Interplay of Oct4 with Sox2 and Sox17: a molecular switch from stem cell pluripotency to specifying a cardiac fate

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Oct4 exerts a dose-dependent dual action, as both a gatekeeper for stem cell pluripotency and in driving cells toward specific lineages. Here, we identify the molecular mechanism underlying this dual function. BMP2- or transgene-induced Oct4 up-regulation drives human embryonic and induced pluripotent stem cells to become cardiac progenitors. When embryonic stem cell pluripotency is achieved, Oct4 switches from the *Sox2* to the *Sox17* promoter. This switch allows the cells to turn off the pluripotency Oct4-Sox2 loop and to turn on the *Sox17* promoter. This powerful process generates a subset of endoderm-expressing *Sox17* and *Hex*, both regulators of paracrine signals for cardiogenesis (i.e., Wnt, BMP2) released into the medium surrounding colonies of embryonic stem cells. Our data thus reveal a novel molecular Oct4- and Sox17-mediated mechanism that disrupts the stem cell microenvironment favoring pluripotency to provide a novel paracrine endodermal environment in which cell lineage is determined and commits the cells to a cardiogenic fate.

Introduction

Embryonic stem cells (ESCs), derived from the inner cell mass of the blastocyst or induced pluripotent stem cells (iPSCs) derived from reprogrammed somatic cells retain the ability to self-renew in culture and the potential to differentiate into any cell lineage. The ESC-specific protein, Oct4, is one of the most ancient transcription factors (TFs) and is expressed very early during embryonic development (Smith, 1991). In mouse ESCs, together with Sox2 and Nanog, Oct4 cooperatively maintains pluripotency through a tightly regulated transcriptional loop (Loh et al., 2006; Niwa, 2007). However, a new function of this TF has recently emerged in the process of cell lineage determination. In fact, the level of Oct4 in ESCs determines its dual function (Niwa et al., 2000). The mechanism of that process remained unknown. We demonstrated in vitro and in vivo a gene dosage-dependent function of Oct4, driving the ESC or the epiblast toward a mesodermal cardiogenic fate (Zeineddine et al., 2006).

However, the genetic and epigenetic mechanisms underlying the dual function of Oct4, maintaining pluripotency or inducing lineage progression, has remained puzzling. Furthermore, whether this concept applies to human pluripotent cells is also questionable.

Results and discussion

We chose the cardiac lineage, determined as early as within the epiblast (Tam and Schoenwolf, 1999), to analyze the dual function of Oct4. First, we tested whether BMP2-induced cardiac commitment and differentiation of HESC (Tomescot et al., 2007) was associated with modulation of Oct4. Expression of both human Oct4 isoforms, Oct4-iA, maintaining cell pluripotency (Lee et al., 2006), and Oct4-iB of still unknown function, was monitored by real-time quantitative PCR (RT-Q-PCR). Oct4-iA was up-regulated threefold in response to BMP2. Expression of Oct4-iB remained unchanged (Fig. 1 A). We then used a HESC line harboring a reporter gene (HUES-9 pOct4/GFP,

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Abbreviations used in this paper: CM, conditioned medium; cTnT, cardiac troponin T; EB, embryoid body; ESC, embryonic stem cell; HCC, high content cell; HESC, human ESC; iPSC, induced pluripotent stem cell; Oct4-iA-OEC, Oct4-iA–overexpressing cells; *p*, promoter; RT-Q-PCR, real-time quantitative PCR; TF, transcription factor.

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Oct4*p* driving EGFP) (Fig. 1 B, inset) to investigate BMP2-mediated regulation of the Oct4*p*. First, to ensure that *GFP* was under the tight control of the Oct4*p*, the HUES-9 pOct4/GFP cell line was nucleofected with COUP-TFI, a repressor of Oct4 (Ben-Shushan et al., 1995). GFP was switched off in cells expressing COUP-TFI, as shown by poor GFP distribution within colonies when compared with a fully green mock colony (Fig. S1 A). Furthermore, overexpression of Oct4-iA in the HUES-9 pOct4/GFP line increased GFP expression as expected from regulation of *Oct4p* by its own protein (Fig. S1 B). Stimulation of this line with BMP2 up-regulated *GFP* mRNAs (Fig. 1 B) and FACS revealed a 70% increase in the highly positive GFP population (Fig. 1 C).

To investigate whether a rise in Oct4-iA induces loss in cell pluripotency and promotes cell lineage specification, HESCs were nucleofected with *Oct4-iA*, or *EGFP* cDNA (mock cells). Cells were cultured for 4 d with FGF2. *Oct4-iA*-OEC (35 times), twofold more protein (Fig. 1 E, inset), did not change expression of Oct4-iB (Fig. 1 E). Indeed, only the 48-kD (Oct4-iA), but not the 35-kD band (Oct4-iB), was increased (Fig. 1 E, inset). SSEA-1 was first used as an early marker of HESC loss of pluripotency (Hoffman and Carpenter, 2005). Less than 1% of mock cells (EGFP nucleofected) but 68% of Oct4-nucleofected cells expressed SSEA-1 (Fig. 1 D). This percentage (68%), normalized to the one of cell nucleofection assessed by scoring GFP^+ cells (42%) (Fig. 1 D, inset), suggests that Oct4-iA-OEC as well as neighboring cells had entered a differentiation program. To examine which lineage was induced by Oct4, gene expression was monitored by Q-PCR. Oct4-iA-OEC expressed both mesodermal (*Brachyury, Tbx6*) and cardiac (*Mesp1/2, Tbx20, Tbx5, Mef2C, Nkx2.5, cardiac* α*-actin*) markers (Fig. 1 E). Endodermal genes *Hex* and *Sox17* were also switched on by Oct4-iA (Fig. 1 F). Furthermore, the corresponding proteins Sox17, Nkx2.5, and Mef2c were present (Fig. 1 G). High content cell (HCC) imaging assay allowed us to monitor more than 2,500 cells and revealed that 48% of cells expressed Sox17, indicating that all nucleofected cells expressed the protein (when normalized to percentage of Oct4-iA nucleofection 42%, Fig. 1 D). Up to 20% (i,e., 48% of nucleofected cells) expressed Mef2c, and 31% (74% of nucleofected cells) Nkx2.5 (Fig. 1 G). Very low expressions of the hematopoietic CD45, of the endothelial CD31, CD34 markers were detected (Fig. S1 C). Thus, PCR, immunofluorescence, and FACS data demonstrate that up-regulation of Oct4iA forces HESC to exit pluripotency to adopt a cardiovascular fate. Furthermore, the cardiogenic action of Oct4-iA was translated into a full cardiac differentiation program. While mock-nucleofected cells gave rise to cardiomyocytes expressing actinin and cardiac troponin T (cTnT), the later proteins were not yet organized in sarcomeric units 4 wk after embryoid body (EB) formation. In contrast, EBs generated from Oct4-iA-OEC featured 3.1 ± 0.2 ($n = 4$) as many $cTnT^+$ and $actinin^+$ myocytes as in mock EBs, as assessed by measuring the anti-cTnT and anti-actinin fluorescent areas within whole EBs. Furthermore, the cardiomyocytes were assembled in strands and featured organized and adult-size sarcomeres (2 μm) (Fig. 1 H). Next, we hypothesized that, to trigger specification to a cell lineage, increased Oct4 should disrupt the Sox2/Oct4 pluripotency loop. A potential candidate to replace Sox2 as an Oct4 target, namely Sox17, recently reported as essential for early cardiogenesis (Liu et al., 2007), was expressed in Oct4-iA-OEC (Fig. 1, F and G). We therefore tested the presence of Oct4 on Sox17*p*. ChIP assays designed to pull down Oct4-bound chromatin revealed that BMP2 led to a 10-fold decrease in enrichment of DNA fragments containing the *Sox2* distal enhancer (Chew et al., 2005) and a 300-fold increase in the enrichment of DNA fragments containing a region of the *Sox17p* within the 700-bp upstream of the transcription start site (Fig. 2, A and B). This result obtained in the HUES-24 line was confirmed in two other HESC lines (H9.2 and I4). This was accompanied with induction of *Sox17* in BMP2-treated cells (Fig. 2 B, right inset). Oct4-iA-OEC featured a loss in Oct4-iA binding *Sox2* DNA including the distal enhancer and a gain in binding *Sox17p* (Fig. 2, C and D). In line with these data, ChIP from Oct4-iA-OEC using anti-modified-H3 antibodies revealed significant changes in methylation and acetylation of H3 associated with both *Sox2* and *Sox17* enhancer and promoter, respectively, when compared with mock cells (i.e., GFP nucleofected). Although the ratio of methylations of K4 versus that of K27 of H3, as well as acetylation of H3K9 associated with *Sox2* distal enhancer was decreased, these were increased for the *Sox17p*. This pointed to repression of *Sox2* and activation of *Sox17p*, respectively (Fig. 2 E). Furthermore, the Oct4/Sox2 interaction in control was lost upon up-regulation of Oct4-iA (Fig. 2 F). These transcriptional and epigenetic events led to Sox17 expression in BMP2-stimulated HESC (Fig. 2 G). A similar effect was observed in Oct4-iA-OEC (Fig. 1 G). To gain more insight into the molecular mechanism of the switch of Oct4-iA from the *Sox2p* to the *Sox17p*, we manipulated the level of expression of Sox2 in Oct4-iA-OEC, surmising that a stoichiometric competition occurs between Sox2 and Sox17. A displacement of Oct4/Sox2 complex on *Sox2* distal enhancer would permit Oct4 binding to *Sox17p*, turning on the gene and the protein, which would reinforce *Sox17* expression by forming an Oct4/Sox17 complex on its promoter. When Sox2 was up-regulated in cells nucleofected with the cDNA (Fig. S1 D), the gain in enrichment of Oct4-iA on the *Sox17p* was lost. When Sox2 was down-regulated using a shRNA (Chew et al., 2005) (Fig. S1, D and E), Oct4-iA binding to the *Sox17p* was dramatically increased (Fig. 2 H). We next looked for Oct4–Sox17 interaction in END-2 cells, an endodermal cell line expressing Sox17 (Mummery et al., 1991). Using coimmunoprecipitation after overexpression of Oct4-iA in this cell line, we found that Sox17 binds Oct4 (Fig. 2 I). Altogether, our findings point to Sox17, a novel target of Oct4 also interacting with it, to compete with Sox2 to switch HESC from a pluripotent toward an endodermal/mesodermal fate. To clarify whether Sox17 accounts for the switch of HESC from pluripotency to mesodermal and cardiac commitment of ESC, we used a shRNA approach. *Sox17* ShRNA was nucleofected in HESC together with Oct4-iA cDNA. *Sox17* mRNA was then reduced in the presence of an increased level of Oct4. The protein was also three times less induced by Oct4 overexpression (Fig. S1 F). The amount of Sox17 upon Oct4-iA up-regulation was thus too limited to significantly trigger cardiogenesis (Fig. 3 A). Similarly, BMP2, which induces *Sox17* together with mesodermal and cardiac genes, could no longer induce these genes in the presence of

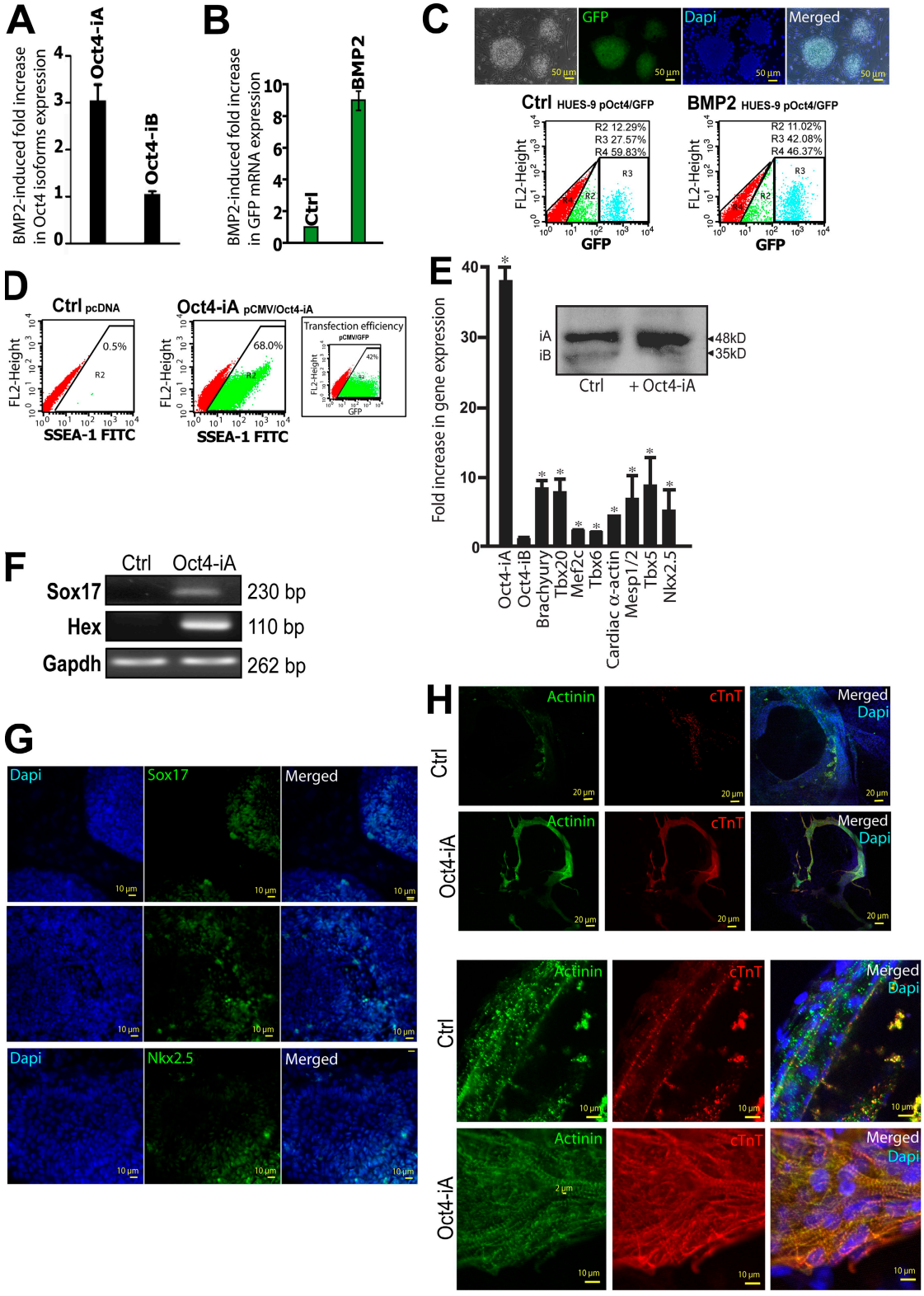

Figure 1. **Overexpression of Oct4-iA induces cardiogenesis.** HUES-24 (A) or HUES-9 pOct4/GFP (B) control or treated for 48 h with BMP2. (A) *Oct4* isoforms Q-PCR. (B) Q-PCR *of GFP* cDNA (n = 2–3). (C) GFP FACS in HUES-9 pOct4/GFP cells (top) nontreated (left) or treated (right) with BMP2. (D–F) Cells nucleofected with *Oct4-iA* or *pCMV-GFP* and cultured for 4 d. (D) FACS of GFP (inset = nucleofection efficiency) and SSEA-1 in mock cells (pcDNA backbone, left) and Oct4-iA-OEC (right). (E) Q-PCR of induced genes. (F) Q-PCR of *Sox17* and *Hex* (amplicons on gel) (means ± SEM [n = 3–6] normalized to huGAPDH). *, Statistically significant ($P \leq 0.01$). (G) Immunofluorescence of anti-Sox17, -Mef2c, and -Nkx2.5 of Oct4-iA OEC scanned by an arrayscan. Bars, 20 µm. (H) Immunofluorescence of anti-sarcomeric actinin and anti-cTnT of d-30 EBs generated from mock or Oct4-iA OECs.

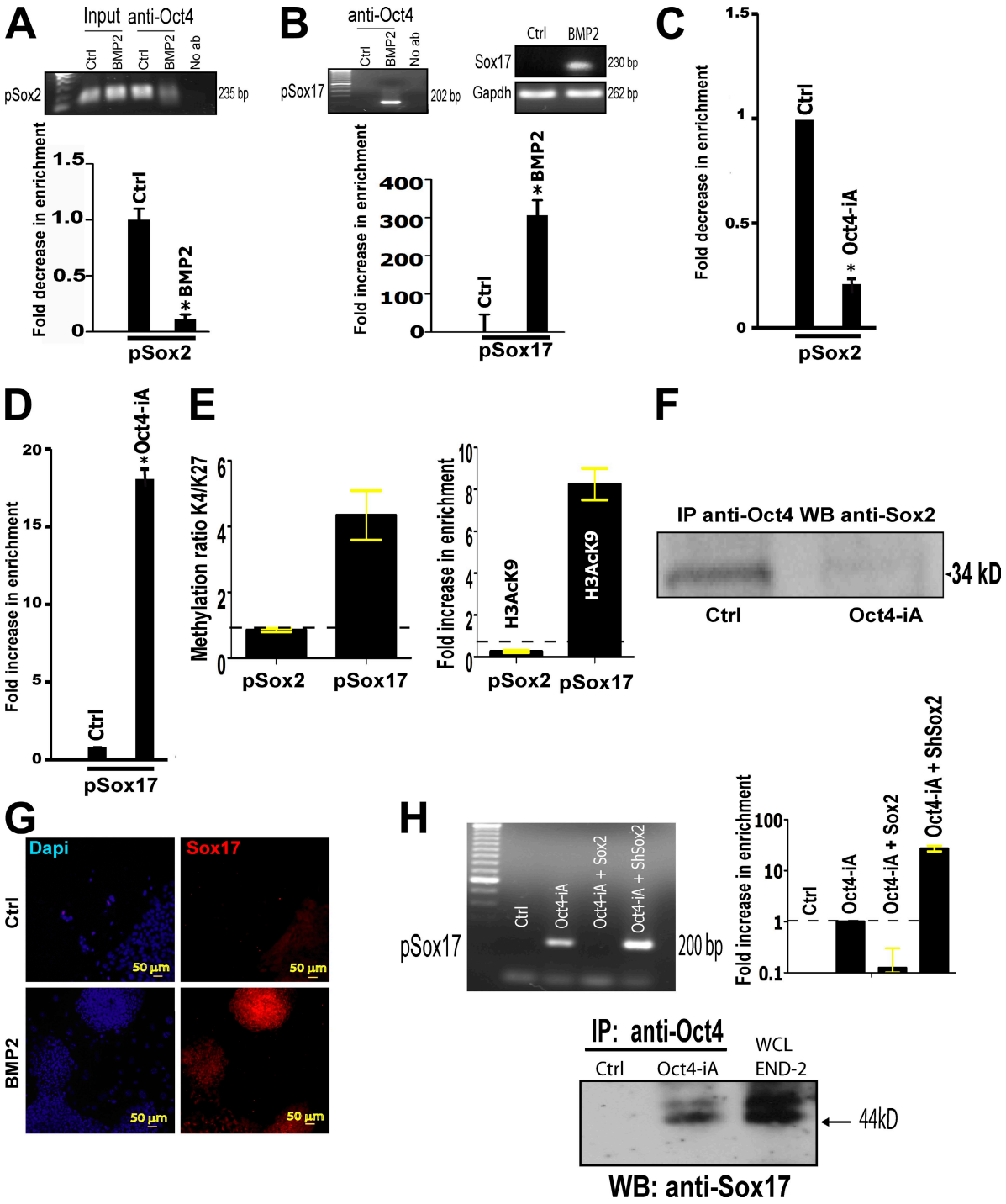

Figure 2. **Oct4 interaction with Sox17 promoter and protein at the expense of Sox2.** Ctrl HESC or treated for 48 h with BMP2, and used for anti-Oct4 ChIP. *Sox2* distal enhancer (A, pSox2) or *Sox17p* (B, p*Sox17*) were amplified in RT-Q-PCR (insets = products on gel). (B, right inset) RT-Q-PCR for *Sox17* in cells treated or not with BMP2. (C and D) anti-Oct4 ChIP in *Oct4-iA*-OECs. p*Sox2* or p*Sox17* was amplified in Q-PCR (n = 3, means ± SEM). (E) Anti-H3trimeK4, -H3trimeK27 and -H3acetylK9 ChIP in *Oct4-iA*-OECs. pSoxs were amplified in Q-PCR. Results are expressed as enrichment (H3AcK9) or as a ratio of enrichment (K4/K27). Data are normalized to inputs and to controls (chromatin from GFP-nucleofected cells) from two experiments (median ± errors). (F) Anti-Sox2 Western blots from Ctrl or Oct4-iA-OEC chromatin. (G) Immunofluorescence of anti-Sox17 and DAPI in Ctrl or BMP2-stimulated HESC. (H) Anti-Oct4 ChIP analysis of p*Sox17*. Cells were nucleofected with GFP cDNA (Ctrl) or Oct4-iA cDNA alone or together with *Sox2* cDNA or *Sox2* ShRNA before ChIP. Q-PCR of p*Sox17* (gel of amplicons on the left). The enrichment in ShRNASox2$^+$ Oct4-OEC was normalized to the one of Oct4-iA-OECs (set to 1). Results are expressed as the median ± errors from two experiments. (I) END-2 cells expressing Sox17 were nucleofected with Oct4-iA and cultured for 2 d. Immunoprecipitation of anti-Oct4 and Western blot of anti-Sox17. END-2 whole-cell lysate was run as a positive control.

Sox17 ShRNA (Fig. S1 G). However, Sox17 shRNA did not prevent the loss of *Sox2* DNA elements bound to Oct4-iA when overexpressed. Interestingly, under the same condition (i.e., Sox17 silencing), the *Sox17p* was no longer occupied by Oct4-iA (Fig. 3 B). Thus, collectively, these ChIP experiments (Figs. 2 and 3) showed the occupancy of *Sox17p* by Oct4. They further revealed

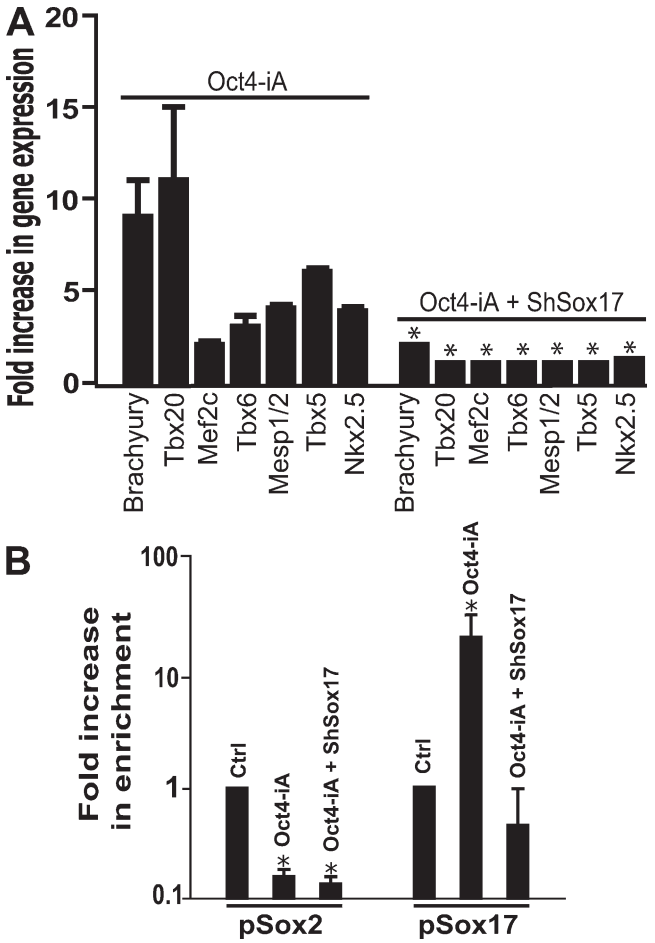

Figure 3. **Sox17 mediates Oct4-triggered cardiogenic commitment of HESC.** *Oct4-iA* cDNA alone or together with Sox17 ShRNA was nucleofected in HESC (A) Q-PCR of genes ($n = 3$). (B) Anti-Oct4ChIP-Q-PCR analysis of *Sox2* distal enhancer and *Sox17p* ($n = 3$, mean ± SEM).

a predominance of K4 over K27 methylations, and an increase in K9 acetylation on H3 in the vicinity of the promoter, thus favoring an active chromatin state. This leads to gene and protein expression. The opposite scenario occurs on the *Sox2* distal enhancer (loss of Oct4 occupancy of the enhancer, increase in K27 methylation, and a decrease in K9 acetylation of H3). Manipulating the levels of Sox2 and Sox17 further pointed to a competition between both Soxs as shown by the capability of Oct4 to form a complex with Sox17. We can further surmise that the Oct4/Sox2 ratio is instrumental in creating various complexes with specific Sox proteins and/or DNA elements. At a normal level of Oct4 or Oct4/Sox2 ratio, it targets the Oct4–Sox2 enhancer, maintaining the transcriptional Oct4/Sox2/Nanog loop and thus cell pluripotency. At a higher Oct4 level or at a low level of Sox2, the POU factor targets the *Sox17p* triggering expression of the protein, forming a more stabilized Oct4/Sox17 complex on the *Sox17p*. This mechanism drives the cells toward specific endo/mesodermal fates. Sox17 is known to target genes encoding cardiogenic factors such as Wnts (Zorn et al., 1999). Wnt is also a trigger of BMP2 (Kasai et al., 2005). To test whether Oct4-iA and Sox17 operate in a cell non-autonomous manner, the conditioned medium (CM) from *Oct4-iA*-OEC was collected to test its potential to induce cardiogenesis. CM from Oct4-iA-OEC triggers in wild-type HESC expression of *Brachyury*, *Mesp1/2, Tbx20, Tbx5, Tbx6, Nkx2.5*, and *cardiac α-actin*, as well as *Oct4-iA* (Fig. 4 A). CM from cells overexpressing *GFP* used as a control did not show any gene induction. Furthermore, CM from Oct4-iA-OEC applied to wild-type cells triggered a switch of Oct4-iA binding from the *Sox2* distal enhancer to the *Sox17p* (Fig. 4 B). We also mixed in the same well HUES-9 pOct4/GFP cells nucleofected with Oct4-iA cDNA with mock cells at different ratios (0:1, 1:1, 3:1, 9:1, respectively). After 4 d of co-culture, mock cell colonies were dissected out and used in real-time PCR. Expression of *Tbx6 Mesp1*, *Isl1*, *Nkx2.5*, *Tbx5* was significantly induced in mock cells when they were mixed with at least three times as many Oct4-iA-OE HUES-9 pOct4/GFP cells as mock cells (3:1 ratio) (Fig. S2 A). In another set of experiments, mixed cells were fixed and stained with an anti-Nkx2.5 antibody. These experiments showed that $Nkx2.5^+$ cells were mainly mock HESC neighboring GFP^+ cells (Fig. S2 B), further confirming that Oct4-iA-OEC exert their cardiogenic function through secretion of cardiogenic factors. We hypothesized that BMP2 or/and Wnt, both direct or indirect targets of Sox17/Hex pathway, as well as Nodal, a Sox17 inducer, might be cardiogenic candidates released by OctiA- and Sox17-OEC. Thus, HESC were nucleofected with *Oct4-iA* cDNA and then cultured for 4 d in the absence or in the presence of 150 ng/ml Dipkopf (DKK), 100 ng/ml Noggin, or 10 ng/ml Lefty to prevent Wnt, BMP2, or Nodal signaling, respectively. Fig. 4 C shows that both DKK and Noggin, but not Lefty, prevented Oct4-iA–induced expression of *Brachyury, Mesp, Tbx20*, *Tbx5*, *Tbx6*, *and Nkx2.5*. Challenging HESC with BMP2 (10 ng/ml) together with Wnt3a (50 ng/ml) significantly improved the effect of BMP2 on early cardiac gene expression as well as on BMP2 and Wnt3a expression (Fig. S2 C). In line with these data, Oct4-iA-OEC expressed *BMP2* and *Wnt3a* (Fig. 4 D). Thus, BMP2 and Wnt3a are the cardiogenic factors released by Oct4 induced $Sox17^+$ cells. Four other findings confirmed this claim. First, phosphorylated Smad recognized by an anti-phosphoSmad1,5,8 antibody was barely detectable in mock cells cultured alone, but observed into nuclei of Oct4-iA-OEC in wells including 50% (i.e., nucleofection efficiency) of *Oct4-iA*-OEC and 50% of non-nucleofected cells (Fig. S3 B). Second, anti-Smad4 ChIP experiments revealed a binding of Smad to both the Nkx2.5 and Tbx6 promoters, two targets of BMP2 (Fig. S3 A) in Oct4-iA-OEC. Third, Wnt3a signaling pathway was activated in Oct4-iA-OEC, as visualized by nuclear localization of β-catenin in contrast to the membrane staining observed in mock cells (Fig. S3 B). Finally, both anti-BMP2 and anti-Wnt3a antibodies added for 2 d in the medium of Oct4-iA-OEC prevented expression of genes marking the mesoderm (*Tbx6*), the cardiogenic mesoderm (*Mesp1*), and cardiac progenitors (*Tbx5*) (unpublished data). To further investigate whether cells expressing Sox17 exerted their cardiogenic action through an autocrine and/or paracrine mechanism, HUES-9-pOct4/GFP cells were plated in microwells and stimulated for 4 d with BMP2. Cells expressing GFP were stained for Sox17 and Mesp1/2, the earliest cardiac marker. Cells not challenged with BMP2 did not express Sox17 or Mesp1/2 (Fig. 4 E, top). Cells challenged with BMP2 expressed both Sox17 and Mesp1/2. Careful observation of cells revealed

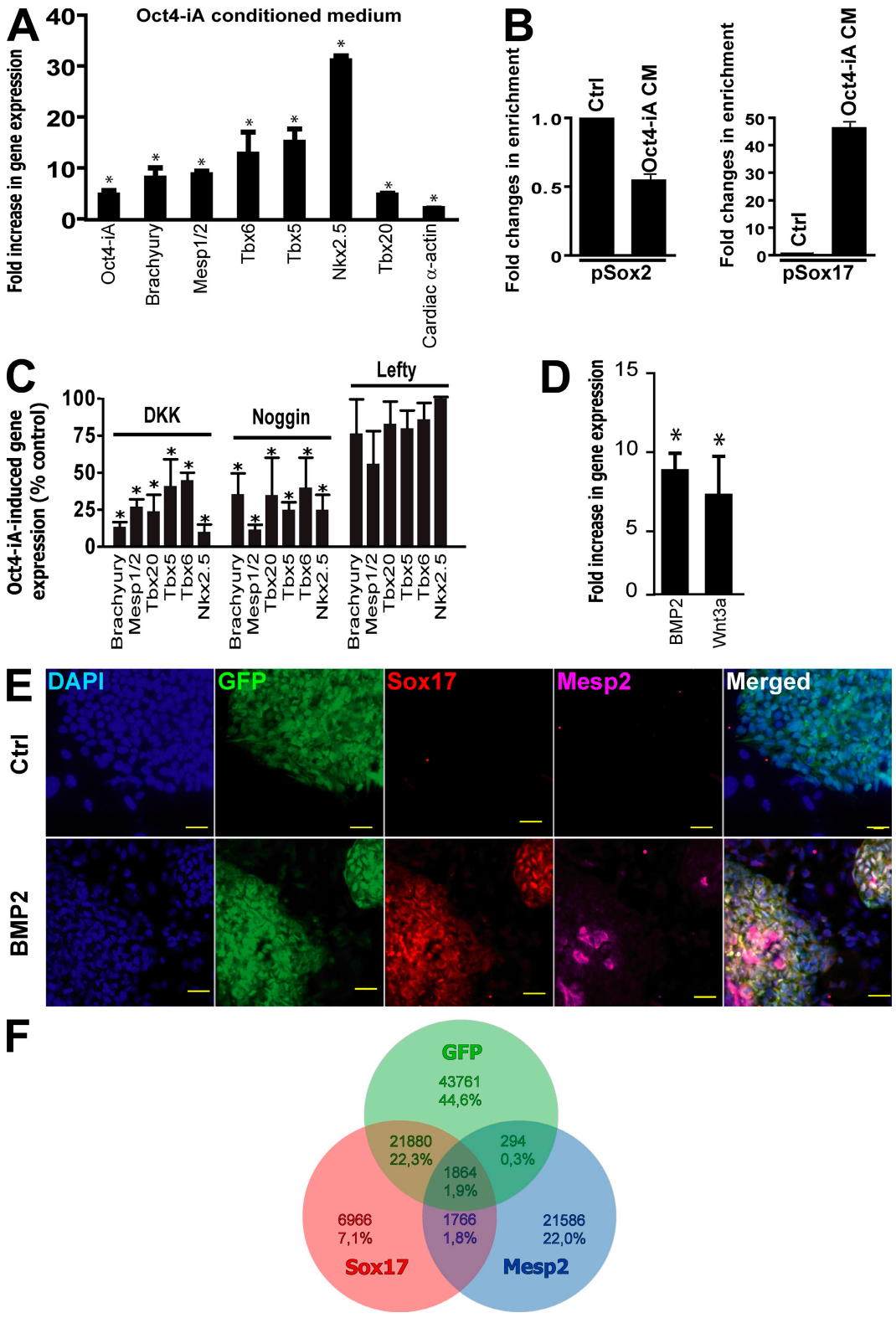

Figure 4. **Overexpression of Oct4-iA induces secretion of paracrine factors.** (A) Q-PCR of genes (n = 3–5). (B) Anti-Oct4 ChIP analysis of *Sox2* distal enhancer and *Sox17p* (pSox) in wild-type HESC treated for 4 d with CM of Oct4-iA-OEC. CM from GFP-nucleofected mock cells was used as control (experiment in duplicate). (C) HESC nucleofected with *Oct4-iA* or *GFP* (mock cells) and cultured for 4 d in the absence or presence of DKK, Noggin, or Lefty. (D) Q-PCR of *BMP2* and *Wnt3a* in Oct4iA-OEC. (E) anti-Sox17 and -Mesp2 immunofluorescence of Ctrl and BMP2-treated HUES-9 pOct4/GFP cells. (F) Venn diagram for the number of cells positive for GFP, Sox17, and Mesp2 alone or together. Ctrl or BMP2-challenged HUES-9 pOct4/GFP cells in 96-well plates were stained with anti-Sox17 and -Mesp2 antibodies. Numbers in the diagram indicate the total number of cells and the percentage. *, Significantly different from control ($P \leq 0.001$).

that a few BMP2-stimulated cells expressed both Sox17 and Mesp1/2, whereas most of them expressed only Sox17 or Mesp1/2. This differential expression of Sox17 and Mesp1/2 was observed in the same or neighboring cell colonies. To further quantify the phenomenon, we set up a high-content imaging assay. 32 wells and 50 fields per well were scanned for expression of GFP, Sox17, and Mesp1/2. Cells expressing GFP, Sox17, Mesp1/2 alone or expressing two or three markers were separately scored. The Venn diagram (Fig. 4 F) first revealed that ∼50% of cells responded to BMP2, as 44% did not express Sox17 and/or Mesp1/2. Half of responder cells (33% of total) expressed Sox17 and the other half (26% of total cells) expressed Mesp1/2. The diagram clearly shows that most of the cells expressed only Sox17, with many still highly GFP^+ or only Mesp2 having lost GFP. A minority of the cells expressed Sox17 and Mesp1/2; almost no cell expressed the three markers. Although 40–50% cells were nucleofected and overexpressed Oct4-iA, 40–60% also expressed several markers including Mef2c and Nkx2.5, which together confer to the cells a cardiac fate (Fig. 1 G), further pointing to a robust paracrine effect of the latter. These findings suggest that the dual function of Oct4 is mediated by a paracrine phenomenon mediated by both BMP2 and Wnt3a. This claim is supported by three series of experiments: first, inhibitors or blocking antibodies, suggesting the presence in the medium of Sox17 expressing cells of both Wnt, known to be a target of Sox17 (Zorn et al., 1999) and BMP2, which cooperates with Wnt pathway (Crease et al., 1998; Kasai et al., 2005; Sumi et al., 2008); second, the BMP2 and Wnt signaling pathways were both activated in wells containing Oct4-iA–overexpressing cells, as revealed by intranuclear localization of both p-Smad1,5,8 and β-catenin in these cells together with the binding of Smad4 to the *Nkx2.5p* and *Tbx6p*; and third, expression of *BMP2* and *Wnt3a* mRNAs by Oct4-OEC. Indeed, both Wnt and BMP2 are well-known cardiogenic factors (Ménard et al., 2004; Liu et al., 2007). Wnt exerts a cardiogenic action early on during embryogenesis to establish the primitive streak/mesendoderm and then BMP2 together with Wnt drive the cells toward the posterior primitive streak and mesoderm (Bakre et al., 2007; Sumi et al., 2008). Furthermore, Wnt in the absence of Activin does not promote the hematopoietic lineage (Nostro et al., 2008) as well as Sox17 prevents the development of ectoderm (Séguin et al., 2008). Then, BMP2 takes over the cardiogenic task, Wnt becoming a cardiogenic inhibitor (Naito et al., 2006). The cardiogenic factors released by Oct4-induced $Sox17^+$ cells may exert their action in an autocrine, and/or in a paracrine manner on neighboring Sox17-negative cells driving them from an undifferentiated to a mesodermal cardiogenic fate. Using HCC imaging to monitor expression of Sox17 and Mesp2 in BMP2-induced Oct4-iA-OEC revealed that one third of Oct4-iA-OEC expressed Sox17 as expected from a direct targeting of Sox17 by the POU factor, whereas many cells expressing Mesp2 did not express any longer Oct4 or Sox17. This observation argues more for a paracrine effect, although we cannot exclude a kinetic effect, cells going through a endo/mesendodermal stage ($Sox17^+$) and then to the cardiogenic mesoderm ($Mesp1/2^+$) turning off Sox17 in line with the inhibitory effect of Mesp1/2 on Sox17 (Bondue et al., 2008).

Our data thus revealed a novel Oct4/Sox17-mediated molecular mechanism that disrupts the microenvironment that favors cell pluripotency and prevents differentiation, to provide a novel paracrine environment more prone to commit the cells toward a cardiac lineage. iPSC are derived from somatic cells reprogrammed using Oct4, Sox2, Nanog, and Lin28 or Myc (Takahashi et al., 2007). We wondered whether manipulating the Oct4-iA level in such cells could also drive them through the Sox2/Sox17 switch toward a cardiogenic fate. Thus, iPSCs were nucleofected with *Oct4-iA* cDNA and both gene expression and *Sox17p* occupancy were monitored by Q-PCR. Fig. S3 C shows that 5 d after nucleofection, iPSC expressing 10 times more *Oct4-iA* mRNA than GFP nucleofected cells changed of morphology, displaying more flat and irregular colonies in comparison with compact colonies in mock cells expressing GFP. These cells expressed mesodermal and cardiac markers including *Brachyury*, *Mesp1/2*, *Tbx20*, *Tbx5*, and *Nkx2.5*, as well as *Sox17* (Fig. S3 D). Oct4-iA switched from the *Sox2* to the *Sox17p* (Fig. S3 E). This was associated with up-regulation of *Sox17* (Fig. S3 D, inset) and of both *Wnt3a* and *BMP2* mRNAs (Fig. S3 F).

Thus, we have found a novel molecular and cellular circuit in which Oct4 and Sox17 work in combination to drive human pluripotent stem cells toward an endodermal or mesendodermal fate, and in turn toward the fate of cardiac progenitors. This circuit is functional within an ESC colony or "niche", BMP2 acting first in cells surrounding the colony, likely generating a gradient from the outer to the inner part of colonies rather secreting factors such as GDF3 maintaining a basal level of Oct4 and cell pluripotency (Peerani et al., 2007). Then, mesendo/endodermal $Sox17^+$ cells amplify the differentiation process by secreting cardiogenic factors (i.e., Wnt3a, BMP2), further acting on the colonies to direct the cells toward a cardiogenic fate (Fig. 5). This molecular and cellular circuitry is likely to occur during the process of somatic cell reprogramming using Oct4 as the main reprogramming inducer, pointing to the importance of an accurate Oct4/Sox2 dosage in these experiments. Oct4 dosage within the nucleus is thus crucial to build specific bridges between different (i.e., Sox2 or Sox17) chromatin domains, resulting in generation of "transcription factories" working either to maintain ES cell pluripotency or to drive them toward a cardiogenic fate.

Materials and methods

Culture and cardiac commitment of human pluripotent stem cells

Two HESC lines and one HiPSC line 11 (Maherali et al., 2008), using human dermal fibroblasts infected by lentivirus harboring the cDNAs encoding Oct4, Sox2, Lin 28, Klf4, and Nanog, were used throughout this study without any difference in results. HUES-24 and HUES-9 pOct4/GFP (a transgenic cell line generated using BAC) and iPS cell were cultured on mouse embryonic fibroblasts (MEFs) prepared from E14 mouse embryos as described previously (Tomescot et al. 2007). HESC were treated for 48 h with 10 ng/ml BMP2 in the presence of 1 µM SU5402, an FGF receptor inhibitor, in KOSR-DMEM. HESC (both HUES-9 and HUES-24) were used within no more than 10 passages (P28-P38). Cells are phenotyped every 10 passages using anti-SSEA-3/4, TRA-1-60, and TRA-1-80 antibodies (Millipore). Less than 5% of cells were positive for SSEA-1 (Millipore). Karyotype was found normal and stable in the course of the experiments. EBs were generated from mock (GFP)–nucleofected or Oct4-iA–nucleofected in DMEM added with 20% FCS. Cells were let in suspension for 5 d to allow for their aggregation and then EBs were plated on gelatin-coated dishes for the next 3 wks. The blocking anti-BMP2 and anti-Wnt3a antibodies

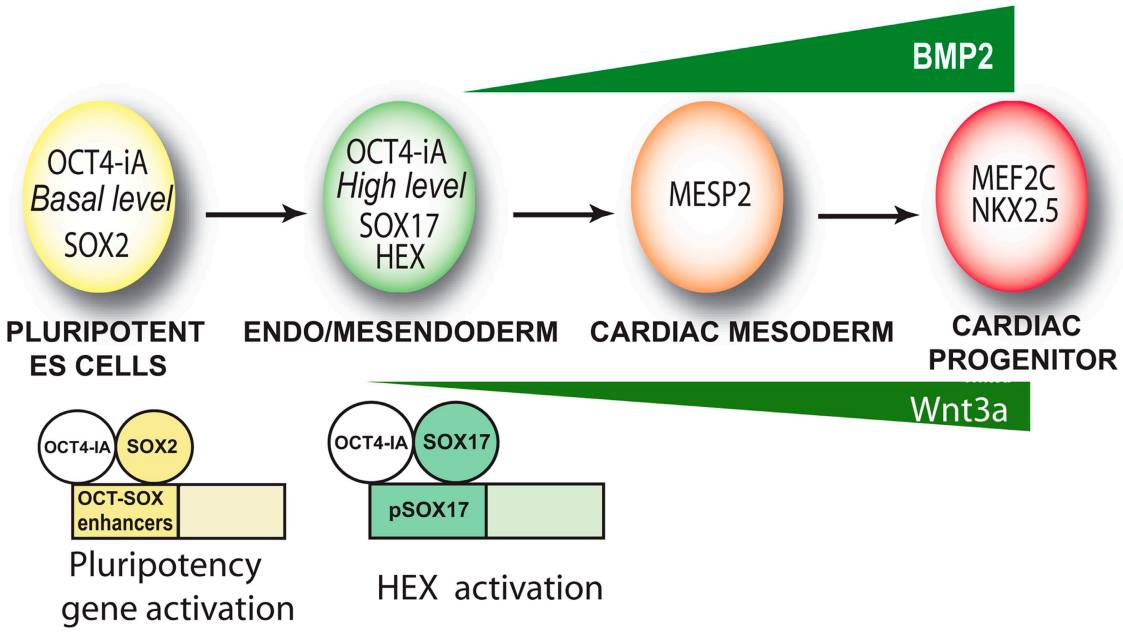

Figure 5. **The Sox17/Oct4 circuit is functional within a stem cell colony or "niche".** Oct4 and Sox17 work in combination to drive HuPSC toward a mesendodermal fate, and through secretion of BMP2 and wnt3a toward the fate of cardiac progenitors.

(MAB3552 and MAB1324, respectively; R&D Systems), used at a concentration of 7.5 µg/ml medium, were added to mock or Oct4-iA–nucleofected cells for 2 d before RNA extraction and RT-Q-PCR of Tbx6, Mesp1, and Tbx5 genes.

RT-Q-PCR by SYBR green detection

RNA was extracted from ES cells using a QIAGEN or Zymo Research (Proteingene) kit or a Zymo Research RNA MicroPrep (Proteingene) for singles colonies. 1 µg of RNA was reverse-transcribed using the SuperScriptII reverse transcription (Invitrogen) and oligo(16)dT. Q-PCR was performed using a Light Cycler LC 1.5 or 480 (Roche) according to the manufacturer. Melting curves were used to determine the specificity of PCR products, confirmed using conventional gel electrophoresis and sequencing. Data were analyzed according to Pfaffl (2001). Primers specific for human genes are described in Tomescot et al. (2007) and are available on request.

Primers to amplify enhancer/promoter regions were: Sox17 promoter: forward, 5′-actttcacagtccaggaacggagt-3′ and reverse 5′-ggcttcctt-ggagaaaggcaat-3′ targeting a region within the 700-bp region upstream the transcription start site; Sox2: distal enhancer forward, 5′-attagtct-gctcttcctcggaatggttgg-3′ and reverse, 5′-tgatgcttgttaaaaacgcttcgctcc-3′. Nkx2.5 promoter: forward 5′-cagtcttgggagctcaagact-3′ and reverse 5′-cagatccccaagcttactagc-3′; Tbx6 promoter: forward 5′-taacccgttcct-gccccacct-3′ and reverse 5′-tccgcttgagctccccttcc-3′.

Chromatin immunoprecipitation (ChIP) assay

ChIP was performed according the Q2ChIP (Dahl and Collas, 2007) or Fast ChIP protocol (Nelson et al., 2006). Data were also confirmed using a standard ChIP procedure as described previously (Zeineddine et al., 2006). The antibodies used were anti-Oct4 (Santa Cruz Biotechnology, Inc.), anti-Smad4 (Santa Cruz Biotechnology, Inc.) and anti-H3triMeK4, triMeK27, and acetylK9 (UBI). Q-PCR was used to amplify the DNA elements as described above. Absolute enrichment was calculated assuming that at most 1% of nucleosome was immunoprecipitated (Dahl and Collas, 2007). Genomic region was thus considered enriched if 10-ng immunoprecipitation samples showed a greater enrichment when compared with 0.1 ng of input DNA. Data in all the text and figures are normalized to a control condition (absolute enrichment set to one) and are thus representative of a relative enrichment in one experimental condition (BMP2 treatment or Oct4 up-regulation) versus the control (non-treated cells or mock cells).

DNA constructs

Human Sox17 ShRNA targeted the following Sox17 cDNA sequence: 5′-gcaggtgaagcggctgaag-3′. This was synthesized as a sense and antisense oligonucleotide, annealed and subcloned in pSuper vector (Ambion). The DNA constructs were nucleofected in HESCs, using Amaxa specific nucleofector solution I, as recommended by the manufacturer.

Oct4-iA was amplified from RNA extracted from HESC as described in Lee et al. (2006) and subcloned in a pcDNA vector.

Cell immunofluorescence and imaging

Cell immunofluorescence was performed as described previously (Zeineddine et al., 2006). The anti-Sox17 antibody was from R&D Systems (Mab1924); anti-Nkx2.5 antibody from R&D Systems (MAB2444 clone 259416); anti-Mef2c from Aviva; anti-CD31, CD45, and CD34 from Becton Dickinson; anti–phospho-Smad1/5/8 from Cell Signaling Technology; anti–β-catenin from BD Biosciences; anti-sarcomeric actinin from Sigma-Aldrich; and anti-cTnt from Abcam. Slides were mounted using Fluoromount-G (Electron Microscopy Science).

Cardiac TnT and α-actinin fluorescent areas were measured in EBs using a thresholding and setting the cTnT and α-actinin fluorescent areas as regions of interest (ROI) within whole EBs observed at 4x to measure the number of pixels within these ROIs with ImageJ software (National Institutes of Health, Bethesda, MD).

Images were acquired at room temperature with an epifluorescence microscope (AxioImager; Carl Zeiss, Inc.) using an Achroplan 10x objective (NA 0.25) (Fig. 1 C), a microscope (Axiostar; Carl Zeiss, Inc.) using an N-Achroplan objective (20x, NA 0.45) (Fig. 1 G), or a laser-scanning microscope (LSM510 Meta; Carl Zeiss, Inc.) using an Achroplan objective 10x (NA 0.25) and Fluar 40x oil (NA 1.3) zoom 2x (Fig. 1 H), and visualized without any processing by LSM browser software (Carl Zeiss, Inc.) or (Fig. 2) a microscope (Multiphoton Radiance 2000MP; Bio-Rad Laboratories) attached to a Nikon Eclipse with a 10x PL-APO (NA 0.45) at room temperature and visualized with Bio-Rad Laboratories software and ImageJ without any processing.

FACS analysis

HESC were trypsinized and washed twice with PBS, filtered through a 70-µm mesh filter before FACS analysis using FACS Calibur (Becton Dickinson) and CELL QUEST software.

Protein immunoprecipitation and Western blots

END-2 cells were cultured in DMEM, supplemented with 10% FCS. Cells were nucleofected with Oct4-iA cDNA using the kit V (Amaxa). Cells were lysed in RIPA buffer. Co-Immunoprecipitation was performed in RIPA buffer and Western blot analysis was conducted as reported previously (Pucéat et al., 1998). The anti-Oct4 antibodies used were from Santa Cruz Biotechnology, Inc. Sox2 and Oct4 Western blots were performed using the anti-Sox2 from Santa Cruz Biotechnology, Inc., and anti-Oct4 recognizing both Oct4-iA and -iB.

Screening of immunostained cells by high content imaging

Immunofluorescence scan of BMP2-treated HUES-9 pOct4/GFP or Oct4iA nucleofected HESC stained with anti-Sox17 and Alexa 546–conjugated anti–mouse IgG or anti-Mesp2 and anti-Alexa 680–conjugated anti–rabbit IgG antibodies or anti-Nkx2.5 and anti-Alexa 488–conjugated anti–rabbit IgG antibodies or anti-Mef2c and anti-Alexa 488–conjugated anti–mouse IgG antibodies: HESC were plated in 96-wells plates on MEF and treated or not with 10 ng/ml BMP2 and SU5402 for 4 d. Other cells were nucleofected with Oct4iA cDNA and plated in Labtech. After immunostaining, the HC imaging 96-well plates (cells in PBS) were scanned with the Arrayscan (Cellomics Thermo Fisher Scientific attached to an inverted microscope [Carl Zeiss, Inc.] and using 20x N-Achroplan objective, NA 0.45, at room temperature) using the Cell Health Profiling Bioapplication. The fluorescence threshold was determined from the background obtained in non-BMP2–stimulated cells or mock cells and set as a fixed threshold value to scan the wells of BMP2-treated cells or Oct4iA–nucleofected cells. In BMP2 experiments, 50 fields/well and 32 wells were scanned giving a total of 98,120 cells selected according the morphology, size, and the proximity of their nuclei (i.e., to discriminate HESC colonies from feeder cells). Different types of events were scored using the cell feature parameters and the Boolean operators. The visualization of images and analysis were then performed using the vHCS software.

Online supplemental material

Fig. S1: characterization of HUES-9 pOct4/GFP clone. Non-cardiac potential of differentiation of Oct4-OEC. KO of Sox2/Sox17 and consequences on BMP2-induced gene expression. Fig. S2: paracrine action of Oct4-overexpressing cells. Fig. S3: Oct4-overexpressing cells activate Smad and β-catenin pathways; The Oct4/Sox17 network is conserved in iPSCs. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.200901040/DC1.

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