

Fig. 2. In vitro chondrogenesis of OP9 cells. A: Time-course analysis of growth factors-induced matrix production in OP9 cells. Macroscopic view of OP9 chondrogenic nodules which were generated after pellet culture for 1–10 weeks in the GM or the CM supplemented with growth factors as indicated. BMP2 drastically enhanced TGF-β3-induced matrix production of OP9 cells. B,C: Microscopic view of OP9 chondrogenic nodules in the pellet culture exposed to growth factors as indicated for 1 week (B) or 3 weeks (C). D: OP9 chondrogenic pellet exposed to TGF-β3 and BMP2 for 3 weeks, a: Hematoxylin and Eosin stain; b: Toluidine blue stain; c: Alcian blue stain. Scale bars: 5 mm (A), 200 μm (B,C), 100 μm (D).

with procedures analogous to those used for KUM5 cells. BMP4, BMP6, and BMP7 enhanced the TGF-β3-induced differentiation in a manner similar to BMP2 (Fig. 2B,C). Unlike its effect in KUM5 cells, PDGF did not inhibit TGF-β3- and BMP4-induced differentiation, as determined by toluidine blue staining (Fig. 2Be,Ce). To confirm the chondrogenetic

differentiation histologically, we examined the ultrastructural analysis of the cartilaginous micromasses. Extracellular matrix was abundantly deposited over OP9 cells, or the surface of the generated micromass (Fig. 3D). The cells covering the micromass showed a flattened shape (Fig. 3E). The OP9 chondrocytes inside the micromass showed an oval or round structure, had cellular processes, and were embedded in the hypertrophic chondrocytes. Abundant rough endoplasmic reticulum and a small number of mitochondria were observed in the OP9 chondrocytes (Fig. 3F).

Cell Surface Markers in KUM5 and OP9 Cells

To characterize the KUM5 and OP9 cells, we analyzed the cell surface markers by using flowcytometry. KUM5 cells were positive (more than tenfold compared to the isotype control) for CD9, CD105 (endoglin), Sca-1 and Ly-6C, marginal for CD106 (VCAM-1) and CD140a (PDGFR α), and negative for c-kit (CD117), Flk-1, CD31 (PECAM-1), CD34, CD144 (VE-cadherin), CD45 (leukocyte common antigen), CD49d (integrin $\alpha 4$), CD90 (Thy-1), CD102, CD14, Ly-6G, and CD41 (Fig. 4A). OP9 cells were strongly positive for CD140a, CD106, and CD9, weakly positive for Sca-1, and negative for CD105, c-kit, Flk-1, CD31, CD34, CD144, CD45, CD49d, CD90, CD102, CD14, Ly-6C, Ly-6G, and CD41 (Fig. 4B). Next, we performed hierarchical clustering by analyzing the global gene expression pattern for cell type classification and cell function prediction. When 244 cell surface marker genes are used for analysis, KUM5 and OP9 formed one cluster independent of seven other marrow stromal cells (Fig. 4C, Supplementary Table I, <http://1954.jukuin-keio.ac.jp/umezawa/sugiki/pca>). We then performed PCA to determine whether it is possible to discriminate OP9 and KUM5 from other cells in three-dimensional expression space. Using the same gene sets for clustering analysis, KUM5 and OP9 cells can clearly separated from the other seven cell lines (Fig. 4D). The similarity of the in vitro phenotype of KUM5 and OP9 cells was supported by the results of grouping the marrow stromal cells into sub-categories in terms of cell surface markers.

Global Outlook by Hierarchical Clustering and PCA by Fat- and Cartilage-Associated Genes

We also performed hierarchical clustering and PCA on the expression pattern of fat- and

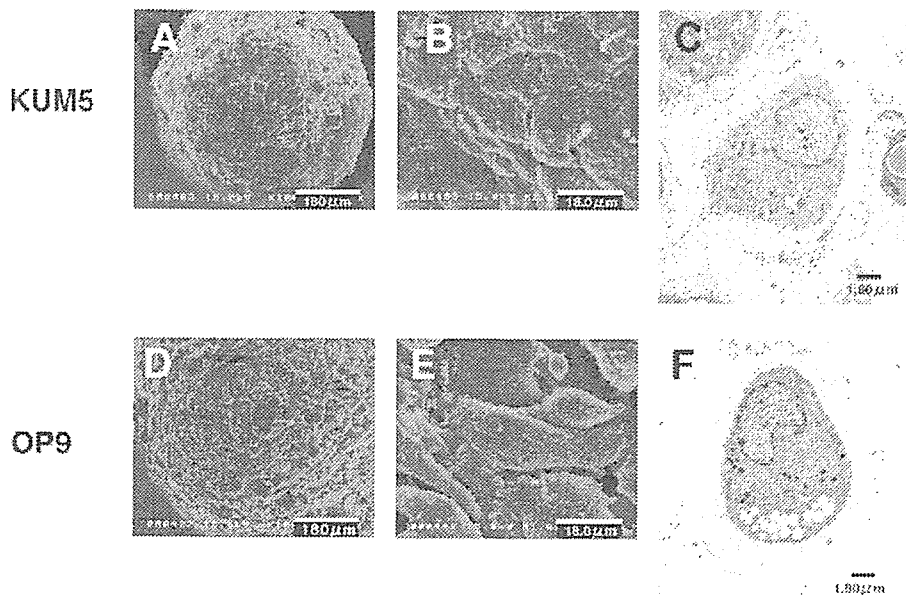


Fig. 3. Ultrastructural analysis of the *in vitro* chondrogenic micromass. Micromasses of KUM5 cells (A–C) and OP9 cells (D–F) were generated by culturing in the CM supplemented with TGF- β 3 for 3 weeks. (A,B,D,E), SEM; (C,F), TEM.

cartilage-associated genes. Using 34 fat-associated genes (Supplementary Table II), KUM5 and OP9 were separated and show smaller distance by both hierarchical clustering and PCA, implying that the KUM5 and OP9 cells have similar characteristics compared with other seven marrow stromal cells (Fig. 5A–D). In contrast, the analysis of 36 cartilage-associated gene expression data (Fig. 5E, Supplementary Table III) demonstrated that these two cell lines were not grouped into the same subcategory. Both cells showed “P: positive” expression in *sox9* and $\alpha 1(\text{II})$ procollagen genes, and OP9 cells expressed cartilage-specific and -associated genes such as the $\alpha 1(\text{II})$ procollagen, $\alpha 1(\text{XI})$ procollagen, cartilage oligomeric matrix proteins, and proline arginine-rich end leucine-rich repeat genes at higher levels, when compared to KUM5 cells (Table I). These results imply that OP9 cells are differentiated chondrocytes as a default state while KUM5 cells are oligopotent mesenchymal cells that have a tendency to differentiate into chondrocytes.

In Vivo Chondrogenesis

To examine the chondrogenic activity of KUM5 cells, we injected KUM5 cells at confluence without any treatment (i.e., without TGF- β 3 and BMP2 treatment) into mice sub-

cutaneously (Fig. 6A). KUM5 cells generated cartilage-like structures within 1 week and complete cartilage at 3 weeks, and the generated cartilage exhibited metachromasia with toluidine blue staining. Interestingly, the cartilage generated by KUM5 cells showed endochondral ossification at 4 weeks. We then implanted the KUM5 chondrogenic micromass after pellet culture into the subcutaneous tissue just beneath the cutaneous muscle (Fig. 6B). The KUM5 cartilage was formed within 1 week and it exhibited typical chondrogenic structures: post-mitotic daughter cells in the cell nest, hypertrophic chondrocytes, and abundant metachromatic matrix with toluidine blue staining. The immunohistochemical analysis showed that KUM5 cartilage stained positive for chondrocyte-specific type II collagen (Fig. 6C), while only a slight amount of type II collagen was detected in the *in vitro* pelleted micromass culture. Ultrastructural analysis revealed that KUM5 chondrocytes implanted into the subcutaneous tissue of nude mice were embedded in the lacunae cavities and had abundant endoplasmic reticulum and a small number of mitochondria (Fig. 6D), and collagen fibers were produced around the lacunae cavity of the KUM5 chondrocytes, as is the case of the *in vitro* conditions (Fig. 6E).

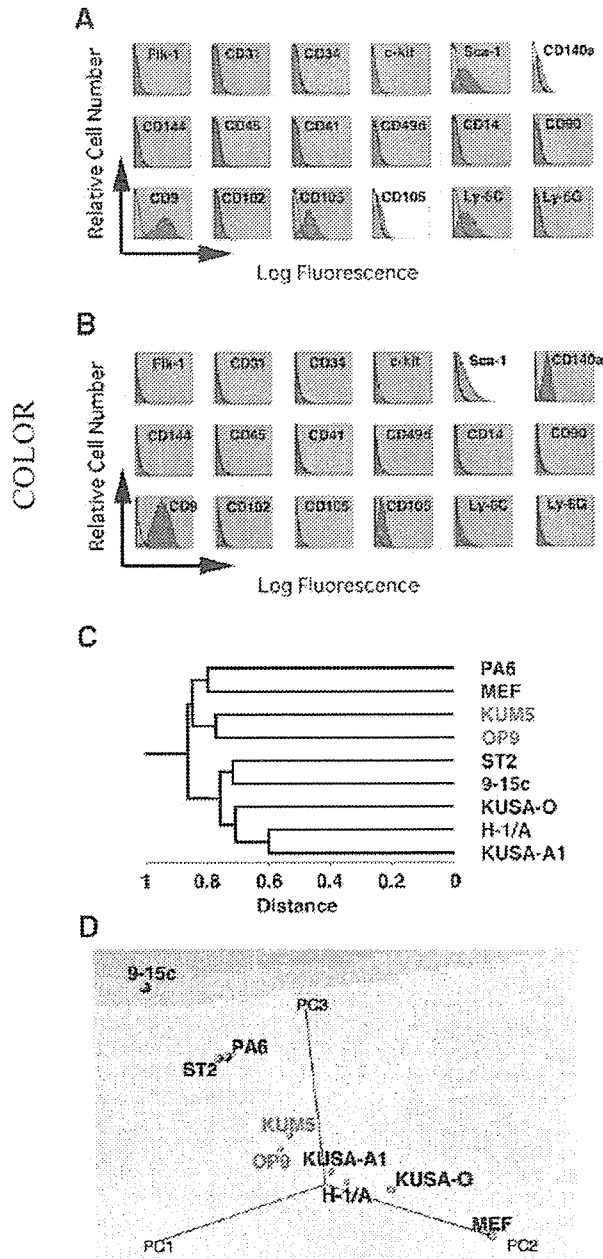


Fig. 4. Expression profiling, hierarchical clustering, and principal component analysis (PCA) of cell surface markers in marrow stromal cells. A,B: Flow cytometric analysis of cell surface markers in KUM5 cells (A) and OP9 cells (B). Red and pink colors indicate positive and marginal expression, respectively, and blue color indicates negative expression. C: Dendrogram revealing clustering profile of nine marrow stromal cells using 244 surface marker genes (Supplementary Table I). D: The rotated and dimensionally reduced gene expression data. Nine marrow stromal cells are plotted onto the 1st, 2nd, and 3rd principal component using 244 surface marker genes. These results indicate that KUM5 and OP9 cells were grouped into the same subcategory.

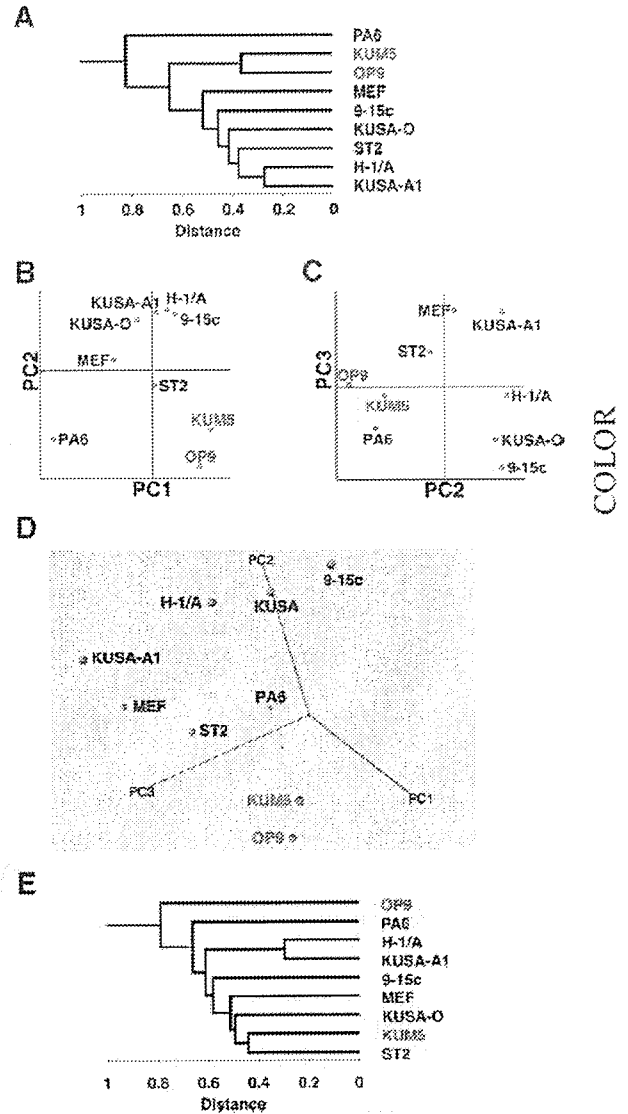


Fig. 5. Hierarchical clustering and PCA of fat- and cartilage-associated gene expression in marrow stromal cells. A: Dendrogram revealing clustering profile of 9 marrow stromal cells using 34 fat-associated genes (Supplementary Table II). B–D: PCA on expression levels of 34 fat-associated genes. The gene expression data from 9 marrow stromal cells were analyzed. Nine marrow stromal cells are plotted onto 2D-representation, PC1 and PC2 axes (B) or PC2 and PC3 axes (C), and 3D-representation (D). These results indicate that KUM5 and OP9 cells were grouped into the same subcategory. E: Dendrogram revealing clustering profile of 9 marrow stromal cells using 36 cartilage-associated genes (Supplementary Table III).

To determine the chondrogenic activity of OP9 cells in vivo, we directly injected them into the subcutaneous tissue. The OP9 cells without any induction did not generate cartilage. We then implanted the OP9 chondrogenic

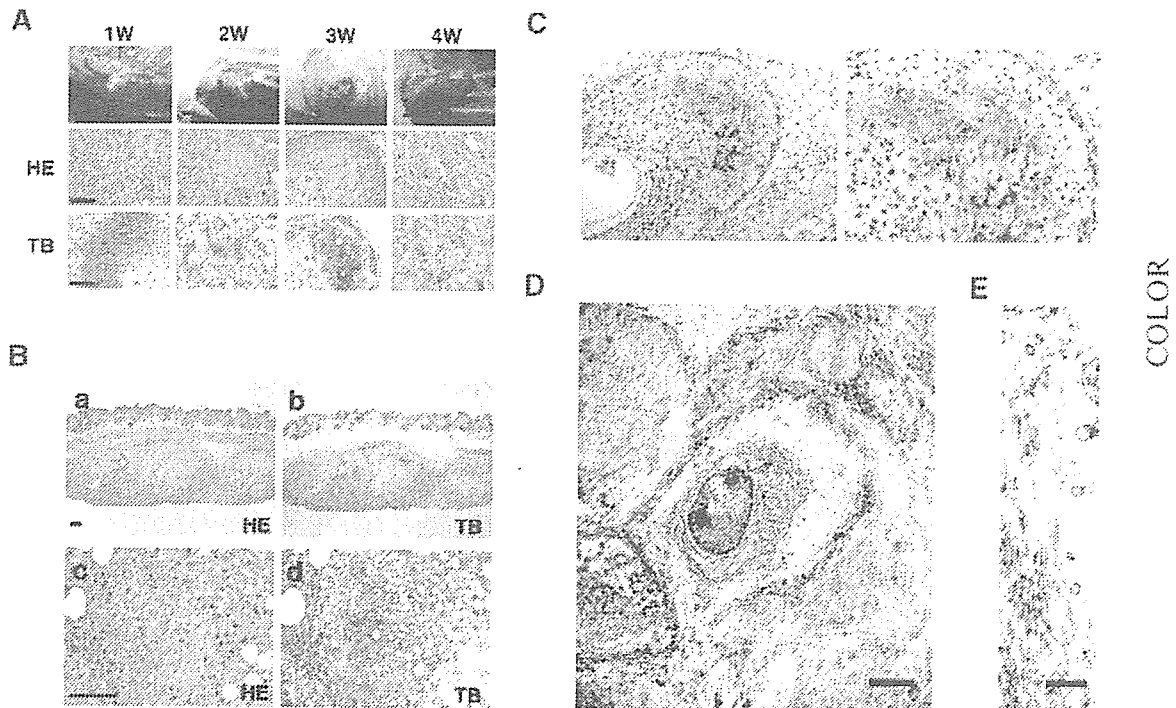


Fig. 6. In vivo chondrogenesis of KUM5 cells. A: Macroscopic view (top), hematoxylin and eosin stain (HE) (middle) and toluidine blue stain (TB) (bottom) analysis at 1, 2, 3, and 4 week (w)-cultivation in vivo after direct injection of KUM5 cells. B: KUM5 chondrogenic nodules, that were generated after pellet culture for 7 days in the CM supplemented with TGF- β 3 and BMP2, were implanted just beneath the cutaneous muscle in the subcutaneous tissue and were cultivated in vivo for 3 weeks. Panels c and d are higher magnifications of a and b, respectively.

C: Expression of chondrocyte-specific collagen type II. The KUM5 chondrogenic nodules were sectioned after 2 week-in vivo cultivation and stained with collagen type II-specific antibody. D,E: Ultrastructural analysis (TEM) of KUM5 implants. KUM5 cells were implanted into the subcutaneous tissue of Balb/c nu/nu mice, and the generated cartilage was resected 2 weeks after implantation. Scale bars: 2 mm (A, top row), 100 μ m (A, middle and bottom row), 100 μ m (B), 2 μ m (D), 1 μ m (E).

micromass after the pellet culture into the subcutaneous tissue just beneath the cutaneous muscle (Fig. 7A,B). The OP9 cartilage was formed at 2 and 4 weeks, and abundant metachromatic matrix was observed with the toluidine blue stain. The immunohistochemical analysis shows that OP9 cartilage stains positive for the chondrocyte-specific type II collagen (Fig. 7C).

Sorting of Chondroblasts by Chondrocyte-Specific Cis-Regulatory Element of the Collagen α 2(XI) Gene

Although the KUM5 cells used in this study were derived from a single-cell origin or clone, it could be argued that both cells responsive and non-responsive to chondrogenic induction were present [Ko et al., 1990]. In this sense, KUM5 cells might have been a largely heterogeneous cell population. Even cells derived from a single clone have been shown to be heterogeneous in

terms of differentiation capacity and stages [Muraglia et al., 2000]. To validate the chondrogenic differentiation observed here, a homogeneous population of committed cell obtained after induction should be isolated. Therefore, for the purpose of sorting chondrogenically committed cells, we transfected KUM5 cells with a Venus-expression vector under the control of the Col α 2(XI) promoter, analyzed the transfected cells, and collected Venus-positive cells (Fig. 8A–D). The sorted cells were assessed for in vitro (Fig. 9A–F) and in vivo chondrogenesis (Fig. 9G–I). The cells again showed metachromatic chondrogenic micromasses with toluidine blue staining in vitro (Fig. 9B). Direct injection of the cells resulted in the cartilage formation within 1 week and obvious enchondral ossification at the periphery of the cartilage at 4 weeks (Fig. 9G). Again, ultrastructural analysis revealed that KUM5 chondrocytes implanted into the subcutaneous

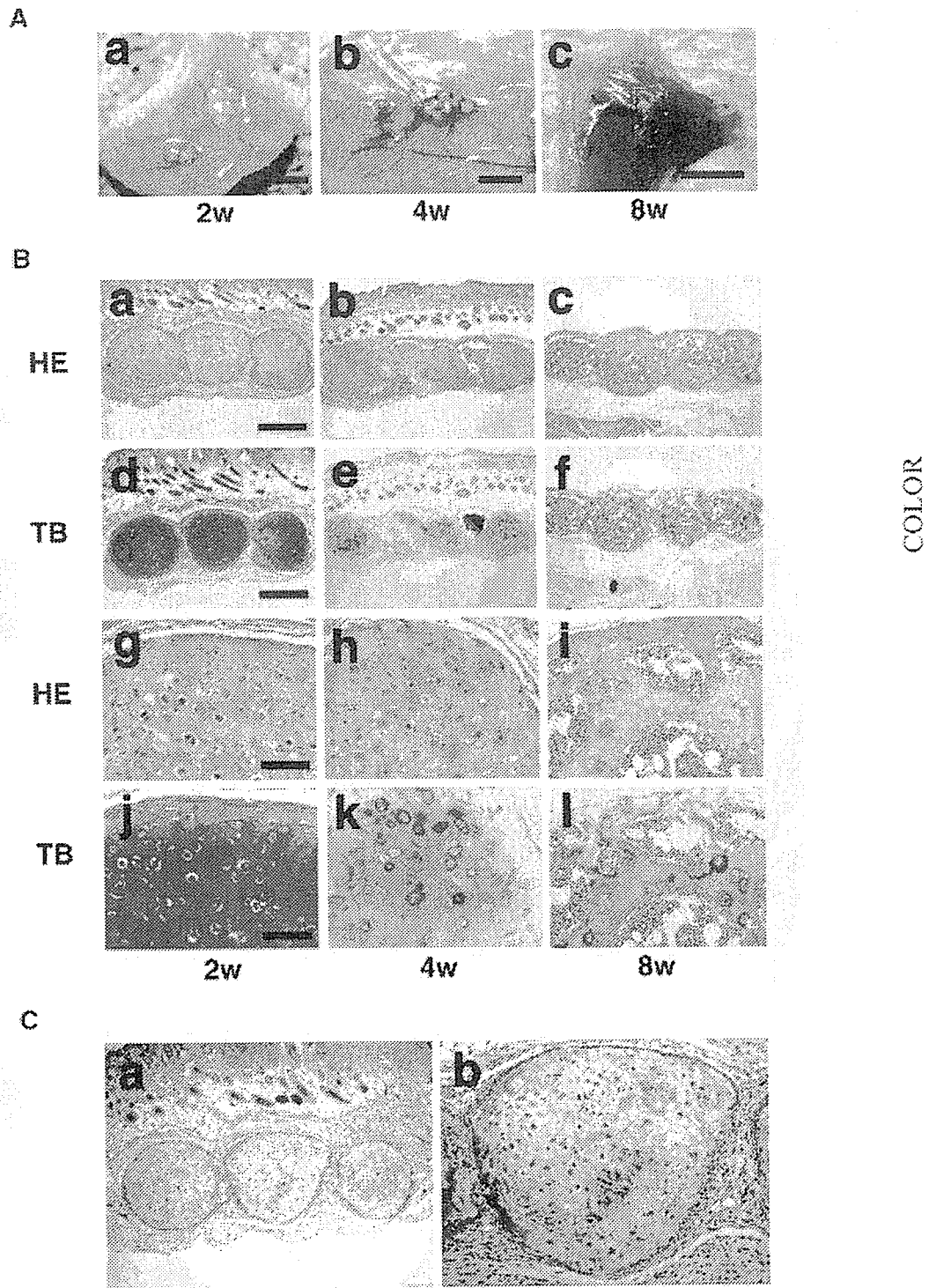


Fig. 7. In vivo chondrogenesis of OP9 cells. In vivo chondrogenesis was examined by implantation of OP9 chondrogenic nodules. OP9 chondrogenic nodules, which were generated after pellet culture for 7 days in the CM supplemented with TGF- β 3 and BMP2, were implanted just beneath the cutaneous muscle in the subcutaneous tissue and were cultivated in vivo for the number of weeks indicated. A: Macroscopic view of OP9 cartilage after 2 (a), 4 (b), and 8 (c)-week-in vivo cultivation.

B: Histological analysis of OP9 cartilage after 2 (a,d,g,j), 4 (b,e,h,k), and 8 (c,f,i,l)-week-in vivo cultivation. (a,b,c,g,h,i), HE stain; (d,e,f,j,k,l), TB stain. Panels g-l are higher magnifications of a-f, respectively. C: Immunohistochemical analysis of the in vivo OP9 chondrogenic nodules after 2-week-in vivo cultivation stained positive for collagen type II. Scale bars: 2 mm (A), 500 μ m (Ba-f), 100 μ m (Bg-l).

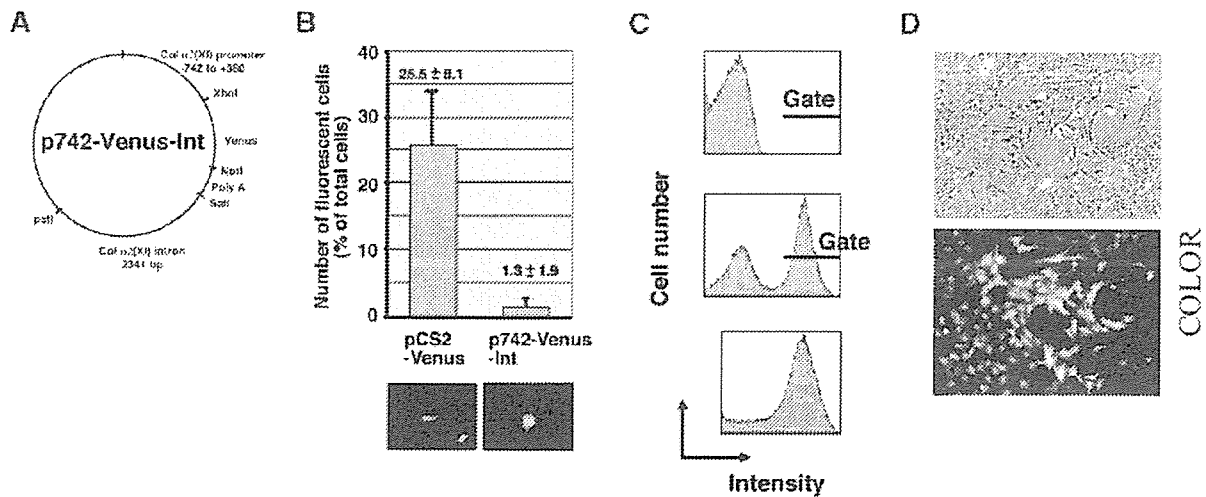


Fig. 8. Isolation of KUM5 chondroblasts using the chondroblast-specific cis-regulatory element. A: The p742-Venus-Int plasmid containing the fluorescent Venus gene driven by the cis-regulatory elements of the $\alpha 2(XI)$ collagen gene. B: The number of fluorescent KUM5 cells (upper) after transfection with the p742-Venus-Int plasmid or pCS2-Venus containing the Venus gene driven by the CMV-promoter. Fluorescent photomicrograph of KUM5 cells after the first sorting (lower). C: Flowcytometric analysis of KUM5 cells after transfection with the p742-Venus-Int

plasmid (top); The fluorescence-positive cells were sorted, propagated, and analyzed (middle). Again, the propagated fluorescence-positive cells were sorted, propagated, and analyzed (bottom). The "gate" for sorting is shown by the horizontal bar in the upper and middle panels. More than 80% of cells became positive after the final sorting. D: Phase contrast micrograph (upper) and fluorescent photomicrograph (lower) of the finally sorted cells (the lower panel of C).

tissue of nude mice were embedded in the hypertrophic chondrocytes and had abundant endoplasmic reticulum and a small number of mitochondria (Fig. 9H,I). The post-mitotic daughter cells in the cell nest, which are often observed in cartilage, were also detected (Fig. 9I).

DISCUSSION

In this study, we focus on the chondrogenic differentiation *in vitro* and *in vivo* using the two cell lines, KUM5 and OP9. The chondrogenic process is determined by the sequential expression of matrix component, and the differential response of differentiating cells to the growth factors may be attributed to the differentiating stages that depend on the expression patterns of the gene set as is the case for hematopoietic cells. The process of the chondrogenic differentiation is influenced by a number of growth factors including TGF- β and/or BMPs. Three isoforms of TGF- β have been known to have the ability to induce the chondrogenic differentiation. Both TGF- $\beta 2$ and - $\beta 3$ are more effective than TGF- $\beta 1$ in promoting chondrogenesis, and TGF- $\beta 3$ accelerates production of cartilagi-

nous extracellular matrix in differentiating mesenchymal stem cells [Barry et al., 2001].

This study was undertaken to obtain mesenchymal stem cells with chondrogenic potential that retain critical *in vivo* cell functions, as do mammary gland epithelial cells, skin keratinocytes, and pigmented epithelial cells. To achieve this, we attempted to identify marrow-derived cells with chondrogenic nature and immortality without transformation among the cells obtained by the limiting-dilution method [Umezawa et al., 1992], defining "immortality" simply as indefinite cell division.

OP9 cells are known to serve as a niche or a specific microenvironment for the regulation of self-renewal and differentiation of stem cells [Nakano, 1996], and the question is raised of whether marrow stromal cells or marrow-derived mesenchymal cells with chondrogenic potential are capable of constituting a microenvironment for stem cells. It is inconceivable that cartilage can form a niche for cells in the living body based on structural and morphological considerations; however, a cell with chondrogenic or adipo-chondrogenic potential may serve as a niche not only in the case of OP9 cells but also as a general concept, at least *in vitro*.

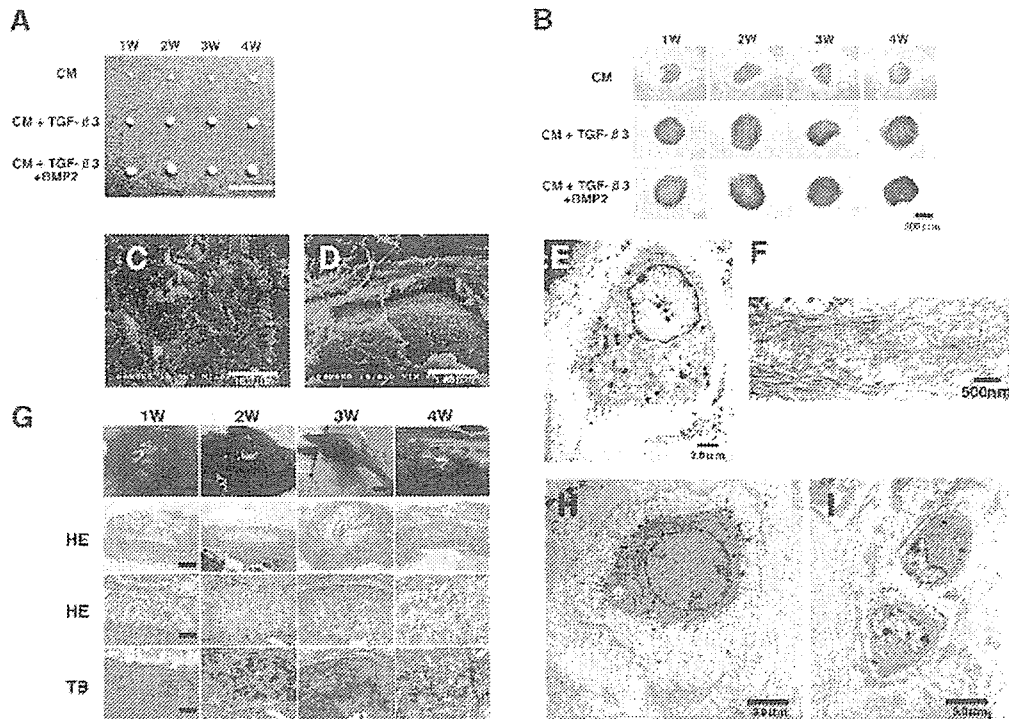


Fig. 9. In vitro and in vivo chondrogenesis of KUM5 cells sorted according to the activity of the chondrocyte-specific cis-regulatory element. **A,B:** Macroscopic view of the chondrogenic nodules which were generated after pellet culture of the finally sorted KUM5 cells for 1–4 weeks in the CM supplemented with growth factors as indicated (**A**) and toluidine blue stained section (**B**). **C–F:** Ultrastructural analysis of the micromasses of KUM5 cells sorted according to the activity of the Col $\alpha 2(XI)$ cis-regulatory element (KUM5-Venus) after culturing in the CM supplemented with TGF- $\beta 3$ for 3 weeks. (**C,D**), SEM; (**E,F**), TEM. **G:** In vivo chondrogenesis was examined 1–4 weeks after direct

injection of the finally sorted KUM5 cells. From top to bottom: Macroscopic view, scale bars: 2 mm; histological analysis, scale bar: 600 μm , HE stain; histological analysis, scale bar: 120 μm , HE stain; histological analysis, scale bar: 120 μm , TB stain. **H,I:** Ultrastructural analysis (TEM) of the sorted KUM5 cartilage. The sorted KUM5 cells were implanted into the subcutaneous tissue of Balb/c nu/nu mice, and the generated cartilage was resected 2 weeks after implantation. Scale bars: 5 mm (**A**), 500 μm (**B**), 2 mm (**G**, top row), 500 μm (**G**, 2nd row), 100 μm (**G**, 3rd and bottom row).

COLOR

The sequence of enchondral or perichondral ossification by KUM5 and OP9 cells was as follows: deposition of homogeneous matrix surrounding the small nests of the injected cells that subsequently became positive for type II collagen and exhibited metachromasia with toluidine blue staining, trapping them in the secreted homogeneous matrix, and the appearance of small nests of isogenous chondrocytes that probably resulted from repeated cell division. At a later stage, that is, 4–8 weeks after injection, the peripheral region of the generated cartilage became ossified. Importantly, the chondrogenesis by KUM5 and OP9 cells was irreversible and reproducible, and the implanted cells never transformed into malignant cells, formed any abnormal extracellular matrices, or induced any significant inflammatory reactions. It is again noteworthy that the

osteogenesis by these two different lines of cells was mediated by chondrogenesis, and it was therefore considered to be chondral ossification. Thus, the unique characteristics of these two cell lines provide an opportunity to analyze the process of enchondral or perichondral ossification in an experimental system in detail.

In fetal life, primary ossification centers form by one of two processes: enchondral ossification or membranous ossification. Enchondral ossification refers to bony replacement of cartilage and is the mode of formation of the long bones. During membranous ossification mesenchymal cells form membranes within which ossification occurs and this is the mode of formation of the scapula and skull and, in part, of the clavicle and pelvis. After birth, bone growth continues by both enchondral and membranous ossification. Further enchondral ossification occurs in

the physes and results in continuous longitudinal growth of the long bones until skeletal maturity. KUM5 and OP9 cells were obtained from long bone and calvaria, respectively, and showed enchondral ossification. We have also reported that KUSA-A1 cells form bone by membranous ossification *in vivo*, and thus we have three different types of cells showing distinctive *in vivo* characteristics. The process of chondrogenesis or enchondral ossification may also serve as a model for chondromatosis and osteochondromatosis in a joint cavity.

The expression pattern of chondrocyte-specific genes in OP9 and KUM5 cells is different from that in ATDC5 cells, which are a mouse embryonal carcinoma-derived chondrogenic cell line. ATDC5 cells exhibit a multistep differentiation process encompassing the stages from chondrogenesis to enchondral ossification [Shukunami et al., 1996]. Early-phase differentiation is characterized by the expression of type II collagen, followed by induction of the aggrecan gene. Late stage differentiation is characterized by the start of expression of short-chain collagen type X genes. By contrast, marrow-derived mesenchymal stem cells express the aggrecan genes at an early stage and then type II collagen during chondrogenic differentiation [Pittenger et al., 1999]. Surprisingly, gene expression pattern determined by the gene chip analysis was consistent with protein levels of cell surface molecules; this consistency indicates that the expression profiling is valid. Expression of "structural proteins" on Gene Ontology, including the extracellular matrix, was much higher by OP9 and KUM5 cells than by non-chondrogenic cells such as KUSA-A1 osteoblasts, H-1/A preadipocytes, and 9-15c mesenchymal stem cells, implying that the OP9 and KUM5 cells are mainly engaged in synthesizing extracellular matrix.

Can we inhibit enchondral or perichondral ossification after the completion of chondrogenesis? This is a challenge for the future, probably the not-too-distant future. We could not prevent the generated hyaline cartilage from ossifying at present even after selection based on the chondrocyte-specific cis-regulatory element of the collagen $\alpha 2(\text{XI})$ gene, probably due to the inability to inhibit vasculogenesis from the neighboring connective tissue. However, these established murine marrow-derived mesenchymal cells with *in vivo* chondrogenic activity and expression profiles provide a powerful model for

studies of chondrogenic differentiation and our further understanding of cartilage regeneration. Bone marrow-derived chondroblasts with chondrogenic potential are useful candidate cell sources in addition to dedifferentiated chondrocytes obtained from cartilage for transplantation in osteoarthritis and rheumatoid arthritis.

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Research Article

Single-cell-derived mesenchymal stem cells overexpressing Csx/Nkx2.5 and GATA4 undergo the stochastic cardiomyogenic fate and behave like transient amplifying cells

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ABSTRACT

Bone marrow-derived stromal cells can give rise to cardiomyocytes as well as adipocytes, osteocytes, and chondrocytes in vitro. The existence of mesenchymal stem cells has been proposed, but it remains unclear if a single-cell-derived stem cell stochastically commits toward a cardiac lineage. By single-cell marking, we performed a follow-up study of individual cells during the differentiation of 9-15c mesenchymal stromal cells derived from bone marrow cells. Three types of cells, i.e., cardiac myoblasts, cardiac progenitors and multipotent stem cells were differentiated from a single cell, implying that cardiomyocytes are generated stochastically from a single-cell-derived stem cell. We also demonstrated that overexpression of Csx/Nkx2.5 and GATA4, precardiac mesodermal transcription factors, enhanced cardiomyogenic differentiation of 9-15c cells, and the frequency of cardiomyogenic differentiation was increased by co-culturing with fetal cardiomyocytes. Single-cell-derived mesenchymal stem cells overexpressing Csx/Nkx2.5 and GATA4 behaved like cardiac transient amplifying cells, and still retained their plasticity in vivo.

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Introduction

Cell-based therapy is a novel therapeutic strategy, based on the concept of the cell-mediated restoration of damaged or diseased tissue. Candidate cell sources include embryonic stem (ES) cells, hematopoietic stem cells (HSCs), neural stem cells (NSCs), mesenchymal stem cells (MSCs) [1], and so on. Clinical trials with MSCs have been performed in patients with

graft-versus-host disease through immunomodulatory effects [2], and osteogenesis imperfecta [3,4], and MSCs are expected to be one of the most available cells. The source of MSCs includes bone marrow [5], adipose tissue [6], umbilical cord [7] and placenta [8].

Bone marrow-derived stromal cells [9] can differentiate into mesenchymal progenitors, including osteoblasts [10], chondroblasts [11], skeletal myoblasts [12], adipoblasts [13],

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and neurons [14,15] when placed in appropriate *in vitro* and *in vivo* environments. We have shown that bone marrow-derived stromal cells are also able to differentiate into cardiomyocytes *in vitro* and *in vivo* [13,14,16,17]. However, the characteristics of the cells that can differentiate into cardiomyocytes are poorly understood, and how the progeny of multipotent cells adopt one fate among several possible fates remains a fundamental question.

Hematopoietic stem cells are defined as cells that are capable of self-renewal to maintain a long-term supply of progeny and are capable of differentiating into multiple hematopoietic lineages [18]. Retroviral labeling of individual cells is one of the useful clonal assays to monitor lineage commitment at the single cell level [16,17,19]. At present, several models have been proposed in which hematopoietic lineage determination is driven intrinsically [20], extrinsically [21], or both [22]. We therefore performed retroviral labeling experiments of bone marrow-derived stromal cells to investigate whether cardiomyocytes are generated from committed cardiac precursor cells or uncommitted stem cells.

In the present study, we provide evidence that cardiomyocytes are stochastically differentiated from MSCs, and we demonstrate that forced expression of cardiomyocyte-specific transcription factors, *i.e.*, *Csx/Nkx2.5* and *GATA4*, destined these MSCs to a cardiomyocytic lineage.

Materials and methods

Cell culture

9-15c cells were used as a source of uncommitted stem cells in this study [23,24]. 9-15c cells are available through one of the cell banks (JHSF cell bank: http://www.jhsf.or.jp/English/index_gc.html; RIKEN cell bank: <http://www.brc.riken.go.jp/lab/cell/english/guide.shtml>). 9-15c cells were cultured using methods described previously [25]. The cells were cultured in Iscove's modified Dulbecco's medium (IMDM) supplemented with 20% fetal bovine serum and penicillin (100 μ g/ml)/streptomycin (100 μ g/ml)/amphotericin B (250 ng/ml) at 33°C with 5% CO₂.

Primary cultures of cardiac myocytes were prepared from the hearts of 16-day-old fetal C3H/HeJ mice (CLEA Japan, Inc., Tokyo, Japan) according to the method of Simpson *et al.* [26] with minor modifications. In brief, cardiomyocytes were dissociated into single isolated cells by trypsinization and the cells were plated in culture medium (IMDM with 20% fetal bovine serum).

Cloning of *Csx/Nkx2.5* and *GATA4* cDNAs

The full open reading frames of mouse *Csx/Nkx2.5* and *GATA4* cDNAs were cloned by RT-PCR from poly(A) RNA obtained from the hearts of fetal mice using the following primers: *Csx/Nkx2.5*, sense: 5'-TGAAACCTGCGTCGCCAC-CATGT-3', antisense: 5'-GGCTCTTTCCTACCAGGCTCGG-3'; *GATA4*, sense: 5'-TAGTTCTTGCTGCCTCGTGCTCA-3', antisense: 5'-GGCGCTGATTACGCGGTGATTATG-3'. The PCR products were subcloned into pGEM-T vector (Promega). DNA sequencing confirmed that the plasmids contained the full-

length fragments of the mouse *Csx/Nkx2.5* and *GATA4* coding regions.

Retroviral transduction

The retroviral vectors pCLNCX (Imgenex), pCLPCX and pCLHCX were used. pCLPCX was constructed from pCLNCX by replacing the neomycin resistance gene with a puromycin resistance gene (pPUR; CLONTECH). pCLHCX was constructed from pCLNCX by replacing the neomycin resistance gene with a hygromycin resistance gene (pcDNA3.1/Hygro(+); Invitrogen). Fragments containing the EGFP, *Csx/Nkx2.5*, and *GATA4* genes were cloned into pCLNCX, pCLPCX, or pCLHCX. Each of these DNAs and pCMV-Eco (kindly provided by Nikunj Somia) were transfected into the producer cells (293 gag pol; kindly provided by Nikunj Somia) using TransFast (Promega). Two days after the transfection, the culture supernatant was filtered through a 0.45- μ m filter. 9-15c cells were treated with viruses and hexadimethine bromide (polybrene) (Sigma) (8 μ g/ml) for 4–6 h. To generate stably expressing cells, 9-15c cells were cultured in the presence of 300 μ g/ml G418, 300 ng/ml puromycin or 300 μ g/ml hygromycin. The mixtures of drug-resistant clones were used to average the clonal variation of the transfected gene expression.

Cardiomyogenic induction

To induce differentiation, cells were initially plated at a density of 2×10^4 cells/ml. The cells were treated with 3 μ M 5-azacytidine (Sigma) for 24 h the next day. In some experiments, PDGF-BB (Peprotech) and retinoic acid (Sigma) were added to the culture dish coated with fibronectin (BD Biosciences) to give a final concentration of 10 ng/ml and 1 nM, respectively, for 6 days. Total number of beating cells was estimated under phase contrast microscopy.

RT-PCR

Total RNA was extracted from adult mouse hearts, skeletal muscles and cultured cells with an RNeasy kit (QIAGEN), and cDNA was made using the SuperScript First-strand Synthesis System (Invitrogen) from 1 μ g of total RNA. First-strand cDNA was diluted 20 fold and 1 μ l of cDNA was used for each PCR reaction. The following primer sets for cardiomyocyte-associated genes were used: atrial natriuretic peptide (ANP), sense: 5'-TTCCTCGTCTTGCCCTTTTGG-3', antisense: 5'-GCTGGATCTTCGTAGGCTCCG-3'; cardiac troponin I (cTnI), sense: 5'-GATCCTGTTCTCTGCCTCTGGA-3', antisense: 5'-TCATCCACTTTGTCCACCCGAG-3'; fast troponin I (fTnI), sense: 5'-GAAGCGCAACAGGGCCATCACG-3', antisense: 5'-CCACGTCACGCAGGTCCCGTTC-3'; *Csx/Nkx2.5*, sense: 5'-TGGCGTCTGGGGACCTGTCTG-3', antisense: 5'-GAGTCTGGTTCCTGCCGCTGTC-3'; *GATA4*, sense: 5'-TACATGGCCGACGTGGGAGCA-3', antisense: 5'-TGGAGT-TACCGCTGGAGGCAC-3'; exogenous *GATA4*, sense: 5'-CCAGAAAACGGAAGCCCAAGAA-3' (the sequence derived from mouse *GATA4* gene), antisense: 5'-GCTTGCCAAACCTA-CAGGTGGG-3' (the sequence derived from pCLPCX vector); adiponectin, sense: 5'-CTGAAGAGCTAGCTCCTGCTTTG-3', antisense: 5'-GAAGAGAACGGCCTTGCTCTTC-3'; glyceraldehyde-

3-phosphate dehydrogenase (G3PDH), sense: 5'-CCCATCAC-CATCTTCCAGGAGC-3', antisense: 5'-TTCACCACCTTCTT-GATGTCATCATA-3'. G3PDH was used as an internal control. PCR was performed with TaKaRa Ex-Taq (TAKARA SHUZO CO., LTD) for 30–35 cycles, with each cycle consisting of 94°C for 1 min, 61–68°C for 1 min, and 72°C for 2 min, with an additional 7 min incubation at 72°C after completion of the final cycle.

RT-PCR samples were electrophoresed through agarose gels and stained with ethidium bromide and visualized through a UV light digital imaging system. Densities of electrophoresis bands were analyzed using ScnImage software (Scion Corporation).

Western blot analyses

Western blots were performed using whole-cell extracts according to the standard protocol [27]. Aliquots (30 μ g) of whole-cell extracts were electrophoresed in SDS-polyacrylamide gels and transferred onto Immobilon-P polyvinylidene difluoride membrane (Millipore) by electroblotting. After treatment in blocking buffer, membranes were sequentially probed with the antibodies against Nkx2.5 (sc-8697, Santa Cruz) or Gata4 (sc-9053, Santa Cruz), and then with HRP-conjugated anti-goat or rabbit IgG. The bands were revealed using the ECL Plus standard protocol (Amersham Pharmacia Biotechnology).

Cellular transplantation

Following priming by 5-azacytidine for 24 h, the cells were cultured for an additional 3 days. Then the cells were harvested with 0.05% trypsin and 0.25 mM EDTA, and

suspended as single cells at a concentration of 1×10^5 cells/ μ l with PBS. The cell viability in suspension, determined by 0.05% erythrosine dye exclusion, was 90% to 95%. After general anesthesia of the recipient mice by an intraperitoneal injection of 0.05 mg/g body weight pentobarbitone, cell transplantation was performed into the quadrant muscles of syngeneic adult recipient C3H/HeJ mice (CLEA Japan, Inc., Tokyo, Japan), aged 8 to 10 weeks old at a dose of 1×10^6 and 1×10^8 cells per mouse. All animals received humane care in compliance with the "Principles of Laboratory Animal Care" formulated by Keio University School of Medicine and the National Research Institute for Child Health and Development, and the experimental procedures were approved by the Laboratory Animal Care and Use Committee of Keio University School of Medicine.

Histological analyses

Tissues were fixed in 10% neutral buffered formalin and embedded in paraffin. Tissue sections (6 μ m) were mounted on poly-L-lysine-coated slides. After deparaffinization with xylene, tissues were rinsed in acetone or ethanol. Slides were incubated in 0.3% H₂O₂ for 30 min. After washing in PBS, tissues were preblocked for 30 min with 5% normal swine serum. They were incubated overnight at 4°C with mouse monoclonal antibody against recombinant GFP (CLONTECH Laboratories, Inc.) diluted 1:500. After rinsing in PBS, the slides were incubated with horseradish peroxidase-conjugated swine anti-mouse immunoglobulin diluted 1:100 with 1% BSA in PBS, and washed in cold PBS. Staining was developed using a solution containing DAB and 0.01% H₂O₂ in 0.05 M Tris-HCl buffer, pH 6.7. Slides were counterstained with hematoxylin. Slices with positive signals for EGFP were further stained

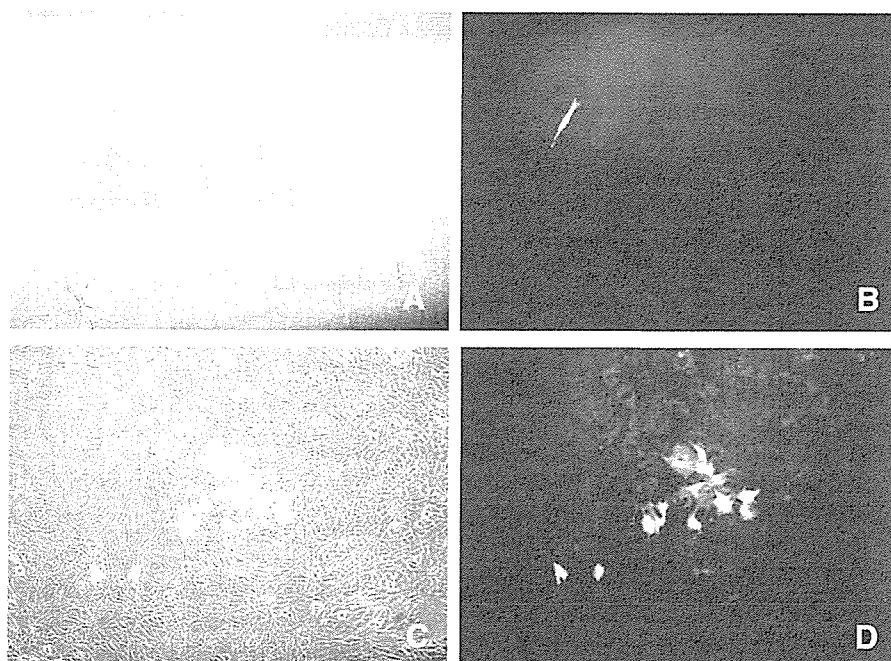


Fig. 1 – Single cell marking by infection of retrovirus carrying EGFP. Phase contrast photomicrograph (A, C) and fluorescent photomicrograph (B, D) of 9-15c cells 1 day (A, B) or 7 days (C, D) after infection with retroviruses carrying EGFP. EGFP-positive single cell-derived cells were clustered.

with anti-CD31 (PECAM-1) antibody (M-20, Santa Cruz Biotechnology, Inc, California, USA).

Frozen sections (6 μm) of the samples were used to detect the donor cells and the differentiation status by examination under a fluorescence microscope. After fixation with acetone and blocking with PBS containing 5% rabbit serum, anti-CD31 or anti-desmin (Bio-Science Products AG, Switzerland) antibodies was used as the first antibody, and rat anti-mouse IgG antibody conjugated with tetramethylrhodamine isothiocyanate (T4280, Sigma, Missouri, USA) and goat anti-mouse IgG antibody conjugated with rhodamine (M116, Leinco Technology, Inc., MO, USA) were used as the second antibody, respectively.

Results

Single-cell marking of 9-15c cells

9-15c cells are mesenchymal stem cells [23,24] capable of differentiating into cardiomyocytes in vitro with the use of 5-azacytidine. To determine if cardiomyocytes were generated from committed cardiac precursor cells or uncommitted stem cells during the differentiation of 9-15c cells, we carried out a single-cell marking experiment. Following retrovirus-mediated EGFP gene infection, a single EGFP-labeled cell could be detected at Day 1 after infection (Figs. 1A, B). The fate of

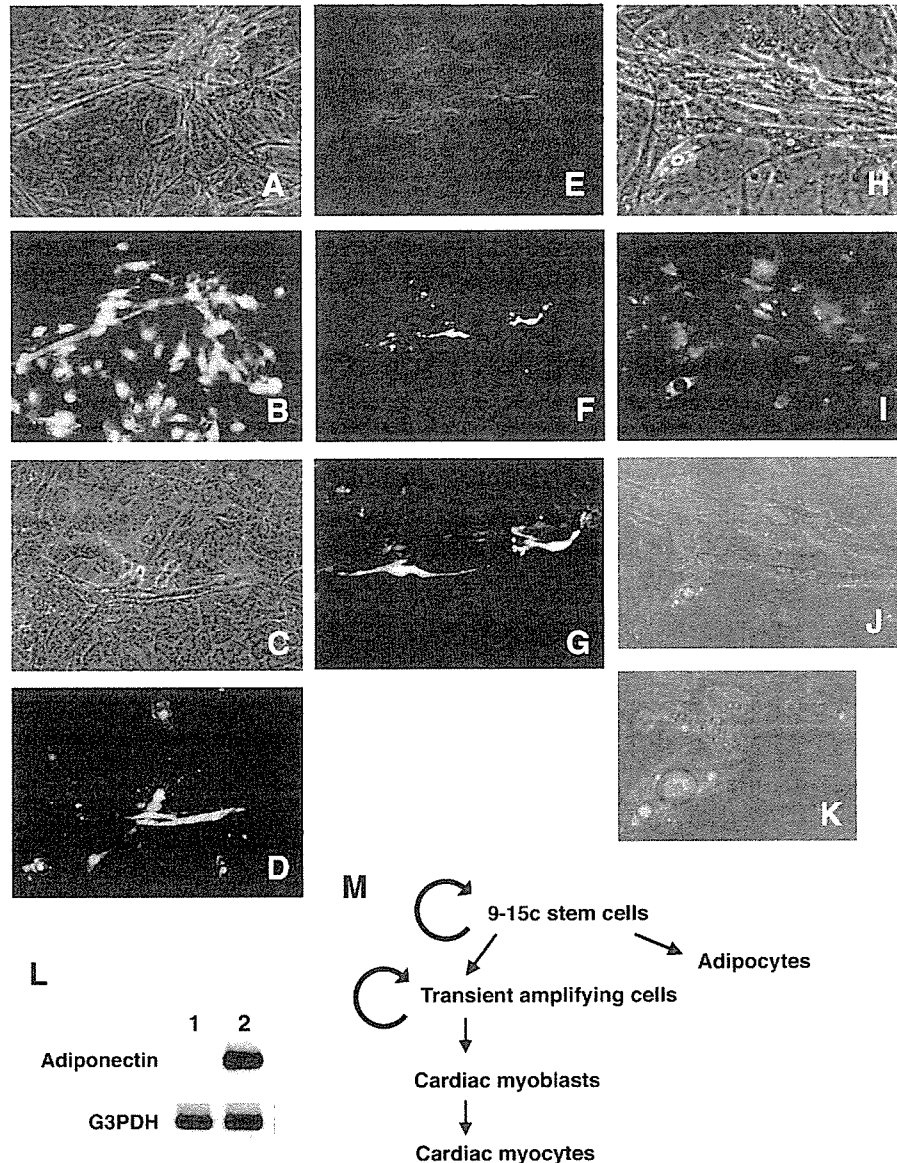


Fig. 2 – Bipotency, i.e., cardiomyogenic and adipogenic differentiation, of single cell-derived cells. Single-cell-derived 9-15c cells marked by EGFP exhibited cardiomyogenic and adipogenic differentiation after exposure to 5-azacytidine. (A–B) Cardiomyogenic and undifferentiated EGFP-marked, single-cell-derived 9-15c cells; (C–G) Cardiomyogenic differentiation of EGFP-marked, single-cell-derived 9-15c cells; (H–J) Cardiomyogenic and adipogenic differentiation of EGFP-marked, single-cell-derived 9-15c cells. (A, C, E, H, J) Phase contrast photomicrographs; (B, D, F, G, I) fluorescent photomicrographs. (K) Enlargement of the panel J. (L) RT-PCR analysis of the adiponectin and G3PDH genes in 9-15c cells at the growing phase without any treatment (lane 1) and 4 weeks after exposure to 5-azacytidine (lane 2). (M) Scheme of 9-15c cell differentiation.

retrovirally tagged 9-15c cells could be traced by monitoring EGFP throughout the differentiation process after exposure to 5-azacytidine. Seven days later, the EGFP-positive, single-cell-derived cells were clustered (Figs. 1C, D). Four weeks after 5-azacytidine treatment, the EGFP-positive cells were examined for differentiated phenotypes. We identified beating cells as cardiomyocytes and oil-red-positive cells as adipocytes. Three kinds of cell populations were observed: a) a cell population in which cardiomyocytes and undifferentiated stem cells were EGFP-positive (Figs. 2A, B); b) a cell population in which all the EGFP-positive cells were cardiomyocytes (Figs. 2C–G); c) a cell population in which cardiomyocytes, adipocytes and undifferentiated stem cells were EGFP-positive (Figs. 2H–K). RT-PCR analysis shows that these cells express adiponectin (Fig. 2L), suggesting the presence of adipocytes among the differentiated population. These results imply that cardiomyocytes are generated from uncommitted stem cells (Fig. 2M).

9-15c multipotent cells were preferentially destined to generate cardiomyocytes by forced expression of transcription factors *Csx/Nkx2.5* and *GATA4*

In order to elucidate the roles of *Csx/Nkx2.5* and *GATA4* in 9-15c cell differentiation, we infected 9-15c cells with retroviruses carrying *Csx/Nkx2.5* and *GATA4*. We detected *Csx/Nkx2.5* and *GATA4* gene expression in the infected cell by RT-PCR and Western blotting (Figs. 3A and B). *GATA4* gene was originally expressed in 9-15c; we detected the *GATA4* transgene with specific primers, but not the endogenous *GATA4* gene (Fig. 3A).

Four weeks after the induction of differentiation by 5-azacytidine treatment, we examined the efficiency of cardiomyogenic differentiation or the expression of cardiomyogenic markers. The expression of the ANP and cTnI genes was up-regulated in 9-15c cells overexpressing *Csx/Nkx2.5* and *GATA4* (9-15c-CG cells) compared to the uninfected 9-15c cells (Fig. 3C, lanes 5 and 9). When 9-15c-CG cells were treated with PDGF and retinoic acid on dishes coated with fibronectin in addition to 5-azacytidine, the expression of the ANP and cTnI gene was further up-regulated (Fig. 3C, lane 10).

Cell implantation into immunodeficient mice

To investigate whether 9-15c-CG cells differentiate *in vivo*, the cells treated with 10 μ M 5-azacytidine for 24 h were injected into immunodeficient mice (Figs. 4A–F). The donor cells clearly formed striated muscles without a branched structure as well as undifferentiated cells 81 days after implantation. The implanted 9-15c-CG cells clearly expressed desmin (Fig. 4G). The grafted cells also generated neovascularization near the injected site 1 month after injection; the EGFP-positive donor cells could be identified as the endothelium of these vessels (Fig. 4H). Immunohistochemistry with an antibody against CD31, a marker for endothelium, confirmed that the donor cells of the newly formed vessels had differentiated into endothelium (Fig. 4Hb). Engrafted donor cells appeared to maintain the characteristics of stem cells, that is, they continued to produce progeny, *i.e.*, differentiated endothelial cells in this case.

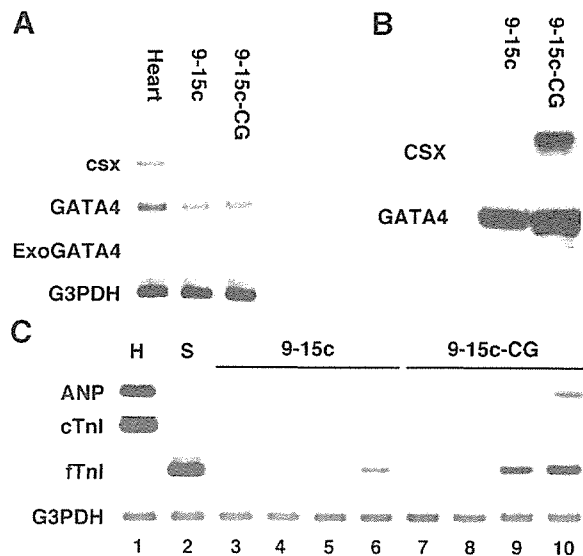


Fig. 3 – Expression of cardiomyocyte-specific or associated genes in 9-15c cells. **A:** RT-PCR analysis of the *Csx*, *GATA4*, exogenous *GATA4* and *G3PDH* genes (from top to bottom) in adult mouse heart, 9-15c cells and 9-15c cells overexpressing the *Csx* and *GATA4* genes (9-15c-CG cells). **B:** Western blotting analysis of the *Csx* and *GATA4* proteins in 9-15c cells and 9-15c-CG cells. **C:** RT-PCR analysis of the ANP, cTnI, and *G3PDH* genes (from top to bottom) in 9-15c cells (lanes 3–6) and 9-15c-CG cells (lanes 7–10). 9-15c cells (lane 3) and 9-15c-CG cells (lane 7) were cultured without any treatment (lanes 4 and 8) or with exposure to 5-azacytidine alone (lanes 5 and 9), or 5-azacytidine, PDGF, retinoic acid, and fibronectin coating on a dish (lanes 6 and 10) for 4 weeks. Heart (lane 1: H) and skeletal muscle (lane 2: S) served as controls.

Enhancement of cardiomyogenic differentiation by the co-cultivation with cardiomyocytes

We co-cultured EGFP-labeled 9-15c-CG cells with cardiomyocytes of fetal mice *in vitro*. Four weeks after 5-azacytidine treatment, EGFP-positive beating cardiomyocytes were increased (Figs. 5A, B). To determine whether factors secreted from the cultured cardiomyocytes promoted cardiomyocytic differentiation, 9-15c cells and 9-15c-CG cells were cultured in growth medium supplemented with conditioned medium from cardiomyocyte cultures. The expression of the ANP and cTnI genes was up-regulated in both 9-15c cells and 9-15c-CG cells with exposure to the conditioned medium of cardiomyocyte cultures (Fig. 5C, lanes 3 and 7). Furthermore, treatment with PDGF and retinoic acid, and fibronectin coating on a dish enhanced cardiomyogenic marker expression in both 9-15c cells and 9-15c-CG cells (Fig. 5C, lanes 4 and 8).

Discussion

Different models arise from different conceptions of the MSCs as in hematopoietic stem cells' differentiation [28,29]. A hierarchical model of MSCs has been proposed based on the *in vitro* differentiation potential of human MSCs as observed

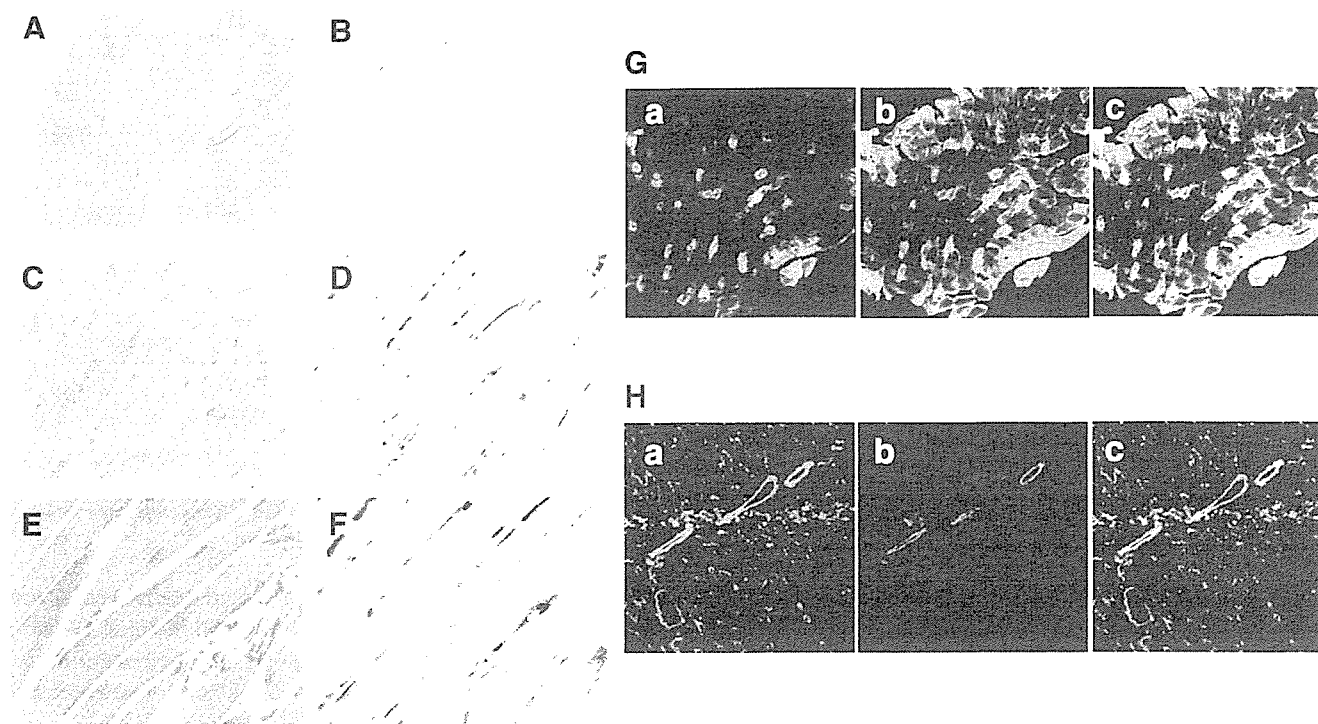


Fig. 4 – Myogenic differentiation of the EGFP-labeled 9-15c-CG cells into the quadriceps femoris muscle. EGFP-labeled 9-15c-CG cells could be recognized morphologically as the skeletal myocytes in the quadriceps femoris muscle 3 months after transplantation (A, C, E: HE staining; B, D, F: immunohistochemistry using anti-GFP antibody). The EGFP-positive donor cells exhibited skeletal myocyte-specific features such as multiple nuclei in the periphery of the cells and striation. Generation of myocytes (G) and endothelial cells (H) by the EGFP-labeled 9-15c cells. The injected donor 9-15c cells labeled with EGFP were detected by green fluorescence. (Ga, Ha) Green fluorescence of EGFP-labeled donor cells. (Gb, Hb) Immunohistochemistry for desmin (Gb, red) or CD31 (Hb, red). (Gc, Hc) The merged images of green fluorescence of injected 9-15c cells and rhodamine of desmin or CD31 clearly demonstrated that 9-15c cells differentiated into myocytes or endothelium. A–F: Longitudinal section; G, H: Cross section.

by clonal analysis [30]. In the present study using single-cell marking, we found that 9-15c cells in culture consisted of a mixture of at least three types of cells, i.e., cardiac myoblasts, cardiac progenitors and multipotent stem cells. Cardiac myoblasts are defined as cells which can differentiate into only cardiac myocytes and have low proliferative potential; cardiac progenitors have proliferative capability and the ability to become cardiomyocytes; multipotent stem cells have both proliferative capability and multipotency. The results obtained in the present study suggest that 9-15c cells are stochastically committed toward the cardiac lineage, and that following this commitment they proliferate as transient amplifying cells and differentiate into cardiac myocytes through the differentiation process, and the hierarchical model applies in the case of 9-15c multipotent cells.

In the present study, we used 5-azacytidine to induce differentiation. 5-azacytidine is a cytosine analog that causes extensive demethylation. The demethylation is attributable to covalent binding of DNA methyltransferase to 5-azacytidine in the DNA [31], with the subsequent reduction of enzyme activity in cells resulting in random loss of methylation at many sites in the genome. Previously, it has been thought that 5-azacytidine activates cardiomyogenic master genes, such as *Nkx2.5/Csx*, *GATA4*, and *MEF-2C*, leading to stochastic trans-

differentiation of MSCs into cardiomyocytes [32,33]. This concept is difficult to account for the existence of cardiac progenitors and multipotent stem cells we identified, and we propose two possibilities how 5-azacytidine works. First, treatment of 5-azacytidine modulates heterochromatin remodeling and leads to dedifferentiation of 9-15c cells. Second, 9-15c cells are stochastically committed toward the cardiac lineage, being independent of treatment of 5-azacytidine. At this time we cannot conclude which is feasible, but it is certain cardiomyocytes are not only transdifferentiated by treatment of 5-azacytidine.

Csx/Nkx2.5 and *GATA4* are two cardiac-enriched transcription factors that are expressed in precardiac mesoderm from the very early developmental stage [34,35]. In the present study, increased frequency of cardiomyogenic differentiation of 9-15c cells was successfully achieved in vitro by forced expression of *Csx/Nkx2.5* and *GATA4*. These results are consistent with a report showing that both *Csx/Nkx2.5* and *GATA4* are required for the cardiac differentiation of P19CL6 cells derived from embryonic teratocarcinoma cells [36]. Cardiomyogenic differentiation, however, could proceed only after treatment with 5-azacytidine in our experimental setting, implying that *Csx/Nkx2.5* and *GATA4* are required but not sufficient for cardiac differentiation. Unknown factors

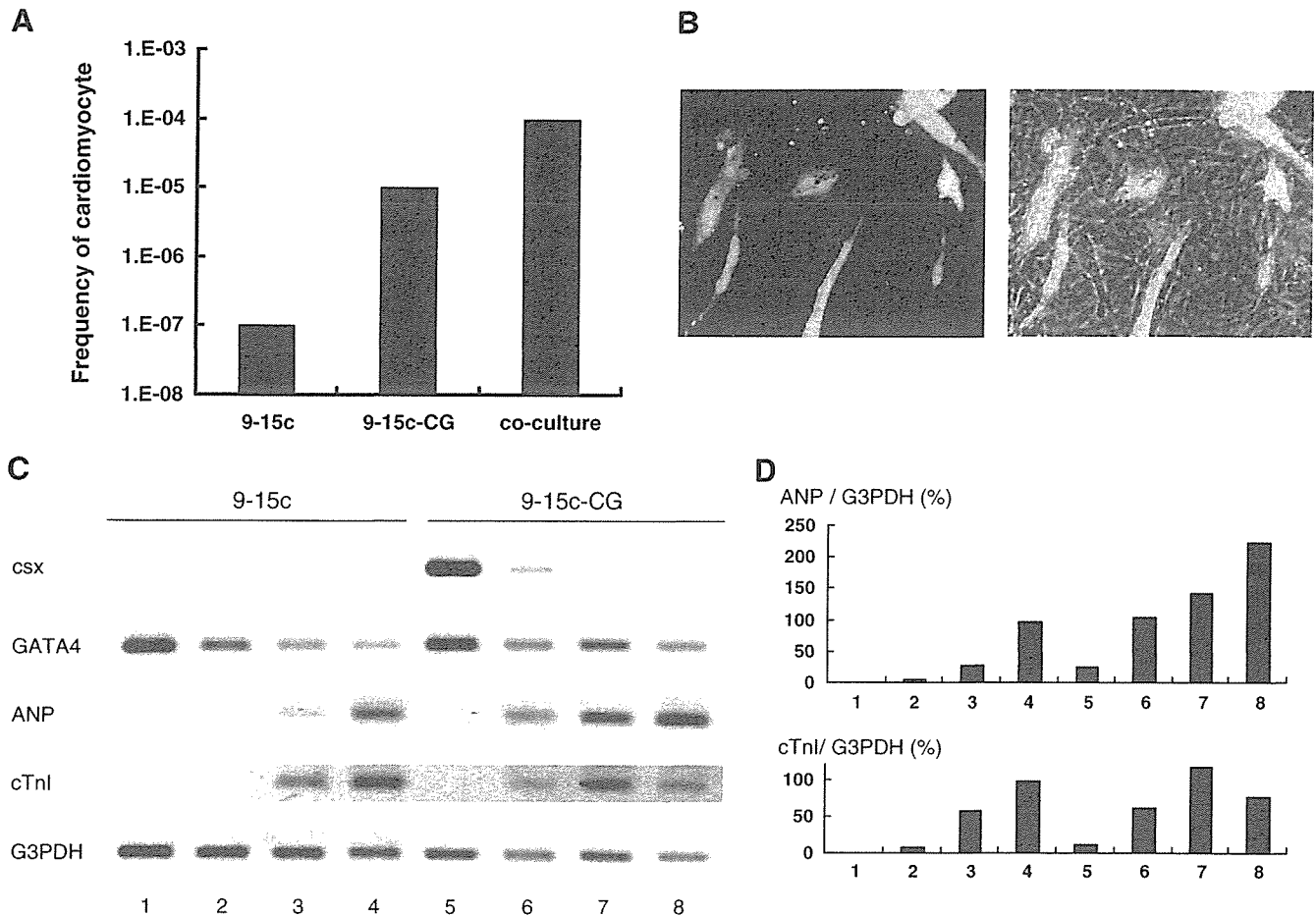


Fig. 5 – Enhancement of cardiomyogenic differentiation of 9-15c cells by co-cultivation with murine fetal cardiomyocytes.
A: Frequencies of cardiomyogenic differentiation in 9-15c cells, 9-15c cells overexpressing the *Csx* and *GATA4* genes (9-15c-CG cells), and 9-15c-CG cells co-cultured with murine fetal cardiomyocytes. **B:** Cardiomyogenic differentiation of EGFP-positive 9-15c-CG cells co-cultured with murine fetal cardiomyocytes. Left: Green fluorescence of EGFP-positive 9-15c-CG cells. Right: Same field visualized by phase-contrast microscopy merged with fluorescence image. **C:** RT-PCR analysis of the *Csx*, *GATA4*, *ANP*, *cTnI* and *G3PDH* genes in 9-15c cells (lanes 1–4) and 9-15c-CG cells (lanes 5–8). 9-15c cells (lane 1) and 9-15c-CG cells (lane 5) were cultured with exposure to 5-azacytidine alone (lanes 2 and 6) or 5-azacytidine and conditioned medium of cardiomyocyte cultures (lanes 3 and 7), or 5-azacytidine, conditioned medium of cardiomyocyte cultures, PDGF, retinoic acid, and fibronectin coating on a dish (lanes 4 and 8) for 4 weeks. **D:** Ratio mRNA expression level of *ANP* and *cTnI* to *G3PDH* in C. The mRNA level of 9-15c cells (lane 4) was regarded as equal to 100%.

induced by 5-azacytidine or microRNAs, whose key roles in stem cell biology are just emerging [37], also seem to be needed.

Adipogenic 3T3-L1 [38], osteogenic MC3T3-E1 [39], and chondrogenic ATDC5 cells [40] have been isolated from stem cells with a mesenchymal nature. In addition, cardiomyogenic precursors may be obtained from stem cells such as cardiac stem cells, embryonic stem cells, and mesenchymal stem cells. Fetal cardiomyocytes are differentiated cardiomyocytes, but not stem cells that can proliferate *in vitro*. Recently, cardiac stem cells capable of clonogenically self-renewing have been isolated from the adult heart [41–43]. Some cardiac stem cells also retain plasticity. The retention of plasticity, i.e., the ability to transdifferentiate into skeletal myocytes and endothelium, of 9-15c cells overexpressing *Csx/Nkx2.5* and *GATA4* supports the idea that these cells may be considered cardiac stem or amplifying cells in terms of differentiation and

self-renewal. On the other hand, *Csx/Nkx2.5* inhibits the myogenic differentiation of C2C12 cells and promotes neuronal differentiation [44]. This unexpected effect of *Csx/Nkx2.5* may be due to differential effects of the gene in different cell types, or of transient versus constitutive expression of the infected gene; dependency of the differentiated phenotypes on the gene expression period is observed for the Notch gene [45,46] and *noggin* gene [47].

Cell transplantation has been attempted to improve cardiac function in severe heart failure; MSCs have been transplanted to functionally restore damaged or diseased tissue in animal models, and mononuclear cells or myoblasts have been injected into ischemic hearts clinically. MSCs are capable of differentiating into many types of cells, and 'cardiomyogenic master genes' are able to enhance the commitment or determine the path to cardiomyogenic differentiation of these MSCs. The stemness of MSCs determined by single-cell

marking in this study needs to be taken into consideration when we are considering mesenchymal stem cell-based therapy: we should pay attention to the possible unexpected differentiation of donor MSCs such as osteogenesis or chondrogenesis in the implanted heart.

In conclusion, we demonstrated that cardiomyocytes were stochastically differentiated from MSCs and that forced expression of *Csx/Nkx2.5* and *GATA4* enhanced the commitment or determined the path to cardiogenic differentiation of these MSCs. Our findings suggest that single-cell-derived MSCs overexpressing *Csx/Nkx2.5* and *GATA4* behave like cardiac transient amplifying cells and that *Csx/Nkx2.5* and *GATA4* could be interesting target molecules for enhancing cardiogenesis of MSCs.

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Review Article

Two MSCs: Marrow stromal cells and mesenchymal stem cells

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Marrow stromal cells (MSC1) are able to generate a series of terminally-differentiated cells *in vitro*. Most experiments are performed with heterogeneous stromal cells obtained by adherence to plastic culture dishes. Since bone marrow-derived stromal cells are purified to a homogeneous population meeting the criteria for non-hematopoietic stem cells, these cells have been termed “mesenchymal stem cells” and have the capability of generating an array of cells. However, “mesenchymal stem cells” (MSC2) are also actual multi-purpose cells capable of differentiating into cells of mesoderm-origin regardless of cell sources. MSC2 can be recovered from a variety of other tissues, such as fat, muscle, menstrual blood, endometrium, placenta, umbilical cord, cord blood, skin, and eye. The terms “mesenchymal stem cell” and “marrow stromal cell” have been used interchangeably in emerging literature to describe cells that can be used in regenerative medicine, thereby introducing a degree of confusion. In this review, we re-organize the understanding of the two MSCs, describe their biology and differentiate between the two.

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Introduction

Two MSCs, i.e., marrow stromal cells (MSC1) and mesenchymal stem cells (MSC2), are attracting a great deal of attention, as they represent a valuable source of cells for use in regenerative medicine, as well as offering an excellent model of cell differentiation in biology. However, confusion exists in the literature due to poor application or misuse of the terms and nomenclature.

In general, mesenchymal stem cells are multi-potential stem cells that can differentiate into a variety of cell types (ref. [\[en.wikipedia.org/wiki/Mesenchymal_stem_cell\]\(http://en.wikipedia.org/wiki/Mesenchymal_stem_cell\)\). They have been shown to differentiate, *in vitro* or *in vivo*, into osteoblasts, chondrocytes, myocytes, adipocytes and neuronal cell among others. Mesenchymal stem cells have traditionally been obtained from bone marrow, and have commonly been referred to as “marrow stromal cells” \(MSC1\).](http://</p></div><div data-bbox=)

While the terms “marrow stromal cell” (or “stromal cell”) and “mesenchymal stem cell” have frequently been used interchangeably, they are increasingly recognized as separate entities as:

1. Stromal cells (MSC1) are a highly-heterogenous cell population, usually derived from bone marrow, consisting of multiple cell types with different potentials for proliferation and differentiation.

2. Mesenchymal stem cells (MSC2) encompass cells derived from other non-marrow tissues, such as fat, muscle, menstrual blood, endometrium, placenta, umbilical cord, cord blood, skin, and eye.

Bone marrow-derived mesenchymal stem cells or bone marrow stromal cells (MSC1) were discovered by Friedenstein in 1976, who described clonal, plastic-adherent cells from bone marrow that were capable of differentiating into osteoblasts, adipocytes, and chondrocytes. More recently, investigators have demonstrated that mesenchymal stem cells (MSC2) *per se* can be recovered from a variety of adult tissues and have the capacity to differentiate into a variety of specialist cell types. This review describes the recent advances in understanding of the two MSC cells, their biology and ongoing investigation and use.

Somatic stem cells

Somatic stem cells have been identified in hematopoietic¹⁾, hepatic²⁾, epidermal³⁾, gastrointestinal⁴⁾, neural^{5,6)}, muscle⁶⁾, and bone marrow⁶⁻⁸⁾ tissues. Many researchers have since demonstrated the developmental pluripotency of these cells. Bone marrow-derived stem cells can be transdifferentiated into multilineage cells, such as muscle⁹⁾ of mesoderm, lung¹⁰⁾ and liver^{10,11)} of endoderm, and brain¹²⁻¹⁵⁾ and skin¹⁰⁾ of ectoderm. Somatic stem cells are more desirable than embryonic stem (ES) cells for cell therapeutics because of ethical considerations and the possible immunologic rejection of ES cells. Mesenchymal stem cells have become the most popular somatic stem cells in medicine and biology, not least because of their high reproductive capability *in vitro*.

Bone marrow stromal cells (MSC1)

The existence of non-hematopoietic cells in bone marrow was first suggested by Cohnheim about 130 years ago¹⁶⁾. Bone marrow-derived stromal cells (MSC1) can differentiate into most somatic cells, including osteoblasts, chondrocytes, myoblasts, cardiomyocytes¹⁷⁻²¹⁾, and adipocytes, when placed in appropriate *in vitro*²⁰⁾ and *in vivo* environments²²⁾, and thus are a useful cell source for regenerative medicine²³⁾. Recent studies suggest that MSC1 can also differentiate into a neuronal lineage²⁴⁾, and murine bone marrow-derived adult progenitor cells can differentiate into dopaminergic neuronal cells^{25,26)}. Since the use of MSC1 entails no ethical or immunological problems, and bone

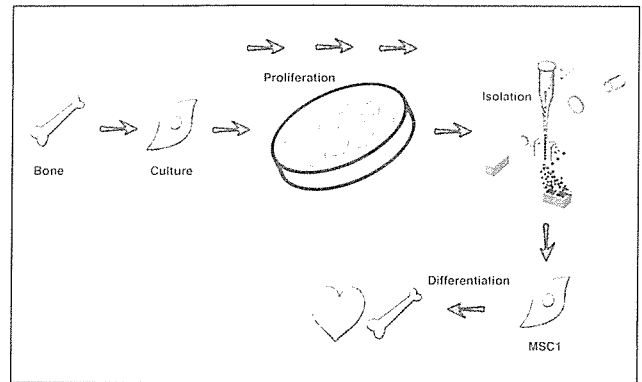


Fig.1 Development and differentiation of mesenchymal stem cells derived from bone marrow

marrow aspiration is an established routine procedure, these cells provide a useful and almost routine source of material for transplantation and tissue repair or regeneration (Fig.1).

1) Osteogenesis

KUSA-A1 cells, a murine marrow stromal cell line, are capable of generating mature bone *in vivo*²⁷⁾. They are a unique, mature osteoblast cell line and serve as a very suitable model for *in vivo* osteogenesis. Bone forms in subcutaneous tissue after subcutaneous injection of the cells into mice. The osteogenesis by KUSA-A1 is not mediated by chondrogenesis and thus is considered to be membranous ossification. Follow-up study on the fate of bone by immortalized osteoblasts shows that the ectopically-generated bone keeps its size and shape for 12 months²¹⁾. Furthermore, the implanted cells do not metastasize like tumor cells. These unique characteristics of KUSA-A1 cells provide an opportunity to analyze the process of membranous ossification in detail.

2) Chondrogenesis

Chondrocytes differentiate from mesenchymal cells during embryonic development²⁸⁾ and the phenotype of the differentiated chondrocyte is characterized by the synthesis, deposition, and maintenance of cartilage-specific extracellular matrix molecules, including type II collagen and aggrecan²⁹⁻³¹⁾. The phenotype of differentiated chondrocytes is rapidly lost since it is unstable in culture³²⁻³⁵⁾. This process is referred to as "dedifferentiation" and is a major impediment to use of mass cell populations for therapy or tissue engineering of damaged cartilage. When isolated chondrocytes are cultured in a monolayer at low density, the typical round chondrocytes morphologically transform into flattened fibroblast-like cells, with profound changes in biochemical and genetic characteristics, including reduced synthesis of type II collagen and cartilage proteins³⁶⁾. When cultured