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Downregulation of LGR5 Expression Inhibits Cardiomyocyte Differentiation and Potentiates Endothelial Differentiation from Human Pluripotent Stem Cells

Rajneesh Jha, Monalisa Singh, Qingling Wu, Cinsley Gentillon, Marcela K. Preininger and Chunhui Xu

INTRODUCTION

Controlled and robust differentiation of cardiomyocytes and endothelial cells from human pluripotent stem cells (hPSCs) is important for their applications in regenerative medicine, disease modeling, and drug discovery (Ebert et al., 2015; Laflamme and Murry, 2011). Differentiation of these cells requires regulation of Wnt signaling in a time- and dose-dependent manner (Murry and Keller, 2008). Wnt signaling needs to be activated at the early stage and subsequently inhibited at the late stage for efficient cardiomyocyte differentiation (Kattman et al., 2011; Lian et al., 2012; Paige et al., 2010; Palpant et al., 2013, 2015), which can be achieved using small molecules (Lian et al., 2012) or growth factors (i.e., activin A and bone morphogenetic protein 4 [BMP4]) (Kattman et al., 2011; Laflamme et al., 2007). Endothelial cell differentiation from hPSCs can be induced by a brief treatment with a Wnt agonist during the first day of differentiation (Lian et al., 2014), but inhibited when the agonist is added after mesodermal commitment (Palpant et al., 2015). Given the critical role of the Wnt signaling, identifying additional molecules regulating Wnt signaling during lineage commitment may enhance efficient differentiation of cardiomyocytes and endothelial cells from hPSCs.

LGR5 is a leucine-rich repeat-containing G-protein-coupled receptor that can bind to R-spondins to potentiate Wnt signaling (Carmon et al., 2011, 2012; de Lau et al., 2011; Glinka et al., 2011). It is a stem cell marker for various tissues (Barker et al., 2007, 2010, 2012; Chai et al., 2012; de Visser et al., 2012; Jaks et al., 2008; Sato et al., 2009), and is overexpressed in cancer stem cells and several types of tumors (Barker et al., 2009; Juntila et al., 2015; McClannahan et al., 2006; Nakata et al., 2013; Tanese et al., 2008). Since R-spondin 3 is essential for cardiac development (Cambier et al., 2014), we speculated that LGR5 may also play a role in hPSC differentiation.

Here, we report that LGR5 expression is transiently upregulated during the early stage of cardiomyocyte differentiation from hPSCs, and that LGR5 promotes cardiomyocyte differentiation and inhibits endothelial cell differentiation from hPSCs.

RESULTS

LGR5 Expression Is Transiently Upregulated during the Early Stage of Cardiomyocyte Differentiation

To understand the role of LGR5 during cardiomyocyte differentiation, we first examined its temporal expression during cardiomyocyte differentiation of H7 human embryonic stem cells (hESCs) induced by activin A and BMP4 (Figures 1A and 1B). As expected, expression of stem cell marker OCT4 was decreased after induction, while expression of mesendodermal marker T (Brachyury) was transiently upregulated at day 2. Subsequently, expression of mesendodermal marker MESPI and cardiac progenitor marker NKX2-5 was increased after day 4, and expression of cardiomyocyte...
marker **TNNT2** (cardiac troponin T) was increased after day 6. Compared with day-0 cells, ~50-fold increased LGR5 mRNA was detected at day 2 and ~170-fold at day 4. After day 5, LGR5 expression gradually decreased but was maintained at levels higher than that of day-0 cells. At the protein level, ~54% of the day-4 cells were positive for LGR5 as detected by flow cytometry (Figure 1C) and LGR5 was detected on cell surface by immunocytochemistry (Figure 1D). Similar LGR5 expression patterns were observed in two other hPSC lines (IMR90 induced pluripotent stem cells [iPSCs] and H9 hESCs) (Figure S1). In addition, parallel cultures of H7 hESCs, IMR90 iPSCs, and H9 hESCs at day 14 contained ~56%–66% cells that were positive for the cardiomyocyte-associated marker α-actinin (Figures 1E, S1E, and S1J).
These data show that increased LGR5 expression occurred during mesendoderm induction (T) and prior to the induction of master regulators of cardiogenesis, MESP1 and NKX2-5, and expression of cardiomyocyte marker TNNT2, suggesting that LGR5 could play a role in specification of mesoderm and cardiovascular progenitors.

Knockdown of LGR5 Does Not Affect Undifferentiated hPSC Growth, but Alters Anterior-Posterior Mesoderm Patterning

To examine the effect of LGR5 knockdown on hPSC growth and differentiation, we first generated stable cell lines by targeting LGR5 using short hairpin RNAs (shRNAs) or scrambled sequences as a control. As expected, the LGR5 mRNA expression was significantly lower in LGR5 shRNA cultures than in control shRNA cultures (Figure S2A). However, cell morphology, growth rate, and expression of stem cell markers were similar between control shRNA cultures and LGR5 shRNA cultures (Figure S2). Next, the LGR5 shRNA and control shRNA cultures were induced for cardiomyocyte differentiation. A time-course analysis showed that LGR5 mRNA levels remained significantly lower in LGR5 shRNA cultures than in control shRNA cultures throughout the differentiation (Figure 2C). At differentiation day 2, the morphology of LGR5 shRNA and control shRNA cultures was similar; however, at day 5, cells from LGR5 shRNA cultures were mostly large and flat while cells from control shRNA cultures were small and densely packed (Figures 2A and 2B). The transient expression patterns of mesendodermal markers T and MIXL1 were similar in LGR5 shRNA cultures and control shRNA cultures: the expression of T increased at day 1 and peaked at day 2 and the expression of MIXL1 peaked at days 1 and 2 (Figure 2D). However, compared with control shRNA cultures, LGR5 shRNA cultures had significantly lower levels of these mesendodermal markers (at days 1, 2, and 3 for T and at day 1 for MIXL1) (Figure 2D). These results suggest that knockdown of LGR5 does not delay mesendodermal induction but reduces the efficiency of mesendodermal induction.

We next examined the expression of genes involved in the development of anterior and posterior mesoderm. Gene expression levels of anterior mesoderm markers EOMES, GSC, and TBX6 were significantly lower in LGR5 shRNA cultures than in control shRNA cultures (at day 2 for GSC and TBX6, and at days 5 and 8 for EOMES) (Figure 2E), whereas the expression of posterior mesoderm markers CDX1 and CDX4 was significantly higher in LGR5 shRNA cultures than in control shRNA cultures at day 2 (Figure 2F). In addition, LGR5 shRNA cultures had significantly lower levels of cardiac mesodermal markers MESP1 and MESP2 and endodermal markers SOX17 and HNF3B than control shRNA cultures at various time points examined (Figures 2G and 2H). These results suggest that knockdown of LGR5 in hPSCs alters the expression of genes involved in anterior-posterior mesoderm patterning and reduces cardiac mesoderm and endoderm differentiation.

Knockdown of LGR5 Inhibits Cardiomyocyte Differentiation from hPSCs

We next investigated the effect of LGR5 knockdown on cardiac progenitor and cardiomyocyte differentiation of IMR90 iPSCs. At days 8 and 14 after cardiac induction, cells from LGR5 shRNA cultures remained mostly large and flat while cells from control shRNA cultures remained densely packed (Figures 3A and 3B). At day 8, the gene expression levels of four out of five cardiac progenitor markers examined (HAND1, MEF2C, NKX2-5, and TBX5 except for ISL1) were significantly lower in LGR5 shRNA cultures than in control shRNA cultures (Figure 3C). While the majority of control shRNA cells started beating at days 8–10 (and persisted until day 14) (Movie S1), very few LGR5 shRNA cells were beating (Movie S2). At day 14, cardiomyocyte purity was significantly lower in LGR5 shRNA cultures than in control shRNA cultures. There were fewer α-actinin/NKX2-5 double-positive cells in LGR5 shRNA cultures than in control shRNA cultures as detected by immunocytochemistry (Figure 3D), and ~8% α-actinin+ cells were present in LGR5 shRNA cultures compared with ~54% in control shRNA cultures as detected by flow cytometry (Figures 3E and 3F). In addition, mRNA levels of cardiomyocyte markers MYH6, MYH7, MYL2, MYL7, and TNNT2 were significantly lower in LGR5 shRNA cultures than in control shRNA cultures at day 14 (Figure 3G).

We also examined the effect of LGR5 knockdown on cardiomyocyte differentiation from another cell line (H9 hESCs) and a different batch of IMR90 iPSCs. Knockdown of LGR5 was observed at both the mRNA level and the protein level for both the cell lines (Figure S1): LGR5 mRNA levels were significantly reduced in LGR5 shRNA cultures compared with control shRNA cultures (Figures S1C and S1H), and the proportion of cells positive for LGR5 protein was reduced to ~1% in LGR5 shRNA cultures at day 2 compared with 3%–10% of the cells in control shRNA cultures (Figures S1B and S1G), and reduced to ~6% in LGR5 shRNA cultures at day 5 compared with ~50% of the cells in control shRNA cultures (Figures S1D and S1I). To determine the effect of LGR5 knockdown on cardiomyocyte differentiation, parallel cultures were maintained until day 14 and examined for purity of cardiomyocytes. Only ~4% and 1% of α-actinin+ cells was detected in LGR5 shRNA cultures compared with ~57% and 56% of α-actinin+ cells detected in control shRNA cultures derived from IMR90 iPSCs and H9 hESCs, respectively (Figures S1E and S1J). These results further confirm that knockdown of LGR5 inhibits cardiomyocyte differentiation.
Knockdown of LGR5 Promotes Endothelial Differentiation

At day 14, LGR5 shRNA cultures were mostly a monolayer of cells with endothelial-like cell morphology, whereas control shRNA cultures contained beating cardiomyocytes (Figure 3B). Given this observation, we characterized endothelial cell differentiation in LGR5 shRNA and control shRNA cultures. We examined the gene expression of HHEX, TAL1, SOX7, and LMO2, markers associated with the development of hemato-endothelial lineages which can give rise to endothelial cells. The expression of TAL1 and SOX7 increased over time during cardiomyocyte differentiation from control shRNA cultures, whereas that of HHEX and LMO2 did not (Figure 4A). Compared with control shRNA cultures, LGR5 shRNA cultures had higher gene expression levels of all four hemato-endothelial markers examined at various time points (Figure 4A). We also examined the expression of endothelial cell markers during differentiation. At differentiation days 8 and 14, the relative mRNA levels of endothelial markers CD31, CD34, and
Figure 3. Knockdown of LGR5 Inhibits Cardiomyocyte Differentiation

(A and B) Morphology of IMR90 iPSCs from control shRNA and LGR5 shRNA cultures at day 8 (A) and day 14 (B). Cells from control shRNA cultures were tightly packed but cells from LGR5 shRNA cultures showed flat monolayer morphology. Scale bars, 200 μm.

(C) qRT-PCR analysis of cardiac transcription factors HAND1, ISL1, MEF2C, NKX2-5, and TBX5 in IMR90 iPSCs at day 8.

(D) Detection of cardiomyocyte markers α-actinin and NKX2-5 in IMR90 iPSCs at day 14 by immunocytochemistry. Scale bar, 100 μm.

(E) Representative flow-cytometry analysis of α-actinin in IMR90 iPSCs at day 14.

(F) Summary of cardiomyocyte differentiation efficiency in IMR90 iPSCs at day 14.

(G) qRT-PCR analysis of cardiomyocyte-associated markers MYH6, MYH7, MYL2, MYL7, and TNNT2 in IMR90 iPSCs at day 14. n = 3–5 independent experiments. Data are presented as mean ± SEM. *p < 0.05; **p < 0.01; ****p < 0.0001. See also Figure S1.
Figure 4. Knockdown of LGR5 Potentiates Endothelial Differentiation

(A) qRT-PCR analysis of genes involved in development of hemato-endothelial lineages HHEX, TAL1, SOX7, and LMO2 in IMR90 iPSCs at days 0, 2, 5, 8, and 14.

(B) qRT-PCR analysis of endothelial cell markers CD31, CD34, and CDH5 in IMR90 iPSCs at days 0, 2, 5, 8, and 14.

(C) Representative flow-cytometry analysis of endothelial cell markers CD31 and VE-cadherin in IMR90 iPSCs at day 14.

(legend continued on next page)
CDH5 (VE-cadherin) were higher in LGR5 shRNA cultures than in control shRNA cultures (Figure 4B). At day 14, 28% of the cells were double positive for CD31 and VE-cadherin proteins in LGR5 shRNA cultures, whereas only ~1–4% of the cells were positive for these markers in control shRNA cultures (Figures 4C and 4D). These endothelial cell markers were found to be localized to cell surface in a subset of cells from LGR5 shRNA cultures (Figures 4E and S3A). These results indicate that knockdown of LGR5 increases the expression of markers associated with hemoto-endothelial lineages and endothelial cells.

We further examined whether the observed endothelial-like cells possessed expected functional characteristics. Following the treatment of differentiated cells at day 14 on Matrigel with vascular endothelial growth factor (VEGF) for 24 hr, cells from LGR5 shRNA cultures formed tube-like networks (a feature of endothelial cells), whereas cells from control shRNA cultures did not (Figure S3B). Analysis of acetylated low-density lipoprotein (Ac-LDL) uptake (another feature of endothelial cells) revealed that a large proportion of the LGR5 shRNA cultures were positive for fluorescently labeled Ac-LDL, but very few cells from control shRNA cultures were positive (Figure S3C). To further confirm these observations, we purified CD31+ endothelial cells (~96%) by fluorescence-activated cell sorting (FACS) from LGR5 shRNA cultures at day 14 (Figure 4F) and then conducted cell-proliferation, tube-formation, and Ac-LDL-uptake assays. These purified CD31+ cells proliferated in endothelial cell medium supplemented with VEGF with a cell population doubling time of ~3 days (Figure 4G), formed tube-like networks that were also positive for VE-cadherin (Figure 4H), and showed robust Ac-LDL uptake (Figure 4I). These results support that the observed endothelial-like cells from LGR5 shRNA cultures were bona fide endothelial cells.

Knockdown of LGR5 Inhibits Proliferation of Differentiated hPSCs at the Early Stage

Since LGR5 is involved in promoting cellular proliferation in other cells (Barker and Clevers, 2010; Barker et al., 2009; Nakata et al., 2013; Schepers et al., 2012; Tanese et al., 2008), we investigated whether modulation of LGR5 expression levels affected proliferation of hPSCs during cardiomyocyte differentiation. Both control shRNA cultures and LGR5 shRNA cultures were subjected to cardiomyocyte differentiation and monitored for cellular proliferation. While there was a comparable number of cells in control shRNA cultures and LGR5 shRNA cultures at the time of induction of differentiation (day 0), cell density assay showed significantly fewer cells in LGR5 shRNA cultures than in control shRNA cultures at differentiation days 5, 8, and 14 (Figure 5A), which is consistent with the morphology of the cultures (Figures 2A, 2B, 3A, and 3B). We also examined the expression of Ki-67, an indicator for cells in active phases of the cell cycle, by flow cytometry. At differentiation day 0, the proportion of Ki-67+ cells was comparable between control shRNA cultures and LGR5 shRNA cultures; >80% of the cells were positive for Ki-67 in these cultures (Figures 5B and SC). However, at differentiation day 5, the proportion of Ki-67+ cells was significantly reduced in LGR5 shRNA cultures compared with control shRNA cultures; ~79% and ~57% Ki-67+ cells were detected in control shRNA and LGR5 shRNA cultures, respectively (Figures 5D and 5E). At days 8 and 14, the proportion of Ki-67+ cells decreased to <20% in both LGR5 shRNA cultures and control shRNA cultures (Figure S4). Consistent with these findings, the transcript levels of proliferation markers including CCND1, MKI67, and PCNA were comparable at day 0 between control shRNA cultures and LGR5 shRNA cultures, but significantly lower at day 5 in LGR5 shRNA cultures than in control shRNA cultures (Figure 5F). These results suggest that in the early stage of differentiation, LGR5 plays a role in the proliferation of cardiac progenitors.

Knockdown of LGR5 Downregulates the Expression of Canonical and Non-canonical Wnt Signaling-Related Genes

Regulation of Wnt signaling drives cardiac differentiation and development (Gessert and Kuhl, 2010). Expression of canonical and non-canonical Wnt signaling-related genes is temporally regulated during cardiomyocyte differentiation (Mazzotta et al., 2016). As expected, the relative levels of canonical Wnt target genes, AXIN2 and LEF1, increased during the early stage of cardiomyocyte differentiation and peaked at 15- and 500-fold higher at differentiation day 3.
compared with those at day 0, respectively (Figure S5A).

Similarly, the expression of canonical Wnt genes WNT3A and WNT8A was transiently upregulated and reached to 1,800- and 6,000-fold higher at day 3 compared with those at day 0 (Figure S5B). The expression of non-canonical Wnt signaling-related gene, WNT11, increased and reached its highest transcript levels at days 8–12 (300-fold higher compared with those at day 0) (Figure S5C). The expression of another non-canonical Wnt signaling-related gene, WNT5A, peaked early from days 2 to 5 and stayed at levels higher than those at day 0 at later time points (Figure S5C).

Since LGR5 is a receptor for R-spondins, which are potent Wnt signal regulators (Cambier et al., 2014), we investigated whether knockdown of LGR5 affects Wnt signaling during cardiomyocyte differentiation. Compared with control shRNA cultures, LGR5 shRNA cultures had significantly reduced expression of the following Wnt signaling-related genes at the early stage: (1) Wnt target genes AXIN2 and LEF1 at days 2 or 5 (Figure 6A), (2) canonical Wnt signaling-related genes WNT3A and WNT8A at day 2 (Figure 6B), and (3) non-canonical Wnt signaling-related genes WNT5A and WNT11 at days 2 and 5 or days 5 and 8 (Figure 6C).

We further investigated the effect of LGR5 knockdown on the activation of β-catenin by analyzing protein level of active β-catenin or its unphosphorylated form at Ser-37 and Thr-41 during the early stage of cardiomyocyte differentiation. In control shRNA cultures, the proportion of cells positive for active β-catenin was ~55% at basal level (day 0), ~91% at differentiation day 1, and ~8% at day 4 (Figure 6D). However, the proportion of cells positive for active β-catenin in LGR5 shRNA cultures was more than...
Figure 6. Knockdown of LGR5 Inhibits the Activation of β-Catenin and the Expression of Wnt Signaling-Related Genes during Cardiomyocyte Differentiation

(A–C) qRT-PCR analysis of Wnt signaling-related genes in control shRNA and LGR5 shRNA IMR90 iPSC cultures at days 0, 2, 5, 8, and 14. (A) Wnt target genes AXIN2 and LEF1; (B) canonical Wnt signaling-related genes WNT3A and WNT8A; and (C) non-canonical Wnt signaling-related genes WNT5A and WNT11.

(D) Flow-cytometry analysis of active β-catenin protein during cardiomyocyte differentiation in control shRNA and LGR5 shRNA IMR90 iPSC cultures at days 0–4.

(E) Immunocytochemistry analysis of active β-catenin protein at day 1 of cardiomyocyte differentiation in control shRNA and LGR5 shRNA IMR90 iPSC cultures. Scale bar, 100 μm.
2- to 4-fold lower at all time points compared with the parallel control shRNA cultures (Figure 6D). Since nuclear translocation of active β-catenin is a hallmark for the activation of canonical Wnt pathway, we also examined the localization of active β-catenin by immunocytochemistry. We found significantly fewer cells positive for active nuclear β-catenin in LGR5 shRNA cultures than in control shRNA cultures at day 1 (Figures 6E and 6F).

Together, these data suggest that knockdown of LGR5 affects the expression of Wnt signaling-related genes and the activation of β-catenin during cardiomyocyte differentiation from hPSCs.

DISCUSSION

Differentiation of cardiomyocytes and endothelial cells is tightly regulated during differentiation of hPSCs, and Wnt signaling pathways are important in regulating both cardiomyocyte and endothelial cell differentiation through ligand-receptor interactions. Therefore, understanding additional molecules involved in Wnt signaling is crucial to controlling efficient cardiomyocyte and endothelial cell differentiation from hPSCs. In this study, we found that expression of LGR5 (which encodes a cell membrane-associated regulator of Wnt signaling) was transiently upregulated during the early stage of cardiomyocyte differentiation from hPSCs. In undifferentiated cells, knockdown of LGR5 did not affect cell growth or gene expression of stem cell markers; however, knockdown of LGR5 reduced mesendoderm induction, altered mesoderm patterning, reduced the expression of cardiac transcription factors, and inhibited cardiomyocyte differentiation. Furthermore, knockdown of LGR5 promoted the differentiation of hPSCs into endothelial cells with typical in vitro functional characteristics, including formation of tube-like structures and Ac-LDL uptake, although further confirmation in animal models is required. Knockdown of LGR5 also inhibited cellular proliferation of early differentiated cells, and decreased the expression of Wnt signaling-related genes and nuclear-localized active β-catenin. These results suggest that LGR5 is critical for controlling differentiation into cardiomyocytes and endothelial cells, possibly by fine-tuning Wnt signaling and regulating progenitor cell proliferation and mesoderm patterning.

LGR5 functions as a growth-promoting molecule, and has been shown to promote cellular proliferation in several stem cell and cancer cell models (Barker and Clevers, 2010; Barker et al., 2009; Nakata et al., 2013; Schepers et al., 2012; Tanese et al., 2008). We found that knockdown of LGR5 in hPSCs did not affect the growth and proliferation of undifferentiated cells. However, knockdown of LGR5 significantly reduced the proliferation of differentiated cells at the early stage and resulted in poor outcome of cardiac differentiation at the late stage. It is possible that reduced proliferation of progenitors in LGR5 knockdown cultures affects the cell density at crucial stages of cardiomyocyte differentiation, preventing the selection and expansion of cardiac progenitors and, consequently, cardiomyocyte differentiation. Thus, the effect of LGR5 knockdown on cardiomyocyte differentiation may be mediated through a cell density-dependent mechanism. However, it is also possible that LGR5 directly affects cell fate decisions, since knockdown of LGR5 alters mesoderm patterning and expression of genes associated with cardiac mesoderm, hematopoietic lineages, and Wnt signaling.

Mesoderm patterning is an essential step in controlling progenitors to differentiate into cardiomyocytes and endothelial cells. Our results show that knockdown of LGR5 reduces the expression of anterior mesoderm markers (EOMES, GSC, and TBX6) but increases the expression of posterior mesoderm markers (CDX1 and CDX4) compared with control shRNA cultures. This expression pattern may contribute to decreased cardiomyocyte differentiation from anterior mesoderm-like cells (Murry and Keller, 2008) and increased endothelial cell differentiation from posterior mesoderm-like cells in LGR5 knockdown cultures.

Knockdown of LGR5 increased the expression of markers associated with hematopoietic lineages, which can differentiate into endothelial cells. These hematopoietic mesodermal markers include: (1) HHEX, which encodes a transcription factor that is expressed specifically in hematopoietic lineages (Kubo et al., 2005; Paz et al., 2010); (2) TAL1 (SCL), which encodes a transcription factor that promotes hematopoietic specification and suppresses cardiogenesis (Org et al., 2015; Real et al., 2012; Van Handel et al., 2012); (3) SOX7, which encodes a transcriptional regulator that binds and activates CDH5, required for the development of both hematopoietic and endothelial cells (Costa et al., 2012; Nelson et al., 2009); and (4) LMO2, which encodes a protein that has a crucial role in hematopoietic development (Landry et al., 2005; Meng et al., 2016; Patterson et al., 2007). Our results raise the possibility that endothelial cells in LGR5 shRNA cultures may be

(F) Summary of percentage of cells positive for nuclear-localized active β-catenin in control shRNA and LGR5 shRNA IMR90 iPSC cultures at day 1.

n = 3 independent experiments. Data are presented as mean ± SEM. *p < 0.05; **p < 0.01; ***p < 0.001; ****p < 0.0001. See also Figure S5.
derived from hemato-endothelial cell lineages. Since hemato-endothelial lineages also give rise to hematopoietic cells, our results encourage future studies to examine the effect of LGR5 knockdown on hematopoietic cell differentiation.

LGR5 is known as both a target and a regulator of Wnt signaling (de Lau et al., 2014). We found that knockdown of LGR5 resulted in a reduction of active β-catenin (nuclear-localized β-catenin) and downregulated the expression of canonical and non-canonical Wnt signaling-related genes at the early stage of differentiation, suggesting that LGR5 is a regulator of Wnt signaling during cardiomyocyte differentiation. Temporal regulation of Wnt signaling has been used to direct hPSC differentiation into cardiomyocytes or endothelial cells. For example, stage-specific activation and inhibition of Wnt signaling are essential for efficient cardiomyocyte differentiation (Kattman et al., 2011; Lian et al., 2012; Mazzotta et al., 2016; Paige et al., 2010; Palpant et al., 2013, 2015). Activation of Wnt signaling by small molecules can lead to high yield of endothelial cell differentiation (Lian et al., 2014), TMEM88, a negative regulator of Wnt/β-catenin signaling, has been shown to regulate cardiomyocyte and endothelial cell differentiation; knockdown of TMEM88 inhibits cardiomyocyte differentiation, but promotes endothelial cell differentiation (Palpant et al., 2013). Since Wnt signaling has a complex temporal role during cardiomyocyte and endothelial cell differentiation, the effect of LGR5 knockdown we observed may be stage specific as well. Future studies using inducible shRNA may reveal the timing of LGR5 expression that is critical for cardiomyocyte and endothelial cell differentiation.

Our results show remarkable changes in efficiency of cardiac and endothelial differentiation of hPSCs upon LGR5 knockdown. Neonatal lethality was observed in Lgr5 null mice that show ankyloglossia and gastrointestinal distension (Morita et al., 2004). The differential contribution of LGR5 genes to human and mouse cardiomyocyte and endothelial cell differentiation remains to be further elucidated. Molecular features of early embryonic development in mice do not always match findings in humans. For example, analysis of human embryos from zygote to blastocyst demonstrates significant difference relative to the mouse in the expression of early lineage-specific genes (Niakan and Eggan, 2013). Human-mouse difference during early embryo development has also been observed in the regulation of metabolism associated with the pluripotent state (Gu et al., 2016). Naïve hESCs have increased glycolytic rate compared with primed hESCs while the opposite is true in mouse-naïve versus primed ESCs, possibly due to discrepancy between human and mouse in nuclear C-MYC levels in naïve versus primed stem cells (Gu et al., 2016).

Conclusion
Together, these results reveal a previously unappreciated role of LGR5 in the differentiation of cardiomyocytes and endothelial cells from hPSCs. LGR5 expression is transiently upregulated during the early stage of cardiomyocyte differentiation from hPSCs, and although LGR5 expression is not required for maintaining hPSCs in the undifferentiated state, knockdown of LGR5 leads to decreased expression of key cardiac transcription factors at the early stage with eventual lack of robust beating cardiomyocytes at the late stage. Knockdown of LGR5 also potentiates differentiation of hPSCs into endothelial-like cells. Therefore, LGR5 is critical in cardiac and endothelial differentiation. These findings will advance our understanding of the molecular underpinnings of efficient differentiation of hPSCs into cardiovascular lineages.

EXPERIMENTAL PROCEDURES

Undifferentiated Cell Cultures and Differentiation of Cardiomyocytes and Endothelial-like Cells
Undifferentiated H7 and H9 hESCs (Thomson et al., 1998) and IMR90 iPSCs (Yu et al., 2007) were maintained as previously described (Xu et al., 2001). For cardiomyocyte differentiation, cells were induced using a growth factor-guided differentiation protocol (Jha et al., 2015). Cells were maintained as undifferentiated cells in mouse embryonic fibroblast-conditioned medium (MEF-CM) supplemented with basic fibroblast growth factor (bFGF) (8 ng/mL). Single cell suspensions were prepared using Versene and seeded at a density of 4 × 10^5 cells in 1 mL of MEF-CM for each well of 24-well Matrigel-coated plates. Cells were fed daily by replacing MEF-CM supplemented with bFGF (8 ng/mL) until cells reached confluence. Usually 2–3 days after seeding at day 0 of induction, medium was replaced with 1 mL of medium (RPMI 1640 with 2% B27 without insulin) supplemented with 100 ng/mL activin A. On the next day (day 1), the medium was replaced with 1 mL of RPMI 1640 medium supplemented with 2% B27 (without insulin) and 10 ng/mL BMP4, and cells were cultured without any medium change for the next 4 days. From day 5 onward, the BMP4-containing medium was replaced with 1 mL of RPMI 1640 with 2% B27 (with insulin) and the medium was changed on alternate days until day 14. Cells were observed daily under a microscope for beating cells, which typically started after day 8. For endothelial cell differentiation, mesoderm induction was accomplished by activin A and BMP4 as described for cardiomyocyte differentiation. At day 8 onward, the medium was replaced with endothelial cell growth medium consisting of M199 Medium (Lonza, #12-118F), 20% fetal bovine serum (FBS), 1% L-glutamine, 1% penicillin/streptomycin, endothelial cell growth supplement (EGCS; Biomedical Technologies #BT-203, final concentration 50 μg/mL), and heparin (Sigma #H3393-10KU, final concentration 100 μg/mL) (Maciag et al., 1981; Thornton et al., 1983). The medium was changed on alternate days until day 14. Cells were pooled from multiple wells (at least 3 wells) for each biological sample and at least triplicates of biological samples were
used for each condition in assays. All cell culture reagents were purchased from Fisher Scientific unless specified.

Preparation of MEIs was approved by the Emory University Institutional Animal Care and Use Committee.

**Knockdown of LGR5**

shRNA plKO.1 plasmid vectors expressing target-specific sequences against human LGR5 (#11586) and non-target scrambled control (#SHC016) were obtained from the RNAi Consortium (TRC, MISSION TRC shRNA library, Sigma). shRNA-mediated gene knockdown was performed by nucleofection of plasmid vectors (for iMB90 iPSCs) or lentiviral transduction (for H9 hESCs and another batch of IMP90 iPSCs). Cells were dissociated using Versene and single cell suspension was washed once with PBS. For nucleofection, 1 × 10⁶ cells were suspended in 100 μL of nucleofection buffer containing 1 μg of plasmids and nucleofected using Amaxa nucleofector II program A033. For lentiviral transduction, 1 × 10⁶ cells were mixed with 1 MOI of viral particles and 6 μM polybrene (Sigma). Cells were immediately collected and seeded in Matrigel-coated 6-well plates containing 1 mL of MEF-CM supplemented with 10 μM Stemolecule Y27632, rock inhibitor (Stemgent). Cells were fed daily with MEF-CM with bFGF (10 ng/mL) for 7 days until reaching around 80%–90% confluence. The cells were then subjected to antibiotic selection for 7 days using 1 μg/mL puromycin (the dose of puromycin was predetermined in a killing curve experiment showing that minimum puromycin concentration killing all hPSCs in 5 days was 1 μg/mL). Stable cell lines were generated from surviving cells that were resistant to puromycin and further expanded in successive passages under puromycin selection. Efficiency of gene knockdown after three passages was examined using qRT-PCR.

**Flow-Cytometry Analysis**

Differentiation of cardiomyocytes was confirmed by intracellular staining of α-actinin using flow cytometry. Differentiated cultures at day 14 were harvested in 0.25% trypsin/EDTA at 37°C for 10 min and subsequently neutralized by 10% FBS in DMEM and washed with PBS. Cells were counted and 1 × 10⁶ cells each were stained for α-actinin and isotype control along with compensation controls including unstained, ethidium monoazide bromide (EMA) only and α-actinin only. Cells were first incubated with 1 μg/mL EMA in staining buffer (2% FBS in PBS) on ice for 15 min, pelleted, resuspended in 1 mL of PBS, and exposed to bright light on ice for 10 min in a horizontally slanted position. After washing, cells were fixed by 4% paraformaldehyde at room temperature for 15 min and permeabilized with 90% ice-cold methanol on ice for 30 min. The cells were then washed, and incubated with the blocking solution consisting of staining buffer supplemented with 20% normal goat serum at room temperature for 30 min. After blocking, cells were incubated for 20 min at room temperature with sarcomeric α-actinin primary antibodies or mouse immunoglobulin G1 isotype control in the blocking solution. Cells were washed and incubated for 15 min at room temperature in the dark with an Alexa 488 conjugated secondary antibody (Table S1). Cells were washed twice and suspended in 200 μL of staining buffer. For staining of LGR5 and endothelial cell surface markers CD31 and VE-cadherin (Table S1), a similar procedure was followed except without cell permeabilization. BD FACS Canto II was used for data acquisition by adjusting voltage and compensation using appropriate excitation and detection channels; fluorescein isothiocyanate and PerCP Cy5.5 channels were used to analyze cells stained for α-actinin and EMA, respectively. Forward versus side scatter quadrants were defined, and at least 10,000 EMA negative (live) events were acquired for each sample. Dot plots were generated upon data analysis using FlowJo software.

**Tube-Formation Assay**

Ice-cold undiluted Matrigel (200 μL) was used to coat each well of 48-well plates and incubated for 40 min at 37°C to allow the gel to solidify. Cultures at day 14 were dissociated using 0.25% trypsin/EDTA solution by incubating at 37°C for 5 min and further neutralized with 10% FBS in DMEM. Cell suspension was centrifuged at 200 × g and cell pellets were resuspended in supplemented basal LaSR medium (DMEM Advanced F12 supplemented with GlutaMAX and L-aspartic acid). Cells were then seeded gently at a density of 2 × 10⁴ cells per well in 200 μL of medium and incubated with (50 ng/mL) or without bFGF at 37°C, 5% CO₂ for 18–24 hr, after which tube formation was confirmed by microscopy (Arnaoutova and Kleinman, 2010).

**Uptake of Acetylated Low-Density Lipoproteins**

Cells were seeded at 10³ cells/cm² in Matrigel-coated 96-well plates 3 days prior to the uptake assay. On the day of the assay, the medium was removed and the cells were washed twice with PBS to remove non-adherent cells. The cells were incubated with 20 μg/mL Ac-LDL-Alexa Fluor 594 (Life Technologies, #L-35353) for 4 hr at 37°C, washed twice with PBS, and further analyzed by fluorescence microscopy for the uptake of fluorescence-labeled Ac-LDL (Niu et al., 2013; Rath et al., 2014).

**Cell Sorting and Expansion of Endothelial Cells**

Day-14 differentiated cells were washed in PBS and dissociated using Accutase (STEMCELL Technologies) for 10 min at 37°C. Cells were gently triturated until single cell suspension was obtained. Cells were spun down at 1,000 × g for 5 min, resuspended in 0.5 mL of PBS containing APC-conjugated CD31 antibody, and incubated on ice for 30 min followed by a single 10-mL PBS wash. FACS Aria II was used to initially exclude debris by gating FSC-SSC and only single cells were further included in the analysis based on width versus height gating parameters. Isolated cells were collected in endothelial cell growth medium MV2 (PromoCell) and used to confirm functional characteristics and cell expansion ability. The purified CD31⁺ cells were expanded in the endothelial cell growth medium supplemented with 50 ng/mL VEGF (PeproTech) for one passage before being examined for cell population doublings.

To further examine the proliferation of CD31⁺ cells, we seeded these purified CD31⁺ cells (2 × 10⁶ cells/cm²) onto laminin-coated plates in the endothelial cell growth medium supplemented with 50 ng/mL VEGF (PeproTech) and counted the cells daily to evaluate cell population doublings over 7 days.

**Statistical Analysis**

At least three sets of independent experiments were performed for each assay, and an unpaired t test was used to compare the control
shRNA group with the LGR5 shRNA group. Data are presented as mean ± SEM.

SUPPLEMENTAL INFORMATION

Supplemental Information includes Supplemental Experimental Procedures, five figures, two tables, and two movies and can be found with this article online at http://dx.doi.org/10.1016/j.stemcr.2017.07.006.

AUTHOR CONTRIBUTIONS

R.J., conception and design, collection and assembly of data, data analysis and interpretation, manuscript writing, and final approval of manuscript. M.S., collection and assembly of data and final approval of manuscript. Q.W., collection and assembly of data and final approval of manuscript. C.G., collection and assembly of data and final approval of manuscript. M.K.P., collection and assembly of data and final approval of manuscript. C.X., conception and design, financial support, data analysis and interpretation, manuscript writing, and final approval of manuscript.

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