The IncRNA DEANR1 Facilitates Human Endoderm Differentiation by Activating FOXA2 Expression

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<th>Jiang, Wei, Yuting Liu, Rui Liu, Kun Zhang, and Yi Zhang. 2015. “The IncRNA DEANR1 Facilitates Human Endoderm Differentiation by Activating FOXA2 Expression.” In Cell Reports 11, no. 1: 137–148. doi:10.1016/j.celrep.2015.03.008.</th>
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<td>Published Version</td>
<td>doi:10.1016/j.celrep.2015.03.008</td>
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The IncRNA \textit{DEANR1} Facilitates Human Endoderm Differentiation by Activating \textit{FOXA2} Expression

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In Brief
Using FACS-based purification and RNA-seq, Jiang et al. comprehensively profile transcriptome dynamics during human endoderm and pancreatic lineage specification and identify hundreds of stage-specific lncRNAs. They further demonstrate that lncRNA \textit{DEANR1} interacts with SMAD2/3 and thus functions in definitive endoderm differentiation through regulating FOXA2.

Accession Numbers
GSE44875

Highlights
- A transcriptome analysis of human endoderm and pancreatic lineage
- Hundreds of dynamically expressed, stage-specific lncRNAs are identified
- \textit{DEANR1} is a functional lncRNA in human endoderm differentiation
- \textit{DEANR1} regulates FOXA2 expression by recruiting SMAD2/3 to FOXA2 promoter
The IncRNA DEANR1 Facilitates Human Endoderm Differentiation by Activating FOXA2 Expression

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INTRODUCTION

Definitive endoderm (DE) specification is one of the first critical steps in early development that generate gastrointestinal tracts and all of the associated organs/tissues, including the pancreas and liver (Zorn and Wells, 2009). Previous studies have shown that human embryonic stem cells (ESCs) and induced pluripotent stem cells (iPSCs) could be induced to differentiate into DE and further into pancreatic progenitors (PPs), as well as islet-like structures exhibiting a partial insulin-secretion function (D’Amour et al., 2006; Jiang et al., 2007; Nostro et al., 2011; Zhang et al., 2006). The derived PPs can be further matured to form well-structured islets that are capable of responding to glucose following transplantation in mouse models (Kroon et al., 2008). However, the in vivo maturation approach was not applicable to clinical studies or suitable for generating large quantities of relevant cells for drug screening until very recently, when two groups reported their success in making functional beta cells in vitro (Pagliuca et al., 2014; Rezania et al., 2014). Additionally, differences between human and mouse endoderm and beta cell development, such as cell-cell interaction and islet structure, have prevented direct translation of the knowledge gained from mouse studies to human applications (McKnight et al., 2010). For instance, a microarray-based transcriptome analysis of human exocrine and endocrine pancreatic cell types not only revealed enrichment of genes important for paracrine signaling but also showed an unexpected abundance of some regulatory proteins, including MAFB in beta cells, distinct from those reported in mouse (Dorrell et al., 2011). Since the study of human development is hampered by limited access to human tissues, particularly of the embryonic stage, understanding cell-lineage-specific differentiation of human ESCs provides an alternative. Indeed, a recent study utilized such a system to investigate human cardiac lineage specification (Paige et al., 2012). Therefore, it is possible that a comprehensive transcriptome characterization of the different developmental stages of endoderm and pancreatic cell lineages would generate a rich resource for understanding the regulatory networks of cell lineage specification and provide additional insights into the mechanism of beta cell differentiation.

The FANTOM and ENCODE projects have revealed that a large proportion of the mammalian genome is transcribed (Carinci et al., 2005; Djebali et al., 2012; Katayama et al., 2005). Thousands of these transcripts are classified as long non-coding RNAs (lncRNAs), with size larger than 200 nucleotides, but very few have been functionally characterized. Biochemically, lncRNAs have been shown to mediate local gene expression in cis, affect multiple gene transcription in trans, and serve as a scaffold for chromatin structure maintenance (Rinn and Chang, 2012; Lifitsky and Bartel, 2013). Functionally, lncRNAs have been shown to regulate diverse biological processes, including X chromosome inactivation, genomic imprinting, cell-cycle regulation, and regulation of stem cell pluripotency (Wang and

SUMMARY

Long non-coding RNAs (lncRNAs) regulate diverse biological processes, including cell lineage specification. Here, we report transcriptome profiling of human endoderm and pancreatic cell lineages using purified cell populations. Analysis of the data sets allows us to identify hundreds of lncRNAs that exhibit differentiation-stage-specific expression patterns. As a first step in characterizing these lncRNAs, we focus on an endoderm-specific lncRNA, definitive endoderm-associated IncRNA1 (DEANR1), and demonstrate that it plays an important role in human endodermal differentiation. DEANR1 contributes to endoderm differentiation by positively regulating expression of the endoderm factor FOXA2. Importantly, overexpression of FOXA2 is able to rescue endoderm differentiation defects caused by DEANR1 depletion. Mechanistically, DEANR1 facilitates FOXA2 activation by facilitating SMAD2/3 recruitment to the FOXA2 promoter. Thus, our study not only reveals a large set of differentiation-stage-specific lncRNAs but also characterizes a functional lncRNA that is important for endoderm differentiation.

INTRODUCTION

Definitive endoderm (DE) specification is one of the first critical steps in early development that generate gastrointestinal tracts and all of the associated organs/tissues, including the pancreas and liver (Zorn and Wells, 2009). Previous studies have shown that human embryonic stem cells (ESCs) and induced pluripotent stem cells (iPSCs) could be induced to differentiate into DE and further into pancreatic progenitors (PPs), as well as islet-like structures exhibiting a partial insulin-secretion function (D’Amour et al., 2006; Jiang et al., 2007; Nostro et al., 2011; Zhang et al., 2006). The derived PPs can be further matured to form well-structured islets that are capable of responding to glucose following transplantation in mouse models (Kroon et al., 2008). However, the in vivo maturation approach was not applicable to clinical studies or suitable for generating large quantities of relevant cells for drug screening until very recently, when two groups reported their success in making functional beta cells in vitro (Pagliuca et al., 2014; Rezania et al., 2014). Additionally, differences between human and mouse endoderm and beta cell development, such as cell-cell interaction and islet structure, have prevented direct translation of the knowledge gained from mouse studies to human applications (McKnight et al., 2010). For instance, a microarray-based transcriptome analysis of human exocrine and endocrine pancreatic cell types not only revealed enrichment of genes important for paracrine signaling but also showed an unexpected abundance of some regulatory proteins, including MAFB in beta cells, distinct from those reported in mouse (Dorrell et al., 2011). Since the study of human development is hampered by limited access to human tissues, particularly of the embryonic stage, understanding cell-lineage-specific differentiation of human ESCs provides an alternative. Indeed, a recent study utilized such a system to investigate human cardiac lineage specification (Paige et al., 2012). Therefore, it is possible that a comprehensive transcriptome characterization of the different developmental stages of endoderm and pancreatic cell lineages would generate a rich resource for understanding the regulatory networks of cell lineage specification and provide additional insights into the mechanism of beta cell differentiation.

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Chang, 2011). Moreover, lncRNAs are less conserved compared with protein coding genes of different species and exhibit tissue- and cell-type-specific expression (Cabili et al., 2011; Derrien et al., 2012). Very recently, Fendrr, an lncRNA that is specifically expressed in lateral mesoderm, was shown to be important for mouse heart and body wall development (Grote et al., 2013; Sauvageau et al., 2013; Braveheart, a mouse- and heart-specific lncRNA, was shown to be required for nascent mesoderm to cardiac fate specification (Klatterhoff et al., 2013); TiNCR, a terminal differentiation-induced lncRNA in human epidermis, was reported to control epidermal differentiation (Kretz et al., 2013); and Inc-DC, an lncRNA that is exclusively expressed in human dendritic cells, was shown to regulate dendritic cell differentiation (Wang et al., 2014). Collectively, these reports support the significance of lncRNAs in cell lineage specification and embryonic development.

Endoderm specification is controlled by a number of signaling pathways and transcriptional factors (Zorn and Wells, 2009), but whether lncRNAs play any role in this process is largely unknown. Interestingly, a recent study reported that during ESC-to-endoderm differentiation, more than 60% of expressed lncRNAs exhibit coordinated expression changes with their associated protein-coding genes (Sigova et al., 2013). Given that lncRNAs are capable of contributing to the regulation of gene expression, they may have a role in endoderm and pancreatic cell lineage specification, which has yet to be defined. Here, we profiled the transcriptome and revealed the dynamic expression pattern of many lncRNAs during endoderm and pancreatic cell lineage specification. We further characterized the function and mechanism of action for an important endoderm-specific lncRNA that we named definitive endoderm-associated lncRNA1 (DEANR1).

RESULTS

Preparation of Purified Cell Samples along the Endoderm and Endocrine Cell Lineage

We previously reported a protocol by which PPs can be generated in vitro by differentiation of human ESCs through the DE stage (Jiang et al., 2011; Zhang et al., 2009). Based on available cell-surface markers of the desired cell types, we prepared purified cell samples along the beta cell lineage, including undifferentiated human ESCs, DE, PPs, and primary adult islet-derived alpha and beta cells. First, we utilized a well-known human ESC surface marker (SSEA-4) combined with a lack-of-lineage markers for DE (Cheng et al., 2012; Nostro et al., 2011), we sorted CD184+/CD117 double-positive cells (as putative DE cells). Next, we sorted CD117, an lncRNA that is exclusively expressed in human dendritic cells, was shown to regulate dendritic cell differentiation (Wang et al., 2014). Collectively, these results support the significance of lncRNAs in cell lineage specification and development, and confirm the reliability of the data sets.

To examine the transcriptome changes that occur between developmentally related stages, we performed a pairwise comparison. Using stringent criteria (log2 [fold change] > 1.5, p value < 0.05 and higher FPKM > 5), we identified hundreds of differentially expressed genes in each comparison. KEGG signal pathway enrichment analysis (Huang et al., 2009) revealed that cell-cycle and related pathways, including metabolism and cancer pathways, were enriched in most differentiation stages (Figure 2C), which is consistent with the observation that the proliferation capacity becomes restricted during cell-fate specification. As expected, several pathways that were previously demonstrated to be involved in pancreatic cell differentiation were enriched in the pairwise analysis. For example, genes of the TGFbeta signaling pathway were enriched in both the human ES-to-DE and DE-to-PP transitions. Interestingly, MAPK and focal adhesion pathways were exclusively enriched in the PP-to-alpha transition, while the ErbB signaling pathway was exclusively enriched in the PP-to-beta transition (Figure 2C). These results suggest that these signaling pathways might coordinate PP-to-alpha/beta cell differentiation. Although previous studies of mice and other vertebrates have reported that multiple signaling pathways are involved in endoderm and pancreatic specification (Zorn and Wells, 2009), these pairwise comparisons may provide valuable information for optimizing in vitro human pancreatic differentiation procedures.

lncRNA Expression during Endoderm and Pancreatic Lineage Specification Is Highly Stage Specific

To identify lncRNAs expressed during human endoderm and pancreatic lineage specification, we mapped RNA-seq data against the GENCODE v14 lncRNA annotation (Derrien et al., 2008, 2011). From multiple primary human islet preparations, we purified beta cells (HP12+/HPa1−) and alpha cells (HP12+/HPa1+) (Figure 1D), qRT-PCR analysis of cell-type-specific factors demonstrated that the cell purification was successful (Figure 1E, Insulin and MAFA mark beta cells, and Glucagon and ARX mark alpha cells).

Expression Dynamics of Protein-Coding Genes during Endoderm and Pancreatic Cell Lineage Specification

To characterize the transcriptional changes that occur during pancreatic beta cell differentiation, we performed RNA sequencing (RNA-seq) using FACS-sorted cells from 11 samples (ES, n = 2; DE, n = 2; PP, n = 3; alpha, n = 2; beta, n = 2) and a modified SMARTseq procedure for Illumina library construction (Yamaguchi et al., 2012) (detailed in Experimental Procedures). For each sample, we generated 24–45 million raw reads, >80% of which mapped uniquely (Figure S1A). Approximately 15,416 human genes were detected under the criteria of FPKM > 1 in replicates. Cluster analysis indicated that the data are highly reproducible (Figure 2A). Inspection of well-known stage-specific markers, such as SOX2, SOX17, SOX9, PDX1, insulin, and glucagon, confirmed their expected stage-specific expression (Figure S1B). The stage-specific expressed genes were enriched for Gene Ontology terms that are consistent with the function of the cells (Figure 2B). Collectively, these results are consistent with human endoderm and pancreatic cell lineage specification and development, and confirm the reliability of the data sets.
Using stringent criteria (FPKM > 1 in each replicate), we identified 1,059 expressed intergenic lncRNAs that were not located within any annotated protein-coding genes (Table S1). Among these lncRNAs, 250 exhibit a stage-specific expression pattern (Figure 3A), 62 are ES specific, 82 are DE specific, 28 are PP specific, 55 are beta specific, and 23 are alpha specific. Representative stage-specific lncRNAs are shown in Figure 3C. Since lncRNAs likely co-express with their neighboring genes (Cabili et al., 2011), we attempted to obtain some insights into the functions of these lncRNAs by asking whether the neighboring protein-coding genes of these lncRNAs (genomic distance of <20 kb) are enriched for any biological processes. A Gene Ontology term analysis revealed that protein-coding genes close to the ES-specific lncRNAs are enriched for regulation of cell division and transcription, and genes close
to DE-specific lncRNAs are enriched for endoderm development, dorsal/ventral pattern formation, and gastrulation (Figure 3B), suggesting a potential role for these lncRNAs in cell-fate determination.

Previous studies have shown that lncRNAs are highly tissue specific (Cabili et al., 2011; Morán et al., 2012). An analysis of the lncRNA expression profiles during endoderm and pancreatic lineage specification indicated that lncRNA expression is highly stage specific: more than 25% of lncRNAs in most of the stages exhibited a stage-specific expression pattern (13.9% for the PP stage), whereas less than 5% of the protein-coding genes were stage specific (Figure 3D). Consistent with previous reports (Cabili et al., 2011; Morán et al., 2012), statistically significant enrichment (\(p < 1 \times 10^{-16}\) for each comparison, chi-square test) of lncRNAs over protein-coding genes was observed during human endoderm and pancreatic lineage specification. To investigate the potential role of these lncRNAs in differentiation, we examined the relationship between the expression of these lncRNAs and their neighboring protein-coding genes during endoderm and pancreatic lineage specification. The expression of lncRNAs and their neighboring genes was highly correlated in ESCs, DE, and PP (Figure 3E); however, the correlation between lncRNAs and their neighboring genes was highly correlated in endoderm and pancreatic lineage specification. The expression of lncRNAs and their neighboring protein-coding genes during these processes (Wang and Chang, 2011), but no lncRNA has been shown to be functionally important for human endoderm and pancreatic lineage specification. To begin to functionally characterize the hundreds of lncRNAs that exhibit stage-specific expression during endoderm and pancreatic lineage specification, we utilized a well-established DE differentiation system to test whether some of these lncRNAs have a role in DE differentiation.

To this end, we applied more stringent criteria (higher FPKM > 5, \(\log_2[\text{fold change}] > 1.5\), \(p < 0.05\)), and identified 38 lncRNAs that are differentially expressed in ESCs and DE cells (13 highly expressed in ESCs and 25 highly expressed in DE cells; Figure 4A; detailed information is provided in Table S2). Among the 25 DE-expressed lncRNAs, 12 are located physically close to protein-coding genes, including the endoderm factors GATA6 and FOXA2. Given that GATA6-associated lncRNAs are divergently transcribed, they likely share a promoter and thus may confound analysis. Therefore, we decided to focus on the FOXA2-associated lncRNA LINC00261. Because this is the first DE-specific lncRNA to be characterized, we renamed LINC00261 as DEANR1 (for definitive endoderm-associated long non-coding RNA).

Our RNA-seq data indicated that DEANR1 is highly expressed in DE, albeit to a lower level than FOXA2 (FPKM: 10 versus 35; Figure 4B). To further characterize the expression pattern of DEANR1, we analyzed its expression level in human ESCs, differentiated neuroectoderm (NE), differentiated embryoid body (EB), and DE cells by qRT-PCR. The results presented in Figure 4C indicate that the expression level of DEANR1 in DE is at least 100-fold higher than in any of the other cell types analyzed. Furthermore, a time-course analysis demonstrated that the expression level of DEANR1 during endoderm differentiation is gradually increased over differentiation (Figure 4D). Based on these results, we conclude that DEANR1 is an lncRNA that is highly expressed in human DE.

**DEANR1 Is Important for Endoderm Differentiation but Is Not Required for ESC Maintenance**

To examine whether DEANR1 is functionally important for endoderm differentiation, we generated two small hairpin RNA (shRNA) constructs targeting different regions of DEANR1. A qRT-PCR analysis demonstrated that both shRNAs achieved...
70%–75% knockdown of DEANR1 in human ESCs (Figure S2A). Importantly, neither knockdown affected human ESC maintenance, as the expression level of pluripotent factors such as SOX2, NANOG, and OCT4 was not altered in the stable knockdown cell lines (Figures S2B and S2C). In addition, neither the morphology nor the growth rate of the stable DEANR1 knockdown cell lines was altered (data not shown). Thus, DEANR1 does not seem to be required for human ESC maintenance, which is consistent with its low expression level in undifferentiated ESCs (Figures 4B and 4C).

To evaluate the effect of DEANR1 knockdown on DE differentiation, we subjected stable DEANR1 knockdown cell lines to endoderm differentiation conditions. A FACS analysis revealed that DEANR1 knockdown cells exhibited a decreased expression of endoderm marker genes, such as FOXA2 and SOX17, after being subjected to endoderm differentiation (Figure 4F). To further analyze the role of DEANR1 in endoderm differentiation, we performed RNA-seq of DEANR1-knockdown cells after subjecting them to endoderm differentiation (Table S3). Compared with differentiated control cells, 632 genes were downregulated and 569 genes were upregulated (Figure 4G) upon DEANR1 knockdown (FDR < 0.001 and fold change > 2). These differentially expressed genes are significantly enriched for DE- and ES-signature genes. Among these, 219 downregulated genes in DEANR1-knockdown cells are DE-signature genes that are expected to be upregulated during endoderm differentiation (Figure 4G, top). Thus, the transcriptome analysis suggested a defective activation of endoderm genes in DEANR1-knockdown cells. A total of 194 upregulated genes in DEANR1-knockdown cells are ES-signature genes that should be downregulated during endoderm differentiation (Figure 4G, bottom). These transcriptome data, together with the differentiation data, suggest that DEANR1 plays an important role in DE differentiation.

DEANR1 Regulates FOXA2 Expression

To identify potential targets of DEANR1 in endoderm differentiation, we collected 47 RNA-seq data sets generated in this study and others (Bramswig et al., 2013; Morán et al.,
Figure 4. Identification of DEANR1 as an Endoderm-Specific IncRNA

(A) Heatmap showing the expression levels of lncRNAs differentially expressed in ESCs and DE cells. Criteria: higher FPKM > 5, log2 (fold change) > 1.5, and p value < 0.05. Red and blue represent high and low expression, respectively. See also Table S2.

(B) Relative enrichment of DEANR1 in DE compared with ESCs shown by FPKM. FOXA2 serves as a control.

(C) Relative expression level of DEANR1 in various cell types quantified by qRT-PCR. Undifferentiated ESCs (ES), differentiated neuroectoderm (NE), spontaneously differentiated embryoid body (EB), and DE samples were compared. The expression level in ES was set as one.

(D) The expression dynamics of DEANR1 during DE differentiation. The mean values are shown and error bars represent the SD from the mean (n = 3). The expression level at day 0 was set as one.

(E) Representative FACS analysis showing a reduced CD117/CD184 double-positive DE cell population upon DEANR1 knockdown.

(F) Representative immunostaining of the DE markers SOX17 and FOXA2 in DE differentiated control and DEANR1 knockdown cells. Scale bar represents 100 μm.

(G) RNA-seq analysis of differentiated DEANR1-knockdown endoderm cells and control endoderm cells. Compared with control (FDR < 0.001 and fold change > 2), 632 genes were downregulated (significantly enriched in DE-signature genes) and 569 genes were upregulated upon DEANR1 knockdown (significantly enriched in ES-signature genes). Among these, 219 downregulated genes in DEANR1-knockdown cells are DE-signature genes that should be upregulated during endoderm differentiation (top), and 194 upregulated genes in DEANR1-knockdown cells are ES-signature genes that should be downregulated during endoderm differentiation (bottom).

See also Figure S2 and Tables S3 and S4.
2012; Xie et al., 2013a, 2013b), and examined the correlation between the expression levels of DEANR1 and transcription factors important for endoderm differentiation, such as MIXL1, SOX17, FOXA2, GSC, EOMES, and GATA6. We found that only expression of FOXA2 was significantly correlated with that of DEANR1 (Figure S3). Interestingly, FOXA2 is also physically close to DEANR1 in its genomic location (Figure 5A). Given that previous studies have demonstrated that IncRNAs can function in cis to regulate expression of adjacent protein-coding genes (Ørom et al., 2010), we examined the possibility that DEANR1 may facilitate DE differentiation by regulating FOXA2 expression. Consistent with this notion, we found that the expression level of DEANR1 was highly correlated with the FOXA2 level in different cell types (Figures 5B and S3). In addition, knockdown of DEANR1 in human ESCs resulted in a dramatic decrease of FOXA2 expression (Figure 5C). A similar effect was also observed in sorted CD184/CD117 double-positive endoderm cells derived from DEANR1-knockdown cells (Figure 5D). A gene-expression analysis in both undifferentiated ESCs (to exclude the differentiation effect) and purified endoderm cells (to bypass the endoderm differentiation defect) supported the notion that DEANR1 regulates FOXA2 expression.
To determine whether FOXA2 is a major functional target of DEANR1 in regulating DE differentiation, we first determined the transcriptome changes in DEANR1-knockdown cells and FOXA2-knockdown cells (80% knockdown efficiency; detailed information is provided in Table S3). Analysis of the RNA-seq data indicated that the changes induced by DEANR1 knockdown and FOXA2 knockdown are highly correlated (Figure 5E). Moreover, the genes affected by DEANR1 knockdown significantly overlap with those affected by FOXA2 knockdown (Figure 6A). Taken together, these data suggest that DEANR1 associates with SMAD2/3 and facilitates its recruitment to the FOXA2 promoter to activate FOXA2 expression.

DISCUSSION

In this study, we performed a comprehensive transcriptome analysis of human endoderm and pancreatic lineage using highly purified samples (Figure 1). We identified hundreds of stage-specific IncRNAs and characterized the function of DEANR1 in endoderm differentiation. Our data suggest that DEANR1 plays an important role in regulating endoderm differentiation. The fact that overexpression of FOXA2 can largely rescue the endoderm differentiation defect caused by DEANR1 depletion suggests that FOXA2 is a major functional target of DEANR1. Furthermore, our data support the notion that DEANR1 regulates FOXA2 transcription in cis. DEANR1 associates with SMAD2/3 and facilitates its binding to the FOXA2 gene promoter to activate FOXA2 expression (Figure 6F), which in turn promotes endoderm differentiation.

Our comprehensive transcriptome analysis of pancreatic beta-cell lineage specification provides insight into the transcriptional dynamics underlying cell fate conversion. First, we observed a decrease in the number of actively transcribed genes during differentiation, particularly in the terminally differentiated islet cell types (Figure S1C), similar to what was observed in a previous study regarding neural differentiation (Wu et al., 2010). Together, the two studies suggest that restriction in gene expression might be a common phenomenon during cell fate specialization. How to silence undesired gene expression during differentiation should be an important question for future investigations. Indeed, two recent studies that profiled the transcriptome and histone K4me3 and K27me3 using human ESC-derived pancreatic intermediate (Xie et al., 2013a) and primary islet cell types (Bramswig et al., 2013) revealed that silencing of transitory genes during lineage progression is associated with reinstatement of Polycomb-dependent repression. Furthermore, DNA methylation-mediated transcription repression has been reported to be essential for maintaining pancreatic beta cell identity (Dhawan et al., 2011). Thus, it is likely that both DNA methylation and H3K27 methylation play an important role in silencing undesired gene expression to achieve cell lineage restriction.

IncRNAs have been reported to participate in diverse biological processes, including ESC maintenance, neural cell differentiation, muscle differentiation, and hematopoiesis (Hu et al., 2012), as well as cardiac development (Grote et al., 2013; Klatenoff et al., 2013) and epidermal differentiation (Kretz et al., 2013). Although a recent study reported the expression of thousands of IncRNAs during endodermal differentiation (Sigova et al., 2013), no specific function has been assigned to any of these IncRNAs during endoderm differentiation. Future characterization of the other endoderm-specific and pancreatic-lineage-specific IncRNAs identified in our study may reveal additional IncRNAs that are important for endoderm and pancreatic
lineage specification. In addition, lncRNAs have been shown to act both in cis and in trans (Rinn and Chang, 2012; Ulltsey and Bartel, 2013). The observation that more than 60% of endoderm-expressed lncRNAs exhibit coordinated expression changes with their adjacent protein-coding genes (Sigova et al., 2013) suggests that cis regulation or local interaction between lncRNAs and their neighboring protein-coding genes may be a common feature of endoderm differentiation. The demonstration that DEANR1 contributes to DE differentiation by regulating its neighboring gene, FOXA2, is consistent with this notion.

Nodal/activin signaling activates the SMAD2/3 pathway and promotes endoderm differentiation (Zorn and Wells, 2009). Secreted Nodal binds and activates ALK4/7, which in turn activates cytosolic SMAD2 and/or SMAD3 by phosphorylation. Phosphorylated SMAD2/3 then enters the nucleus to activate its downstream targets. While the mechanism of SMAD2/3 activation is conserved and well documented, the mechanisms by which SMAD2/3 activate their downstream target genes appears to be cell-context dependent (Feng and Derynck, 2005; Massagué et al., 2005). Although the MH1 domain of SMAD3 is capable of binding to DNA through Smad-binding elements...
with weak affinity, native SMAD target promoters seldom contain such Smad-binding elements, and thus many partners, including DNA-binding proteins, have been reported to form complexes with SMAD2/3 to activate SMAD2/3 target gene expression (Feng and Derynck, 2005; Massagué et al., 2005). In our study, we demonstrated that the association of DEANR1 with SMAD2/3 can facilitate SMAD2/3 binding to the FOXA2 promoter. Based on the data we have obtained so far, we propose a hypothetical model that may explain how DEANR1 contributes to FOXA2 activation and endoderm differentiation (Figure 6F).

It is possible that activation of DEANR1 by an endoderm differentiation signal causes chromatin looping to make the DEANR1 locus spatially close to the FOXA2 promoter. The DEANR1 transcripts can help bring SMAD2/3 to the FOXA2 promoter through a specific interaction with SMAD2/3 and at the same time base pair with a certain region of DNA that encodes DEANR1. Together with the recruitment of other transcription machinery, transcription of FOXA2 can be initiated. We cannot rule out the possibility that other proteins are also required for the binding of DEANR1 to SMAD2/3, since no report has suggested that Smad2 is associated with an intrinsic RNA-binding property, and some RNA-binding proteins have been shown to be able to physically interact with Smad2, Smad3, and Smad4 (Sun et al., 2006). However, adenomatous polyposis coli (APC), a well-studied protein that is involved in the microtubule and Wnt signaling pathway, was recently reported to be an RNA-binding protein (Preitner et al., 2014). Nevertheless, RNA-mediated SMAD2/3 targeting represents an alternative mechanism by which SMAD2/3 are recruited to their targets.

EXPERIMENTAL PROCEDURES

Sample Preparation for RNA-Seq

The following antibodies (all purchased from BD Biosciences) were used to label different cell populations for flow cytometry on a FACSAria II with FACSDiva software (version 6.0; BD Biosciences) as described previously (Dorrell et al., 2011): SSEA4+/CD184 for undifferentiated human ESCs; CD184+/CD117 for DE; CD24+/CD49f for PPs; HP2+/HP1a for beta cells; and HP2+/HP1b for alpha cells. DE cells and PPs were differentiated as previously described (Jiang et al., 2011) with minor modifications. Two individual islet preparations were used to generate alpha1/beta1 and alpha2/beta2 samples for sequencing.

RNA Deep Sequencing and Data Analysis

Total RNA was purified from 1,000 sorted cells using a ZR RNA microPrep kit (Zymo Research). cDNA synthesis and amplification were performed with the SMARTer ultra-low input RNA kit (Clontech). Amplified cDNA (10–40 ng) was then fragmented by a Covaris S2 sonicator (Covaris) and converted to sequencing libraries with barcode in an Illumina Hiseq 2000 instrument (pair-end 100 bp). All obtained reads from each sample were mapped against the human genome (hg19 build) with Bowtie/Tophat and RefSeq gene models) (Harrow et al., 2012; Pruitt et al., 2012) with Cufflinks v2.0.2 (Trapnell et al., 2012). The expression level of each gene was defined as follows:

\[
\text{score} = \frac{\text{mean}_A - (\text{mean}_\text{Other} + 2 \times \text{sd}_\text{Other})}{\text{sd}_\text{Other}}
\]

where meanA is the mean expression of the samples in certain stage, meanOther and sdOther are the mean and SD of the expression levels in the other samples, respectively. Therefore, a positive score indicated that the gene or IncRNAs was expressed in a certain stage at a considerably higher level than in the rest of the stages. A gene or IncRNA with a score of >0.5 was considered as specifically expressed in a certain stage.

Genetic Manipulation

The human ESC line HUES8, cultured without feeder, was used to generate stable knockdown cell lines. A lentiviral vector system containing the murine U6-shRNA cassette and a puromycin selection marker was used to achieve high transfection efficiency. We used two efficient shRNA targeting sites against DEANR1 and one against FOXA2, as follows: DEANR1-shRNA1, GAAAGCTGTAGCCATTCAA (position: 761–779 nt); DEANR1-shRNA2, GCCATTAATTCAGGACACT (position: 2,979–2,997 nt); and FOXA2-shRNA, GCAGGGAAGAAGGATCC.

FISH

Sequential protein staining and RNA detection were performed as previously described (Namekawa and Lee, 2011; Takizawa et al., 2008). In brief, RNA-FISH was performed by using a nick-translated probe (Roche) followed by a tyramide signal amplification kit (Life Technologies). After RNA-FISH, the cells were treated by RNase A and denatured. Nick-translated BAC containing FOXA2 (RP11-842A16) was labeled as a DNA probe.

RNA-Binding Protein Immunoprecipitation and ChIP

An RNA-binding protein immunoprecipitation (RIP) assay was performed using the Magna RIP kit (Millipore) according to the manufacturer’s instruction. Cell lysates from 10 million cells and 2–5 μg of control IgG or antibody against SOX17 (R&D, AF1924), EOMES (Abcam, ab23345), or SMAD2/3 (R&D, AF3797) were used. We validated the RIP assay using the SNRP70 antibody, which can bind to U1 snRNA. A ChIP assay was performed using magnetic beads. Equal amounts of chromatin from each sample and 1 μg of control IgG or antibody against SMAD2/3 were used.

ACCESSION NUMBERS

The data reported in this paper have been deposited to the NCBIGEO and are available under accession number GSE44875.

SUPPLEMENTAL INFORMATION

Supplemental information includes Supplemental Experimental Procedures, three figures, and four tables and can be found with this article online at http://dx.doi.org/10.1016/j.celrep.2015.03.008.

AUTHOR CONTRIBUTIONS

W.J. and Y.Z. conceived the project, designed the experiments, and wrote the manuscript. W.J. performed the experiments. Y.L. performed the bioinformatics analysis. R.L. prepared the low-input library and helped with the bioinformatics analysis. K.Z. assisted in analysis and data interpretation.

ACKNOWLEDGMENTS

We thank Dr. Philip Streeter (Oregon Stem Cell Center) for providing the antibodies against HP1a and HP1b. We also thank Drs. Donghui Zhang and Shinpei Yamaguchi for their help in making Figure 6F. Drs. Azusa Inoue and Shogo Matoeba for advice on RNA-FISH, and Dr. Luis M. Tuesta for a critical reading of the manuscript. This work was supported by NIH grant U01-DK089565 (Y.Z.). W.J. is supported by a Juvenile Diabetes Research Foundation postdoctoral...
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