

c-kit expression identifies cardiovascular precursors in the neonatal heart

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Directed differentiation of embryonic stem cells indicates that mesodermal lineages in the mammalian heart (cardiac, endothelial, and smooth muscle cells) develop from a common, multipotent cardiovascular precursor. To isolate and characterize the lineage potential of a resident pool of cardiovascular progenitor cells (CPCs), we developed BAC transgenic mice in which enhanced green fluorescent protein (EGFP) is placed under control of the c-kit locus (c-kit^{BAC}-EGFP mice). Discrete c-kit-EGFP⁺ cells were observed at different stages of differentiation in embryonic hearts, increasing in number to a maximum at about postnatal day (PN) 2; thereafter, EGFP⁺ cells declined and were rarely observed in the adult heart. EGFP⁺ cells purified from PN 0–5 hearts were nestin⁺ and expanded in culture; 67% of cells were fluorescent after 9 days. Purified cells differentiated into endothelial, cardiac, and smooth muscle cells, and differentiation could be directed by specific growth factors. CPC-derived cardiac myocytes displayed rhythmic beating and action potentials characteristic of multiple cardiac cell types, similar to ES cell-derived cardiomyocytes. Single-cell dilution studies confirmed the potential of individual CPCs to form all 3 cardiovascular lineages. In adult hearts, cryoablation resulted in c-kit-EGFP⁺ expression, peaking 7 days postcryoablation. Expression occurred in endothelial and smooth muscle cells in the revascularizing infarct, and in terminally differentiated cardiomyocytes in the border zone surrounding the infarct. Thus, c-kit expression marks CPC in the neonatal heart that are capable of directed differentiation in vitro; however, c-kit expression in cardiomyocytes in the adult heart after injury does not identify cardiac myogenesis.

bacterial artificial chromosome | progenitor cell | stem cell

The process of early heart cell specification from pluripotent cardiovascular progenitor cells (CPCs) has recently been advanced that a common cardiovascular precursor can give rise to cardiomyocytes, endothelial cells, and smooth muscle cells through directed differentiation of ES cells in vitro, and when these cells are implanted into adult hearts (1–5). Several markers have been reported to identify CPC, including the kinase insert domain protein receptor KDR (also known as Flk-1) (1, 2), the stem cell factor (SCF) receptor c-kit (4–6), the LIM-homeobox transcription factor islet-1 (isl1) (7), and the cardiac transcription factor Nkx2.5 (4). In vitro directed differentiation of ES cells suggests mammalian heart development involves mesoderm specification to a multipotent precursor stage. However, such cells have not been isolated from the heart and shown to undergo multipotent differentiation in vitro, and Nkx2.5-expressing cells isolated from E7.5 and E8.5 mouse embryos could not be induced to expand and differentiate (4).

Used extensively as a marker to identify adult hematopoietic stem cells, c-kit is expressed during various stages of cell lineage commitment in germ, mast, stellate, epithelial, endothelial, and smooth muscle cells (8–10). Isolated c-kit⁺ cells from E9.5 and E10.5 embryos express cardiac and smooth muscle genes in vitro and differentiate to smooth and cardiac myocytes in vivo (4). Here, we report the isolation and characterization of neonatal c-kit⁺ cells from a transgenic mouse in which enhanced green fluorescent protein (EGFP) expression is placed under control of the *kit* locus

within a bacterial artificial chromosome (BAC). EGFP⁺ cells from postnatal c-kit^{BAC}-EGFP mouse hearts expand in culture and differentiate in vitro into cardiac, smooth muscle, and endothelial cells. The study of isolated CPC is likely to provide important information with respect to the genetic status, mechanism of differentiation and commitment, and biological potential of these cells.

Results

Generation of c-kit^{BAC}-EGFP Mice. To facilitate the study of heart precursors known to express c-kit (4–6), we inserted the EGFP coding sequence in frame at the start codon of c-kit (1st exon) (11) within a 186-kb BAC by recombinering methods (Fig. 1A) (12). A founder line was identified by a 1.1-kb PCR amplicon that included c-kit and EGFP DNA (Fig. 1A and B). Neonatal c-kit^{BAC}-EGFP pups displayed intense skin fluorescence consistent with the expression of c-kit in melanocytes (Fig. 1C) (10), and were easily distinguished from nontransgenic littermates by using a hand-held fluorescent light source and filtered goggles [see [supporting information \(SI\) Materials and Methods](#)]. In adult mice strong EGFP fluorescence was observed in a variety of organs in a pattern consistent with endogenous c-kit expression (Fig. 1D); expression was observed in interstitial cells of the intestines and stomach, muscle layer of the uterus and testis. EGFP was detected by immunohistochemistry in Leydig cells and outer layer spermatogonium in the testis, in basket and stellate cells in the molecular layer of the cerebellum, and within the hippocampus (Fig. 1E), consistent with the cell-type-specific expression of c-kit in these tissues (13). As expected from a genetic strategy in which the endogenous locus was not altered, c-kit^{BAC}-EGFP mice display no apparent phenotype.

Spatial and Temporal Expression of EGFP in the Heart. The expression pattern of EGFP was analyzed in heart sections from embryonic [14.5 and 18.5 days post coitus (dpc)], PN 2–3, and adult c-kit^{BAC}-EGFP mice. Fluorescent cells were observed in the atrial and ventricular walls at 14.5 dpc (Fig. 2A *Top*). The total number of EGFP expressing cells increased as the heart expanded in size, peaking shortly after birth (PN 2–3; Fig. 2A *Middle*). Thereafter, the number declined rapidly and c-kit-EGFP⁺ cells were only occasionally observed as mononuclear cells within vascular compartments, or rarely as a striated myocytes within the cardiac intersti-

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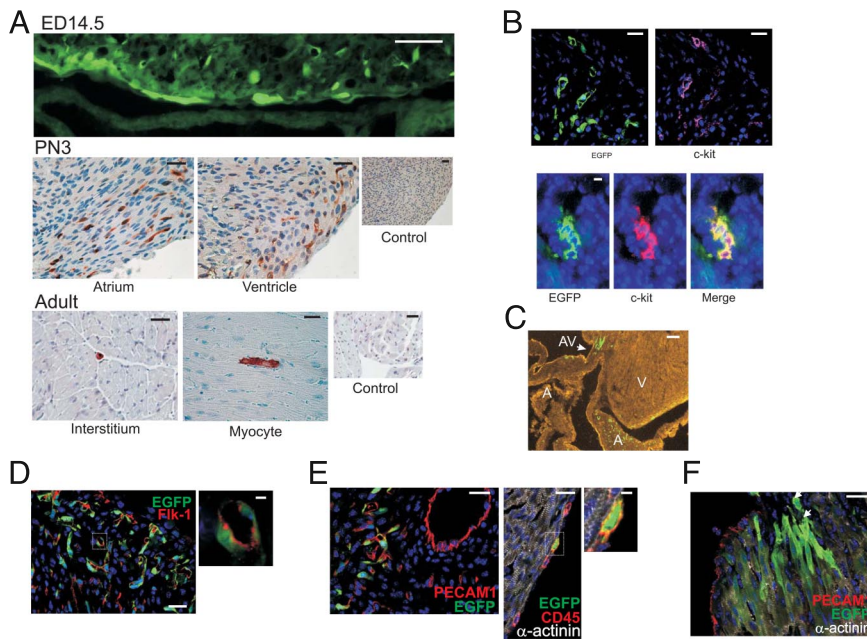


Fig. 2. EGFP expression in *c-kit*^{BAC}-EGFP mouse hearts. (A) EGFP expression in the heart wall of 14.5-dpc embryo (fluorescence) and PN 3 (immuno) neonates. In the adult heart rare immunostained cells were observed. Control, no 1^o antibody. (B) EGFP/*c-kit* expression concordance. Anti-EGFP (green); anti-CD117 (red). Note lack of coexpression (*Upper*) and colocalization within a niche (*Lower*). (C) Native EGFP expression in the atrioventricular region of a PN 2 heart. (D) Some cells coexpressed Flk-1 and EGFP. (E) Some *c-kit*⁺ cells coexpress PECAM1, indicating endothelial commitment. Very bright EGFP-expressing cells were commonly observed in the epicardium; these cells commonly coexpressed the hematopoietic lineage marker CD45. (F) *c-kit*-EGFP⁺ cells in the atrioventricular region showing a gradient of EGFP expression, from less differentiated bright cells (arrows), to less fluorescent striated cells. A, atrium; AV, atrioventricular region; and V, ventricle. Hoechst staining (blue) (B, D–F). (Scale bars: A, 14.5 dpc, 50 μ m, and others, 25 μ m; B, 10 μ m; C, 50 μ m; D, 25 μ m; D *Inset*, 10 μ m; E *Left*, 25 μ m; E *Center*, 20 μ m; E *Right*, 5 μ m; F, 25 μ m.)

morphologies included nodal, atrial, and ventricular characteristics (Fig. 4B). Spontaneously depolarizing phase 0 currents and stable resting potential were observed, as well as atrial- or ventricular-like plateau phases and nodal-type transient depolarizations. Phasic electrical activity included both stable depolarization rates and complex, repeated burst-type activity (18). The latter pattern was observed mainly in networked EGFP⁺ cells, and occasionally in single EGFP cells. AP characteristics were summarized based on the level of resting membrane potential (RMP) (Table S1). Group 1 displayed the most depolarized RMP (-46 ± 2.8 mV), the slowest upstroke velocity (dv/dt , 4.4 ± 1 V/sec), and the longest duration (APD⁹⁰, 123.6 ± 10.5 ms). APs in groups 2 and 3 displayed more stable RMPs (-60 ± 0.6 mV and -75 ± 1 mV, respectively), faster dv/dt (34.5 ± 6.3 and 69.5 ± 9.6 V/sec), and shorter APD⁹⁰ (77.8 ± 7.7 and 66.5 ± 13.9 ms). Significant differences existed between all 3 groups for the parameters mentioned above ($P < 0.05$), with the exception of APD⁹⁰ between groups 2 and 3. No significant difference existed between mean AP frequencies for group 1 (240 ± 34 min⁻¹), group 2 (287 ± 28 min⁻¹), or group 3 (205 ± 30 min⁻¹).

The ion channel dependence of the APs was investigated by using blockers of cardiac fast sodium channels [tetrodotoxin (TTX), 10 μ M], and L-type calcium channels (nifedipine, 1 μ M). TTX abolished APs in a reversible manner (Fig. 4C), indicating the cardiac nature of these currents; nifedipine also inhibited the APs, indicating the importance of L-type Ca²⁺ channels (Fig. 4D). Taken together, these data indicate the cardiac phenotype of spontaneously contracting *c-kit*-EGFP⁺-derived cells.

Lineage Potential of *c-kit*⁺-EGFP Precursor Cells. To determine whether individual *c-kit*-EGFP⁺ cells are multipotent, we sorted sEGFP cells and cultured them for 9–16 days under conditions designed to promote cardiovascular lineage differentiation. Wells were stained for cardiac, smooth muscle, or endothelial markers, and the fraction of positive cells counted in all wells. Cardiac differentiation was markedly favored in media containing bFGF, with $\approx 15\%$ of cells expressing the troponin T, compared with $< 3\%$ in media containing tumor growth factor- $\beta 1$ (TGF- $\beta 1$) or vascular endothelial growth factor (VEGF) (Fig. 5). Addition of VEGF to the media enhanced the expansion of endothelial and smooth muscle cells, and the latter effect was more potent than that observed in TGF- $\beta 1$ media. TGF- $\beta 1$, which promotes smooth

muscle differentiation (2, 4), significantly decreased in cardiac myogenesis. Thus, *c-kit*^{BAC}-EGFP cells from neonatal hearts can be manipulated *in vitro* to selectively expand the 3 cardiovascular lineages.

Because the above results could reflect induced expansion of precommitted cells or selective differentiation of multipotent precursors, we performed limiting dilution studies to determine the fate of individual clonal populations. Cells were plated to yield one cell per well and cultured for 21 days; $\approx 15\%$ of the individual cells counted on day 3 survived and expanded during the culture period (Fig. 5B). Separate immunostaining of the expanded populations revealed individual committed cardiac, smooth muscle, and endothelial cells among cells that did not express these markers (Fig. 5C). The above result, in which cells of all 3 lineages were detected, was repeated in 19 separate dilution experiments. Costaining for α SMA and PECAM1 or troponin T and PECAM1 clearly demonstrated smooth muscle and endothelial or cardiac and endothelial lineages arising in clonal expansions (Fig. 5D). *In vitro* expansion of single clones to all 3 cardiovascular lineages indicates that *c-kit*-EGFP⁺ cells from neonatal hearts include a population of undifferentiated cells similar to ES cell-derived cardiovascular precursor cells (2, 4, 7).

Reexpression of *c-kit*-EGFP⁺ after Injury. To analyze *c-kit* expression following myocardial injury, we induced cryolesions in the left ventricle of adult *c-kit*^{BAC}-EGFP mice (19). Seven days after cryolesion there was marked expression of fluorescent cells in the infarct and the border zone, with fluorescent cells often associated with vessels within the infarcts, and modestly fluorescent striated cardiomyocytes surrounding the border zone (Fig. 6A). In sham-operated mice rare EGFP⁺ cells were equally distributed throughout the myocardium. EGFP expression increased by day 3, peaked at 7 days, and declined at 21 days postinjury.

EGFP⁺ cells within the infarct were found preferentially in contributing to blood vessels (Fig. 6B *Left* and *Inset*). Luminal EGFP cells in vessels were PECAM1 positive (Fig. 6B *Right*), whereas cells surrounding larger vessels stained for α -SMA (data not shown), thus contributing to the endothelium and smooth muscle layer of vessels. Single endothelial cells formed lumens, consistent with early angiogenesis. Fluorescent cells within vessels were still observed 21 days after the lesion. By contrast, the pattern of EGFP expression in the border zone was different, with modest,

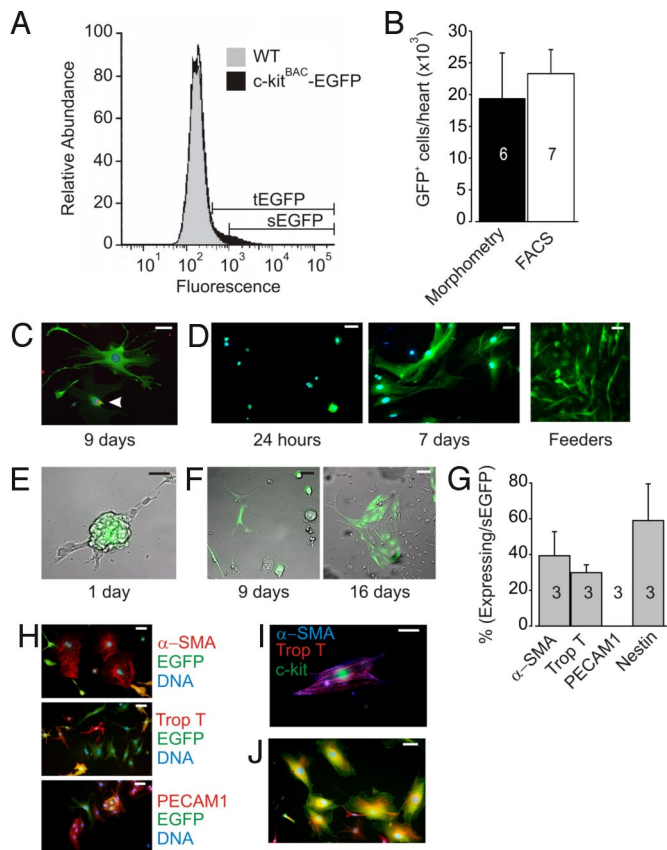


Fig. 3. Isolation and expansion of FACS sorted cardiac c-kit-EGFP cells. (A) Representative FACS from PN c-kit^{BAC}-EGFP and WT littermate hearts. WT and EGFP histograms were normalized to same maximum. tEGFP overlaps with brightly autofluorescent WT cells; sEGFP identifies a pure c-kit-EGFP⁺ population of cells 5 times brighter than background fluorescence. (B) Morphometry and FACS estimate of EGFP⁺ cells in neonatal hearts. (C) EGFP expression and PCNA (red) staining indicates cycling in c-kit sEGFP⁺ cells cultured for 9 days in basic media. Arrow indicates PCNA staining. (D) EGFP expressing cells at 24 h (Left) and 9 days (Center) post-FACS. Note differences in cell size and shape. At right tEGFP cells plated on feeders expand rapidly (3 days) in a network pattern. (E) Merged bright-field and fluorescent image show after 1 day in culture some tEGFP cells form clusters. (F) Images taken from the same field of 9 days (Left) and 16 days (Right) post-sEGFP⁺ plating in basic media shows expansion of cells. Images are merged fluorescent and bright field. Some cells at both 9 and 16 days are no longer fluorescent. (G) Distribution of committed cells 24 h post-FACS (tEGFP cells). Note lack of endothelial cells (PECAM1) and equal distribution of smooth muscle (α SMA) and cardiac cells (troponin T). Nestin staining suggests a population of undifferentiated cells. Number of experiments is indicated in bars. (H) Costaining 9–16 days post-FACS (sEGFP cells). (I) c-kit (green) cell expressing both α SMA (blue) and troponin T (red) markers. Merge of α SMA and troponin T yields purple. (J) Nestin (red) and c-kit (green) costaining in cells cultured for 9 days. (H and I) DAPI staining (blue). (Scale bar: C, 20 μ m; D–F, H, and J, 50 μ m; I, 10 μ m.)

EGFP expression in striated cardiomyocytes (Fig. 6C) and robust expression in elongated fibroblasts. EGFP⁺ cardiomyocytes did not express phosphohistone H3 (pHH3), a marker of cell proliferation, and the number of these cells peaked at day 7 and declined to the level of sham control by day 21 (Fig. 6D). Neither mitotic figures nor immature cardiomyocytes were observed postcryoablation. Troponin T-positive cells were never observed within the infarct, indicating a lack of cardiac myogenesis. pHH3⁺ fibroblasts and leukocytes were observed within the infarct and at the border zone, only \approx 1% of pHH3⁺ cells were also c-kit⁺. Thus, c-kit expression is observed in cells associated with the early revascularization and fibrosis of the infarcted heart, declining within a few weeks after injury, and is also seen in differentiated myocytes, but the latter is not associated with myocyte proliferation.

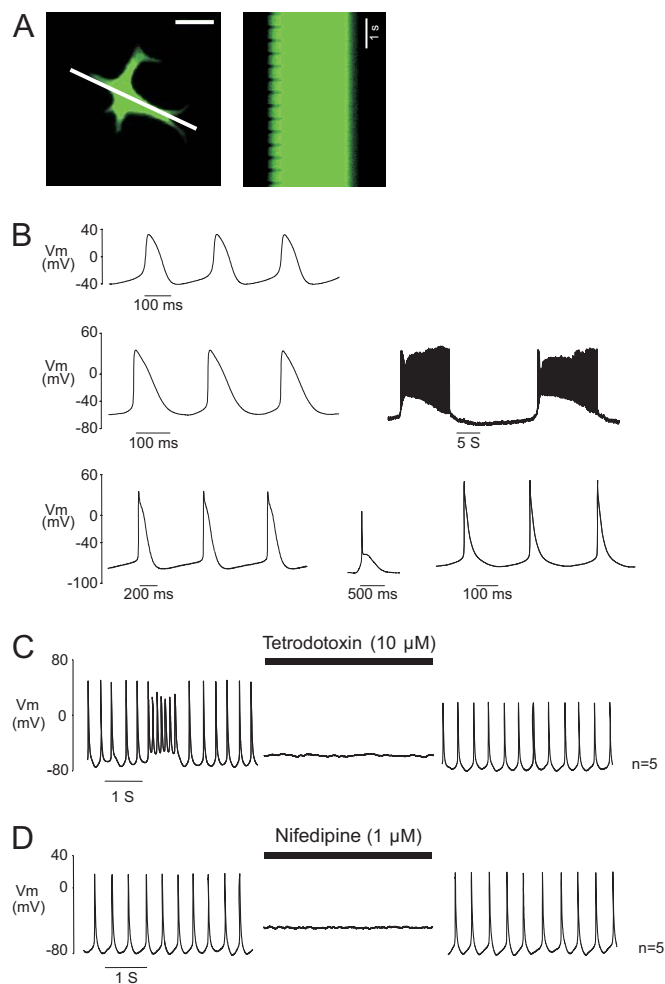


Fig. 4. Cardiac phenotype of spontaneously beating c-kit⁺-EGFP cells. (A) Single, contractile EGFP expressing cell at left in single frame from a time series. Line through image indicates area used for sequential scans of fluorescence shown at right. Left edge of line scan shows rhythmic contraction of the top left cell extension at \approx 2 Hz. (Scale bar: 25 μ m.) (B) APs ranged from nodal-like (Top), to more atrial (Middle) or ventricular (Bottom) morphologies. Note prominent diastolic depolarization phases. Networked c-kit-EGFP⁺ cells fired rhythmic burst-like activity, interrupted by periods of quiescence accompanied by prominent membrane hyperpolarization. (C) TTX (10 μ M, $n = 5$) or (D) Nifedipine (1 μ M, $n = 5$), reversibly abolished APs.

Discussion

Recent evidence suggests that within the developing heart a resident population of CPC exists, with the capacity to differentiate into multiple cardiovascular cell lineages (4). C-kit expression appears to characterize a developmental stage of one subset of these cardiovascular precursor cells (1), but studies in mouse (4) and human (2, 3) ES cell-derived precursors suggest that a c-kit-negative stage precedes commitment. To examine the role of c-kit expression in CPCs, and to facilitate their isolation and analysis, we created BAC transgenic mice in which EGFP is placed under the transcriptional control of the c-kit locus to achieve high expression levels and outstanding transcriptional fidelity (20, 21). Bernex *et al.* (22) and Wouters *et al.* (23) knocked reporters into the c-kit locus, but did not examine cardiac expression, and the dominant nature of the c-kit locus complicates this strategy. A minimal c-kit promoter strategy yielded similar results with the concordance of CD117 and anti-GFP staining that declined after birth (24, 25). We show that embryonic and postnatal c-kit⁺ cells are in a mixed developmental state within the developing heart (Fig. 2), as predicted for a

attach or partial digestion of the PECAM1 epitope during enzymatic dissociation.

Our attempts to culture single purified FACS sorted c-kit⁺ cells resulted in cell death in ES media. Switching to a medium containing bFGF, a growth factor associated with mesodermal cell survival, cell proliferation, and angiogenesis (4), produced viable cells that expanded and produced differentiated mesenchymal cells in culture. Wu *et al.* (4) also tried to culture FACS sorted Nkx2.5⁺ cells from 7.5- to 8.5-dpc hearts in similar ES cell media without success. The addition of bFGF appears to be necessary for the propagation of c-kit⁺ cells in culture (Fig. 5A).

The above results could suggest either the presence of multipotential cardiovascular precursors within the purified cell population, or the selective survival and expansion of precommitted populations under appropriate in vitro conditions. To determine whether c-kit-EGFP⁺ cells include uncommitted precursors, we undertook clonal analysis by plating cells at limiting dilutions that yielded individual cells within multiwell plates. The absence of attachment factors and conditioning substances resulted in relatively low viability of clones; however, individual surviving cells were observed to expand into clonal colonies and were probed for lineage commitment 21–25 days after plating. Evidence of commitment to all 3 cardiovascular lineages was observed in these clonal populations, although the majority of cells did not express any lineage-specific markers (Fig. 5C). The presence of uncommitted cells within these colonies suggests that the results are not simply explained by expansion of a previously committed cell, that definitive evidence of multilineage potential was obtained by costaining of these clonal populations (Fig. 5D). Differentiation of individual cells to both muscle (cardiac and smooth) and endothelium was observed, definitively establishing the multilineage potential of neonatal c-kit-EGFP⁺ cells. These results are similar to those reported by Moretti *et al.* (7), who clonally amplified Isl1⁺ cells from ED8–8.5 heart cell cultures, and showed that a rare number of these cells differentiated into endothelium, cardiac, and smooth muscle cells. These Isl1⁺ and/or Nkx2.5⁺ cells, isolated from hearts at a markedly earlier stage of development, do not express c-kit (15), and our results confirm a lack of Isl1 staining in c-kit^{BAC}-EGFP⁺ cells.

Recent work (25) demonstrated that pressure overload results in augmented expression of c-kit in cardiomyocytes. Such expression could reflect cardiomyogenesis from c-kit⁺ CPc, or could be the result of c-kit reexpression in committed myocytes. We show that c-kit expression in the adult injured

heart is associated with fibrous and vascular infarct repair, but not myogenesis. C-kit expression is detectable within 3 days postinjury, peaks at 7 days, and declines within a 4-week period to near baseline. EGFP⁺ expression in cardiomyocytes was only observed in striated, terminally differentiated cells. The lack of EGFP⁺ myocytes within the infarct zone, absence of immature (nonstriated) troponin T-positive myocytes, and lack of mitotic figures or pHH3 staining in EGFP⁺ myocytes indicate that cryoinjury does not provoke cardiomyogenesis through activation of c-kit. Rather, these factors indicate that c-kit reexpression occurs in differentiated cardiomyocytes at regions surrounding cardiac injury, activated by local conditions such as hypoxia or inflammatory cytokines, because these cells are not seen at remote regions. Thus, rather than unequivocally identifying adult cardiac precursors, c-kit reexpression in adult cardiac myocytes appears to play a role in the transcriptional activation of fetal/neonatal genes that are induced during cardiac stress (25).

In summary, we describe the purification of a population of cells that includes mesodermally derived cardiovascular precursors, as well as cells in early stages of cardiovascular development. Our results indicate that true CPcs persist through embryonic development and that the PN heart contains significant numbers of these cells, which decline rapidly in the first weeks after birth. Isolated CPcs differentiate into rhythmically contracting cell networks, and individual cells display complex electrical activity. C-kit-EGFP⁺ cells can be expanded in vitro, although the multipotency of expanded and passaged EGFP⁺ cells remains to be demonstrated. Finally, c-kit-EGFP⁺ cells are observed transiently in damaged heart tissue, but do not identify prominent reactivation of resident CPcs in the adult heart. Neonatal c-kit-EGFP⁺ cells may prove useful for determination of the genetic basis of CPc status and provide a model for the directed differentiation of pluripotent cells for cardiac cell-based therapy.

Materials and Methods

Generation of Tg(RP24-330G11-EGFP)1Mik Mice and Neonatal Heart Characterization. Detailed BAC targeting strategy, PCR genotyping FACS, culturing parameters, electrophysiology, and immunohistochemistry characterization of c-kit-EGFP⁺ cells are found in *SI Materials and Methods*.

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