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Short communication

Investigation of telomere length dynamics in induced pluripotent stem cells using quantitative fluorescence *in situ* hybridization

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ABSTRACT

Here we attempted to clarify telomere metabolism in parental cells and their derived clonal human induced pluripotent stem cells (iPSCs) at different passages using quantitative fluorescence *in situ* hybridization (Q-FISH). Our methodology involved estimation of the individual telomere lengths of chromosomal arms in individual cells within each clone in relation to telomere fluorescence units (TFUs) determined by Q-FISH. TFUs were very variable within the same metaphase spread and within the same cell. TFUs of the established iPSCs derived from human amnion (hAM933 iPSCs), expressed as mean values of the median TFUs of 20 karyotypes, were significantly longer than those of the parental cells, although the telomere extension rates varied quite significantly among the clones. Twenty metaphase spreads from hAM933 iPSCs demonstrated no chromosomal instability. The iPSCs established from fetal lung fibroblasts (MRC-5) did not exhibit telomere shortening and chromosomal instability as the number of passages increased. However, the telomeres of other iPSCs derived from MRC-5 became shorter as the number of passages increased, and one (5%) of 20 metaphase spreads showed chromosomal abnormalities including X trisomy at an early stage and all 20 showed abnormalities including X and 12 trisomies at the late stage.

1. Introduction

Telomeres are repetitive G-rich DNA sequences found at the ends of linear eukaryotic chromosomes and appear to play a key role in preventing genomic instability (Blackburn, 2001; de Lange, 2005). Telomeres in human cells show shortening due mainly to mitosis *in vitro* (Vaziri et al., 1994), and aging *in vivo* (Aida et al., 2008). Telomere lengths of cultured fibroblasts (Takubo et al., 2010) and human tissues (Aida et al., 2008) show marked heterogeneity among individual telomeres and in terms of mean or median values in individual cells. Telomere length heterogeneity and telomerase expression among induced pluripotent stem cells (iPSCs) have been reported previously (Wang et al., 2012).

iPSCs are derived from somatic cells and, like embryonic stem cells, possess the capacity to differentiate into cell derivatives of all three germ layers (Takahashi and Yamanaka, 2006; Takahashi et al., 2007). iPSCs have been generated from somatic cells derived from aged organisms, including both mouse and human (Takahashi and Yamanaka, 2006; Takahashi et al., 2007). iPSCs have considerable therapeutic promise, as well as providing a potent *in vitro* model for studying biological processes (Apostolou and Hochedlinger, 2011). It has been reported that direct reprogramming of somatic cells to a pluripotent condition is accompanied by telomerase activation and telomere elongation (Park et al., 2008; Takahashi and Yamanaka, 2006; Takahashi et al., 2007). However, there is very little detailed information about telomere metabolism in individual iPSCs.

Studies using Southern blotting (Takahashi et al., 2007) or semi-quantitative fluorescence *in situ* hybridization (FISH) (Suhr et al.,

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2009) have indicated that some iPSCs may display significantly elongated telomeres, whereas telomere elongation or shortening may be evident in some lines but not in others. Terminal restriction fragment (TRF) analysis by Southern blotting does not estimate pure telomere length due to the fact that the TRF has subtelomere components (Aubert et al., 2012). iPSCs are usually cultured on feeder cells (irradiated mouse cells), and therefore the samples obtained are always admixtures of iPSCs and feeder cells, making it difficult to obtain DNA from pure iPSCs after multiple passages. Accordingly, instead of Southern blotting, we have used the quantitative fluorescence *in situ* hybridization (Q-FISH) method to measure iPSC telomere length.

We have also measured individual telomere lengths of chromosomal arms in human fibroblast strains by Q-FISH to clarify the morphologic signs of chromosomal instability (Takubo et al., 2010). Our findings indicated a linear correlation between telomere fluorescence units (TFUs) estimated by Q-FISH and telomere length measured by Southern blotting (Takubo et al., 2010). Few previous studies have attempted to examine telomere metabolism in human iPSCs after various numbers of passages or in quantitative terms using an assay such as Q-FISH (Liu et al., 2012). Here, therefore, using Q-FISH, we attempted to clarify the telomere metabolism of iPSCs and the parental cells from which they were derived at different passages using cloned iPSCs. In terms of the linear correlation between TFUs determined by Q-FISH, we estimated telomere lengths of individual cells by measuring the TFUs of telomere lengths of chromosomal arms in individual cells.

2. Materials and methods

2.1. Ethics statement

Human amnion cells were collected by scraping tissue from surgical specimens, with signed informed consent from the donors concerned, and under ethical approval from the Institutional Review Board of the National Institute for Child Health and Development, Japan. The surgical specimens were irreversibly de-identified. All experiments involving the handling of human cells and tissues were performed in line with tenets of the Declaration of Helsinki.

2.2. Human cell culture

Human amniotic membrane (hAM)-derived cells were independently established in our laboratory (Cui et al., 2007, 2011; Nishino et al., 2010, 2011). hAM-derived cells and MRC-5 cells were maintained in Dulbecco's Modified Eagle Medium (DMEM) supplemented with 10% fetal bovine serum and penicillin–streptomycin. Human iPSCs were generated in our laboratory using the procedures described by Yamanaka and colleagues (Cui et al., 2007, 2011; Nishino et al., 2010, 2011; Takahashi and Yamanaka, 2006; Takahashi et al., 2007). The iPSCs were established from hAM-derived cells and MRC-5, and designated hAM933 iPSCs and MRC-5 iPSCs, respectively. They were maintained on irradiated mouse embryonic fibroblasts (MEFs) in iPSellon medium (Cardio Incorporated, Kobe, Japan) supplemented with 10 ng/ml recombinant human basic fibroblast growth factor (bFGF, Wako Pure Chemical Industries, Ltd., Osaka, Japan). We used iPSCs that had been chosen randomly from stable lines in our laboratory.

We measured telomere lengths in the parental cells (hAM933 and MRC-5), two iPSCs (hAM933 iPSCs-2, hAM933 iPSCs-3) derived from different colonies originating from hAM933, and two iPSCs (MRC-5 iPSCs-16 and MRC-5 iPSCs-40) cloned from the same iPSCs (MRC-5 iPSCs) at different passages (MRC-5 iPSCs-16; passages 22 and 59; MRC-5 iPSCs-40; passages 21 and 62) (Table 1).

3. Q-FISH and image analysis

3.1. Probes and counterstaining

For karyotype analysis and quantitative analysis of telomeres, metaphase chromosomes were fixed and then hybridized using the peptide nucleic acid-FISH preparation method described previously (Poon and Lansdorp, 2001a,b).

A Cy3-labeled $(CCCTAA)_3$ peptide nucleic acid probe (telo C) (Fasmac, Atsugi, Catalogue No. F1002, Japan) was used to label the telomeres, and a FITC-labeled CTTCGTTGGAAACGGGGT peptide nucleic acid probe (CENP1; a non-specific centromere probe; Fasmac, custom made, Japan) was used for labeling the centromere. The chromosome preparations were counterstained with 4′,6-diamidino-2-phenylindole (DAPI, Molecular Probes, Eugene, OR, USA).

3.2. Q-FISH and image analysis

Analysis of fluorescence images was performed as described previously (Takubo et al., 2010). Digital images were recorded with a CCD camera, AxioCam MRm (Zeiss, Oberkochen, Germany), mounted on an Axio Imager M1 (Zeiss) epifluorescence microscope equipped with a triple band-pass filter for Cy3/FITC/DAPI (61010 Chroma Technology, Corp., Rockingham, VT, USA) and a 63× oil objective lens (Zeiss EC Plan-NEOFLUAR 63×/1.25 ∞/0.17). Microscope control and image acquisition were performed with the ISIS system (MetaSystems, GmbH, Altlussheim, Germany).

The level of calibration was used to ensure a reliable quantitative estimation of telomere length in the various samples. To correct for daily variations in lamp intensity and alignment, images of fluorescent beads (orange beads, size 0.2 μm, Molecular Probes, Inc.) were acquired just prior to acquisition of the images from the samples. The fluorescence intensities of the beads and telomeres were analyzed using the TFLTelo-V2 software package (Terry Fox Laboratory, BC Cancer Research Centre, Canada).

3.3. Karyotype analysis using the iPSCs FISH samples

The parental cells and all of the iPSCs at early and late passages were subjected to karyotyping of 20 metaphase spreads of FISH samples using telomere measurements for detection of abnormalities (Table 1). Chromosome identification and karyotype designations were performed in accordance with the International System for Human Cytogenetic Nomenclature (Shaffer et al., 2009).

3.4. Measurements of telomere length in metaphase spreads

Using the ISIS karyotyping system, we analyzed the karyotypes of 20 metaphase spreads at early passage (hAM933, passage 3, MRC-5, and MRC-5 iPSCs-16 and 40, passages 22 and passages 21, respectively) and late passage (hAM933 iPSCs-2, passage 25, hAM933 iPSCs-3, passage 27, MRC-5 iPSCs-16, passage 59 and MRC-5 iPSCs-40, passage 62). We then measured the telomere fluorescence intensities of the p- and q-arms of all the chromosomes in the spread individually.

The median TFU value was defined as a representative value for a metaphase spread (184 telomeres), and the mean value of the median values for all metaphase spreads for a single subject was defined as the representative value for that subject. The mean value of the median for all subjects within each of the three groups was defined as the representative value for the subject group.

Table 1
Data for iPSCs, karyotype analyses, and telomere length measurements.

Cell (ID)	Origin	Passages	Karyotype	Mean of median TFU (SD)	Minimum TFU	Ratio after reprogramming and multiple PDL
hAM933	Amnion	3	46, XY[20]	13,936 (1526)	425	1.00
hAM933 iPSCs-2	Amnion	25	46, XY[20]	23,302 (3864)	568	1.67
hAM933 iPSCs-3	Amnion	27	46, XY[20]	19,309 (3334)	471	1.39
MRC-5	Fetal lung fibroblasts	–	46, XY[20]	14,010 (2015)	380	1.00
MRC-5 iPSCs-16	Fetal lung fibroblasts	22	46, XY[20]	19,670 (3501)	766	1.40
MRC-5 iPSCs-16	Fetal lung fibroblasts	59	46, XY[20]	18,613 (3147)	609	1.33
MRC-5 iPSCs-40	Fetal lung fibroblasts	21	46, XY[19],47, XY, +X[1]	25,092 (4384)	700	1.79
MRC-5 iPSCs-40	Fetal lung fibroblasts	62	46, XY, inc[5], 47, XY, +12[8], 47, XY, +mar[4], 47, XY, +X[2], 48, XY +2mar[1]	16,923 (4191)	371	1.21

TFU: telomere fluorescence units; mar: marker chromosome; inc: incomplete.

3.5. Statistical analysis

The telomere lengths in the two groups (parental cells and their iPSCs, and MRC-5 iPSCs-16 and 40 at early and late passages) were compared using the unpaired t test. Fisher's Z test and Pearson's correlation coefficient were used to compare any correlations. For all comparisons, differences at $p < 0.05$ were considered to be significant.

4. Results

4.1. Karyotype analysis

FISH images were obtained for the parental cells established from human amnion (hAM933) and fetal lung fibroblasts (MRC-5), and the iPSCs established from hAM933 and MRC-5, which were designated hAM933 iPSCs-2, hAM933 iPSCs-3, MRC-5 iPSCs-16

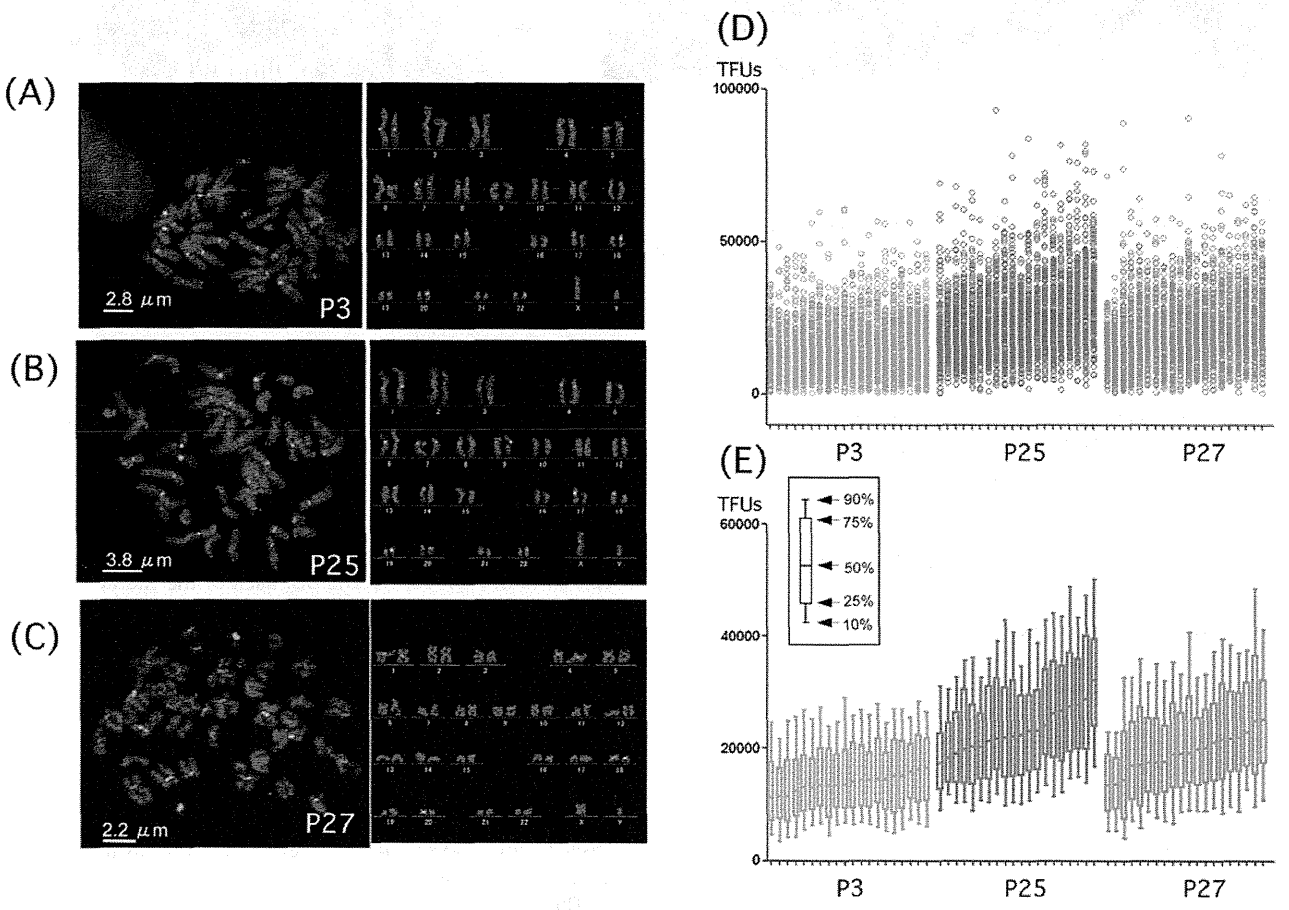

Fig. 1. Karyotype analysis and telomere length measured by Q-FISH and image analyses of hAM933 (A), hAM933 iPSCs-2 (B) and hAM933 iPSCs-3 (C), and telomere fluorescence units (TFUs, D and E) of the p- and q-arms of all constituent chromosomes. No chromosomal instabilities were found. Twenty metaphase spreads from the hAM933 parental cells (A, 3P; passage 3), hAM933 iPSCs-2 (B, 25P; passage 25) and hAM933 iPSCs-3 (C, 27P; passage 27). Cy3, FITC, and DAPI images were observed after assignment of pseudo-colors (red for Cy3, green for FITC and blue for DAPI). The labeling with Cy3 and FITC demonstrated the telomeres and centromeres, respectively. The chromosome preparations were counterstained with DAPI. The telomere fluorescence units (TFUs) of the p- and q-arms of all the chromosomes in the spread were measured individually. The median telomere lengths of 20 metaphase spreads in the parental cells (hAM933, passage 3), hAM933 iPSCs-2 (passage 25) and hAM933 iPSCs-3 (passage 27) are shown as scatter plots for all analyzed data (D) and as box plots (E).

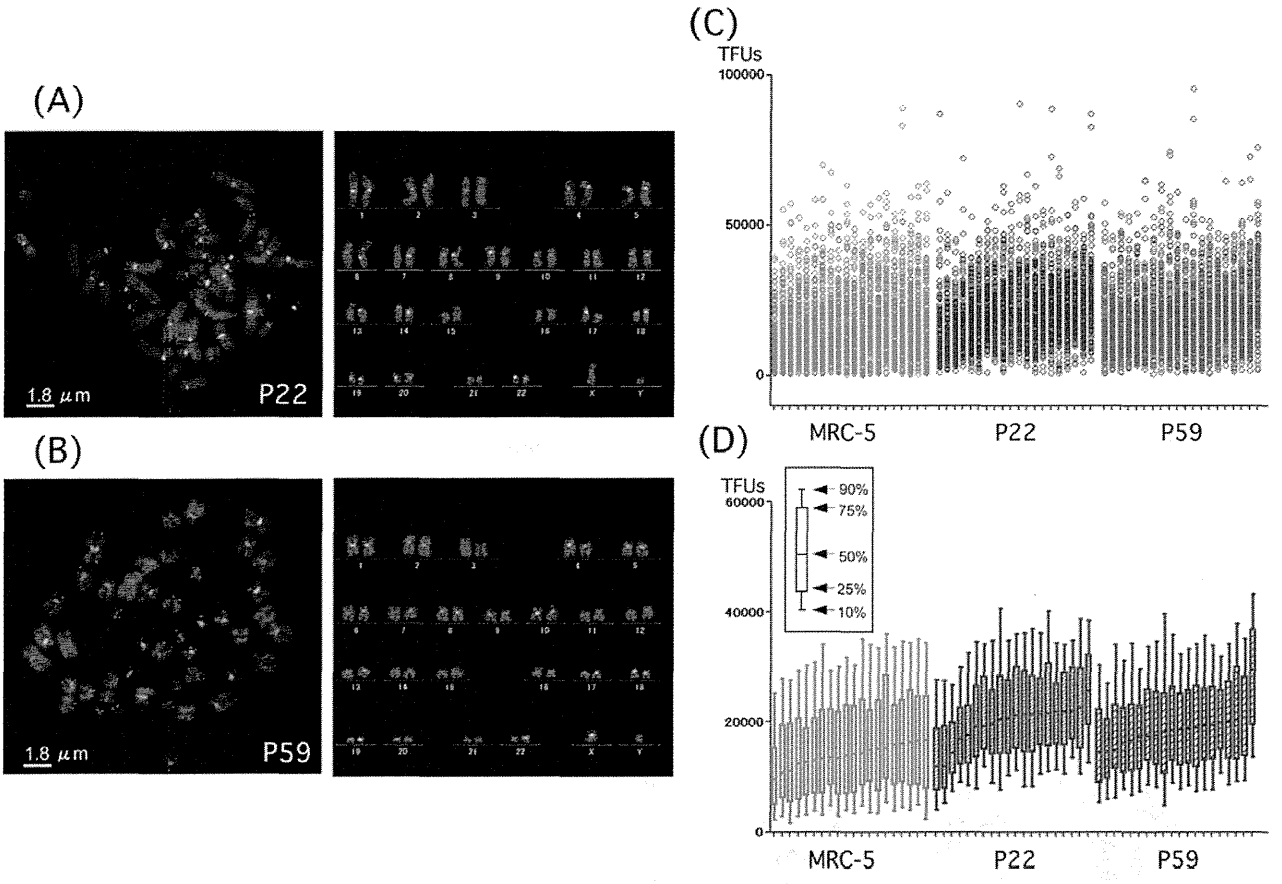

Fig. 2. Karyotype analysis and telomere length measured by Q-FISH and image analyses of MRC-5 iPSCs-16 at passages 22 (A) and 59 (B), and telomere fluorescence units (TFUs, C and D) of the p- and q-arms of all the constituent chromosomes. No chromosomal instability was found. Twenty metaphase spreads of MRC-5 iPSCs-16 at passages 22 and 59 (A, 22P and B, 59P) were examined. Cy3, FITC, and DAPI images were observed after assignment of pseudo-colors (blue for DAPI, red for Cy3 and green for FITC). Labeling with Cy3 and FITC demonstrated the telomere and centromere, respectively. The chromosome preparations were counterstained with DAPI. The telomere fluorescence units (TFUs) of the p- and q-arms of all the chromosomes in the spread were measured individually. The median telomere lengths of 20 metaphase spreads in MRC-5 and MRC-5 iPSCs-16 (passages 22 and 59) are shown as scatter plots for all analyzed data (C) and as box plots (D).

and MRC-5 iPSCs-40 (Nishino et al., 2010, 2011; Cui et al., 2007, 2011). Cy3, FITC, and DAPI images were observed after assignment of pseudo-colors (red for Cy3, green for FITC and blue for DAPI). Twenty metaphase spreads from the parental cells (Fig. 1A), hAM933 iPSCs-2 (passage 25) (Fig. 1B) and hAM933 iPSCs-3 (passage 27) (Fig. 1C), and MRC-5 iPSCs-16 (passages 22 and 59) (Fig. 2A and B) demonstrated no chromosomal instability. None of the 20 parental cell lines, hAM933 iPSCs-2, hAM933 iPSCs-3, or MRC-5 iPSCs-16 (passages 22 and 59) tested showed any abnormality of chromosome number, including X trisomy ($n=1$). However, of the 20 MRC-5 iPSCs-40 (passage 21) cells tested, 19 (95.0%) exhibited normal diploidy and 1 (5.0%) showed chromosomal instability. Of the 20 MRC-5 iPSCs-40 (passage 62) cells tested, all contained abnormal numbers of chromosomes including X ($n=2$) and 12 ($n=8$) trisomies (Fig. 3A and B, Table 1).

4.2. Telomere length (TFU)

We measured telomere lengths in parental cells (hAM933 and MRC-5), two iPSCs (hAM933 iPSCs-2, hAM933 iPSCs-3) derived from different colonies originating from hAM933, and two iPSCs (MRC-5 iPSCs-16 and MRC-5 iPSCs-40) cloned from the same iPSC (MRC-5 iPSCs) at different numbers of passages (MRC-5 iPSCs-16; passages 22 and 59; MRC-5 iPSCs-40; passages 21 and 62) (Table 1).

The median telomere lengths of 20 metaphase spreads in the parental cells, hAM933 iPSCs-2 (passages 25) and hAM933 iPSCs-3 (passages 27), MRC-5 iPSCs-16 (passages 22 and 59), and MRC-5 iPSCs-40 (passages 21 and 62) are shown in Figs. 1D, E, 2C, D, and 3C, D. Scatter plots for all analyzed data are indicated in Figs. 1D, 2C and 3C. The data are summarized as box plots in Figs. 1E, 2D and 3D. Each of the metaphase spreads examined showed marked heterogeneity.

Mean values of the median telomere length in 20 metaphase spreads of parental cells (hAM933 and MRC-5) and all iPSCs are shown in Table 1 and Fig. 4. Mean values for 20 metaphase spreads of the parental cells had a smaller standard deviation than those of iPSCs overall. The established iPSCs, hAM933 iPSCs-2 and hAM933 iPSCs-3, had significantly longer telomeres than hAM933 ($p<0.001$, 1.67 and 1.39), although the telomere extension rate varied quite significantly among the clones ($p<0.001$, 1.67 *versus* 1.39). This observation showed that telomere lengths in an individual iPSC have marked heterogeneity.

The ratios of the mean telomere lengths for medians of 20 metaphase spreads in MRC-5, MRC-5 iPSCs-16 and MRC-5 iPSCs-40, between early and late passages, are shown in Table 1. MRC-5 iPSCs-16 showed no telomere elongation ($p=0.322$, 1.40 and 1.33) as the number of passages increased (22 and 59), whereas MRC-5 iPSCs-40 showed telomere shortening ($p<0.001$, 1.79 and 1.21) as the number of passages increased (21 and 62). The minimum

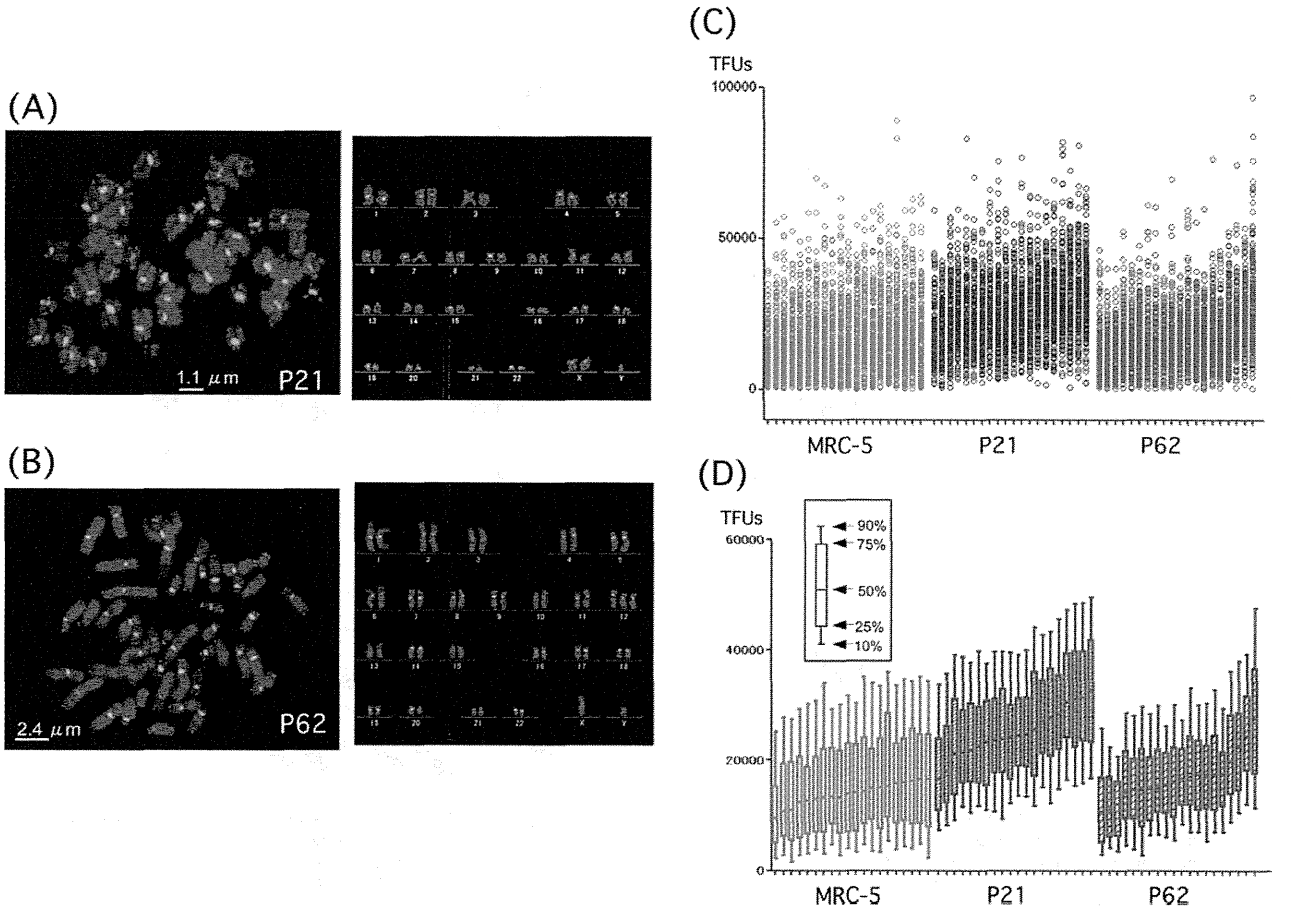

Fig. 3. Karyotype analysis and telomere length measured by Q-FISH and image analyses of MRC-5 iPSCs-40 at passages 21 (A) and 62 (B), and telomere fluorescence units (TFUs, C and D) of the p- and q-arms of all the constituent chromosomes. One (5%) of 20 metaphase spreads showed chromosomal abnormalities including X trisomy at an early stage (A, passages 21) and all 20 showed abnormalities including X and 12 trisomies at the late stage (B, passage 62). Twenty metaphase spreads from MRC-5 iPSCs-40 (21P and 62P; passages 21 and 62) were examined. Cy3, FITC, and DAPI images were observed after assignment of pseudo-colors (blue for DAPI, red for Cy3 and green for FITC). Labeling with Cy3 and FITC demonstrated the telomere and centromere, respectively. The chromosome preparations were counterstained with DAPI. The telomere fluorescence intensities of the p- and q-arms of all the chromosomes in the spread were measured individually. The median telomere lengths of 20 metaphase spreads in MRC-5 and MRC-5 iPSCs-40 (passages 21 and 62) are shown as scatter plots for all analyzed data (C) and as box plots (D).

TFU of MRC-5 iPSC-40 (passage 62, TFU; 371) was smaller than that of MRC-5 (TFU; 380). These results indicated that MRC-5 iPSC-40 with telomere shortening would be susceptible to an abnormal karyotype.

5. Discussion

The initial reports by Yamanaka and others on transcriptional factors directing the reprogramming of somatic cells to a pluripotent state indicated that this event is accompanied by telomerase activation and telomere length extension (Park et al., 2008; Takahashi and Yamanaka, 2006; Takahashi et al., 2007). Activation of telomerase is induced upon establishment of iPSCs, and is dependent on the parental cells of origin. In the present study, the telomeres of parental cells were elongated upon establishment of iPSCs, but the telomere extension rate differed among the clones. These results suggest that establishment of iPSCs induces telomerase activation to various degrees depending on the cell of origin. For telomerase activation, the transcriptional regions of the hTERT need to be switched on, and this process is dependent on the epigenetic information in each individual iPSC. Establishment of iPSCs requires a process of epigenetic reprogramming (Reik, 2007). Epigenetic information is present in the form of DNA methylation, and culture of iPSCs under various conditions can result in stochastic *de novo* methylation (Nishino et al., 2010, 2011). Telomeres become elongated upon establishment of iPSCs, which also acquire telomerase activity and epigenetic changes.

iPSCs are heterogeneous, and also individual iPSCs show a wide range of telomerase expression and telomere length (Wang et al., 2012). Here we found that the iPSCs without telomere shortening showed no significant chromosomal instability as the number of passages increased, whereas the iPSCs with telomere shortening showed significant chromosomal instability with increasing passages. Telomere length represents the potential replicative capacity of a cell, and there is a correlation between the frequency of fusions and telomere length in senescent human cells (Counter et al., 1992; Pereira-Smith and Smith, 1988). Fusions occur between the arms of chromosomes whose telomeres are significantly shorter than average (Aida et al., 2010, 2012; Takubo et al., 2010). We have already developed a method based on estimation of the individual telomere lengths of chromosomal arms of individual cells of different types within independent clones, which exploits the linear correlation between TFUs obtained by Q-FISH and telomere length obtained by Southern blotting (Takubo et al., 2010). Several studies have tried to estimate telomere lengths using tissue sections subjected to Q-FISH (Aida et al., 2008, 2010, 2012; Takubo et al., 2010), and these demonstrated that telomere shortening was associated with an increased incidence of chromosome instability.

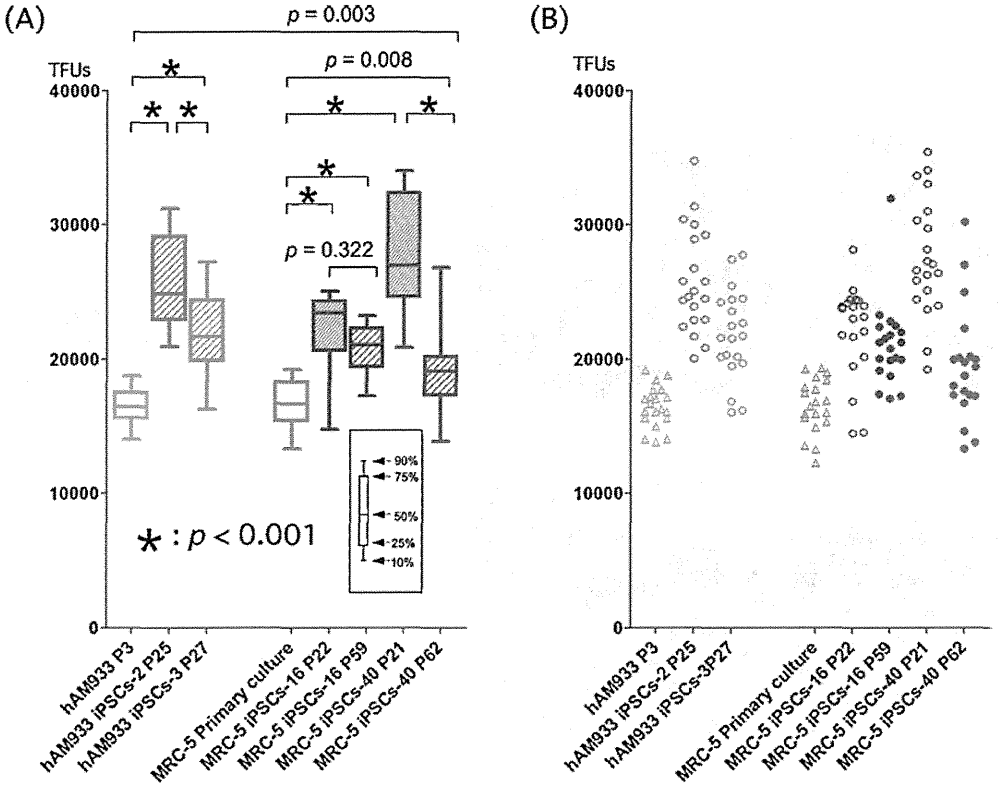

Fig. 4. Mean values of the median telomere length for 20 metaphase spreads in the parental cells (hAM933) and all iPSCs. Box plots (A) and scatter plots for all analyzed data (B). Mean values of 20 metaphase spreads of the parent cells had a smaller S.D. than those of the iPSCs overall. The telomeres of hAM933 iPSCs-2 and hAM933 iPSCs-3 were significantly longer than those of hAM933 ($p < 0.001$, 1.67 and 1.39), although the telomere extension rate varied quite significantly among the clones ($p < 0.001$, 1.67 *versus* 1.39). MRC-5 iPSCs-16 showed no telomere shortening as the number of passages increased (22 and 59) ($p = 0.322$, 1.40 and 1.33), whereas MRC-5 iPSCs-40 showed telomere shortening as the number of passages increased (21 and 62) ($p < 0.001$, 1.79 and 1.21). The mean telomere lengths of the median telomere lengths for 20 metaphase spreads in the parent cells and all iPSCs are shown as scatter plots for box plots (A) and all analyzed data (B).

These studies demonstrating excessive telomere shortening in the background epithelium have also suggested that this is an initial feature in the process of cancerization (Aida et al., 2010, 2012; Takubo et al., 2010). Our present study indicated that although established iPSCs maintain telomerase activity, chromosomal instability can be induced by telomere shortening. This suggests that iPSCs showing telomere shortening associated with an increased number of passages or chromosomal instability should probably not be chosen for experimental or therapeutic purposes.

The establishment of iPSCs appeared to be associated with telomere elongation and activation of telomerase. The heterogeneity of telomerase expression in iPSCs suggests that cellular senescence could be controlled by the chromosomes of individual cells, and that short telomeres arising as a result of limiting levels of telomerase predispose chromosomes to instability. Long-term culture of iPSCs would induce random methylation and convergence, and telomere activation might be influenced by epigenetic regions of hTERT transcription. iPSCs comprise convergent cells in which stochastic methylation, selection and fixation would be dependent on environment conditions. It has been proposed that cell therapy using iPS cells for a variety of patients with genetically complex and heterogeneous diseases would have both advantages and limitations, although iPSCs with alleles from the patient would provide an abundant material for clarifying the molecular mechanisms of disease in a variety of genotypes, thus facilitating the development of tailored therapy (Agarwal and Daley, 2011; Agarwal et al., 2010). If iPSCs are applied for cell therapies in the future, reprogramming techniques will need to consider the expression of specific genes in individual cells. Telomere measurement would also be useful for guaranteeing the quality of iPSCs, and further studies will be necessary to clarify the telomere metabolism of iPSCs in detail.

6. Conclusions

The telomere lengths of iPSC clones, represented as mean values of median telomere fluorescence units, significantly exceeded those of the parental strain, while the telomere extension rates varied significantly between the clones.

iPSCs established from fetal lung fibroblast (MRC-5) did not exhibit telomere shortening and chromosomal instability as the number of passages increased. However, the telomeres of other iPSCs derived from MRC-5 became shorter as the number of passages increased; one (5%) of 20 metaphase spreads showed chromosomal abnormalities including X trisomy at an early stage, and all 20 showed abnormalities including X and 12 trisomies at the late stage.

Conflict of interest statement

The authors have no conflicts of interest to declare in relation to this study.

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RESEARCH ARTICLE Open Access

Large-scale cell production of stem cells for clinical application using the automated cell processing machine

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Abstract

Background: Cell-based regeneration therapies have great potential for application in new areas in clinical medicine, although some obstacles still remain to be overcome for a wide range of clinical applications. One major impediment is the difficulty in large-scale production of cells of interest with reproducibility. Current protocols of cell therapy require a time-consuming and laborious manual process. To solve this problem, we focused on the robotics of an automated and high-throughput cell culture system. Automated robotic cultivation of stem or progenitor cells in clinical trials has not been reported till date. The system AutoCulture® used in this study can automatically replace the culture medium, centrifuge cells, split cells, and take photographs for morphological assessment. We examined the feasibility of this system in a clinical setting.

Results: We observed similar characteristics by both the culture methods in terms of the growth rate, gene expression profile, cell surface profile by fluorescence-activated cell sorting, surface glycan profile, and genomic DNA stability. These results indicate that AutoCulture® is a feasible method for the cultivation of human cells for regenerative medicine.

Conclusions: An automated cell-processing machine will play important roles in cell therapy and have widespread use from application in multicenter trials to provision of off-the-shelf cell products.

Keywords: Automated cell culture system, Cell transplantation, Stem cells, Clinical trial, Cell processing facility

Background

Degenerative diseases affect increasing numbers of people, particularly in developed countries with aging populations. Despite advancements in medicine, modalities to cure advanced diseases are often not available. Therefore, regenerative therapy may become the standard treatment option in cardiovascular medicine. Recent developments in stem cell biology, including those related to induced pluripotent stem cells (iPSCs) and tissue-derived stem/progenitor cells, are a giant leap toward the goal. Recently, myocardium-derived stem/progenitor cells were isolated by several institutes [1-3]. These cell populations have the potential to repair the diseased heart, and clinical trials are currently ongoing.

In tandem with these developments in stem cell biology and the large number of completed and ongoing clinical trials, attempts have been made to commercialize these therapies [4]. The most prominent therapeutic strategy is cell transplantation. However, harvested cells or tissues are usually limited in quantity and stem cells properties may vary from batch to batch, hindering the reliability for clinical applications. Moreover, current cell therapy protocols are laboratory centered and labor intensive, requiring highly skilled personnel and weeks to months to harvest sufficient quantities of stem/progenitor cells from the isolated tissues. These manual procedures are expensive and can result in high phenotypic and yield variability between different trials and institutions [5].

Strategies to validate advanced medicinal products have been established; however, these "best practices" still depend on the ability of personnel to perform them, such as the cultivation of stem/progenitor cells under strictly

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controlled conditions [6]. High process reproducibility can be achieved by automation, and several effective automatic cell culture systems have been reported [7-12]. These automated platforms have the potential to provide cost-effective, large-scale expansion of stem/progenitor cells with consistent phenotype for clinical use and improved operational safety [13]. Progress in robot platforms for cell culture has resulted in several prototypes to implement large-scale expansion and harvesting of stem/progenitor cells with yield and phenotypic reproducibility. An automated culture system by "The Automation Partnership Biosystems (TAP Biosystems)" has cultivated human embryonic stem cells and bone marrow-derived cells [14,15]. Kawasaki Heavy Industries (Tokyo, Japan) has created AutoCulture® (Additional file 1), which can automate many manual steps in cell culture, including media exchange, centrifugation of cells, splitting and passaging, and recording of cell morphology (Figure 1A). To the best of our knowledge, no cell products obtained from an automated culture apparatus have actually been transplanted into humans for regenerative therapy.

Our institute recently completed a phase I clinical trial using autologous cardiac stem cells (CSCs) isolated by manual cell culture techniques to treat ischemic cardiomyopathy [16]. The trial is registered in the Japanese government database for clinical trials using human stem cells and ClinicalTrials.gov, which is a world-wide registry and results database for clinical trials involving humans, as AutoLogous Human CArdiac-Derived Stem Cell to Treat Ischemic cArdiomyopathy (ALCADIA; Identifier: NCT00981006). CSCs are manually cultivated by a single experienced investigator for approximately 1 month to minimize variability of the final cell products. To advance this trial from a single-center to a multi-center randomized trial, we evaluated AutoCulture® by comparing the growth rate, morphology, and phenotype of cells cultivated using this method with those of manually cultured CSCs.

Results

Cellular morphology and growth

Calculations based on the net cell number and doubling time obtained in the ALCADIA trial (Additional file 2)

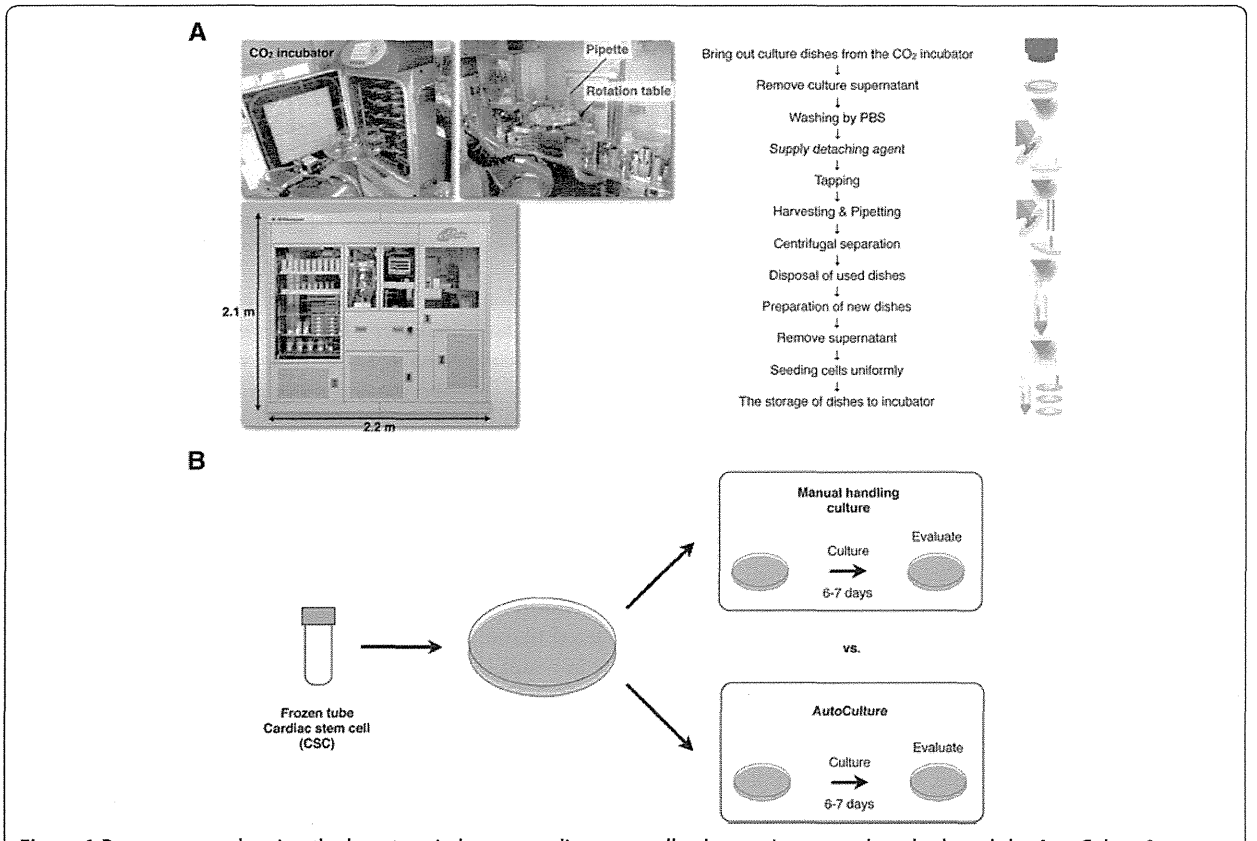

Figure 1 Process maps showing the key steps in human cardiac stem cell culture using manual methods and the AutoCulture® system. **(A)** The automated culture system AutoCulture® by Kawasaki Heavy Industries (left) can automate every step of manual cell culture under current good manufacturing practice (cGMP) grade. **(B)** Schematic representation of the experiment. Human cardiac stem cells (CSCs) were thawed and split into 2 dishes for either manual culture or automated culture using AutoCulture®.

indicated that a culture duration of 2 weeks was sufficient to obtain the appropriate cell number for clinical trial when cells after the second passage (P2) were used as the starting material. Identically seeded culture plates were maintained manually or by automation using AutoCulture® (Figure 1B). The morphology of CSCs cultured using the automated system was similar to that of manually cultured CSCs on day 7 and 14 after seeding (Figure 2A). Under both the conditions, the cells were of similar size, exhibited a low nucleus/cytoplasm ratio, and had a spindle-like shape. In addition, the growth rate was not significantly different, as indicated by cell counts at passage (Figure 2B). Trypan blue staining revealed no significant difference in cell viability between the culture methods. Moreover, both the methods effectively washed out the cells, as indicated by the paucity of adherent cells on discarded culture dishes (data not shown). These results suggest that manual passage was effectively replicated using AutoCulture®.

Gene expression

To investigate the gene expression profiles, RT-PCR analysis was performed according to the shipping criteria for cultivated cells in the current clinical trial (ALCADIA). We examined expression levels of the pluripotency related genes *NANOG*, *OCT4*, *SOX2*, and *REX1* and 2 transcription factor genes involved in cardiomyocyte development, *NKX2.5* and *GATA4* (Figure 2C). The stem cell markers *OCT4*, *REX1*, and *GATA4* were expressed by both cell populations; however, neither *NANOG* nor *NKX2.5* expression was detectable. Moreover, expression levels were not significantly different between the 2 groups on either day 7 or day 14.

Cell surface marker expression profiles

Cell surface markers indicative of CSCs and other phenotypes were detected by fluorescence-activated cell sorting (FACS) (Figure 3A). Under both the culture conditions, the cells were positive for the mesenchymal stem cell (MSC) markers CD29 and CD90 and the vascular endothelial marker CD105 and negative for the hematopoietic lineage marker CD45 and MHC class II. In addition, fluorescent intensities measured by FACS were similar for all positive markers, indicating that equal proportions of cells in both the populations expressed these proteins. Moreover, almost all the cells were CD29 positive, whereas at least 2 populations were distinguished on the basis of CD90 expression. Furthermore, STRO-1, which is expressed by mesenchymal stem cells in the bone marrow, was negative in both the populations. Although the surface expression profiles of CSCs and bone marrow-derived stem cells overlap, STRO-1 expression can discriminate cardiac MSCs from bone marrow-derived MSCs.

Surface glycan expression profile by lectin microarray analysis

Recently, glycan expression profiling has been reported to be an effective cell validation tool to complement phenotype analysis by epigenetic and gene expression analyses

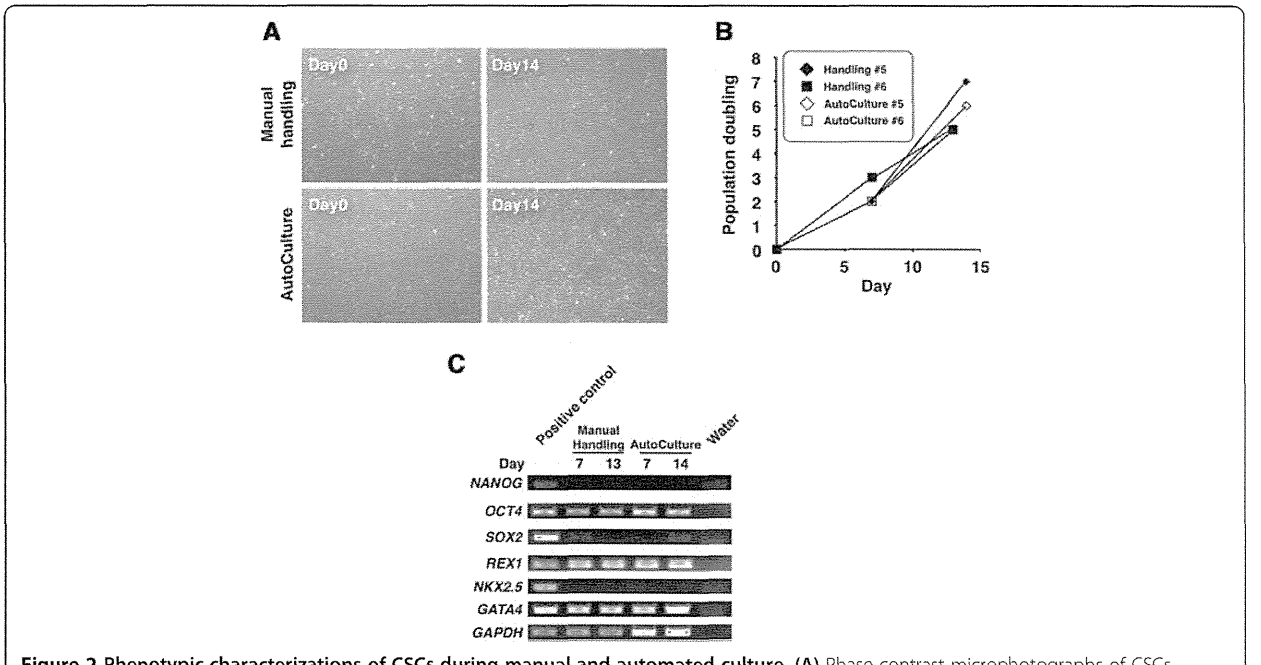

Figure 2 Phenotypic characterizations of CSCs during manual and automated culture. (A) Phase contrast microphotographs of CSCs cultivated either by manual handling (upper panels) or using AutoCulture® (lower panels). **(B)** Growth rates of CSCs under manual or automated culture. **(C)** RT-PCR analysis of genes related to pluripotency and cardiac-specific transcription factors.

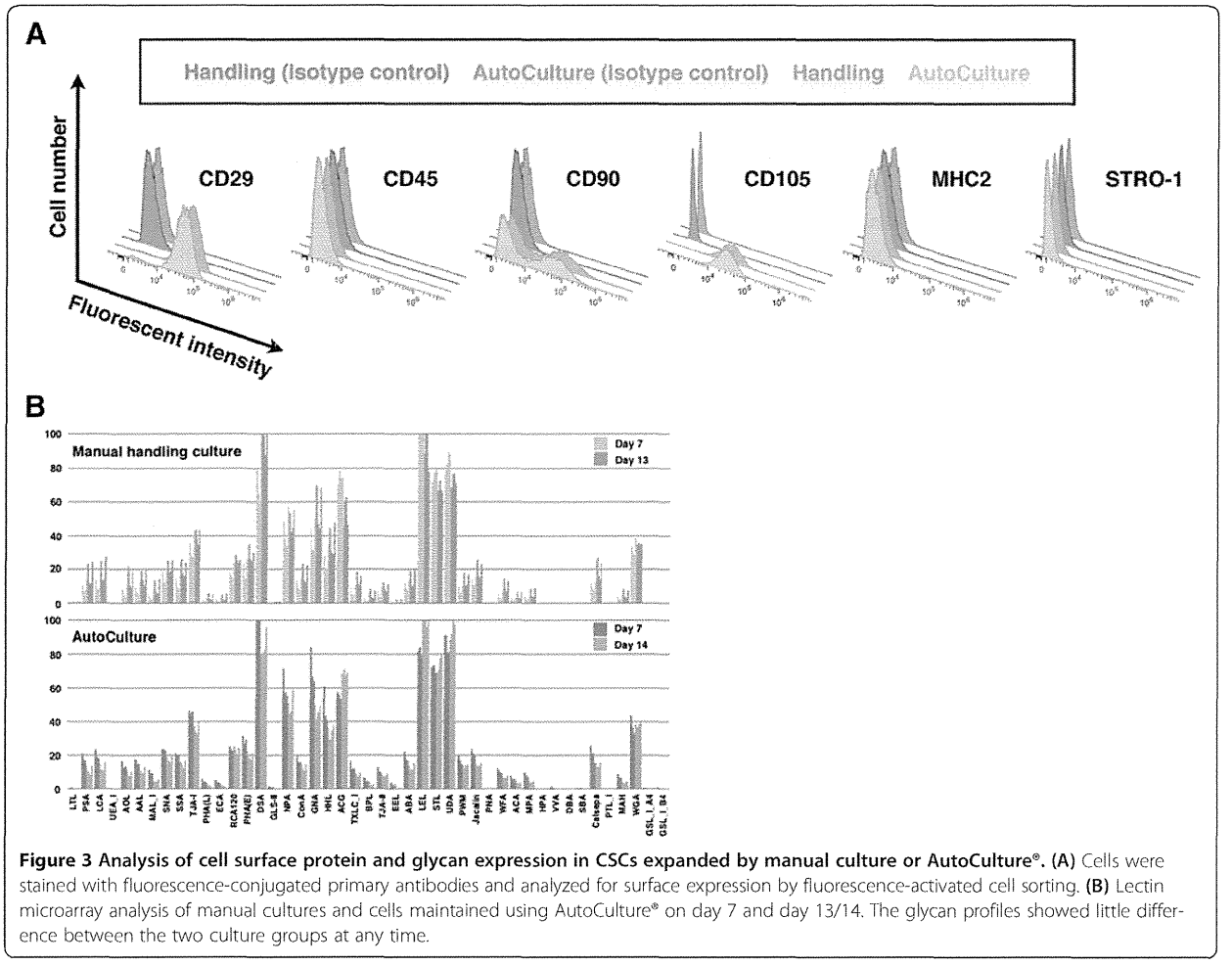

Figure 3 Analysis of cell surface protein and glycan expression in CSCs expanded by manual culture or AutoCulture®. (A) Cells were stained with fluorescence-conjugated primary antibodies and analyzed for surface expression by fluorescence-activated cell sorting. **(B)** Lectin microarray analysis of manual cultures and cells maintained using AutoCulture® on day 7 and day 13/14. The glycan profiles showed little difference between the two culture groups at any time.

[17]. These lectin profiles showed similar patterns, and no significant differences in expression intensities were observed between the 2 culture groups on either day 7 or day 13/14 after seeding (Figure 3B). The washing process used to harvest adherent cells may have profound effects on the cell surface structure and expression. CSCs harvested from the AutoCulture® system exhibited similar surface expression profiles and overall viability to those cultured manually.

Analysis of array comparative genomic hybridization (aCGH) and microarray

To detect genomic DNA mutations on AutoCulture®, we performed aCGH analysis (Agilent technologies) on day 7 and day 14 and compared them with the tissue derived from human right atrial appendage (RAA) (Figure 4A). There were no differences in genomic DNA mutation between CSCs in AutoCulture® and RAA. To investigate the global gene expression profile changes between CSCs in manual culture and CSCs in AutoCulture®, we performed a pairwise comparison of gene expression microarray data using NIA array analysis [18]. The results revealed a similar gene pattern between them (Figure 4B, Additional file 3). The "Symbol" of 162 gene probes was left blank in 258 overexpressed gene probes.

Discussion

Cell-based regenerative medicine is still in the early stages of development [19,20]. The quality of cells for transplant depends on the ability of skilled personnel to isolate, expand, and harvest cultured cells. For consistency of cell yield and phenotype, it is imperative that methodological consistency is strictly maintained. Automation greatly enhances the consistency of culture conditions and may thus reduce the variability in cell quality that is one of the great impediments to the widespread application of cell-based therapy till date. In this study, we used the automated cell culture system AutoCulture® to expand human CSCs isolated from the RAA for use in the ALCADIA clinical trial designed to assess the safety of cell-based therapy for patients with ischemic cardiomyopathy. RAA-derived cells containing CSCs exhibited similar growth rates and gene

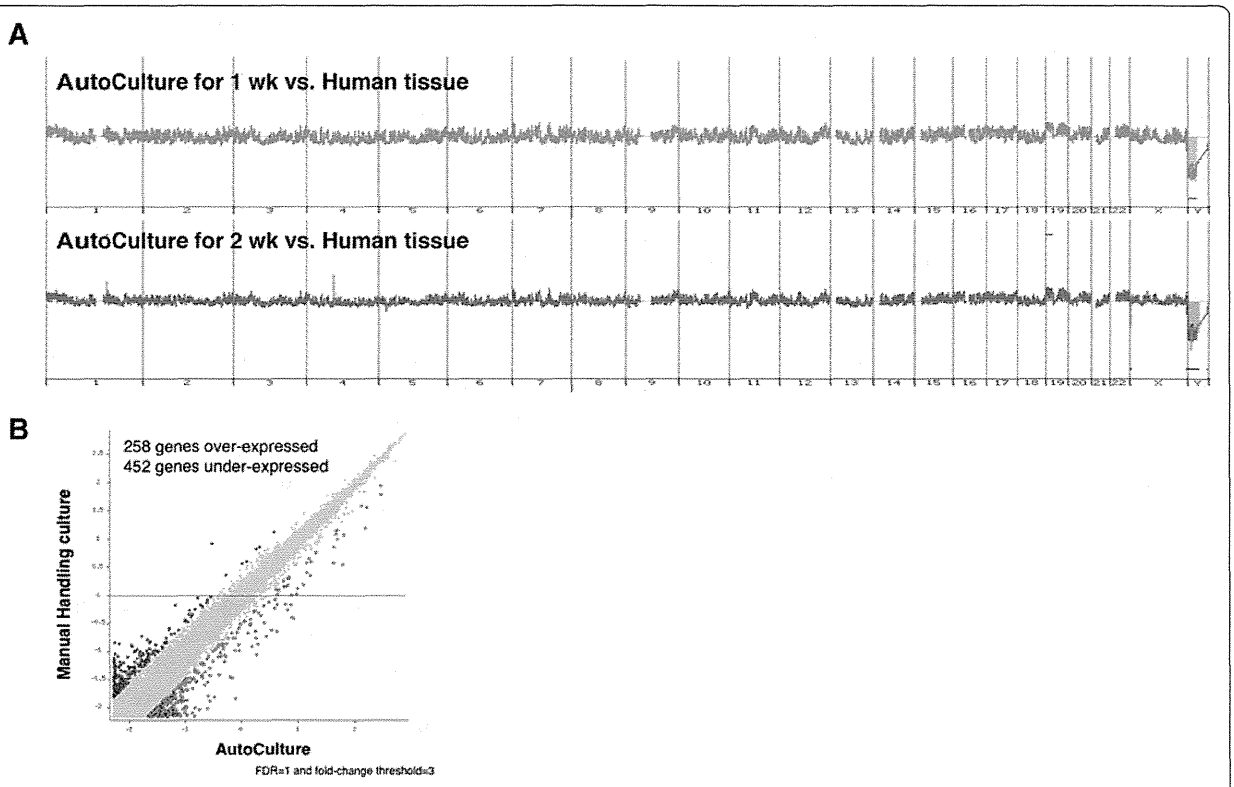

Figure 4 Global analysis of gene expression and genomic DNA mutations. (A) Comparison of array comparative genomic hybridization analysis. Human gDNA (from RAA) was compared to gDNA extracted from CSCs cultivated using AutoCulture® after 1 and 2 weeks using CGH arrays (arrays G4413A). **(B)** Microarray analysis of gene expression profiles. The pairwise scatter plot presents differences in gene expression on day 7 after seeding between manually cultured CSCs and those cultured using AutoCulture®. Grey dots represent transcripts with a subthreshold difference in expression. Red or green dots indicate those with at least a 3-fold difference in expression levels between the two groups. Gene expression levels are depicted on a log2 scale. The number of differentially expressed genes is indicated above.

expression profiles between manual and automated cultures. Thus, the AutoCulture® system effectively replicated manual culture and demonstrated scalability and stability in addition to safety and cost-effectiveness. Indeed, we found no significant differences in phenotype between the two culture methods. Cells in both the populations had similar morphologies, mean growth rates, and expression levels of genes associated with pluripotency and the mesenchymal lineage. In addition, the surface glycan profile was virtually identical, while aCGH analysis revealed no difference in genomic DNA mutation frequency. Finally, the approximately 41,000-probe Agilent Whole Human Genome Microarray chip G4112F showed that only approximately 1% of transcripts measured were significantly under- or overexpressed. The successful transfer of manual to automated cell culture may be attributable to the high flexibility of the machine, which can faithfully copy every step and condition, including media changes, splitting, and passaging in a controlled environment.

AutoCulture® is an all-in-one automated cell culture system consisting of robot arms, tube and flask decappers, flask holders, flask tappers, media pumps, a pipette head, a centrifugal separator, a rotating plate, and a CO_2 incubator. In addition to media change and passage, it permits routine observation. To automate these culture steps, it is necessary to program the humidity, temperature, volume and flow of liquid, and robot arm motion that transfers flasks from or into the CO_2 incubator or flask holder. Another automated cell culture platform, TAP CompacT, was also shown to be an effective system for culture of adherent cells by the Healthcare Engineering group [14]. However, the lack of a centrifugal separator in that system may result in differences between the manual and automated processes, possibly explaining why automation resulted in a smaller population of STRO-1+ cells and overall lower cell yield after the first passage [21]. STRO-1 expression is not a necessary or specific marker for stem or progenitor cells, and somatic stem cells may be more resistant to nutritional and chemical stress [22]. Residual trypsin in the culture media may have adversely affected the survival of differentiated cells, but it is not clear whether stem or progenitor cells can survive or not. On the other hand, the AutoCulture® system efficiently removes trypsin/EDTA by washing and centrifugation. There were no significant

differences in the surface marker expression profile or the mean rate of proliferation between these cells and those maintained manually, strongly suggesting that both populations of RAA-derived CSCs contain equal properties.

The AutoCulture® system can save labor and costs by expanding the scale of production and maintaining uniformity of results. In addition, this system can simultaneously cultivate different cells without cross-contamination because it can be equipped with a connecting hatch to multiple CO_2 incubators. Large-scale production and multi-sample cell culture capacity for cell transplantation may be a prerequisite for commercialization of cell products under current good manufacturing practice (cGMP) grade. Production methods for cell therapy should be designed to ensure that the end product is standardized and safe. cGMP is a quality assurance system that ensures that the cell product meets preset specifications with minimal lot-to-lot variability [23]. It requires traceability of raw materials used in cell culture and validated standard operating procedures (SOPs) throughout the process [24,25]. Current good tissue practice (cGTP) is intended to prevent human cells, tissues, and cellular and tissue-based products from contamination by infectious disease agents and to ensure that these cells and tissues maintain their integrity and function. The controlled environment of a carefully designed, constructed, validated, and maintained clean room will minimize the risks of environmental contamination and decrease the possibility of cross-contamination [26]. Based on cGMP, aseptic handling and filling of raw materials should be performed in a grade A environment (class 100) with a grade B background (class 1,000). Clean room disciplines, gowning procedures, cleaning programs, and maintenance of air handling units are included in SOPs. Environmental monitoring is essential in clean room quality control. Proper cleaning, maintenance, repair, and attire are major issues for cGMP [27].

Construction and maintenance of a cGMP facility is so expensive that it may be difficult to conform to these standards on a large scale without automation. Unlike manual culture, the robots enabled the environment in the cell culture cabinet to be completely separated from the external environment. Moreover, automated cell culture machines can be equipped with cleaning and monitoring systems to prevent contamination by microorganisms and cross-contamination by other cell types cultured in tandem. These properties may meet the stringent conditions for a human cell processing facility while reducing both construction and maintenance costs.

In Japan, the regulatory path of a regenerative cell therapy using this automated machine will be to obtain an approval for the end products, such as cells or tissues, based on the new guidelines and philosophy at an initial phase. An important requirement for obtaining approval is publication of the safety and reliability of the machine to produce the final biological products in a peer-reviewed journal. The similar properties of cell products between those obtained by machine and those obtained by manual culture, as demonstrated in this study, could support approval of a clinical trial using this machine, which is currently being planned.

Conclusion

AutoCulture® is one of the best candidates to solve the problems inherent in large-scale production and harvesting of human cells for clinical applications. The automated cell processing system can reproduce many complex operations performed by professional staff and can maintain multiple cell lines automatically. Thus, this automation system will be a powerful tool for both clinical trials exploring the potential of autologous or allogeneic cell-based regeneration therapies and for the commercialization.

Methods

Isolation of human CSCs containing atrial appendage

After this study was approved by the ethics committees of Tokyo Metropolitan Geriatric Hospital (ID: #220106), human cardiac tissue samples from RAA were surgically excised from 7 patients (60–75 years old) during cardiac surgery. All patients provided written informed consent. A cell population containing CSCs was acquired according to the current protocol for ALCADIA [28]. In brief, the tissue fragments were cut into 5 × 5-mm pieces and incubated with 0.2% collagenase type II and 0.1% DNase I (Worthington Biochemicals) at 37°C for 30 min. The cells were cultivated in a basic culture medium of Dulbecco's modified Eagle medium (DMEM)/F12 supplemented with 10% fetal bovine serum (FBS) and 40 ng/ml basic fibroblast growth factor (bFGF). The cells were seeded in 60-mm dishes coated with collagen type I. The cultured cells were passaged twice, harvested, and frozen until used in this experiment. P2 cell population was utilized as the starting material for this comparison experiment.

Cell expansion and harvesting

After thawing, the cells derived from the human atrium were seeded at 1×10^5 cells per 100-mm culture dish and cultivated for 5–7 days. The cells were split at 1:10 at 80%–90% confluence. The basic culture medium was replaced every 3 or 4 days. For automated culture, we used the same lot of CSCs. After seeding, the culture dishes were placed in the AutoCulture® chamber and transferred into the internal CO_2 incubator by the robot arm (Figure 1A, Additional file 4). For media replacement, the robot arm retrieved the culture dishes from the incubator and set them on a rotating table. The dish covers were removed by the robot arm, a specified amount of medium was discarded, fresh medium was supplied by a new pipette, the covers were returned,

and the culture dishes was transferred back to the CO_2 incubator. For passage, the old medium was removed and DPBS was pipetted onto the dishes under gentle shaking. After washing in DPBS, AutoCulture® supplied trypsin, oscillated the culture dishes, and returned them to the CO_2 incubator for a 5-min incubation. Following this, the robot arm moved the culture dishes onto the rotation table, added a prespecified volume of the basic culture media, and transferred the cell suspension from each dish to a separate 50-ml centrifuge tube. The cell suspension was centrifuged at 200 × *g* for 5 min at room temperature, and the supernatant was discarded. Fresh basic culture medium was supplied to the cell pellet, which was then resuspended. The washed cell suspension was subcultured at approximately 1:10 onto new culture dishes and returned to the CO_2 incubator.

Reverse transcription-polymerase chain reaction (RT-PCR)

Total RNA was extracted from cell populations containing CSCs, from human iPSCs, and raw human heart tissue samples using the RNeasy Plus Mini Kit (QIAGEN) as positive/negative control. Total RNA from human iPSCs and the human heart (Clontech Laboratories) was used as the positive control for each primer. Total RNA (500 ng per reaction) was converted to cDNA using the Transcriptor High Fidelity cDNA Synthesis Kit (Roche Applied Science) according to the manufacturer's protocol. Primers for the cardiac-specific transcription factors *NKX2.5* and *GATA4*; the stem cell markers *NANOG*, *OCT3/4*, *SOX2*, and *REX1*; and the housekeeping gene *GAPDH* were obtained from PrimerBank (Additional file 5).

Flow cytometric analysis

The cells (1×10^6 per reaction) were stained in autoMACS Running Buffer (Miltenyi Biotec.) with fluorescence-conjugated primary antibodies for 30 min at 4°C. The cells were then analyzed on the Attune Acoustic Focusing Cytometer (Applied Biosystem), and the data were analyzed using FlowJo 8.8.7 software (TOMY Digital Biology). Antibodies used for phenotyping included anti-human CD29-PE, CD90-PE, CD105-FITC, STRO-1-FITC, CD45-PE, and MHC class II-PE. Isotype controls were FITC-conjugated mouse IgG_1, PE-conjugated mouse IgG_1, and FITC-conjugated mouse IgM.

Lectin microarray analysis

Proteins were extracted from each cell population in hydrophobic and hydrophilic fractions using the CelLytic MEM Protein Extraction Kit (Sigma-Aldrich), as described previously [29]. Lectin microarray analysis was performed as described previously, with only minor modifications [30]. The glycoprotein (200 ng) was labeled with Cy3 monoreactive dye (GE Healthcare) in DPBS containing 0.5% Triton X-100 (PBSTx) at room temperature for 1 h. The Cy3-labeled glycoprotein solution (60 μl) was applied to the LecChip (GP Bioscience), which has triplicate spots specific for 45 lectins on each glass slide. An evanescent-field fluorescence scanner (GlycoStationTM Reader) was used to analyze the LecChip. All data were analyzed with GlycoStationTM Tools Signal Capture 1.0 and GlycoStationTM Tools Pro 1.0 software (GP Bioscience). To expand the dynamic range, the data were subjected to a gain-merging procedure, and the merged data were then normalized with max-normalization, as described previously [29].

aCGH analysis

Genomic DNA from the heart tissue and cultured cells was isolated using the DNeasy Blood & Tissue Kit (QIAGEN). Labeled test and reference DNAs were combined, denatured, preannealed with Cot-1 DNA (Invitrogen) and blocking agent, and then hybridized to the arrays (SurePrint G3 Human CGH Microarray 2x400K, Agilent Technologies). After hybridization and washing, the arrays were scanned at 3-μm resolution using an Agilent G2505C scanner. Images were analyzed with Feature Extraction software 10.7.3.1 (Agilent Technologies) using the CGH 107 Sep09 protocol for background subtraction and normalization.

Gene expression analysis

Gene expression analysis was performed using the Agilent Whole Human Genome Microarray chip G4112F (Agilent Technologies), which contains >41,000 probes. Raw data were normalized and analyzed by GeneSpring GX11 software (Silicon Genetics). Pairwise scatter plot analysis of the global gene expression profiles of both manually cultured cells and autocultured cells was performed on day 7 after thawing. The number of differentially expressed genes is indicated over each scatter plot. The NIA Array [18] web tool was used for pairwise scatter plot analysis. Gene expression microarray data have been submitted under accession number GSE 44032. Analysis of microarray experiments was conducted using the Aberration Detection Method-2 statistical algorithm (Agilent Technologies) on the basis of the combined log2 ratios at a threshold of 6.0. The data were centralized, and calls with average log2 ratios <0.3219 were filtered to exclude false positives.

Additional files

Additional file 1: Document 1. Specialization of the automated cell processing machine (Auto Culture®).

Additional file 2: Document 2. Quantitative cellular aspects for ALCADIA clinical trial.

Additional file 3: Table S1. Results of microarray analysis of CSCs in manual culture and AutoCulture®. To investigate the differences in global gene expression profile between CSCs in manual culture and CSCs in AutoCulture®, we performed a pairwise comparison of gene expression

microarray data using NIA array analysis. The results revealed similar gene expression patterns between them.

Additional file 4: Movie 1. AutoCulture®.Movie of the culture robot in AutoCulture®.

Additional file 5: Table S2. RT-PCR primer sequences. RT-PCR primer sequences were obtained from PrimerBank (http://pga.mgh.harvard.edu/primerbank/).

Abbreviation

CSC: Cardiac stem cells; FACS: Fluorescence-activated cell sorting; MSCs: Mesenchymal stem cells; aCGH: Array comparative genomic hybridization; RAA: Right atrial appendage; cGMP: Current good manufacturing practice; SOPs: Standard operating procedures; cGTP: Current good tissue practice; bFGF: Basic fibroblast growth factor.

Competing interests

DK, MYI, KM, TK, YI, MT, AU and SG declare that they have no competing interests. KW and TS are employees of Kawasaki Heavy Industries, Ltd.

Authors' contributions

DK, MT, AU, and SG designed the research; DK, KW, YI, KM, MYI, and performed the experiments; DK, MT, and SG analyzed the data; and DK, TK, YI, and SG wrote the manuscript. All authors read and approved the final manuscript.

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Noncanonical NOTCH Signaling Limits Self-Renewal of Human Epithelial and Induced Pluripotent Stem Cells through ROCK Activation

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Noncanonical NOTCH Signaling Limits Self-Renewal of Human Epithelial and Induced Pluripotent Stem Cells through ROCK Activation

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NOTCH plays essential roles in cell fate specification during embryonic development and in adult tissue maintenance. In keratinocytes, it is a key inducer of differentiation. ROCK, an effector of the small GTPase Rho, is also implicated in keratinocyte differentiation, and its inhibition efficiently potentiates immortalization of human keratinocytes and greatly improves survival of dissociated human pluripotent stem cells. However, the molecular basis for ROCK activation is not fully established in these contexts. Here we provide evidence that intracellular forms of NOTCH1 trigger the immediate activation of ROCK1 independent of its transcriptional activity, promoting differentiation and resulting in decreased clonogenicity of normal human keratinocytes. Knockdown of NOTCH1 abrogated ROCK1 activation and conferred sustained clonogenicity upon differentiation stimuli. Treatment with a ROCK inhibitor, Y-27632, or ROCK1 silencing substantially rescued the growth defect induced by activated NOTCH1. Furthermore, we revealed that impaired self-renewal of human induced pluripotent stem cells upon dissociation is, at least in part, attributable to NOTCH-dependent ROCK activation. Thus, the present study unveils a novel NOTCH-ROCK pathway critical for cellular differentiation and loss of self-renewal capacity in a subset of immature cells.

Notch is an evolutionarily conserved cell surface receptor that plays essential roles in cell fate decisions as well as maintenance of self-renewing tissue organization (1–3). Notch proteins are expressed in most adult tissues, and the biological consequence of Notch activation is critically dependent on the cell type and the cellular context (4–7). In keratinocytes, Notch1 has been shown to be a key inducer of differentiation (8–11). Keratinocyte-specific conditional deletion of the *Notch1* gene results in epidermal hyperproliferation and tumor formation in mice, thus indicating a tumor-suppressive role of Notch1 in mammalian postnatal epidermis (12). The Notch receptor is generally activated by interaction with its ligands displayed on the neighboring cell surface. Cell-cell contact is a strong inducer of keratinocyte differentiation in culture, where Notch1 acts as a critical determinant in the transition from proliferation to differentiation (13, 14). Due to *cis* inhibition of Notch by its ligand when these are expressed on the same cell surface (15, 16), the relative increase in expression levels of the Notch receptor over its ligand is also shown to be a pivotal cue to activate Notch signaling and generate distinct cell fates among neighboring cells (17). We previously demonstrated that p53 and TAp63 transactivate *Notch1* gene expression and induce keratinocyte differentiation, while ΔNp63 is a transcriptional repressor of the *Notch1* gene and inhibits keratinocyte differentiation (14, 18). p63, especially ΔNp63α, is a master regulator of development and maintenance of stratified epithelia (19, 20). ΔNp63α expresses predominantly in the basal proliferating compartment, where Notch1 signaling is suppressed (21). In suprabasal layers, downregulation of ΔNp63α by miR-203 or another factor(s) (22–24) evokes activation of Notch1 signaling, which in turn further downmodulates ΔNp63α expression so as to induce differentiation (9, 21). The Notch1 precursor (~300 kDa) is processed by furin protease in the Golgi apparatus and transported to the cell surface as a mature heterodimeric complex (~120/~180 kDa) that is held by Ca^{2+}-dependent noncovalent interaction (25). Ligand binding dissociates the Notch1 extracellular domain (~180 kDa) by *trans* endocytosis. The residual transmembrane domain (~120 kDa) is sequentially cleaved by tumor necrosis factor alpha-converting enzyme/metalloprotease (TACE) and γ-secretase, resulting in release of the Notch1 intracellular domain (~110 kDa) into the cytosol (3). EDTA is reported to activate Notch signaling through disruption of the heterodimeric complex of Notch1 (25) and thus used as a tool to study Notch1 signaling (26–28). In canonical Notch1 signaling, the liberated Notch1 intracellular domain (~110 kDa) translocates into the nucleus to activate Notch-responsive genes, such as Hes1, by making a complex with CSL family members {CBF1 and RBP-Jκ in mammals, Suppressor of hairless [Su(H)] in *Drosophila*, and Lag1 in *Caenorhabditis elegans*} and its transcriptional coactivator Mastermind (MAM). Besides this canonical pathway, accumulating evidence suggests noncanonical cytoplasmic Notch functions (29–31).

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Rho-associated coiled-coil protein kinases (ROCKs) (also known as Rho kinases [ROKs]) are effectors of the small GTPase Rho and belong to a family of protein serine/threonine kinases (32–34). Activated ROCK proteins regulate actomyosin cytoskeletal dynamics and contractility through phosphorylation of multiple downstream targets, such as myosin phosphatase (MYPT1), to drive cell motility. In keratinocytes, ROCK proteins play a role in differentiation (35, 36), and their selective inhibitor, Y-27632, completely inhibits differentiation as well as stratification of keratinocytes in organotypic raft culture (37). Y-27632 also enables efficient immortalization of not only human primary keratinocytes but also several other primary human epithelial cells in the presence of fibroblast feeders (37, 38), although molecular details supporting immortalization remain elusive.

In addition, Y-27632 has been shown to increase the survival rate and cloning efficiency of human embryonic stem cells (hESCs) dissociated with EDTA (39) through blocking the Rho-ROCK-myosin light chain signaling cascade (40, 41). However, the precise mechanisms by which EDTA activates ROCK have not been elucidated (41, 42).

These results let us hypothesize a possible link between NOTCH1 and ROCK activation. Here we show a novel function of NOTCH1 as a critical upstream regulator of ROCK1 and its relevance to loss of self-renewal capacity in human keratinocytes as well as human induced pluripotent stem (hiPS) cells.

MATERIALS AND METHODS

Cell culture. Normal human cervical keratinocytes (HCKs) were obtained with written consent from a patient who underwent abdominal surgery for a gynecological disease other than cervical cancer and were retrovirally transduced with the catalytic subunit of human telomerase reverse transcriptase (hTERT) for immortalization (HCK1Ts) (14). HCK1Ts were cultured in serum-free keratinocyte-SF medium supplemented with 5 ng/ml epidermal growth factor (EGF) and 50 μg/ml of bovine pituitary extract (Invitrogen, Life Technologies, Saint Aubin, France). Primary human dermal keratinocytes (HDKs) were purchased from Cell Applications Inc. (San Diego, CA). Primary human foreskin keratinocytes (HFKs) were obtained from Denise A. Galloway (Fred Hutchinson Cancer Research Center, Seattle, WA). HDKs and HFKs were cultured in serum-free keratinocyte-SF medium supplemented with 5 ng/ml EGF and 50 μg/ml of bovine pituitary extract (Invitrogen, Life Technologies). Human endometrium cells were collected by scraping tissues from surgical specimens, with signed informed consent and with ethical approval of the Institutional Review Board of the National Institute for Child Health and Development, Japan. All experiments involving human cells and tissues were performed in line with Tenets of the Declaration of Helsinki. Human iPS cell lines, MRC-hiPSCs and UtE-hiPSCs, were established from MRC-5 fetal lung fibroblasts (43) and UtE1104 endometrium-derived cells (44), respectively, via procedures described by Takahashi et al. (45) with slight modification (46, 47). Human iPS cells were maintained in iPSellon medium (Cardio Incorporated, Osaka, Japan) supplemented with 10 ng/ml recombinant human basic fibroblast growth factor (bFGF) (Wako Pure Chemical Industries, Ltd., Osaka, Japan) in the presence of irradiated mouse embryonic fibroblast (MEF) feeders.

Retroviral vector construction and transduction. Retroviral vector plasmids were constructed using the Gateway system according to the manufacturer's instructions (Invitrogen). Segments of the intracellular domain of human NOTCH1 (ICN1), a truncated form of MAML1 corresponding to amino acids 13 to 74 fused to N-terminal hemagglutinin (HA) tag (MAML61-3HA), and c-MYC were cloned and recombined into retroviral expression vectors to generate pCLXSN-ICN1 (14), pCLXSN-MAML61-3HA (48, 49), and pCMSCVpuro-c-MYC (50). Human ROCK1, ROCK1ΔC241, ROCK1-D1113A, ROCK1-K105A, ICN1-ERT, ICN2-ERT2, RhoA, and enhanced green fluorescent protein (EGFP) were cloned into a lentiviral vector, CSII-TRE-Tight-RfA, in which the elongation factor promoter in CSII-EF-RfA (a gift from Hiroyuki Miyoshi, RIKEN, BioResource Center) was replaced with the tetracycline-responsive promoter from pTRE-Tight (Clontech, Mountain View, CA). The Notch1 short hairpin RNA (shRNA) vectors were described previously (14, 18). To generate ROCK1- or ROCK2-specific shRNA expression vectors pCL-SI-MSCVpuro-ROCK1Ri-1,-2,-3 and pCL-SI-MSCVpuro-ROCK2Ri-1,-2,-3, the following sequences were chosen as the targeted sites: 5′-GTACTTGTATGAAGATGA-3′ (51), 5′-GGTATATGCTATGAAGCTT-3′, and 5′-GCGAAATGGTGTAGAAGAA-3′ for ROCK1 and 5′-GAAACTAATAGGACACTAAC-3′ (52), 5′-GGTTTATGCTATGAAGCTT-3′, and 5′-GGATAAACATGGACATCTA-3′ for ROCK2. The retroviral vector and packaging constructs pCL-GagPol and pEF6/env (10A1) or the lentiviral vector and packaging constructs pCAG-HIVgp and pCMV-VSV-G-RSV-Rev were cotransfected into 293FT cells (Invitrogen) using TransIT-293 (Mirus Co., Madison, WI) according to the manufacturer's instructions, and the culture fluid was harvested at 60 to 72 h posttransfection. Titers of the recombinant viruses were determined by drug resistance with HeLa cells or a real-time PCR method (TaKaRa, Otsu, Japan) to detect the viral RNA genome, yielding titers equivalent to greater than 1×10^6 CFU/ml. Following addition of the recombinant viral fluid to cells in the presence of 4 μg/ml Polybrene, infected cells were selected in the presence of 0.5 μg/ml puromycin or 50 μg/ml G418, and promptly after drug selection, pooled cell populations were used for most subsequent experiments.

Tet-On keratinocytes. HCK1T cells were stably transduced with Tet-On ADV and tTS expression vectors, encoding the rtTA-Advanced transactivator and transcriptional silencer, respectively (Clontech). The resultant HCK1T Tet-On cells were then introduced with CSII-TRE-Tight-ROCK1, ROCK1ΔC241, ROCK1-D1113A, ROCK1-K105A, ICN1-ERT, ICN2-ERT2, RhoA (constitutive active and dominant negative forms), and EGFP by retroviral gene transfer. Induction of these transgenes was routinely achieved by treatment with 1 μg/ml doxycycline (DOX) for 72 h.

Inhibitors. The following pharmacological inhibitors were used: cycloheximide (CHX) (239764; Calbiochem, Darmstadt, Germany), z-VAD-fmk (caspase inhibitor IV) (219007; Calbiochem), γ-secretase inhibitor IX (DAPT) (565784; Calbiochem), Y-27632 (08945-84; Nacalai Tesque, Kyoto, Japan), C3 ADP-ribosyltransferase (Rho inhibitor) (CT04; Cytoskeleton, Inc., Denver, CO), and blebbistatin (sc-203532; Santa Cruz Biotechnology, Santa Cruz, CA). Cells were pretreated with inhibitors for 2.5 h. For DAPT, in addition to pretreatment, cells were incubated with this inhibitor during and after exposure to EDTA or differentiation stimuli for up to 48 h.

Induction of keratinocyte differentiation. At 48 h after plating, HCK1T cells were treated with 2.5 mM EDTA in phosphate-buffered saline without Ca^{2+} and Mg^{2+} [PBS(−)] for 10 min or exposed to 0.7% and 5% bovine serum albumin (BSA) or 10% serum-containing medium in the presence of 10 μg/ml of bovine pituitary extract. To induce ligand-dependent NOTCH activation, HCK1T cells were harvested in subconfluent and 7-day-postconfluent states. HCK1T cells were also introduced with ICN1 by retroviral gene transfer to induce differentiation.

Dissociation of human iPS cells. First, hiPSC colonies were treated with collagenase IV solution at 37°C for 10 min. The detached hiPSC clumps were recovered, incubated with 0.005% trypsin–2.5 mM EDTA solution at 37°C for 5 min, and dissociated into single cells by pipetting. The dissociated cells were counted with Vi-CELL (Beckman Coulter, Brea, CA) and seeded onto MEF feeders.

Immunoblotting. Whole-cell protein extracts were used for analysis, and immunoblotting was conducted as described previously (14). Primary antibodies against Notch1 (sc-6014; Santa Cruz Biotechnology), activated Notch1 (cleaved Notch1 Val1744 2421; Cell Signaling Technology, Danvers, MA), Notch2 (clone C651.6DbHN; Developmental Studies Hybridoma Bank, University of Iowa), Hes1 (Toray Industries, Inc., To-

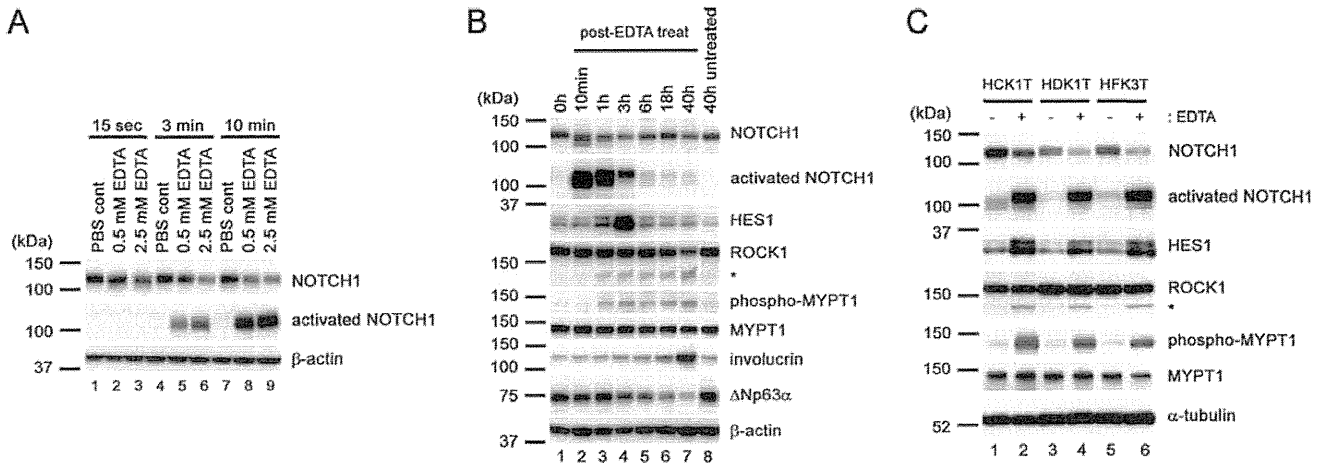

FIG 1 Immediate activation of ROCK1 following release of the NOTCH1 intracellular fragment in normal human keratinocytes. (A) HCK1T cells were either left untreated (PBS cont) or treated with 0.5 or 2.5 mM EDTA in PBS(−) for indicated time points. Cell lysates were prepared and analyzed by immunoblotting with the indicated antibodies. (B) HCK1T cells were either left untreated or treated with 2.5 mM EDTA in PBS(−) for 10 min at 37°C. After washing twice with PBS(−), cells were incubated with keratinocyte-SF medium. Cell lysates were prepared at the indicated time points after EDTA treatment. Extracts were analyzed by immunoblotting with the indicated antibodies. The band corresponding to the furin-processed transmembrane domain of NOTCH1 with a molecular mass of 120 kDa is shown as NOTCH1 here. An asterisk indicates a smaller fragment of ROCK1 protein with a molecular mass of ~130 kDa. (C) Keratinocytes from cervix (HCK1T), dermis (HDK1T), and foreskin (HFK1T) were either left untreated or treated with 2.5 mM EDTA for 10 min. After washing twice with PBS(−), cells were incubated with keratinocyte-SF medium for 3 h. Extracts were analyzed by immunoblotting with the indicated antibodies.

kyo, Japan), Hey1 (sc-16424; Santa Cruz Biotechnology), involucrin (clone SY5; Sigma, Saint-Quentin Fallavier, France), loricrin (AF 62; Covance, Princeton, NJ), Rock1 (sc-5560; Santa Cruz Biotechnology), phospho-MYPT1 (07-251; Merck-Millipore, Billerica, MA), MYPT1 (07-672; Merck-Millipore), Rock2 (sc-5561; Santa Cruz Biotechnology), p63 (clone 4A4; Santa Cruz Biotechnology), caspase-3 (9662; Cell Signaling Technology), poly(ADP-ribose) polymerase (PARP) (9542; Cell Signaling Technology), OCT3/4 (sc-5279; Santa Cruz Biotechnology), HA tag

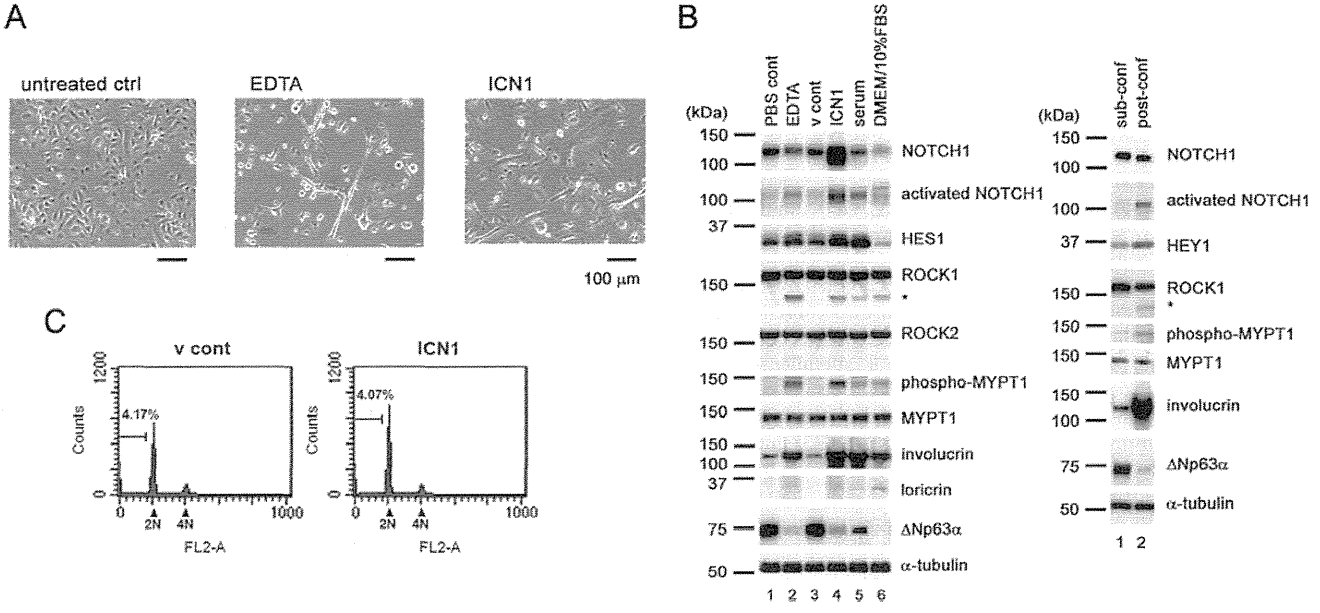

FIG 2 Expression of the NOTCH1 intracellular domain, serum exposure, and cell-cell contact cause ROCK activation and cellular differentiation in normal keratinocytes. (A) HCK1T cells were either left untreated or treated with 2.5 mM EDTA and incubated with keratinocyte-SF medium after treatment. HCK1T cells were transduced with the constitutively active form of NOTCH1 (ICN1). Typical areas were photographed at 3 days posttreatment or posttransduction. Scale bars represent 100 μm. (B) HCK1T cells were either left untreated or treated with 2.5 mM EDTA and incubated with keratinocyte-SF medium after treatment. HCK1T cells were transduced with the constitutively active form of NOTCH1 (ICN1) or control (v cont). HCK1T cells were exposed to serum-containing keratinocyte-SF medium (serum) or Dulbecco modified Eagle medium with 10% fetal bovine serum (DMEM–10% FBS). Cell lysates were harvested at 3 days posttreatment or posttransduction. HCK1T cells were also harvested in subconfluent and 7-day-postconfluent states. Extracts were analyzed by immunoblotting with the indicated antibodies. (C) HCK1T cells were transduced with the constitutively active form of NOTCH1 (ICN1) or control (v cont). At 3 days posttransduction, cells were collected and DNA content was analyzed by flow cytometry. The percentage of apoptotic cells displaying a sub-G_1 DNA content is shown between markers.