricular myosin heavy chain (vmhc)* in the anterior lateral plate mesoderm correlate with the spatial organization of atrial and ventricular precursors within this tissue (Berdougo et al., 2003; Schoenebeck et al., 2007; Yelon et al., 1999). These initial populations of atrial and ventricular cells are later joined by late-differentiating cells that contribute to the venous and arterial poles of the heart and assume atrial
and ventricular identity accordingly (de Pater et al., 2009; Hami et al., 2011; Kelly, 2012; Lacic and Scott, 2011; Zhou et al., 2011).

The allocation of progenitor cells into atrial and ventricular lineages is subsequently reinforced by chamber-specific transcription factors that promote the maintenance of atrial and ventricular characteristics. In mice, the atrial transcription factor COUP-TFII regulates the atrial gene expression program (Wu et al., 2013). Tissue-specific deletion of COUP-TFII in differentiated myocardium results in ventricularized atria that express ventricular markers and exhibit electrical activity similar to that of ventricular cells. Likewise, the ventricular transcription factors Irx4 and Hey2 are both required to prevent ectopic activation of atrial genes in the ventricular myocardium (Bao et al., 1999; Bruneau et al., 2001; Bruneau et al., 2000; Koibuchi and Chin, 2007; Xin et al., 2007). Thus, atrial and ventricular chamber identities are relatively plastic and require active enforcement by chamber-specific transcription factors; however, it is not yet clear how the chamber-specific expression of these factors is established.

Our recent work in zebrafish has indicated that Nkx transcription factors play important roles in controlling regionalized expression of Irx4 and Hey2 and in maintaining ventricular identity (Targoff et al., 2013). Both irx4a and hey2 are downregulated in nfx2.5; nfx2.7 double mutants; furthermore, loss of nfx gene function leads to gradual reduction of vmhc expression and simultaneous gain of amhc expression within the ventricle, ultimately yielding an expanded atrium, a diminished ventricle, and ectopic amhc-expressing cells within the ventricular remnant. In addition, nfx genes promote the attainment of ventricular characteristics in the late-differentiating cells that append to the arterial pole (George et al., 2015). Thus, nfx genes seem to sit near the top of the transcriptional hierarchy that insures
retention of ventricular identity in both early-differentiating and late-differentiating cardiomyocytes.

We now seek to define the signaling pathways that act upstream of nkx genes to control the maintenance of ventricular identity. One appealing candidate is the FGF signaling pathway, since prior studies have demonstrated its influence on the induction of nkx2.5 expression and on the regulation of ventricular size. In zebrafish, chick, and Xenopus, nkx2.5 expression in the anterior lateral plate mesoderm is significantly reduced when the FGF pathway is inhibited (Alsan and Schultheiss, 2002; Keren-Politansky et al., 2009; Reifers et al., 2000; Simões et al., 2011). Additionally, inhibiting FGF signaling during gastrulation in zebrafish reduces the number of cells in both cardiac chambers, with a stronger impact on the ventricle (Marques et al., 2008). This early influence of FGF signaling is echoed at later stages, when FGF signaling promotes the accretion of late-differentiating cells to the arterial pole of the ventricle (de Pater et al., 2009; Lazic and Scott, 2011; Marques et al., 2008; Zeng and Yelon, 2014). Similarly, in mouse, a hypomorphic allele of Fgf8 or tissue-specific deletion of Fgf8 results in formation of a hypoplastic right ventricle and outflow tract (Abu-Issa et al., 2002; Ilagan et al., 2006; Park et al., 2006).

Here, we demonstrate a previously unappreciated role for FGF signaling during ventricular development: in addition to promoting the allocation of an appropriate number of ventricular cardiomyocytes, FGF signaling insures that these cells properly maintain their ventricle-specific characteristics. We find that inhibiting FGF signaling subsequent to the onset of chamber-specific differentiation leads to a gradual accumulation of atrial cells, a corresponding loss of ventricular cells, and a progressive increase in the appearance of ectopic amhc-expressing cells in the ventricle. Examination of the dynamic localization of Vmhc and Amhc, as well as
analysis of *amhc*-expressing cells using a photoconvertible reporter transgene, suggests that sustained FGF signaling is required to repress the acquisition of atrial traits by ventricular cardiomyocytes. This role of FGF signaling influences the retention of ventricular characteristics both in the early-differentiating cells that form the initial ventricle and in the late-differentiating cells that contribute to the arterial pole. Finally, we demonstrate that FGF signaling acts upstream of *nkx* genes to execute its important function in enforcing ventricular identity. Together, our studies provide insight into the mechanisms regulating plasticity and commitment of ventricular cardiomyocytes, both of which are fundamentally important for strategies in cardiac regenerative medicine.
RESULTS

Inhibition of FGF signaling results in ectopic amhc expression in the ventricle

Zebrfish fgf8a mutants have small hearts with severe deficiencies in the size of both the atrium and the ventricle (Marques et al., 2008; Reifers et al., 2000). Our prior work has shown that FGF signaling plays an early role in promoting the production of both atrial and ventricular cardiomyocytes, with a particularly potent effect on ventricular cardiomyocytes (Marques et al., 2008). This function of FGF signaling accounts for the small cardiac chambers in fgf8a mutants, but there remains an unexplained aspect of the fgf8a mutant phenotype: in contrast to wild-type hearts (Fig. 1A,E), fgf8a mutant hearts express amhc not only in the atrium, but also in a separate cluster of cardiomyocytes in the ventricle, clearly outside of the normal domain of amhc expression (Fig. 1B,F). (Here, we will refer to these as "ectopic amhc-expressing cells".) This scenario is reminiscent of the phenotype of nkx2.5 mutants, which initially exhibit normal expression patterns of amhc and vmhc, but then display ectopic amhc-expressing cells at later stages (George et al., 2015; Targoff et al., 2013). We therefore explored whether this aspect of the fgf8a mutant phenotype reflected a later role for FGF signaling in preventing inappropriate amhc expression, in addition to its earlier influence on the initial production of ventricular cells.

To evaluate whether FGF signaling plays a relatively late role in repressing ectopic amhc expression, we inhibited the FGF pathway at stages after the onset of atrial and ventricular differentiation. Since expression of both amhc and vmhc is initiated by 18 hours post-fertilization (hpf) (Fig. S1), we chose to reduce FGF signaling from this stage onward. We employed two methods to manipulate FGF
signaling: heat-induced expression of a dominant-negative form of Fgfr1, using the transgene \textit{Tg(hsp70l:dnfgfr1-EGFP)} (Lee et al., 2005) (hereafter referred to as \textit{Tg(hsp70:dnfgfr1)}), and exposure to the FGFR antagonist SU5402 (Mohammadi et al., 1997). Using either method, inhibition of FGF signaling starting at 18 hpf consistently generated ectopic \textit{amhc}-expressing cells, most notably in the ventricular inner curvature and near the arterial pole (Fig. 1C-D,G-H). These data show that FGF signaling prevents inappropriate \textit{amhc} expression in the ventricle; moreover, FGF signaling has a sustained influence on ventricular development, beyond its previously demonstrated role in the early embryo (Marques et al., 2008).

At 18 hpf, \textit{fgf8a} is expressed in and near ventricular precursors, and it continues to be expressed in the ventricle through 48 hpf (Reifers et al., 2000). This persistence of \textit{fgf8a} expression prompted us to investigate the duration over which FGF signaling is required to prevent ventricular expression of \textit{amhc}. As seen at 18 hpf, administration of heat shock to \textit{Tg(hsp70:dnfgfr1)} embryos at 24 or 28 hpf also generated ectopic \textit{amhc}-expressing cells (Fig. 2), whereas ectopic \textit{amhc}-expressing cells were not seen in embryos after heat shock at 29, 30, or 31 hpf (data not shown, \(n\geq10\) for each stage). Additionally, we observed differences in the potency of the effect of expressing \textit{Tg(hsp70:dnfgfr1)} at 18, 24, and 28 hpf. While all embryos heat shocked at 18 hpf (\(n=15/15\)) and nearly all embryos heat shocked at 24 hpf (\(n=22/24\)) displayed ectopic \textit{amhc}-expressing cells, only a small number of embryos heat shocked at 28 hpf (\(n=6/36\)) exhibited this phenotype. Also, while embryos heat shocked at 18 hpf typically displayed ectopic \textit{amhc}-expressing cells both in the inner curvature and at the arterial pole (Fig. 1C,G), fewer ectopic \textit{amhc}-expressing cells were detected, primarily at the arterial pole, after heat shock at 24 hpf (Fig. 2B,E), and even fewer ectopic \textit{amhc}-expressing cells were seen at the arterial pole after
heat shock at 28 hpf (Fig. 2C,F). Together, these results suggest that FGF signaling is required until approximately 28 hpf to repress ectopic expression of amhc within the ventricle, although this requirement tapers over time.

**Loss of FGF signaling results in progressive accumulation of atrial cells and simultaneous loss of ventricular cells**

In addition to creating ectopic amhc-expressing cells in the ventricle, loss of FGF signaling at 18 hpf also alters chamber morphology, such that the atrium appears abnormally dilated and the ventricle appears abnormally compact (Fig. 1E,G,H). These aberrant morphologies seem to be the consequence of an altered number of cardiomyocytes in each chamber: for example, following heat shock at 18 hpf, Tg(hsp70:dnfgfr1) embryos exhibited an increased number of Amhc+ cells and a decreased number of Amhc- cells at 50 hpf (Fig. 3E-G), while their total number of cardiomyocytes remained the same (Fig. 3G). This phenotype emerged gradually over time in Tg(hsp70:dnfgfr1) embryos. In the linear heart tube, only a modest increase in the number of Amhc+ cells was detectable (Fig. 3A,B,G). This excess of Amhc+ cells became more substantial by 36 hpf (Fig. 3C,D,G) and was most notable at 50 hpf (Fig. 3E-G). At all stages examined, we found reciprocal changes in the numbers of Amhc+ and Amhc- cells, such that the total number of cardiomyocytes was not significantly altered (Fig. 3G). Moreover, the observed increase in Amhc+ cells was primarily driven by changes within the atrial chamber, with ectopic Amhc+ cells in the ventricle providing only a minor contribution to the total Amhc+ number. At 26.5 hpf, we occasionally saw one ectopic Amhc+ cell in Tg(hsp70:dnfgfr1) embryos, and, at 36 and 50 hpf, ectopic cells constituted around 10% of the total
Amhc⁺ population (Table S1). Thus, in addition to preventing ectopic *amhc* expression in the ventricle, FGF signaling also plays an important role in preserving the relative proportions of the ventricle and the atrium. Intriguingly, the gradual and reciprocal shift in chamber proportions observed in *Tg(hsp70:dnfgfr1)* embryos echoes the phenotype seen in *nkx*-deficient embryos, in which cardiomyocytes appear to undergo a ventricular-to-atrial transformation (Targoff et al., 2013). This similarity suggests that FGF signaling, like *nkx* genes, promotes the maintenance of chamber proportions, possibly by preventing a conversion from ventricular to atrial identity.

**Loss of FGF signaling results in increased expression of *amhc* and decreased expression of *vmhc* in the ventricle**

Bearing in mind the notion that a shift in chamber proportions could result from a ventricular-to-atrial fate transformation (Targoff et al., 2013), we wondered whether the appearance of ectopic *amhc*-expressing cells in embryos lacking FGF signaling might also reflect a defect in maintaining ventricular identity. Does aberrant *amhc* expression arise within resident ventricular cardiomyocytes, or do the ectopic *amhc*-expressing cells originate elsewhere and then enter the ventricle? As a first step toward understanding the origins of the ectopic *amhc*-expressing cells, we investigated the dynamics of *amhc* and *vmhc* expression following inhibition of FGF signaling. Our analysis in *Tg(hsp70:dnfgfr1)* embryos indicated that ectopic *amhc*-expressing cells emerged with a characteristic spatial organization in the ventricle (Fig. 4A-H). These cells first appeared between 26-29 hpf along the inner curvature of the ventricle (Fig. 4E,F) and were later observed both along the inner curvature and at the arterial pole (Fig. 4G,H). Expression of *vmhc* was compromised in a
reciprocal fashion when FGF signaling was inhibited (Fig. 4I-P). Reduced vmhc expression became apparent between 26-29 hpf (Fig. 4M,N), and, at later stages, vmhc expression appeared excluded from the portions of the ventricle that contained ectopic amhc expression (Fig. 4O,P). Together, the dynamics of amhc and vmhc expression in Tg(hsp70:dnfgfr1) embryos suggest that FGF signaling not only prevents ectopic amhc expression in the ventricle but also preserves ventricular expression of vmhc.

Given that FGF signaling inhibits amhc expression and promotes vmhc expression in the ventricle, we investigated whether it is also capable of repressing amhc expression and inducing ectopic vmhc expression in the atrium. For these studies, we employed the transgene Tg(hsp70:ca-fgfr1), which facilitates activation of FGF signaling through heat-inducible expression of a constitutively active form of Fgfr1 (Marques et al., 2008). Although activation of Tg(hsp70:ca-fgfr1) at early stages can generate a surplus of cardiomyocytes (Marques et al., 2008; Sorrell and Waxman, 2011), we found that induction of transgene expression at 18 hpf did not alter the distribution of amhc expression (Fig. S2A,B), nor did it introduce ectopic vmhc expression (Fig. S2C,D). Thus, FGF signaling is not sufficient to regulate amhc or vmhc expression in the context of the atrium; its role in controlling the expression of amhc and vmhc seems to be restricted to the ventricle.

The complementary loss of vmhc expression and gain of amhc expression in the ventricle of Tg(hsp70:dnfgfr1) embryos led us to examine whether these reciprocal changes take place in the same cells. To test this, we examined the dynamics of Amhc and Vmhc protein localization (Fig. 5 and Fig. S3). When FGF signaling was reduced, the ventricle contained Vmhc, and not Amhc, at 26 hpf (Fig. 5A-D). However, at 28 hpf, Amhc was detectable within Vmhc+ cells located along
the inner curvature (Fig. 5E-H). At later stages, Vmhc+Amhc+ cells became increasingly prevalent both in the inner curvature and at the arterial pole of the ventricle (Fig. 5I-L), and these cells seemed to exhibit increasingly heightened levels of Amhc (Fig. 5M-P).

The observed patterns of amhc and vmhc expression (Fig. 4) and Amhc and Vmhc localization (Fig. 5) point to gradual changes in ventricular traits following the loss of FGF signaling. Our results are consistent with a scenario in which reduced FGF signaling causes resident ventricular cardiomyocytes to activate amhc expression and to lose vmhc expression. Downregulation of vmhc is more clearly illustrated through examination of transcripts (Fig. 4I-P), whereas perdurance of Vmhc protein is likely to explain the persistence of Vmhc+Amhc+ cells (Fig. 5I-P). Thus, our data suggest that FGF signaling acts to promote the maintenance of ventricular cardiomyocyte characteristics, both by repressing amhc expression and by promoting vmhc expression. At the same time, these results do not rule out other possible mechanisms through which FGF signaling could prevent the appearance of ectopic amhc-expressing cells.
**Ectopic amhc-expressing cells are not derived from the atrium**

Some of the ectopic amhc-expressing cells in embryos with reduced FGF signaling reside in positions adjacent to the atrium (Figs. 1C,D, 4F-H), raising the question of whether any of these cells are derived from atrial cardiomyocytes or from the atrioventricular canal (AVC). Prior studies have demonstrated that injury to the larval ventricle can cause atrial cardiomyocytes to transdifferentiate into ventricular cardiomyocytes in order to replenish the damaged tissue (Zhang et al., 2013). To test the possibility that a similar mechanism recruits cells from the atrium into the ventricle when FGF signaling is inhibited, we labeled amhc-expressing cells and followed them over time. To do so, we generated transgenic lines carrying a photoconvertible reporter, Tg(amhc:dendra) (Fig. S4), which expresses the fluorescent protein Dendra under the control of a previously characterized amhc promoter (Zhang et al., 2013).

To analyze whether ectopic amhc-expressing cells in the ventricle originate from the atrium or AVC, we exposed Tg(amhc:dendra) embryos to SU5402 at 18 hpf, performed photoconversion at 26 hpf, and evaluated the fluorescence of the ectopic amhc-expressing cells at 48 hpf (Fig. 6). We chose to perform photoconversion at 26 hpf since the ventricle of SU5402-treated embryos is typically devoid of amhc expression at this stage (Fig. S4C,D); moreover, Dendra fluorescence in Tg(amhc:dendra) embryos is robust enough at 26 hpf to insure successful detection of its photoconverted red form at the experimental endpoint (Fig. S4A,B). In DMSO-treated control embryos, Dendra was found only in the atrium, and atrial cells exhibited both green and red fluorescence (Fig. 6A-D). In contrast, SU5402-treated embryos contained Dendra both in the atrium and in
groups of ectopic cells within the ventricle (Fig. 6E-L). In all of the SU5402-treated embryos examined (n=15), we identified Dendra$^+$ cells in the ventricular inner curvature or at the arterial pole that displayed green, but not red, fluorescence, indicating that these cells had not been expressing \textit{amhc} at the time of photoconversion. In the majority of these embryos (n=10/15), all of the Dendra$^+$ cells seen in the inner curvature and at the arterial pole exhibited only green fluorescence (Fig. 6E-L). However, in a few embryos (n=5/15), the observed group of green-only Dendra$^+$ cells was accompanied by 1-3 doubly fluorescent Dendra$^+$ cells. These relatively rare examples of doubly fluorescent Dendra$^+$ cells likely represent cases in which a few cells had already initiated ectopic \textit{amhc} expression at the time of photoconversion. Altogether, our data indicate that the vast majority of the ectopic \textit{amhc}-expressing cells induced by loss of FGF signaling are not derived from \textit{amhc}-expressing cells in the atrium or AVC.

\textbf{FGF signaling inhibits \textit{amhc} expression in both early-differentiating and late-differentiating ventricular cardiomyocytes}

Since some of the ectopic \textit{amhc}-expressing cells in embryos with reduced FGF signaling reside near the arterial pole, we wondered whether any of these might be derived from the late-differentiating second heart field (SHF) progenitor cells that normally construct this portion of the ventricle (de Pater et al., 2009; Hami et al., 2011; Lazic and Scott, 2011; Zhou et al., 2011). If so, this would parallel a previous finding in \textit{nkx2.5} mutants, in which some of the ectopic \textit{amhc}-expressing cells in the ventricle are late-differentiating cardiomyocytes (George et al., 2015). To begin investigating whether FGF signaling influences ventricular characteristics in late-differentiating cells, we first examined whether SHF progenitor cells were present in
embryos subjected to our experimental conditions. Prior studies have shown that strong inhibition of FGF signaling with a high dose of SU5402 (10 μm) beginning at 24 hpf can nearly eliminate the formation of mef2cb-expressing SHF progenitor cells (Lazic and Scott, 2011; Zeng and Yelon, 2014). However, our strategies for reduction of FGF signaling at 18 hpf, either by heat shock of Tg(hsp70:dnfgrf1) embryos or by exposure to a lower dose of SU5402 (5 μm), did not affect mef2cb expression in the SHF progenitor population (Fig. S5 and data not shown). In addition, as in control embryos (Fig. 7A-D), SHF progenitor cells went on to contribute late-differentiating cardiomyocytes to the arterial pole in Tg(hsp70:dnfgrf1) embryos (Fig. 7E-H), as shown by an established developmental timing assay that can distinguish early-differentiating from late-differentiating cardiomyocytes (de Pater et al., 2009).

To test whether ectopic amhc-expressing cells at the arterial pole represent early-differentiating or late-differentiating cardiomyocytes, we performed an adapted developmental timing assay that employs the transgenes Tg(myl7:dsredt4) and Tg(amhc:egfp). In control embryos expressing these transgenes at 48 hpf, eGFP is found in the atrium, and DsRed is found in early-differentiating, but not late-differentiating, cardiomyocytes (Fig. 8A-D). In contrast, when FGF signaling is reduced, eGFP is found both in the atrium and ectopically in the ventricle (Fig. 8E-L). In all of the SU5402-treated embryos examined (n=10), the ventricle contained eGFP+DsRed+ cardiomyocytes (arrows in Fig. 8E-L), which we categorized as early-differentiating. In addition, the majority of these embryos (n=7/10) also contained some eGFP+ cells at the arterial pole that lacked DsRed and were therefore categorized as late-differentiating (arrowheads in Fig. 8E-L).
Synthesizing all of our data, we propose that both early-differentiating and late-differentiating ventricular cardiomyocytes can become ectopic amhc-expressing cells when FGF signaling is reduced. In addition to the results from our developmental timing assay (Fig. 8E-L), the locations of the observed ectopic cells are consistent with their derivation from both of these populations. Late-differentiating cardiomyocytes populate the arterial pole (de Pater et al., 2009; Hami et al., 2011; Lazic and Scott, 2011; Zhou et al., 2011), whereas early-differentiating cells construct the inner curvature (de Pater et al., 2009; Zhou et al., 2011), and we routinely found ectopic amhc expression in each of these areas (e.g. Fig. 8E-L). We also found ectopic amhc-expressing cells in the proximal portion of the ventricle (e.g. Fig. 8E), another early-differentiating territory (de Pater et al., 2009). Notably, ectopic amhc-expressing cells in this region were also evident in a separate set of experiments in which we mosaically expressed the Tg(hsp70:dnfgfr1) construct in clusters of ventricular cardiomyocytes: in these mosaics, dnfgfr1-expressing cells in the proximal ventricle were found to be Amhc⁺ (Fig. 8M-P). The timeframe during which we observed the appearance of ectopic amhc-expressing cells also fits with the timing of the early and late phases of ventricular differentiation: in embryos with reduced FGF signaling, we could first detect ectopic Amhc within Vmhc⁺ cells in the early-differentiating inner curvature as early as 28 hpf (e.g. Fig. 5E-H), whereas more ectopic cells appeared at the arterial pole after 30 hpf (e.g. Fig. 5I-L), when late-differentiating cells are typically added (Lazic and Scott, 2011). Taken together, our results suggest that FGF signaling plays important and similar roles in both populations of ventricular cells: the FGF pathway represses atrial traits and maintains ventricular characteristics in both early-differentiating and late-differentiating cardiomyocytes.
FGF signaling functions upstream of \textit{nkn} genes to repress ectopic \textit{amhc} expression

In embryos with reduced FGF signaling, as in embryos lacking Nkx transcription factors (George et al., 2015; Targoff et al., 2013), we observe gradual diminishment of the ventricle, gradual enlargement of the atrium, and the appearance of ectopic \textit{amhc} expression in both early-differentiating and late-differentiating ventricular cardiomyocytes. These similarities suggest that FGF signaling and \textit{nkn} genes play comparable roles in the maintenance of ventricular identity. In addition, we found that treatment with a low dose of SU5402 (4 $\mu$m) can subtly enhance the appearance of ectopic \textit{amhc} expression in \textit{nkn}2.5 mutant embryos (Fig. S6), suggesting that FGF signaling and \textit{nkn} genes may operate in the same pathway.

Since FGF signaling has been shown to promote \textit{nkn}2.5 expression in the anterior lateral plate mesoderm of the early embryo (Alsan and Schultheiss, 2002; Keren-Politansky et al., 2009; Reifers et al., 2000; Simões et al., 2011), we examined the expression of \textit{nkn}2.5 and \textit{nkn}2.7 in the hearts of embryos with reduced FGF signaling. In contrast to control siblings, cardiac expression of \textit{nkn}2.5 and \textit{nkn}2.7 was reduced within the ventricle of \textit{Tg(hsp70:dnfgfr1)} embryos following heat shock at 18 hpf (Fig. 9A-D). As \textit{nkn}2.5 and \textit{nkn}2.7 expression are established prior to 18 hpf (Lee et al., 1996), these results suggest that FGF signaling is required to maintain expression of \textit{nkn} genes.

To test the hypothesis that FGF signaling functions upstream of \textit{nkn} genes to prevent ventricular expression of \textit{amhc}, we examined whether overexpression of \textit{nkn}2.5 can inhibit the formation of ectopic \textit{amhc}-expressing cells in embryos with reduced FGF signaling. We employed a previously characterized transgene,
Tg(hsp70l:nkx2.5-EGFP) (abbreviated as Tg(hsp70:nkx2.5)) (George et al., 2015), to induce nkx2.5 expression. Prior studies using this transgene have shown that overexpression of nkx2.5 can rescue the defects in chamber proportionality and repress ectopic amhc expression in nkx2.5 mutants (George et al., 2015). In our experiments, Tg(hsp70:nkx2.5) embryos were treated with SU5402 from 18 hpf and subsequently heat shocked at 24 hpf. We found that 84% of nontransgenic embryos treated with SU5402 had ectopic amhc-expressing cells, whereas only 64% of Tg(hsp70:nkx2.5) embryos exhibited any ectopic amhc expression (Fig. 9E-H). This decrease in the frequency of detecting ectopic amhc expression, while modest, is statistically significant (p=0.0019, Fisher’s exact test) and seems to represent a partial rescue of the SU5402-treated phenotype. Therefore, our results suggest that FGF signaling functions upstream of nkx2.5 in a pathway that insures the maintenance of ventricular identity.
DISCUSSION

Taken together, our data demonstrate that the FGF signaling pathway plays a crucial role in maintaining the characteristics of the developing ventricle. We propose a model in which FGF signaling acts to reinforce the assignment of ventricular identity, both by repressing expression of atrial genes and by promoting expression of ventricular genes. For early-differentiating cells, FGF signaling is required to maintain the appropriate number of cardiomyocytes in the ventricle, as well as to preserve the ventricular characteristics of these cells. For late-differentiating cells, FGF signaling is required to promote their accretion to the arterial pole (de Pater et al., 2009; Lazic and Scott, 2011; Marques et al., 2008; Zeng and Yelon, 2014), as well as to regulate their presentation of appropriate ventricular traits. Thus, sustained FGF signaling suppresses myocardial plasticity and preserves the integrity of the ventricular chamber.

Our studies provide several new insights regarding the nature of ventricular plasticity and commitment. Beyond defining a new role for FGF signaling in enforcing ventricular character, our work has also shed light on the spatial distribution and temporal limitations of ventricular plasticity. Spatially, our results reveal that distinct regions within the ventricle are differentially susceptible to the loss of FGF signaling: for example, we more frequently observe ectopic *amhc*-expressing cells in the inner curvature than in the outer curvature of the ventricle. This differential distribution may signify spatial heterogeneity in the degree to which cells are committed to the ventricular differentiation pathway, with the more primitive myocardium of the inner curvature being more malleable than the working myocardium of the outer curvature. Perhaps commonalities in the programs of gene
expression within the inner curvature and within the arterial pole underlie their similar
dependence on sustained FGF signaling. Temporally, our data indicate a defined
time window during which the ventricular myocardium is vulnerable to the effects of
reduced FGF signaling. Together with prior studies that indicate that nkg2.5 acts to
maintain ventricular identity during a similar timeframe (George et al., 2015), these
findings may reflect the timing of a transition from plasticity to commitment within the
ventricular myocardium. Similarly, a recent study in Xenopus suggested that
ventricular fate can be influenced over a relatively broad time window and that the
responsiveness of ventricular precursors to inductive signals is gradually lost over
time (Caporilli and Latinkic, 2016). In future studies, it will be intriguing to seek the
differences in gene expression that presumably underlie the spatial heterogeneity
and temporal progression of commitment to a ventricular identity.

In addition, our work adds a new facet to our understanding of SHF
development. Numerous studies have focused on the signaling pathways that
regulate the production, proliferation, or differentiation of SHF-derived progenitor
cells (e.g. de Pater et al., 2009; Dyer and Kirby, 2009; Ilagan et al., 2006; Lazic and
Scott, 2011; Park et al., 2006; Tirosh-Finkel et al., 2010; Zeng and Yelon, 2014;
Zhou et al., 2011), but the signals that confer the appropriate chamber-specific
characteristics to these late-differentiating cells have not been characterized.
Strikingly, we find that reduction of FGF signaling causes late-differentiating cells to
inappropriately initiate amhc expression, suggesting either misassignment to an
atrial identity or failure to maintain the ventricular differentiation program. Thus, our
analysis of FGF signaling provides the first demonstration of a pathway that plays a
key role in enforcing ventricular identity in late-differentiating cardiomyocytes.
We note that our studies rely on the expression of vmhc and amhc as proxies for ventricular and atrial identity. Even though neither of these genes is strictly chamber-specific (Berdougo et al., 2003; Foglia et al., 2016; Yelon et al., 1999), they serve here as representatives of larger gene expression programs in the ventricle and the atrium. It would be interesting to evaluate whether the ectopic amhc-expressing cells in the ventricle also express additional atrial genes; unfortunately, amhc is the most robust marker of its type that is currently available. The mechanisms regulating vmhc and amhc expression are undoubtedly relevant to the control of chamber identity, but it will also be valuable for future studies to expand the roster of ventricular and atrial markers and thereby extend our comprehension of the breadth of influence of FGF signaling.

We envision a pathway in which FGF signaling acts upstream of nkx genes, which in turn regulate the downstream effectors irx4 and hey2 (Targoff et al., 2013). Our findings regarding the function of FGF signaling in both early-differentiating and late-differentiating ventricular cardiomyocytes echo what has previously been observed in zebrafish nkx-deficient embryos (George et al., 2015; Targoff et al., 2013). Moreover, our data suggest that FGF signaling acts through nkx2.5 to execute its function in repressing ectopic amhc expression. However, although we observed a statistically significant improvement in SU5402-treated embryos upon overexpression of nkx2.5, this result represents only a partial rescue. One possible explanation for this outcome is that we are failing to induce the level of nkx2.5 expression that is required for thorough repression of ectopic amhc. Alternatively, perhaps both nkx2.5 and nkx2.7 are required to prevent ectopic amhc expression. Since these two genes are not entirely redundant in function (George et al., 2015), overexpression of nkx2.5 may not be able to compensate for reduced activity of
both. Lastly, FGF signaling may act through additional downstream effector genes, beyond *nkx2.5* and *nkx2.7*, to repress ectopic *amhc* and maintain ventricular identity. Identification of these putative downstream effectors of the FGF pathway, as well as elucidation of the mechanism through which FGF signaling promotes *nkx* gene expression, will be important future endeavors.

More broadly, our insights into the signaling pathways that reinforce chamber identity have important implications for approaches to cardiac regenerative medicine. Efforts toward the *in vitro* differentiation of homogeneous populations of mature cardiomyocytes are moving increasingly toward protocols that employ cocktails of small molecules to manipulate signaling pathways and modify chromatin (e.g. Cao et al., 2016). As these protocols are further refined, it will be crucial to control not only the pathways that direct chamber-specific lineage decisions but also the pathways that reinforce commitment to chamber identity. Our work suggests that regulation of the FGF signaling pathway will be an important element of future regenerative medicine strategies that aim to harness the inherent plasticity of ventricular cardiomyocytes.
MATERIALS AND METHODS

Zebrafish

We used the following zebrafish strains: Tg(hsp70l:dnfgfr1-EGFP)pd1 (Lee et al., 2005), Tg(hsp70:ca-fgfr1)pd3 (Marques et al., 2008), Tg(amhc:egfp)s358 (Zhang et al., 2013), Tg(myl7:H2A-mCherry)sd12 (Schumacher et al., 2013), Tg(myl7:egfp)twu277 (Huang et al., 2003), Tg(myl7:dsredt4)sk74 (Garavito-Aguilar et al., 2010), Tg(hsp70:nkx2.5-EGFP)fcu1 (George et al., 2015), nkx2.5\textsuperscript{vu179} (Targoff et al., 2013), and fgf8a\textsuperscript{ti282a} (Reifers et al., 1998). The fgf8a\textsuperscript{ti282a} mutation alters splicing and may not be a null allele, since low levels of wild-type transcript can be detected in mutant embryos (Reifers et al., 1998). All zebrafish work followed IACUC-approved protocols.

Immunofluorescence and in situ hybridization

Whole-mount immunofluorescence was performed as previously described (Alexander et al., 1998), using the antibodies in Table S2. Previously described protocols were also used for in situ hybridization (Thomas et al., 2008) and fluorescent in situ hybridization in combination with immunofluorescence (Zeng and Yelon, 2014), using established probes for amhc (myh6; ZDB-GENE-031112-1), vmhc (ZDB-GENE-991123-5), myl7 (ZDB-GENE-991019-3), nkx2.5 (ZDB-GENE-980526-321), nkx2.7 (ZDB-GENE-990415-179), and mef2cb (ZDB-GENE-04901-7). All data represent at least two technical replicates of each experiment.
Cardiomyocyte counting

To count cardiomyocytes in Figure 3, we employed embryos carrying the transgenes Tg(hsp70l: dnfgfr1-EGFP) and Tg(myl7:H2A-mCherry). We counted both Amhc\(^+\) and Amhc\(^-\) cardiomyocyte nuclei using an established protocol (Schoenebeck et al., 2007) and employed a two-tailed, unpaired t-test to compare data sets. To estimate the numbers of ectopic amhc-expressing cells in Figures 1 and 2, we scored morphologically evident cells in which the NBT/BCIP precipitate surrounded a presumed nucleus, as in prior studies (Thomas et al., 2008).

Photoconversion

To generate Tg(amhc:dendra), we placed the Dendra coding sequence downstream of the previously characterized amhc promoter (Zhang et al., 2013). Transgenic founders were established using standard techniques for I-SceI-mediated transgenesis (Soroldoni et al., 2009). F1 and F2 progeny of two different founders with comparable expression levels were used.

We treated Tg(amhc:dendra) embryos with either SU5402 or DMSO at 18 hpf, and subsequently performed photoconversion at 26 hpf through exposure to a series of 30 second intervals of UV light, using a DAPI filter set on a Zeiss Axioimager microscope. Exposure continued for up to 120 seconds, until all Tg(amhc:dendra)-expressing cells exhibited red fluorescence. Embryos were maintained in either SU5402 or DMSO until 48 hpf.
**Imaging**

Images were captured using a Zeiss Axioimager and Axiocam and were processed using Zeiss Axiovision and Adobe Creative Suite software. Confocal imaging was performed with a Leica SP5 confocal laser-scanning microscope and analyzed using Imaris software (Bitplane).

**Heat shock**

Embryos from outcrosses of fish heterozygous for Tg(hsp70l:dnfgfr1-EGFP), Tg(hsp70l:ca-fgfr1), or Tg(hsp70l:nkx2.5-EGFP) were kept at 28.5°C prior to heat shock. To perform heat shock, embryos were added to 500 mL of E3, pre-equilibrated to 37.5°C. Tg(hsp70l:dnfgfr1-EGFP) clutches were incubated at 37.5°C for 22 min; in most of our experiments with this transgene, we administered heat shock at 18 hpf, since treatment at this timepoint proved to be the most potent (Fig. 1 and Fig. 2). Tg(hsp70l:ca-fgfr1) clutches were incubated at 37.5°C for 60 min at 18 hpf. Rescue experiments were conducted by first treating Tg(hsp70l:nkx2.5-EGFP) embryos with SU5402 at 18 hpf, followed by heat shock at 24 hpf at 37.5°C for 60 min.

Following heat shock, embryos carrying Tg(hsp70l:dnfgfr1-EGFP) or Tg(hsp70l:nkx2.5-EGFP) were identified by eGFP induction, and embryos carrying Tg(hsp70l:ca-fgfr1) were identified by red fluorescence in the lens. For all experiments employing heat shock, nontransgenic siblings served as controls.
**SU5402**

SU5402 treatments were performed as previously described (Marques et al., 2008). A 10 mM stock of SU5402 (Tocris and Sigma) in DMSO was diluted to a working concentration of 5 μM in E3 medium. Control embryos were treated with a corresponding dilution of DMSO in E3. Up to 12 embryos were housed in 1 mL in a glass vial.

We chose to use 5 μM SU5402 after comparing the effects of a range of doses. This concentration caused a consistent cardiac phenotype without notable toxicity. Higher concentrations were more potent and led to Amhc being found throughout the heart, consistent with prior observations (Reifers et al., 2000), but these doses also caused considerable embryonic toxicity.

In all assays performed, SU5402 treatment and heat-induced expression of *dnfgr1* produced comparable results. However, *Tg(hsp70l:dnfgr1-EGFP)* embryos were used whenever possible, since they exhibited a more consistent phenotype. In some experiments (Fig. 5, Fig. 6, and Fig. 8A-L), we took advantage of SU5402 treatments in order to avoid complications resulting from perdurance of the GFP reporter within *Tg(hsp70l:dnfgr1-EGFP)*.

**Mosaic expression**

For mosaic studies, wild-type embryos at the one-cell stage were injected with 30 pg of *Tg(hsp70l:dnfgr1-EGFP)* (Lee et al., 2005) plasmid. Embryos were heat shocked at 18 hpf and fixed for immunofluorescence at 48 hpf.
ACKNOWLEDGMENTS

We thank K. Cooper, S.A. Wasserman, and members of the Yelon laboratory for thoughtful input.

COMPETING INTERESTS

No competing interests declared.

AUTHOR CONTRIBUTIONS

AP and DY designed these studies; AP, XXZ, PS, SM, and DY performed experiments; VG, KLT and NCC generated reagents; AP and DY analyzed the data; and AP and DY wrote the manuscript with input from all authors.

FUNDING

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REFERENCES


Figure 1.

Inhibition of FGF signaling results in ectopic *amhc* expression in the ventricle.

(A-D) In situ hybridization depicts *amhc* expression in frontal views at 48 hpf. (A) Wild-type embryos express *amhc* in the atrium. Similar phenotypes are seen in all controls examined: wild-type siblings of *fgf8a* mutants, nontransgenic siblings following heat shock, and DMSO-treated siblings. (B) In *fgf8a* mutants, *amhc* expression is found not only in the atrium but also in a small cluster of ventricular cells (arrowhead; n=32/46 mutants). (C) More ectopic *amhc*-expressing cells are induced in *Tg(hsp70:dnfgfr1)* embryos following heat shock at 18 hpf (n=15/15); these cells are typically seen along the inner curvature (arrow) and at the arterial pole (arrowhead) of the ventricle. (D) Similarly, ectopic *amhc*-expressing cells can be induced by exposure to SU5402 starting at 18 hpf (arrowhead; n=15/15). The relatively mild phenotype of *fgf8a* mutants (B), compared with the more striking
presence of ectopic cells in *Tg(hsp70:dnfgfr1)-expressing and SU5402-treated embryos (C,D), suggests that additional FGF ligands may work together with *fgf8a* to prevent inappropriate *amhc* expression.

(E-H) Immunofluorescence with MF20 (marks the myocardium; red) and S46 (recognizes Amhc; green) shows cardiac morphology and Amhc localization in lateral views at 48 hpf. In contrast to wild-type (E), ectopic Amhc (arrowheads) is seen in *fgf8a* mutants (F), *Tg(hsp70:dnfgfr1)* embryos after heat shock at 18 hpf (G), and embryos treated with SU5402 from 18-30 hpf (H) (n>10 each).

Scale bars: 50 μm.
Figure 2.

Defining a time interval during which FGF signaling prevents ectopic *amhc* expression.

(A-C) In situ hybridization depicts *amhc* expression in frontal views of nontransgenic (A) and *Tg(hsp70:dnfgfr1)* (B,C) embryos at 50 hpf. Heat shock at 24 hpf (A,B) induces ectopic *amhc*-expressing cells in nearly all *Tg(hsp70:dnfgfr1)* embryos (B, n=22/24), whereas ectopic cells are induced less frequently with heat shock at 28 hpf (C, n=6/36). Heat shock at 18 hpf gives rise to approximately 20-30 ectopic *amhc*-expressing cells (Fig. 1C), heat shock at 24 hpf induces approximately 5-10 ectopic *amhc*-expressing cells (B, arrowhead), and approximately 2-3 ectopic cells are produced with heat shock at 28 hpf (C, arrowhead).
(D-F) Three-dimensional reconstructions of immunofluorescence, as in Fig. 1E-H, of nontransgenic (D) and Tg(hsp70:dnfgfr1) (E,F) embryos. While Tg(hsp70:dnfgfr1) embryos heat shocked at 18 hpf (Fig. 1G) typically display ectopic amhc-expressing cells in the ventricular inner curvature and at the arterial pole, Tg(hsp70:dnfgfr1) embryos heat shocked at 24 (E) and 28 hpf (F) primarily exhibit ectopic cells at the arterial pole (arrowheads) (n=15 for nontransgenic, n=10 per condition for Tg(hsp70:dnfgfr1)).

Scale bars: 50 μm.
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- **Amhc⁻**: Light gray bars
- **Amhc⁺**: Dark gray bars

- * indicates significant difference
Figure 3.

Progressive accumulation of Amhc⁺ cells and decrease in Amhc⁻ cells in embryos with reduced FGF signaling.

(A-F) Immunofluorescence for Amhc (green) and mCherry (red) allows counting of Amhc⁺ and Amhc⁻ cardiomyocytes in nontransgenic (A,C,E) and Tg(hsp70:dnfgfr1) embryos (B,D,F) carrying Tg(myl7:2A-mCherry). Images depict hearts flattened to facilitate visualization of individual myocardial nuclei at 26.5 (A,B), 36 (C,D), and 50 hpf (E,F). Heat-induced expression of dnfgfr1 at 18 hpf results in a gradual shift in chamber proportions that leads to an enlarged atrium and a reduced ventricle. In addition, there is a visible increase in the presence of Amhc⁺ cells within the ventricle over time.

(G) Bar graphs indicate numbers of Amhc⁺ (grey) and Amhc⁻ (white) cardiomyocytes, as well as the total number of cardiomyocytes (mean±s.d.); asterisks indicate statistically significant differences from nontransgenic (p<0.0001). Cell counts reveal a gradual increase in numbers of Amhc⁺ cells and a corresponding decrease in numbers of Amhc⁻ cells in hearts of Tg(hsp70:dnfgfr1) embryos (26.5 hpf: n=8 for nontransgenic, n=6 for Tg(hsp70:dnfgfr1); 36 hpf: n=11 for nontransgenic, n=9 for Tg(hsp70:dnfgfr1); 50 hpf: n=8 for nontransgenic, n=12 for Tg(hsp70:dnfgfr1)). See Table S1 for the number of ectopic Amhc⁺ cells in a subset of these embryos.

Scale bar: 50 μm.
Figure 4.

Increased expression of *amhc* and reduced expression of *vmhc* in the ventricle of embryos with reduced FGF signaling.

(A-P) In situ hybridization depicts *amhc* (A-H) and *vmhc* (I-P) expression in dorsal (A,B,E,F,I,J,M,N) and frontal (C,D,G,H,K,L,O,P) views, following heat shock at 18 hpf.

(A-H) In contrast to nontransgenic embryos (A-D), *Tg(hsp70:dnfgfr1)* embryos (E-H) fail to restrict *amhc* to the atrium (n>10 each). (E) At 26.5 hpf, *amhc*-expressing cells
can be seen infringing the boundary between the atrium and the ventricle. (F) By 29.5 hpf, amhc levels in ectopic cells are upregulated (arrowhead). (G,H) A prominent population of ectopic cells is found at the inner curvature and arterial pole of the ventricle (arrowhead).

(I-P) While vmhc is robustly expressed in the ventricle of nontransgenic embryos (I-L), this expression pattern is disrupted in Tg(hsp70:dnfgfr1) embryos (M-P) (n>10 each). (M,N) At early stages, Tg(hsp70:dnfgfr1) embryos display lower levels of vmhc expression in regions adjacent to the atrium. (O,P) As development proceeds, vmhc levels at the arterial pole become reduced or absent (arrowheads); moreover, the vmhc expression pattern appears reciprocal to that of ectopic amhc in the ventricle.

Scale bars: 50 μm.
Figure 5.

Increased colocalization of Vmhc and Amhc in the ventricle when FGF signaling is inhibited.

(A-P) Immunofluorescence depicts Vmhc (red) and Amhc (green) localization in embryos treated with SU5402 from 18 hpf. Lateral views are three-dimensional reconstructions (A,E,I,M) or magnified single optical sections, showing both channels (B,F,J,N), green only (C,G,K,O), or red only (D,H,L,P). See Fig. S3 for DMSO-treated control embryos.
(A–D) At 26 hpf, the SU5402-treated ventricle contains only Vmhc (n=10).

(E–H) By 28 hpf, Amhc is evident within some Vmhc+ cells, particularly along the inner curvature (arrowheads; n=9). We presume that these cells are early-differentiating cardiomyocytes, since late-differentiating cardiomyocytes normally contribute to the heart after 30 hpf (Lazic and Scott, 2011).

(I–L) By 32 hpf, increasing numbers of Amhc+Vmhc+ cells are visible in the ventricle (arrowheads; n=11).

(M–P) By 48 hpf, higher levels of Amhc accumulate in ectopic cells (arrowheads), in concert with diminishing levels of Vmhc (n=9).

Scale bars: 50 μm.
Figure 6.

Ectopic amhc-expressing cells are not derived from the atrium or AVC.

(A-L) Dendra fluorescence in live DMSO-treated (A-D) and SU5402-treated (E-L) Tg(amhc:dendra) embryos at 48 hpf, following photoconversion at 26 hpf; two representative SU5402-treated embryos are shown. Images are three-dimensional reconstructions (A-C,E-G,I-K) or single optical sections (D,H,L); lateral views, anterior to the right. (D,H,L) Overlay illustrates location of Dendra\(^+\) cells within the heart; white dashes outline the ventricle. See Fig. S4 for additional information regarding experimental design.

(A-D) In DMSO-treated controls, Dendra is found only in the atrium and AVC. Both green and red forms of Dendra are visible, as illustrated in single channel and merged views (n=10).
(E-L) SU5402-treated embryos exhibit Dendra$^+$ cells in the ventricle, in distinct clusters at the arterial pole and in the inner curvature (arrowheads). Cells at the arterial pole and inner curvature fluoresce green, but not red (arrowheads; n=15). Dendra$^+$ cells are also found in and near the AVC (arrows), as seen in controls (A-D), reflecting the wild-type expression of amhc in this area (Foglia et al., 2016).

Scale bars: 50 μm (A,I); 100 μm (E).
Late-differentiating cardiomyocytes contribute to the heart after inhibition of FGF signaling.

(A-H) Three-dimensional reconstructions (A,E) and single optical sections (B-D,F-H) of live embryos carrying Tg(myl7:egfp) and Tg(myl7:dsredt4), lateral views at 40 hpf, after heat shock at 18 hpf. Due to the differential protein-folding kinetics of eGFP and dsRed (Lepilina et al., 2006), reporter transgene expression distinguishes early-differentiating (eGFP+dsRed+) and late-differentiating cardiomyocytes (eGFP+dsRed−) (de Pater et al., 2009). As in nontransgenic embryos (A-D, n=6), late-differentiating cardiomyocytes (eGFP+dsRed−, dotted outlines) contribute to the arterial pole (brackets) in Tg(hsp70:dnfgr1) embryos (E-H, n=8).

Scale bar: 30 μm.
Figure 8.

FGF signaling influences the identity of both early-differentiating and late-differentiating ventricular cardiomyocytes.

(A-L) Three-dimensional reconstructions (A,E,I) and single optical sections (B-D,F-H,J-L) of live $Tg(\text{amhc:egfp})$; $Tg(\text{myl7:dsredt4})$ embryos, lateral views at 48 hpf, after exposure to DMSO (A-D) or SU5402 (E-L) from 18 hpf.
(A-D) As expected, control embryos display eGFP in the atrium and not in the ventricle, and the arterial pole (bracket) is composed of late-differentiating cardiomyocytes (DsRed⁺) (n=5).

(E-L) In SU5402-treated embryos, eGFP is routinely found in the ventricle (n=10). Two representative embryos (E-H, I-L) illustrate detection of eGFP both in early-differentiating cardiomyocytes (arrows, eGFP⁺DsRed⁺; n=10/10) and in late-differentiating cardiomyocytes (arrowheads, eGFP⁺DsRed⁻; n=7/10).

(M-P) Immunofluorescence for MF20 (magenta), GFP (green), and Amhc (red) at 48 hpf indicates mosaic expression of dnfgfr1-egfp in the ventricle of an embryo that was injected with the Tg(hsp70:dnfgfr1) construct and then heat shocked at 18 hpf; three-dimensional reconstruction (M) and single optical sections (N-P). The dnfgfr1-egfp-expressing cells in the proximal ventricle exhibit variegated levels of Amhc (P; n=3).

Scale bars: 30 μm.
### H

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Figure 9.

FGF signaling functions upstream of *nkr* genes to repress *amhc* expression in the ventricle.

(A-D) In situ hybridization depicts *nkx2.5* (A,B) and *nkx2.7* (C,D) expression in dorsal views at 26.5 hpf, following heat shock at 18 hpf. Nontransgenic embryos (A,C) exhibit robust expression of *nkx2.5* (n=24) and *nkx2.7* (n=12), and *Tg(hsp70:dnfgfr1)* embryos (B,D) exhibit reduced expression of *nkx2.5* (n=24) and *nkx2.7* (n=12). This reflects a reduced amount of ventricular tissue in *Tg(hsp70:dnfgfr1)* embryos (compare to Fig. 4M), as well as lower expression levels within this tissue.

(E-G) In situ hybridization depicts *amhc* expression at 48 hpf in nontransgenic (F) and *Tg(hsp70:nkx2.5)* (E,G) embryos treated with DMSO (E) or SU5402 (F,G); frontal views. In some cases (G), overexpression of *nkx2.5* represses ectopic *amhc* expression in *Tg(hsp70:nkx2.5)* embryos that were treated with SU5402 at 18 hpf and subsequently heat shocked at 24 hpf.

(H) Table reports the results of experiments gauging whether *amhc* expression in the ventricle of SU5402-treated embryos can be repressed by overexpression of *nkx2.5*. Asterisk indicates a statistically significant difference in the frequency of detecting ectopic *amhc* expression, compared to nontransgenic siblings (p=0.0019, Fisher’s exact test), representing partial rescue of the SU5402-treated phenotype. The degree of rescue was not enhanced when we used embryos carrying two copies of *Tg(hsp70:nkx2.5)* or when we administered two rounds of heat shock (data not shown).

Scale bars: 50 μm
### SUPPLEMENTAL FIGURES

**FIGURE S1**

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Supplemental Figure S1.

Expression of both *vmhc* and *amhc* is initiated by 18 hpf.

(A-I) In situ hybridization depicts expression of *myl7* (A,D,G), *vmhc* (B,E,H), and *amhc* (C,F,I) in dorsal views of wild-type embryos from 14-20 hpf (n=10 for each condition). *myl7* is expressed in all differentiated cardiomyocytes (Yelon et al., 1999). At 14 hpf, a subset of *myl7*-expressing cells express *vmhc* (B) and *amhc* is not yet expressed (C) (Yelon et al., 1999). By 18 hpf, cardiac fusion is underway, and *vmhc* (E) and *amhc* (F) are expressed in relatively medial and lateral populations of cardiomyocytes, corresponding to the locations of ventricular and atrial precursors (Schoenebeck et al., 2007). By 20 hpf, cardiomyocytes fuse at the midline to form a cardiac cone (Yelon et al., 1999), and *vmhc* (H) and *amhc* (I) expression are expressed in relatively central and peripheral populations of ventricular and atrial cardiomyocytes (Berdougo et al., 2003).

We do not consider either *vmhc* or *amhc* to be expressed in a strictly chamber-specific fashion: for example, low levels of *vmhc* are present in atrial cells at early stages (Berdougo et al., 2003; Yelon et al., 1999), and a subset of cells at the apex of the ventricle have been shown to express *amhc* (Foglia et al., 2016). Even so, the differences between the *vmhc* and *amhc* expression patterns point to the initiation of distinct differentiation programs in ventricular and atrial precursor populations, beginning as early as 18 hpf.

Scale bar: 50 μm.
Supplemental Figure S2.

Distribution of amhc and vmhc expression is unaffected by increased FGF signaling.

(A-D) In situ hybridization depicts frontal views of amhc (A,B) and vmhc (C,D) expression at 50 hpf, following heat shock at 18 hpf. Nontransgenic embryos (A,C) show stereotypical expression patterns of amhc and vmhc (n=10). Increased FGF signaling in Tg(hsp70:ca-fgfr1) embryos (B,D) results in slight morphological changes,
consistent with prior observations (Marques et al., 2008). However, increased FGF signaling does not repress amhc in the atrium or result in ectopic vmhc expression (n=10).

Scale bar: 50 μm.
Supplemental Figure S3.

Vmhc antibody marks expected locations of vmhc expression within the heart.

(A-L) Immunofluorescence depicts Vmhc (red) and Amhc (green) localization in wild-type embryos treated with DMSO at 18 hpf. Images are three-dimensional reconstructions of lateral views at 26-48 hpf, showing both channels (A,D,G,J), green only (B,E,H,K), or red only (C,F,I,L). The Vmhc antibody marks the expected locations of vmhc expression within the heart (n=10 for 26.5 hpf; n=8 for 28 hpf; n=8 for 32 hpf; n=8 for 48 hpf). Vmhc immunostaining recapitulates expression of the reporter transgene Tg(vmhc:mCherry-NTR) (Zhang et al., 2013), as well as expression of vmhc itself (Fig. 4I-L). Vmhc is robustly detected in the ventricle, with low levels in the atrium that diminish over time, as has been previously shown for expression of vmhc (Fig. 4I-L) (Yelon et al., 1999).

Scale bar: 50 μm.
**Supplemental Figure S4.**

**Tg(amhc:dendra) facilitates tracking of amhc-expressing cells.**

**(A-B)** *Tg(amhc:dendra)* hearts before (A) and after (B) photoconversion at 26 hpf, lateral views. *Tg(amhc:dendra)* expression recapitulates the expression of the reporter transgene *Tg(amhc:eGFP)* (Zhang et al., 2013) and the expression of *amhc* itself (Fig. 4A-D): it is expressed throughout the atrium. Upon photoconversion, Dendra fluorescence is converted from green to red. Photoconversion at 26 hpf permits labeling of *amhc*-expressing cells throughout the atrium, and these photoconverted cells can then be detected at later stages (Fig. 6).

**(C-D)** In situ hybridization depicts *amhc* expression in dorsal views of DMSO-treated and SU5402-treated embryos at 26 hpf. At 26 hpf, *amhc* expression in SU5402-treated embryos (D) is limited to the atrium; ectopic *amhc*-expressing cells are not yet visible at this stage.
(E) Timeline of experimental design. Since amhc expression is not found in the ventricle of SU5402-treated embryos at 26 hpf, photoconversion at this stage permits examination of whether the ectopic amhc-expressing cells that appear later are derived from within the atrium or the AVC.

Scale bars: 50 μm.
Supplemental Figure S5.

**SHF progenitor cells are present after inhibition of FGF signaling.**

(A-B) MF20 immunofluorescence and *mef2cb* in situ hybridization (green) in lateral views at 30 hpf, after heat shock at 18 hpf. *mef2cb* (green, arrowheads) is expressed in SHF progenitor cells residing next to the differentiated myocardium (red) in both nontransgenic (A, n=8) and *Tg(hsp70:dnfgfr1)* (B, n=8) embryos.

Scale bar: 50 μm.
Supplemental Figure S6.

Subtle enhancement of the *nkh2.5* mutant phenotype by treatment with a low dose of SU5402.

(A-D) In situ hybridization depicts frontal views of *amhc* expression in wild-type (A,B) and *nkh2.5* homozygous mutant (C,D) embryos at 48 hpf. Embryos were treated with DMSO (A,C) or 4 µm SU5402 (B,D) from 18 hpf until 30 hpf. In wild-type embryos, this
relatively low dose of SU5402 altered cardiac morphology but did not induce ectopic
$amhc$-expressing cells (B). However, in a few $nkx2.5$ mutants, this dose of SU5402
resulted in the increased presence of ectopic $amhc$ in the ventricle (arrowhead, D); this
example is representative of 9 similar embryos observed in a total of 135 progeny from
4 independent intercrosses of $nkx2.5$ heterozygotes. This subtle enhancement of the
$nkx2.5$ mutant phenotype (C) suggests that FGF signaling may act in the same pathway
as the $nkx$ genes to repress the inappropriate expression of $amhc$.

Scale bar: 50 μm.
Supplemental Table S1.

Ectopic Amhc\(^+\) cells constitute a small fraction of the total number of Amhc\(^+\) cells in *Tg(hsp70:dnfgfr1)* embryos after heat shock at 18 hpf.

<table>
<thead>
<tr>
<th>Stage</th>
<th>Number of ectopic Amhc(^+) cells</th>
<th>n</th>
<th>Total number of Amhc(^+) cells</th>
<th>n</th>
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<tbody>
<tr>
<td>26.5 hpf</td>
<td>0.6 ± 0.6</td>
<td>5*</td>
<td>139.5 ± 2.9</td>
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<tr>
<td>36 hpf</td>
<td>13.2 ± 5.3</td>
<td>5*</td>
<td>152.8 ± 36.6</td>
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<tr>
<td>50 hpf</td>
<td>26.3 ± 6.7</td>
<td>6*</td>
<td>195.4 ± 16.2</td>
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* Includes only embryos in which the locations of the Amhc\(^+\) cells were unambiguous.
### Supplemental Table S2.

**Antibodies used for immunofluorescence.**

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<th>Antibody</th>
<th>Vendor</th>
<th>Product</th>
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<td>Thermo Fisher</td>
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<td>SouthernBiotech</td>
<td>1090-02</td>
<td>1:100</td>
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