GFRA2 Identifies Cardiac Progenitors and Mediates Cardiomyocyte Differentiation in a RET-Independent Signaling Pathway

**Highlights**

- Gfra2 is specific for cardiac progenitors (CPs) among mesodermal cells
- GFRA2 enables isolation of multipotent or unipotent CPs in mouse and human
- Gfra2 and the related molecule Gfra1 play a vital role in heart development
- The GFRA1/2 signal in heart development is independent of established ligands

**In Brief**

Ishida et al. show that GPI-anchored neurotrophic factor receptor Gfra2 specifically marks cardiac progenitor cells (CPs) in mouse and human, providing a method for isolating CPs. Unexpectedly, Gfra2 plays a significant role in heart development via a non-canonical signaling pathway that is independent of known ligands and the co-receptor RET tyrosine kinase.

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GFRA2 Identifies Cardiac Progenitors and Mediates Cardiomyocyte Differentiation in a RET-Independent Signaling Pathway

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SUMMARY

A surface marker that distinctly identifies cardiac progenitors (CPs) is essential for the robust isolation of these cells, circumventing the necessity of genetic modification. Here, we demonstrate that a Glycosylphosphatidylinositol-anchor containing neurotrophic factor receptor, Glial cell line-derived neurotrophic factor receptor alpha 2 (Gfra2), specifically marks CPs. Gfra2 expression facilitates the isolation of CPs by fluorescence activated cell sorting from differentiating mouse and human pluripotent stem cells. Gfra2 mutants reveal an important role for GFRA2 in cardiomyocyte differentiation and development both in vitro and in vivo. Mechanistically, the cardiac GFRA2 signaling pathway is distinct from the canonical pathway dependent on the RET tyrosine kinase and its established ligands. Collectively, our findings establish a platform for investigating the biology of CPs as a foundation for future development of CP transplantation for treating heart failure.

INTRODUCTION

The heart is the first morphologically distinct developing organ in vertebrates. The primordial heart is derived from the anterior part of the lateral plate mesoderm as cardiac progenitors (CPs) being one of the earliest populations emerging from the primitive streak at gastrulation (Kinder et al., 1999; Rana et al., 2013). Lineage tracing experiments have led to the identification of CPs in the first (FHF) and second heart field (SHF) according to their anatomical origin and destiny (Rana et al., 2013). Recently, studies have delineated the complex molecular mechanisms underlying cardiomyocyte differentiation (Kathiriya et al., 2015; Paige et al., 2015); however, our knowledge of the precise spatiotemporal mechanisms that regulate the segregation, identity, and fate of CPs remains incomplete. A major hurdle is the paucity of reliable and specific markers to identify CPs, especially for the robust isolation of living CPs using cell sorting, circumventing the requirement of genetic modification for tagging CPs. Previous reports have demonstrated that Kinase insert domain receptor (KDR, also known as Flk-1), platelet-derived growth factor receptor alpha (PDGFRA), KIT, C-X-C chemokine receptor type 4 (CXCR4), and/or Prion protein (PrnP) can be used in defined combinations to identify and harvest CPs (Bonde et al., 2011; Hidaka et al., 2010; Kattman et al., 2006, 2011; Nelson et al., 2008; Yang et al., 2008). In vitro clonal-tracing studies have revealed that both KDR/PDGFRα* and KDRlow/ KITneg cell populations contain highly enriched multipotent progenitors producing not only cardiomyocytes but also endothelial and smooth muscle cells in mouse and human, respectively (Kattman et al., 2006, 2011; Yang et al., 2008). Moreover, since the expression pattern of each of these factors in the embryo is dynamic and not specific for the cardiac lineage (Hidaka et al., 2010; Kataoka et al., 1997; McGrath et al., 1999; Yang et al., 2008), concerns have been raised about the purity of CPs harvested using these markers. More recently, a cell-surface protein, hyperpolarization-activated cyclic nucleotide-gated potassium channel 4 (HCN4), has been reported to be
transiently specific for FHF CPs during the earliest phase of cardiomyogenesis (Später et al., 2013). However, because there is no commercially available antibody against the extracellular domain of this molecule, its use in cell-sorting experiments is limited. Thus, identification of a CP-specific surface antigen for which an antibody is readily available is essential for furthering our understanding of the critical early events in heart development.

In this study, we found that Glial cell line-derived neurotrophic factor receptor alpha 2 (Gfra2) specifically marks CPs of the FHF and SHF in mouse and human (Airaksinen and Saarma, 2002; Paratcha and Ledda, 2008). The specificity and expression pattern of Gfra2 provides a reliable means to isolate stage-specific CPs with high purity. Strikingly, Gfra2 is essential for heart development, whereas Gfra1, another member of the Gfra receptor family, is functionally redundant. Finally, we demonstrate that the pathway by which GFRA1/2 modulates heart development is independent of the classical Gfra receptor family signaling pathway via the RET proto-oncogene.

RESULTS

Gfra2 Specifically Marks Both FHF and SHF CPs

According to previous single-cell expression profiling of mouse embryonic CPs between days 7.5 and 8.0 post-conception (E7.5–E8.0), we observed that Gfra2, a specific receptor for a neurotrophic factor Neurturin (NRTN), was expressed in CPs but not in embryonic stem cells (ESCs) (42.31 ± 22.53 SEM of CPs versus 0.00 of ESCs in Reads Per Millions, respectively) (Brouilette et al., 2012; Kokkinopoulos et al., 2015). This was consistent with the data demonstrating that Gfra2 was co-expressed within the cardiac mesoderm expressing Mesp1 (Bondue et al., 2011). To confirm the expression pattern of Gfra2 in mouse embryos, we conducted whole-mount in situ hybridization (WISH) analyses in serial stages of early mouse embryos and found that Gfra2 was detected from the Early Atlantico Bud stage simultaneously with one of the earliest markers of CPs, Isl1, and was clearly expressed in the cardiac crescent from E7.5 to E8.5 (Figures 1A and S1A) (Downs and Davies, 1993; Kokkinopoulos et al., 2015). Single-cell expression profiling suggests that Isl1 precedes Gfra2, because Isl1-expressing CPs had a higher incidence of expression of Gfra2 after they had started to express a common marker for the FHF and SHF, Nkx2-5, as they further differentiated (Figure S1B) (Kokkinopoulos et al., 2015). Thereafter, Gfra2 was downregulated in the heart field by the tenomisome stage (E8.75) upon formation of the heart tube (Figure 1A). Immunofluorescence micrographs indicated that Gfra2 protein was prominently detected in the early headfold (EHF) stage CPs (Figure 1B) (Downs and Davies, 1993). Serial sections of the three-somite stage embryos revealed that Gfra2 co-localized with Nkx2-5, TBX5, HCN4 (the FHF), and ISL1 (the SHF) (Figures 1C and S1C) (Cai et al., 2003; Devine et al., 2014; Kokkinopoulos et al., 2015; Liang et al., 2013; Später et al., 2013; Stanley et al., 2002). Therefore, Gfra2 can be considered a marker of CPs within both the FHF and SHF in mouse embryos.

GFRA2 Predominantly Identifies CPs Derived from Pluripotent Stem Cells

Next, to clarify whether GFRA2 marks CPs derived from pluripotent stem cells, we investigated the expression of Gfra2 during cardiac differentiation of mouse ESCs. Quantitative real-time reverse transcription PCR (qPCR) demonstrated that Gfra2 was transiently expressed with its peak at differentiation day 7, before the initiation of spontaneous beating of differentiated cardiomyocytes (Figure 2A). Flow cytometry using an antibody raised against the extracellular domain of GFRA2 revealed that GFRA2 could be identified between differentiation days 4–9, among the PDGFRA positive mesodermal cells (Figures 2B and S2A). Upon culturing the separately isolated cell populations of GFRA2+/PDGFRA+, GFRA2+/PDGFRA−, and GFRA2−/PDGFRA− at differentiation day 7 by fluorescent activated cell sorting (FACS), the majority of GFRA2+/PDGFRA+ cells differentiated into TNNT2+ and ACTN1 (α-ACTININ) cardiomyocytes, without a propensity for differentiation to endothelial cells and smooth muscle cells (Figures 2C–2F, S2B, and S2C; Movie S1). By contrast, the other cell populations rarely contained such cardiac cells. These results suggest that GFRA2+/PDGFRA+ cells at day 7 are already committed to a cardiomyocyte fate but remain as precursor cells without terminal differentiation. The expression of Nkx2-5 (common), TBX5 (FHF), HCN4 (FHF), and ISL1 (SHF) in GFRA2+/PDGFRA+ cells demonstrated that GFRA2+/PDGFRA+ CPs reside in both the FHF and SHF (Figures 2G and S2D) (Cai et al., 2003; Devine et al., 2014; Kokkinopoulos et al., 2015; Liang et al., 2013; Später et al., 2013; Stanley et al., 2002). These data were consistent with our histological results in mouse embryos (Figures 1C and S1C).

To further characterize GFRA2+ cells during cardiac differentiation, we investigated the relationship between GFRA2 expression and the well-validated earliest CPs of the KDR+/PDGFRA+ population in differentiating mouse ESCs (Kattman et al., 2006, 2011). KDR and PDGFRA were already expressed by day 3 of differentiation as previously described (Kattman et al., 2011), and KDR expression was downregulated in the PDGFRA+ population at day 6 (Figure 3A). Of note, from day 4 to 5, almost the entire KDR+/PDGFRA+ population expressed GFRA2. Thus, GFRA2 could also mark the earliest mouse CPs in cardiac differentiating ESCs. When we isolated a GFRA2+/KDR+/PDGFRA+ triple-positive population on day 4 and cultured the cells for a further 7 days, they gave rise not only to cardiomyocytes, but also to endothelial cells (Figure 3B). Given that GFRA2 marked KDR+/PDGFRA+ CPs on differentiation day 4, the earliest GFRA2+ CPs would be expected to be multipotent based on previous reports (Bondue et al., 2011; Kattman et al., 2011). Thereafter, KDR expression would be limited to the endothelial lineage, with cardiomyogenic cells having lost KDR expression after day 6 of differentiation (Figures 3A, S2E, and S2F). Taken together, our findings clearly demonstrate that GFRA2 facilitates the robust isolation of CPs from differentiating mouse ESCs.

GFRA2 Marks Human CPs from Differentiating Human Pluripotent Stem Cells

To challenge whether human GFRA2 can be used for CP isolation from human pluripotent stem cells, we investigated the expression of human GFRA2 during the cardiac differentiation of human
Figure 1. GFRA2 Is Expressed in the First and Second Heart Field Cardiac Progenitor Cells

(A) Whole-mount in situ hybridization (WISH) of Gfra2 in E7.25–8.75 early allantoic bud (EB) stage to the ten-somite (S) stage embryos. Gfra2 was expressed in the cardiac crescent (arrows). Once the heart tube is formed and the looping initiated, Gfra2 is downregulated (red arrowheads). Gfra2 was also expressed in migrating neural crest cells and the rhombomere 4 (white arrowheads). n = 3. Scale bar, 250 μm. EHF, early headfold; LHF, late headfold.

(B and C) Immunohistochemical (IHC) images of GFRA2 in an EHF and three-somite stage embryo. GFRA2 was expressed in the mesodermal regions corresponding to the heart field. n = 4. Scale bar, 50 μm. FHF, first heart field; SHF, second heart field.

See also Figure S1.
Figure 2. GFRA2+/PDGFRA+ Cells Derived from Mouse ESCs Are Unipotent Cardiac Precursors

(A) qPCR analyses of Gfra2, Mesp1, T (Brachyury), Nkx2-5, Tbx5, and Myl2. The peak of Gfra2 expression was observed just before the initiation of spontaneous beating of cardiomyocytes. Note that mesodermal induction represented by Mesp1 and T peaked at day 3 and sarcomeric protein synthesis of cardiomyocyte was apparent from day 8. Data are representative of biological triplicates with technical duplicates as mean ± SEM.

(B) Flow cytometrical (Flo) analyses show transient expression of GFRA2 during cardiomyocyte differentiation. GFRA2 was detected in the PDGFRA+ mesodermal population from day 4 to day 9.

(C) FACS isolation at day 7 of differentiation. GFRA2+/PDGFRA+ (G+P+), GFRA2-/PDGFRA+ (G-/P+), GFRA2-/PDGFRA- (G-/P-) populations were separately isolated.

(D) Immunocytochemistry (ICC) of TNNT2 in FACS-isolated cells after an additional 5 days culture in differentiation media. The condensed high DAPI signals represent dead cells. We counterstained with TUBA1A (α-tubulin) to delineate the live cells and found that most of G+P+ cells differentiated into TNNT2+ cardiomyocytes. Scale bar, 100 μm.

(E and F) Flow cytometrical (Flo) analyses for TNNT2 revealed that most of the G+P+ cells (93.6% ± 3.1%) differentiated into cardiomyocytes. n = 3.

(G) Quantitative analyses by Flo for HCN4, NKK2-5, Tbx5, and ISL1 in GFRA2+ CPs at day 7. Bar graph represents the proportion of FHF and SHF as mean ± SEM. n = 3.

See also Figure S2 and Movie S1.
ESCs or induced pluripotent stem cells (iPSCs) (Burridge et al., 2011). Consistent with our results for the mouse, qPCR analyses showed human GFRA2 was induced with a peak just before the appearance of spontaneously beating cardiomyocytes at day 8 of differentiation, both in ESCs and iPSCs (Figures 4A and S3A). We also identified the hGFRA2+/hPDGFRA+ cell population at day 8 by flow cytometry, with FACS-isolated hGFRA2+/hPDGFRA+ cells efficiently differentiating into TNNT2+ cardiomyocytes when cultured for an additional 5 days (Figures 4B–4D and S3B–S3D). These TNNT2+ cardiomyocytes demonstrated spontaneous beating (Movie S2). The expression profiles of FACS-purified hGFRA2+/hPDGFRA+ cells suggest that this population contains both the FHF and SHF CPs, similarly as in the case of mouse ESCs (Figures 2G, 4E, and S2D). Thus, labeling with antibodies raised to human GFRA2 also enables the isolation of a CP population from human pluripotent stem cells, without the need of lineage tagging by genetic modification.

To elucidate additional details concerning the earliest phase of hGFRA2+ CPs in human cardiac differentiation, we performed flow cytometry using hGFRA2, hPDGFRA, hKDR, and hKIT antibodies at day 4 of differentiation. We found that the proportion of hGFRA2+ expressing cells among the multipotent CP-enriched population of hKDRlow+/hPDGFRA+ cells were less than in the case of mouse (Figures 3A and 4F) (Kattman et al., 2011). As expected, the hKDRlow+/hPDGFRA+ population was hKIT negative, whereas hKDR+/hPDGFRA+ population was hKIT positive (Figure 4F) (Yang et al., 2008). By separating isolated hGFRA2+/hKDRlow+/hPDGFRA+/hKITneg and hGFRA2neg/hKDRlow+/hPDGFRA+/hKITneg populations, we found that the GFRA2 negative population almost lacked cardiomyogenic ability (Figure S3E). To confirm multipotency of human GFRA2 positive cells, we performed clonal lineage-tracing experiments. A single hGFRA2+/hKDRlow+/hPDGFRA+/hKITneg cell at day 4 was cloned by FACS and cultured for 2 weeks. RT-PCR using cardiomyocyte (hTNNT2), endothelial cell (hPECAM), and smooth muscle cell (hMYH11) markers clearly indicated the existence of the multiple cell lineages derived from a single cell, which strongly supports the multipotency of hGFRA2+/hKDRlow+/hPDGFRA+/hKITneg cells (Figure 4G). This is consistent with the data from mouse ESCs and previous work (Kattman et al., 2006, 2011; Yang et al., 2008). After differentiation day 4, as cardiomyocyte differentiation progressed, GFRA2+/hPDGFRA+ CPs lost KDR expression by day 8 as observed in mouse ESCs differentiation (Figure S3F). Taken together, as in the mouse, hGFRA2+/hKDRlow+/hPDGFRA+/hKITneg CPs at day 4 are multipotent CPs, and hGFRA2neg/hKDRlow+/hPDGFRA+/hKITneg at day 8 are unipotent cardiac precursors.

A Non-canonical Signaling Cascade via GFRA1/2 Is Indispensable for Cardiomyocyte Differentiation of Pluripotent Stem Cells

To elucidate a physiological function of GFRA2 in cardiac differentiation, we generated Gfra2 knockout (KO) mouse ESC lines...
using the CRISPR/Cas9 genome editing system (Figures 5 and S4) (Cong et al., 2013; Wang et al., 2013). After 10 days of cardiac differentiation, two independent lines of Gfra2-KO ESCs did not show significant defects in cardiomyocyte differentiation, although a minor decrease in the number of differentiated cardiomyocytes was observed without statistical significance (Figures 5 A–5C). This is consistent with the phenotype of KO mice that showed no cardiac defects (Airaksinen and Saarma, 2002; Hiltunen et al., 2000; Paratcha and Ledda, 2008; Rossi et al., 1999, 2003). Since GFRA1, another member of GFRA-family receptor whose specific ligand is glial cell line-derived neurotrophic factor (GDNF), might be functionally redundant, we generated compound mutant of $\text{Gfra1}/2$ double-KO (DKO) ESCs (Airaksinen and Saarma, 2002; Baloh et al., 2000). Whereas Gfra1 KO lines exhibited no significant defect in cardiomyocyte differentiation (Enomoto et al., 1998), the simultaneous ablation of Gfra1 in addition to Gfra2 significantly suppressed cardiomyocyte differentiation (Figures 5A–5C and S4A–S4E). It is unlikely that an off-target mutation is responsible for this phenotype, because two independent single guidance (sg) RNA targeting different portions of the gene resulted in an indistinguishable phenotype (Figures S4 C and S4D) (Enomoto et al., 1998; Fu et al., 2013; Hiltunen et al., 2000; Rossi et al., 1999, 2003). Thus, Gfra1/2 are required for cardiomyocyte differentiation in vitro, and Gfra1 is functionally redundant for Gfra2. Interestingly, we found that Gfra1 expression was significantly increased in Gfra2 KO ESCs (Figure 5D), By contrast, Gfra2 expression was unchanged in Gfra1 KO ESCs. This result suggests that the loss of Gfra2 can be compensated for by upregulated Gfra1, whereas Gfra1 appears to be dispensable for cardiac differentiation (Baloh et al., 2000; Paratcha and Ledda, 2008; Scott and Ibanez, 2001). This suggestion is supported by the fact that Gfra1 is not expressed in the heart field in vivo (Figure S5A).

The canonical signaling cascade acting via GFRA2 depends on a single-pass transmembrane protein, RET tyrosine kinase (Airaksinen and Saarma, 2002). When the specific ligand, neurturin (NRTN) binds GFRA2, the RET tyrosine kinase is activated by GFRA2/NRTN, to elicit a biological response. To confirm

![Image](image-url)
whether the GFRA2 signaling pathway affecting cardiomyocyte differentiation depends on RET, we generated Ret KO ESCs lines. As expected from the phenotypes of KO mice, targeting of Ret did not result in significantly impaired cardiomyocyte differentiation (Figures 5A–5C, S4A, and S4B) (Airaksinen and Saarma, 2002; Baloh et al., 2000; Paratcha and Ledda, 2008; Schuchardt et al., 1994). This observation is also supported by the fact that RET was not expressed in the heart fields (Figure S5A). In addition, the KO lines of Nrtn, Gdnf, and Nrtn/Gdnf also did not show any statistically significant difference in cardiomyocyte differentiation efficiency compared to WT. N.S., not significant versus WT. Bar graph represents mean ± SEM. n = 3. (E and F) Flow cytometrical analyses of TNNT2 in differentiation day 10 ESC lines. G&N, Gdnf, and Nrtn. Gdnf- and Nrtn-null ESC lines did not show any statistically significant difference in cardiomyocyte differentiation efficiency compared to WT. N.S., not significant versus WT. Bar graph represents mean ± SEM. n = 3. (F) Immunofluorescent images of TNNT2 in ESC lines at differentiation day 10. Scale bar, 100 μm.

operating in the absence of any secreted ligands and RET (Paratcha and Ledda, 2008; Paratcha et al., 2003; Sjöstrand et al., 2007). Although NCAM1 was not expressed in the heart field (Figure S5A), we cannot exclude the possibility that another cell adhesion molecule mediates a similar signal pathway. To confirm whether a similar pathway is responsible for the cardiac signaling of GFRA2, we investigated the phosphorylation of FAK, FYN, and its downstream ERK1/2 in Gfra1/2 DKO ESCs during cardiomyocyte differentiation (Figure S6). Western blot analyses demonstrated that FAK phosphorylation was slightly but significantly elevated in Gfra1/2 DKO ESCs, whereas FYN and ERK1/2 phosphorylation were unaffected (Figure S6A). Since the NCAM1/GFRA1 signal pathway first activates FYN and phosphorylated-FYN activates FAK (Paratcha et al., 2003), it is unlikely that a signal similar to the NCAM1/GFRA1 signal mediated by a cell adhesion molecule is operating. Thus, it suggests that FAK phosphorylation in Gfra1/2 DKO ESCs becomes elevated by an unknown mechanism. We further tested whether the attenuation of elevated FAK could rescue the phenotype of Gfra1/2 DKO ESCs, since it has been previously reported that activated FAK signaling impaired cardiomyocyte differentiation (Hakuno et al., 2005). We administered the FAK inhibitor PF-573228 to Gfra1/2 DKO ESCs during their differentiation. However, the...
efficiency of cardiomyocyte differentiation showed no improvement even though FAK phosphorylation was kept within physiological levels (Figures S6B and S6C). Therefore, the upregulation of FAK signaling was not primarily responsible for the defect of Gfra1/2DKO ESCs. This signaling pathway operating via GFRA2 during cardiomyogenesis must activate effectors of an alternative and critical circuit for cardiomyocyte differentiation.

Gfra1/2 Are Required for Ventricular Compaction In Vivo
To exclude the possibility that the phenotype observed in Gfra1/2 DKO ESCs is an in vitro phenomenon, we generated Gfra1/2 DKO mouse embryos by the direct injection of Gfra1-targeted sgRNA, Gfra2-targeted sgRNA, and Cas9 mRNA into zygotes.

(A) Genotype of the Gfra1/2 DKO mouse embryos generated by the direct injection of Gfra1-targeted sgRNA, Gfra2-targeted sgRNA, and Cas9 mRNA into zygotes.

(B) WISH analyses of differentiated cardiomyocyte marker Nppa in Gfra1/2 DKO and WT littermate embryos at E8.5. Nppa expressions disappeared in DKO embryos (red arrows). Scale bar, 250 μm.

(C) H&E staining for the hearts of Gfra1/2 DKO E17.5 embryos. The compaction layers of myocytes were thin, and the alignments of cardiomyocytes were impaired in Gfra1/2 DKO embryos as compared to the control hearts (mCherry sgRNA and Cas9 mRNA transduced embryos) and Gfra1/2 compound heterozygote mutant. Gfra1 null resulted in kidney agenesis as previously described (black arrowheads, No), whereas the well-developed kidney was observed in the heterozygotes and WT (black arrows, +) (Enomoto et al., 1998). The mutation of each embryo induced by CRISPR/Cas9 is shown in Figure S7B. IVS, intraventricular septum; RV, right ventricle; LV, left ventricle. Scale bar, 500 μm in whole-heart images and 100 μm in higher magnification. See also Figure S7.

just after heart tube formation, since embryonic defects or lethality would preclude the analysis of later stage embryos. Embryos containing multiples of three base insertions/deletions inside the exon were discarded from the analysis because the presence of functional protein production could not be refuted (Figure 6 A). We examined cardiomyocyte differentiation of Gfra1/2 DKO embryos by WISH using a marker of differentiated cardiomyocytes, Nppa (also known as ANF) (Bruneau et al., 2001; Christoffels et al., 2000). As expected from our ESC experiments, Gfra1/2 DKO embryos exhibited a significant reduction of Nppa (Figure 6B), suggesting the cardiomyocyte differentiation process was significantly affected. As expected from the data of Gfra2 KO ESCs (Figure 5D), Gfra2 single-KO embryos showed significant but transiently elevated Gfra1 expression by E8.5 in the heart field (Figure S7A). However, despite the fact that cardiomyocyte differentiation was impaired, the macro- and micro-anatomical morphology of the formed heart tube appeared unaffected in any DKO embryos (Figures 6B and S7B). This suggests that the reduction of Nppa in Gfra1/2 DKO embryos simply reflected a delay of cardiomyocyte differentiation. To clarify this, we analyzed the Gfra1/2 DKO embryos at E17.5 (Figures 6C, S7C, and S7D). Surprisingly, DKO embryos had the capacity to develop up to this stage without edema, and developed hearts were also observed (Figure 6C). This indicates that sufficient cardiomyocyte differentiation occurred in DKO embryos to support the fetal circulation. Further histological examination
unexpectedly revealed that Gfra1/2 DKO hearts at E17.5 suffered from noncompaction cardiomyopathy (Figures 6C and S7D). Excessively prominent trabeculations and deep intra-trabecular recesses, which are characteristic features of noncompaction cardiomyopathy, were apparent, but no other congenital heart disease in DKO embryos was observed. However, the structure of sarcomeres and mitochondria were not altered (Figures 7A and S7C), suggesting that noncompaction was not caused by the abnormality of sarcomeres and mitochondria (Towbin et al., 2015). The absence of Gfra1/2 and Ntrn at the sites of trabeculation and compaction suggests that RET-dependent and -independent Gfra1/2 signal pathways do not directly or locally regulate trabeculation and compaction (Figures S7A, S7E, and S7F). Importantly, we found that NOTCH1 in total protein and its downstream molecules BMP10 and ERBB4 were missing in DKO hearts at E9.5 (Figure 7B). NOTCH signaling is essential for proliferation and differentiation of ventricular cardiomyocytes through which proper trabeculated and compacted myocardial layers are formed, and mutants with NOTCH signaling defects exhibit a noncompaction phenotype (de la Pompa and Epstein, 2012; Grego-Bessa et al., 2007; Luxán et al., 2013; Zhang et al., 2013). Thus, the ventricular noncompaction observed in DKO embryos likely resulted from altered NOTCH signaling (Figures 7B and 7C).

Taken together, these results suggest that GFRα1/2 plays an important function in normal mammalian heart development, especially for ventricular wall compaction, but an unknown mechanism could compensate for cardiomyocyte differentiation due to the lack of GFRα1/2 in vivo. Thus, taken together, our data reveal a non-canonical signal cascade via GFRα1/2 is indispensable for heart development in vivo.

DISCUSSION

Here, we report a surface marker, GFRα2, that is specific for CPs in mouse and human. We show that the expression of
Gfra2 is initiated among both FHF and SHF CPs in vivo and in vitro just before the initiation of spontaneous beating of cardiomyocytes. Gfra2 is downregulated after CPs terminally differentiate to cardiomyocytes. The use of an antibody specific for GFRα2 protein made it possible for us to harvest human and mouse CPs derived from pluripotent stem cells. Physiologically, Gfra2 plays an important role in heart development in vitro as well as in vivo, but, in the absence of Gfra2, ectopic activation of Gfra1 can functionally compensate for its loss. Of note, our data suggest that an alternative non-canonical signaling cascade transmits GFRα1/2 activation to CP function, and that this is distinct from the canonical signaling pathway dependent on RET.

In differentiating ESCs, it is known that KDR<sup>low+/PDGFRA+</sup> or KDR<sup>low+/KIT<sup>neg</sup></sup> cells constitute multipotent CPs which give rise to cardiomyocytes, smooth muscle cells, and endothelial cells, based on previously reported clonal tracing experiments (Bondue et al., 2011; Kattman et al., 2006, 2011; Yang et al., 2008). However, it remains an open question as to whether all of these cells or only a proportion of these cells are CPs. In this study, we found that almost all mouse KDR<sup>low+/PDGFRA+</sup> express GFRα2 (Figure 3). However, the situation is likely somewhat different in human. The proportion of hGFRα2-expressing cells among hKDR<sup>low+/PDGFRA+</sup> population is much lower (Figure 4F). As expected, hKDR<sup>low+/PDGFRA+</sup> cells are negative for KIT (Yang et al., 2008). Of note, most hGFRα2-negative hKDR<sup>low+/PDGFRA+</sup> cells failed to differentiate to cardiac cells (Figure S3E), which strongly supports the specificity of hGFRα2 for human CPs. Thus, in humans, the additional usage of hGFRα2 labeling is superior to the previously proposed protocols to isolate multipotent CPs with high purity. Furthermore, the use of GFRα2 labeling in addition to KDR and PDGFRA will enrich for more mature unipotent CPs which cannot be isolated with previous protocols dependent on KDR expression. It is interesting that these unipotent late-stage GFRα2<sup>+</sup> CPs represent not only the FHF, represented by HC4N/TB5 and already known as unipotent, but also the SHF identified through expression of ISL1, because the SHF CPs are generally thought as multipotent (Figures 2G, 4E, S2D, and S2E) (Devine et al., 2014; Evans et al., 2010; Kelly and Evans, 2010; Kokkinopoulos et al., 2015; Lescroart et al., 2014; Später et al., 2013). This evidence indicates that the late-stage expression of GFRα2 expression of GFRα2 excludes the multipotent SHF but includes the already committed but not fully differentiated SHF lineage. Thus, here we propose a strategy to isolate stage-specific human and mouse CPs with GFRα2, PDGFRA, and KDR (Figure 7D). GFRα2<sup>+/KDR<sup>low+/PDGFRA+</sup> triple-positive CPs would be multipotent cardiovascular progenitors. As CPs begin to commit but not yet terminally differentiate to cardiomyocytes, they lose KDR expression so that a GFRα2<sup>+/KDR<sup>low+/PDGFRA+</sup> double-positive population represents a cardiomyocyte precursor at a later stage.

We found that Gfra1/2 DKO mouse ESCs showed a severe impairment of cardiomyocyte differentiation. Our data reveal that GFRα2 plays a pivotal role in cardiomyocyte differentiation in vitro that can be compensated by upregulation of GFRα1. Examples of an ectopic upregulation of an evolutionarily duplicated paralogous gene to compensate for loss of a gene have been described (Barbaric et al., 2007). An evolutionarily close relationship between Gfra1 and Gfra2 suggests that a preserved common enhancer drives Gfra1 if Gfra2 is not expressed in CPs, whereas a high level of Gfra2 primarily suppresses Gfra1 (Barbaric et al., 2007; Hätinen et al., 2007). However, the phenotype of KO of the known ligands for GFRα1 and 2, Gdnf and NrtN, or KO of its co-receptor Ret did not show any defect of cardiomyocyte differentiation (Figures 5, S4, and S5). Interestingly, we observed a tendency of a slightly reduced yield of cardiomyocytes in single KO of Gfra1, Gfra2, and Ret, although not to a statistically significant degree (Figure 5B). Given the evidence that previously reported KO mice of each gene also did not show any heart defect (Enomoto et al., 1998; Heuckereth et al., 1999; Rossi et al., 1999; Sánchez et al., 1996), the role of classic RET-dependent GFRα1/2 signals are unlikely to be vital for heart development. In addition, whereas an alternative GFRα1 signal pathway via NCAM1/FYN/FAK is known (Paratcha et al., 2003; Sjöstrand et al., 2007), our data showed that NCAM1, FYN, and FAK were not involved in the cardiac differentiation defect in the Gfra1/2 DKO (Figure S8). Thus, the pathway by which GFRα2 modulates heart development is likely to be distinct from previously established pathways. To uncover the nature of this alternative non-canonical signaling pathway acting via GFRα1/2, further investigation is required, to identify molecules interacting directly with GFRα2 in the context of cardiac differentiation.

In contrast to the in vitro phenotype, the loss-of-function of Gfra1/2 showed a different phenotype in vivo. In E8.5 DKO embryos, Nppa expression disappeared, which is likely consistent with the impaired in vitro cardiomyocyte differentiation of DKO ESCs. However, viable E17.5 DKO embryos possessing a developed heart were observed, indicating that cardiomyocyte differentiation itself occurred to form a functional fetal heart in vivo. Indeed, although missing Nppa, the heart tube of E8.5 DKO embryos seemed morphologically normal (Figures 6B and S7B). This evidence is inconsistent with the in vitro phenotype of ablated cardiomyocyte differentiation in DKO ESCs. Thus, the disappearance of Nppa in E8.5 DKO embryos might simply represent the delay of cardiomyocyte differentiation or anomalous sequential events inside the cardiomyocytes in DKO embryos. We propose that an unknown compensatory mechanism functions in vivo to circumvent the lack of GFRα1/2 to promote cardiomyocyte differentiation. Although the differentiation protocol for ESCs used in this study provides a strong drive toward cardiomyocytes with a defined set of growth factors (Kattman et al., 2011; Wamstad et al., 2012), these conditions are probably insufficient to perfectly mimic the in vivo environment for cardiomyocyte differentiation.

E17.5 DKO embryos showed noncompaction cardiomyopathy without other congenital heart diseases (Towbin et al., 2015; Zhang et al., 2013). We speculate that these DKO mice would not survive after birth because of the extremely thin compact layer of the ventricular wall. However, absence of edema in E17.5 DKO embryos suggests that the contractile apparatus in DKO cardiomyocytes at least developed sufficiently to support the fetal circulation. Unfortunately, germline deletion of Gfra1 does not allow neonates to survive due to kidney agenesis (Figure 6C) (Enomoto et al., 1998; Sánchez et al., 1996). Thus, to confirm the perinatal prognosis, a conditional knockout will be required.
Importantly, we found that NOTCH1 and its downstream targets, BMP10 and ERBB4, were significantly downregulated in DKO embryos, and that this might be responsible for the non-compaction defect (Figures 7B and 7C) (Grego-Bessa et al., 2007; Luxán et al., 2013; Zhang et al., 2013). Given the lack of Nppa expression in NOTCH signal mutants (Luxán et al., 2013), it is concluded that the altered NOTCH signal in the endocardium promotes the downregulation of Nppa in DKO embryos. Surprisingly, Gfra2 is expressed by CPs, but not at the sites of trabeculation or compaction (Figures 1, S1, S7E, and S7F). Thus, the defect within the endocardium is cell autonomously induced by the loss of Gfra1/2 in multipotent CPs and is likely primarily required for ventricular noncompaction, although we cannot exclude a possibility that additional defects within the myocardium of DKO embryos may also contribute to this phenotype (Figure 7C).

Taken together, an alternative signaling pathway via GFRα1/2 is indispensable for proper heart development, although the mechanism underlying the signaling pathway of cardiac differentiation mediated by GFRα2 has yet to be elucidated. Future work, involving the clarification of the mechanistic details of this signaling pathway should provide deeper insight into cardiomyocyte differentiation, the biology of CPs, normal trabeculation, and compaction of ventricular myocytes.

EXPERIMENTAL PROCEDURES

The details are given in the Supplemental Experimental Procedures.

Animals

All animal procedures in this project were carried out under the project licenses 70/7254 and 70/2452 and 27-028-001 approved by the Home Office according to the Animals (Scientific Procedures) Act 1986 in the UK and Osaka University Animal Ethical Committee in Japan, respectively.

Cell Culture and Differentiation

Cardiomyocyte induction for mouse E14tg2a ESCs (Magin et al., 1992; Smith and Hooper, 1987) was performed according to standard protocols as previously described (Kattman et al., 2011). Cardiomyocyte induction from human HUES7 ESCs or iPSCs was undertaken as previously described (Burridge et al., 2011). Human ESCs were used under the license of the UK Steering Committee (reference number; SSCS13-25). Human iPSCs (iPS-HS1M) were originally established by D.M. using human dermal fibroblasts (HDFs) from a healthy donor under informed consent (Health Research Authority approval 13/LO/0224), for a study to be described elsewhere (D.M., T. McKay, L.D., and A.T., unpublished data).

CRISPR/Cas9-Mediated Genome Editing

The CRISPR/Cas9-mediated genome editing for mouse ESCs and embryos was performed as previously described (Hashimoto and Takemoto, 2015; Wang et al., 2013).

Flow Cytometry/FACS

Cells were sorted as previously described using FACS ARIA II or analyzed by LSR Fortessa II or FACSCanto II (BD Biosciences) with FACSDiva 7.0 software (Kokkinopoulos et al., 2015).

SUPPLEMENTAL INFORMATION

Supplemental Information includes Supplemental Experimental Procedures, seven figures, and two movies and can be found with this article online at http://dx.doi.org/10.1016/j.crep.2016.06.050.

AUTHOR CONTRIBUTIONS

K.Y. planned this project, and H.I. and K.Y. performed the majority of the experiments. K.Y. and H.I. wrote the manuscript. R.S., I.K., S.N., A-K.H., M.S., P.R., and K.O. contributed to mouse ESC experiments. A.P., D.M., S.H., L.D., A.T., and K.O. contributed to human ESCs and human iPSCs experiments. M.H. and H.S. contributed to CRISPR/Cas9-mediated direct genome editing. O.Y. and Y. Sakata contributed to electron microscopy observations. S.K., A-K.H., Y. Sawa, K.O., and K.S. contributed to the discussion of the results.

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