

Collection and Culture of Alveolar Bone Marrow Multipotent Mesenchymal Stromal Cells From Older Individuals

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ABSTRACT

In this work, we examined the culture condition of alveolar bone marrow multipotent mesenchymal stromal cells (ABMMSCs), aiming to apply regenerative therapy to older periodontitis patients. To better understand the character of cultured cells from alveolar bone marrow, the expression profiles of well-known genes and their responses to the induction of osteogenic, chondrogenic, or adipogenic differentiation were examined. Using α MEM-based culture, ABMMSCs could be obtained from older individuals than in previous reports. Interestingly, ABMMSCs expressing Klf4 were able to differentiate into osteoblasts. The prediction of differentiation potential by Klf4 could be a useful guide for further improvement of the culture conditions required to culture ABMMSCs derived from older individuals. *J. Cell. Biochem.* 107: 1198–1204, 2009. © 2009 Wiley-Liss, Inc.

KEY WORDS: REGENERATIVE MEDICINE; ORAL; ALVEOLAR; BONE MARROW; STROMA; OLDER INDIVIDUALS

The choice of stem cell source is a matter of great importance because it directly influences the success of regenerative therapy. While various stem cell sources have been reported [Barrilleaux et al., 2006; Bjerknes and Cheng, 2006; Dominici et al., 2006; Burke et al., 2007; Yu et al., 2008], iliac bone marrow [Matsubara et al., 2005], alveolar bone marrow [Matsubara et al., 2005], dental pulp [Gronthos et al., 2000], and periodontal ligament [Seo et al., 2004] have been examined as stem cells for oral regenerative therapy. Alveolar bone marrow is a realistic candidate because tooth extraction is needed to obtain stem cells from dental pulp and the periodontal ligament. In a previous report, the success of the human alveolar bone marrow multipotent mesenchymal

stromal cells (ABMMSCs) culture was relatively limited to young patients [Matsubara et al., 2005].

In this study, we examined the culture condition of ABMMSCs, aiming to apply regenerative therapy to older periodontitis patients. To better understand the character of ABMMSCs, the expression profiles of well-known genes associated with the maintenance of undifferentiated embryonic stem cells [Ulloa-Montoya et al., 2007; Jiang et al., 2008], and associated with the induction of pluripotent stem cells from somatic cells [Takahashi et al., 2007], osteogenesis [Song and Tuan, 2004; Delorme et al., 2008; Ogata, 2008], chondrogenesis [Song and Tuan, 2004; Delorme et al., 2008], and adipogenesis [Song and Tuan, 2004; Delorme et al., 2008] were

Abbreviations Used: ABMMSCs, alveolar bone marrow multipotent mesenchymal stromal cells; BSP, bone sialoprotein; ESCs, embryonic stem cells; FGF2, fibroblast growth factor 2; IBMMSCs, iliac bone marrow multipotent mesenchymal stromal cells; MAPK, mitogen-activated protein kinase; MSCs, mesenchymal stem cells; α -MEM, α -minimum essential medium; Runx2, runt homeodomain protein 2; SMC, smooth muscle cell.

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investigated. Their responses to the induction of osteogenic, chondrogenic and adipogenic differentiation were also examined.

METHODS

MATERIALS

Dulbecco's modified Eagle's medium (DMEM), Alpha minimum essential medium (α MEM), fetal calf serum (FCS), penicillin and streptomycin, and TrypLETM Express were obtained from Invitrogen (Carlsbad, CA). Fibroblast growth factor 2 (FGF2) was obtained from Sigma-Aldrich (St. Louis, MO).

CELL PREPARATION

The use of all tissue was approved by the Committee on the Use of Human Subjects in Research at Nihon University School of Dentistry at Matsudo (EC03-046 and EC04-001). Human iliac bone marrow multipotent mesenchymal stromal cells (IBMMSCs) were purchased from Cambrex Bio Science (Cat. No.2M-125C) (Walkersville, MD). Cryopreserved samples of IBMMSCs were thawed rapidly in a 37°C water bath, suspended in DMEM or α MEM containing 10% FCS, and plated at a seeding density of approximately 4×10^4 cells/cm². Alveolar bone marrow aspirates were obtained from patients for dental implant treatment. Aspirates were suspended in α MEM and plated at a seeding density of approximately $3.7\text{--}6.2 \times 10^3$ white blood cells/cm² (details shown in Table II). Cells were left undisturbed for 3–9 days until they adhered to culture dishes, excluding the addition of 3 ng/ml FGF2 from day 6 of culture. Medium containing 3 ng/ml FGF2 was then replaced with fresh medium at 3-day intervals. Passages were performed when cells became subconfluent, and cell numbers and population doublings were measured throughout the culture period.

MTT ASSAY

IBMMSCs suspended in DMEM, DMEM supplemented with 40 μ g/ml L-proline and 50 μ g/ml ascorbic acid, or α MEM were plated in sextuplicate at a density of 9.6×10^4 cell/well in 24-well plate (BD Biosciences, San Jose, CA). On day 10, culture medium and non-adherent cells were washed off, MTT (1 mg/ml) was added to each well, and the 24-well plate was incubated for 4 h. The cells were treated with lysis solution (50% dimethylformamide, 20% SDS) and incubated for 2 h. The degree of MTT reduction in each sample was assessed by measuring absorption at 570 nm.

REVERSE TRANSCRIPTION POLYMERASE CHAIN REACTION (RT-PCR)

Total RNAs were extracted from IBMMSCs and ABMMSCs (passage 5–6) using guanidine thiocyanate as described previously [Ogata et al., 1997, 2000]. RT-PCR was carried out with a SuperScript III One-Step RT-PCR system with Platinum Taq High Fidelity (Invitrogen) in a 50 μ l mixture containing 0.1 μ g total RNA, 0.2 μ M of the primer sets (Table I) and 2 \times Reaction Mix according to the manufacturer's instructions. The cycling condition was 1 cycle (cDNA synthesis at 50°C for 30 min, RTase inactivation and pre-denaturation at 94°C for 2 min), 35 cycles (denaturation at 94°C for 30 s, annealing at 55°C for 30 s and extension at 72°C for 30 s) and 1 cycle (final extension at 72°C for 10 min). PCR products were separated by 2% agarose gel and visualized under ultraviolet illumination after ethidium bromide staining.

REAL-TIME PCR

Total RNA (1 μ g) was used as a template for cDNA synthesis. cDNA was prepared using an EXScript RT Reagent Kit. Quantitative real-time PCR was performed using human Runx2, Osterix, Klf4, and GAPDH primer sets (Table I) using the SYBR Premix EX Taq in a

TABLE I. Details for Surveyed Genes and the Primer Pairs for Their Amplification

| Gene symbol | Entrez gene ID | Gene official full name | Primer pairs |
|---------------|----------------|---|---|
| GAPDH | 2597 | Glyceraldehyde-3-phosphate dehydrogenase | Fwd: GCACCGTCAAGGCTGAGAAC Rev: ATGGTGGTGAAGACGCCAGT |
| POU5F1 | 5460 | POU class 5 homeobox 1 | Fwd: GCAATTGCGCAAGCTCCTGAA Rev: AAGCTAAGCTGCAGAGCCTCAAAG |
| SOX2 | 6657 | SRY (sex determining region Y)-box 2 | Fwd: GTGAGCGCCTGCAGTACAA Rev: GCTGCGAGTAGGACATGCTGTAG |
| NANOG | 79923 | Nanog homeobox | Fwd: CAACTGGCCGAAGAATAGCAATG Rev: TGGTTGCTCCAGGTTGAATTGTT |
| KLF4 | 9314 | Kruppel-like factor 4 (gut) | Fwd: AAGAGTTCCCATCTCAAGGCACA Rev: GGGCGAATTTCCATCCACAG |
| MYC | 4609 | v-Myc myelocytomatosis viral oncogene homolog (avian) | Fwd: CGGATTCCTGCTCTCCTCGAC Rev: CCTCCAGCAGAAGGTGATCCA |
| BSP | 3381 | Integrin-binding sialoprotein | Fwd: CTGGCACAGGGTATACAGGGTATG Rev: ACTGGTGCCTTTATGCCTTG |
| RUNX2 | 860 | Runt-related transcription factor 2 | Fwd: ATGTGTGTTTGTTCAGCAGCA Rev: TCCCTAAAGTCACTCGGTATGIGTA |
| OSTERIX | 121340 | Sp7 transcription factor | Fwd: GCCATTCCTGGGCTTGGGTATC Rev: GAAGCCGGAGTGCAGGTATCA |
| FGF4 | 2249 | Fibroblast growth factor 4 | Fwd: GAGCGCAAGGGCAAGCTCTA Rev: ACCTTCATGGTGGGGCGACA |
| PPAR γ | 5468 | Peroxisome proliferator-activated receptor gamma | Fwd: TGGAATTAGATGACAGCGACTTGG Rev: CTGGAGCAGCTTGGCAAACA |
| SOX9 | 6662 | SRY (sex determining region Y)-box 9 | Fwd: TGTATCACTGAGTCATTTGCAGTGT Rev: AAGGTCTGTGCTGAGTGGGCTGAT |
| GDF3 | 9573 | Growth differentiation factor 3 | Fwd: GTACTTCGCTTCTCCAGACCAA Rev: CCTTCTTTGATGGCAGCAGGTT |
| TERT | 7015 | Telomerase reverse transcriptase | Fwd: TGTGCTACGGCGACATGGA Rev: GAGGTGAGGTGTACCAACAAGAA |

TP800 thermal cycler dice real-time system (Takara, Tokyo, Japan). Amplification was performed in 25 μ l final volume containing 2 \times SYBR Premix EX Taq (12.5 μ l), 0.2 μ M forward and reverse primers (0.1 μ l) and 25 ng cDNA (2.5 μ l) for Klf4, Runx2 and 10 ng (1.0 μ l) cDNA for GAPDH. To reduce variability between replicates, PCR premixes, which contained all reagents except for cDNA, were prepared and aliquoted into 0.2 ml Hi-8-tubes (Takara). The thermal cycling conditions were 1 cycle at 95°C for 10 s, 40 cycles at 95°C for 5 s, and 60°C for 30 s. Post-PCR melting curves confirmed the specificity of single-target amplification and fold expressions relative to GAPDH were determined in quadruplicate.

INDUCTION OF OSTEOGENESIS, CHONDROGENESIS, AND ADIPOGENESIS

Osteogenic, chondrogenic, or adipogenic differentiation was induced in cells at passage 5–6 with a Human Mesenchymal Stem Cell Functional Identification Kit (R&D Systems) according to the manufacturer's instructions. Cells were cultured for 21 days in induction medium (Osteogenic; α MED containing 10% FCS, dexamethasone, ascorbate-phosphate and β -glycerolphosphate, Chondrogenic; α MED containing insulin, transferrin, selenious acid, bovine serum albumin, linoleic acid, dexamethasone, ascorbate-phosphate, proline, pyruvate, and TGF- β 3, Adipogenic; α MED containing 10% FCS, hydrocortisone, isobutylmethylxanthine and indomethacin. R&D Systems did not reveal the concentration of drugs in the media). In this period, induction medium was replaced with fresh medium every 3 days. On the 21st day of induction, the cultures were washed with PBS, fixed for 10 min in 4% buffered paraformaldehyde at room temperature and stained with Alizarin Red for osteogenic cells or Oil Red-O for adipogenic cells. For chondrogenic cells, cultures were fixed with 100% ethanol for 10 min at room temperature and stained with Alcian Blue.

STATISTICAL ANALYSIS

MTT light absorption data were analyzed using one-way analysis of variance followed by Bonferroni's multiple *t* tests.

RESULTS

DMEM needed 36 days to expand 4.5×10^6 IBMMSCs to 2.0×10^7 cells. α MED needed only 15 days to expand 1.0×10^7 IBMMSCs to 2.2×10^7 cells. IBMMSCs cultured with DMEM (I-D) were flatter and larger (Fig. 1a) than IBMMSCs cultured with α MED (I- α), which were small and clear (Fig. 1b). IBMMSCs cultured with DMEM supplemented with L-proline and ascorbic acid showed a significantly higher MTT value than those cultured with DMEM ($P < 0.01$), and those cultured with α MED had the highest MTT value ($P < 0.01$) (Fig. 1c).

Three alveolar bone marrow specimens collected from separate individuals were cultured. The details of initial data for each aspirated specimen are shown in Table II. Figure 2 shows population doubling per colony of ABMMSCs in each specimen, and doubling time in the logarithmic phase was approximately 36 h.

Figure 3 shows the results of RT-PCR using I-D, I- α , and ABMMSCs (A-1, A-2, and A-3) cultured with α MED. Remarkably

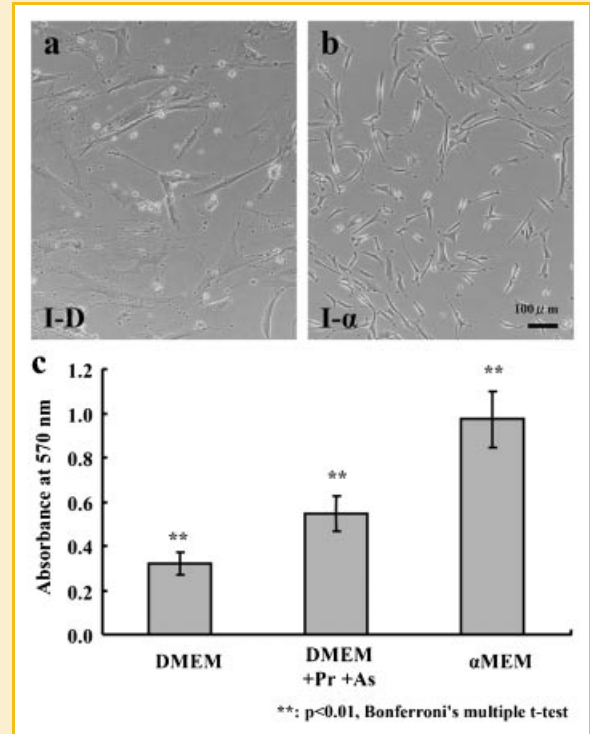


Fig. 1. Phase-contrast micrograph of iliac bone marrow multipotent mesenchymal stromal cells (IBMMSCs) cultured with (a) DMEM (I-D) and (b) α MED (I- α). Two or more days were necessary for DMEM to produce equal numbers of cells compared with α MED, and I-D was flatter and larger than I- α , which was small and clear. c: Difference in the number of primary cultured IBMMSCs among DMEM, DMEM supplemented with L-proline and ascorbic acid (DMEM + Pr + As), and α MED. Significantly more IBMMSCs were cultured with DMEM + Pr + As than with DMEM ($P < 0.01$), and significantly more α MED were cultured than the others ($P < 0.01$).

weak Nanog, c-Myc, bone sialoprotein (BSP) and Runx2, and lack of Klf4 gene expression in I-D. I- α and A-2 showed almost the same tendencies in all examined gene expressions except for Osterix. Weak c-Myc, BSP, Runx2, and Osterix gene expressions in A-1, and weak gene expression of Klf4, c-Myc, and BSP in A-3 were distinct. All specimens expressed POU5F1 and Sox2 at almost the same level, and did not express FGF4, PPAR γ , Sox9, GDF3, and TERT. Quantitative real-time PCR was performed using human Runx2,

TABLE II. Detail Data for Primarily Cultured Alveolar Bone Marrow Aspirates

| | Patient 1 | Patient 2 | Patient 3 |
|--|-------------------|-------------------|-------------------|
| Age | 62 | 57 | 57 |
| Sex | Female | Male | Female |
| Aspirated sample volume (μ l) | 250 | 400 | 30 |
| Total number of red blood cells | 1.2×10^8 | 9.8×10^7 | 9.8×10^7 |
| Total number of white blood cells | 1.2×10^5 | 1.7×10^5 | 9.1×10^4 |
| WBC/RBC | 1/1,000 | 1/578 | 1/1,081 |
| Seeded sample volume (μ l) | 125 | 227 | 30 |
| Seeded sample concentration (WBC/cm ²) | 6.2×10^3 | 3.7×10^3 | 4.6×10^3 |
| Number of colony (day 12) | 5 | 10 | 35 |
| Name of MSCs | ABMMSCs1 | ABMMSCs2 | ABMMSCs3 |

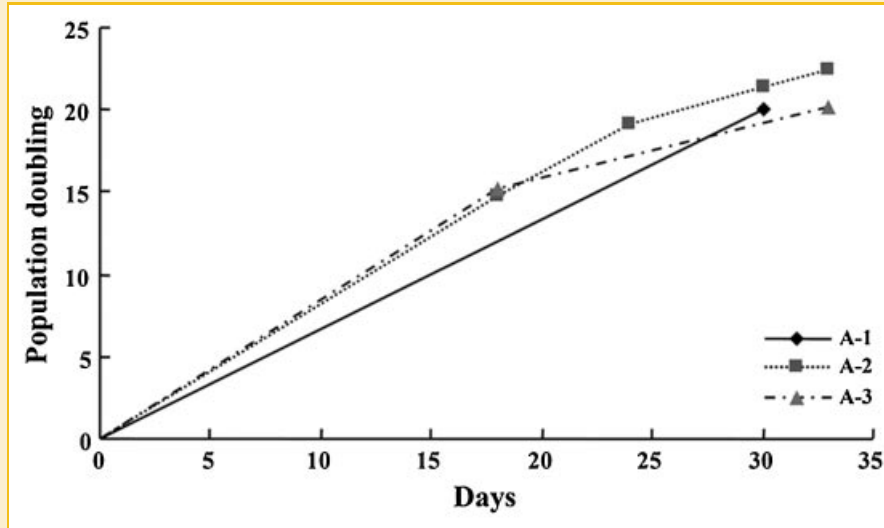


Fig. 2. Population doubling of alveolar bone marrow multipotent mesenchymal stromal cells cultured with α MEM (ABMMSCs- α) in each specimen. Vertical axis indicates base 2 logarithms of accumulated ABMMSCs- α numbers per colony, and horizontal axis indicates days of culture. All cases needed 1 month for ABMMSCs- α to expand up to 2^{20} (approximately 10^6) cells. ABMMSCs- α doubled every approximately 36 h. A-1, A-2, and A-3: ABMMSCs- α from patient 1, 2, and 3.

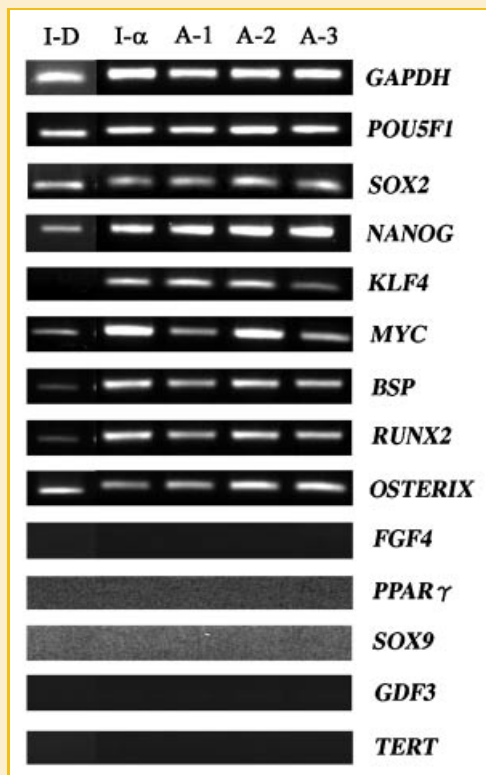


Fig. 3. Gene expression of IBMMSCs cultured with DMEM (I-D) and with α MEM (I- α), and ABMMSCs- α (A-1, A-2, A-3). Each gene was amplified with RT-PCR, and PCR products were separated by agarose gel electrophoresis and visualized under ultraviolet illumination after ethidium bromide staining. Lack of KLF4 gene expression in I-D, remarkably weak c-Myc, BSP, and Runx2 gene expression in A-1, weak gene expression of KLF4, c-Myc, and BSP in A-3.

Osterix, Klf4, and GAPDH primer sets to determine the exact levels of Klf4, Runx2, and Osterix gene expression in these cells. Results of real-time PCR were almost same as RT-PCR (Fig. 4).

Figure 5 shows the response of I-D, I- α , and ABMMSCs to the induction of osteogenic, chondrogenic and adipogenic differentiation. Osteogenic differentiation was strongly induced in I- α and A-1, moderately in A-2, slightly in A-3, and was not induced in I-D. Chondrogenic differentiations were induced in all specimens. Adipogenic differentiations were strongly induced in I- α and A-2, and slightly in A-1 and A-3.

DISCUSSION

Using an α MEM-based culture, ABMMSCs could be obtained from older individuals than in the previous report [Matsubara et al., 2005], and only the medium composition was different from the above report, in which DMEM had been used. In the IBMMSC culture, two or more days were necessary for DMEM to produce equal numbers of cells to α MEM, and moreover, IBMMSCs cultured with DMEM seemed to have the characteristic shape of extremely aged cells (Fig. 1a). DMEM could be a severe culture environment for cells from older individuals.

DMEM contains ferric nitrate and α MEM contains several kinds of amino acids, vitamins, lipoid acids and nucleic acids. The contribution of collagen to the adhesion of cells to the culture dish is expected because the addition of essential components (L-proline and ascorbic acid) for collagen production to DMEM significantly increased primary-cultured IBMMSCs (Fig. 1c). In addition, this was not due to radical-scavenger and reduction efficacy by ascorbic acid (data not shown). It has already been reported that integrin-mediated signaling prevented the anoikis of mesenchymal stem cells (MSCs) [Benoit et al., 2007] and also contributed to MSC survival

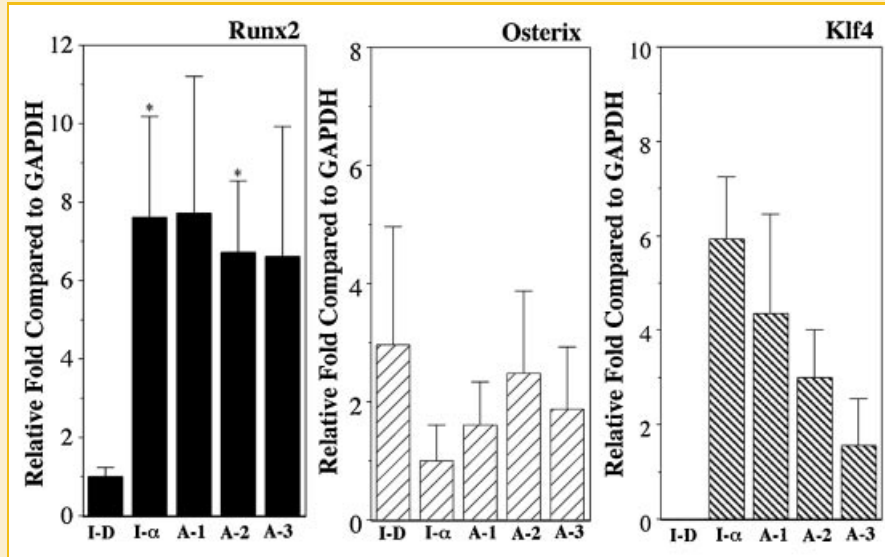


Fig. 4. The expressions of Runx2, Osterix, Klf4, and GAPDH mRNA in the cells were measured by real-time PCR. The relative amounts of mRNA of Runx2, Osterix and Klf4 to GAPDH were calculated. The experiments were performed in quadruplicate for each data point. Quantitative analyses of the quadruplicate data sets are shown with standard errors. Significant differences from control: * $P < 0.1$.

[Song et al., 2007]. Such a mechanism might have functioned in our experiment. Furthermore, the efficacy remained unclear, because significantly more cells were cultured with α MEM than with DMEM. The supportive culture environment due to such efficacies might have enabled the culture of ABMMSCs from older individuals, but further study aiming at a more supportive culture condition is required because there is still room for improvement.

Some tendencies in the gene expression profile and in the response to the induction of differentiation are described as follows. The transcription factors associated with the maintenance of embryonic stem cells (ESCs) undifferentiated state (POU5F1, Sox2, and Nanog) were expressed similarly in all cells, while other ESC-associated genes (TERT and GDF3) were not expressed in all cells. The transcription factors crucial for osteogenesis (Runx2 and Osterix) were expressed in all cells, while adipogenesis-associated PPAR γ and chondrogenesis-associated Sox9 were not expressed in all cells. The details are still unclear, although the above-mentioned gene expressions have been reported in MSCs cultured under various conditions, such as FGF2-containing medium [Song and Tuan, 2004; Alexanian, 2007; Battula et al., 2007; Isenmann et al., 2007; Roche et al., 2007; Ulloa-Montoya et al., 2007; Delorme et al., 2008]. In our culture condition, these genes did not seem to predict the differentiation potential of the cells. FGF4 is known as a soluble factor essential for trophoblast stem cell self-renewal [Niwa et al., 2000]. In adult tissues, FGF4 is locally and specifically expressed in the brain and testis [Yamamoto et al., 2000], regulates neural progenitor cell (NPC) proliferation and neuronal differentiation [Kosaka et al., 2006], and induces spermatogenesis and prevents adriamycin-induced testicular toxicity [Yamamoto et al., 2002]; however FGF4 was not expressed in all cells. c-Myc and BSP tend to be strongly expressed in IBMMSCs cultured with α MEM (I- α) and in ABMMSCs-2 cultured with α MEM (A-2) than in others. The expression of c-Myc promotes normal cell proliferation

[Skaletz-Rorowski et al., 1999] and is found in undifferentiated MSCs [Mugrauer and Ekblom, 1991], although it is up-regulated as a symptom of transformation in senescent MSCs [Rubio et al., 2008]. BSP is non-collagenous protein that has multiple functions, including bone mineralization, and is a major component of mineralized connective tissues [Ogata, 2008]. Both c-Myc and BSP are activated by FGF2 stimulation via the mitogen-activated protein kinase (MAPK) pathway [Skaletz-Rorowski et al., 1999; Shimizu-Sasaki et al., 2001; Shimizu et al., 2006], and the observed similarity of these gene expression tendencies in each sample would be a reflection of the status of MAPK.

In recent years, Klf4 has been focused on as an essential transcription factor for the induction of pluripotent stem cells from somatic cells [Takahashi et al., 2007]. Klf4 binds to GT-rich or CACCC elements on the target gene, forms a complex with histone acetyltransferase or histone deacetylase, and regulates the target gene expression by modulating the chromatin structure in the neighborhood [Evans et al., 2007]. This gene stabilizes the ESC undifferentiated state cooperatively with Klf2 and Klf5, and contributes to the expression of ESC-specific genes [Jiang et al., 2008]. Klf4 also plays an important role in smooth muscle cell (SMC) dedifferentiation in injured blood vessels. c-fos and SMC-specific genes have CARG elements in their promoter region. Usually, the SMC phenotype is maintained by activation of the above genes due to serum response factor binding to the CARG element. The Klf4 binding site exists near the CARG element, and SMC dedifferentiation is induced by gene repression caused by Klf4 binding to CARG box after injury [McDonald et al., 2006; Kawai-Kowase and Owens, 2007]. Klf4 is closely related to the undifferentiated state, and dedifferentiation as described above functions as a tumor suppressor in somatic cells via p21^{cip1/kip1} pathway-dependent cell-cycle arrest when its own DNA is damaged [Ghaleb et al., 2005; McConnell et al., 2007]. Moreover, an important transcription factor for the

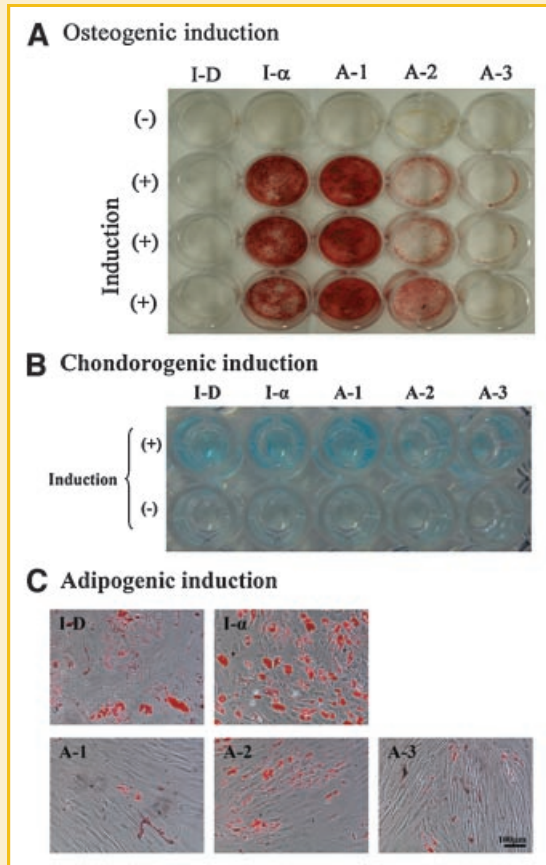


Fig. 5. Response of IBMMSCs cultured with DMEM (I-D) and with α MEM (I- α), and ABMMSCs- α (A-1, A-2, A-3) to induction of (A) osteogenic, (B) chondrogenic and (C) adipogenic differentiation. Osteogenic differentiation (triplicate) was strongly induced in I- α and A-1, moderately in A-2, slightly in A-3, and not in D-I. Chondrogenic differentiation was induced in all specimens. Adipogenic differentiation was strongly induced in I- α and A-2, and slightly in A-1 and A-3. Remarkably, IBMMSCs cultured with α MEM (I- α) and ABMMSCs- α expressing Klf4 (I- α , A-1, A-2, and A-3) were able to differentiate into osteogenic cells (see Fig. 3).

differentiation of osteoblasts, activator protein 1, is regulated by c-fos [Zayzafoon et al., 2005], which is repressed by Klf4 [McDonald et al., 2006; Kawai-Kowase and Owens, 2007]. We hypothesize that MSCs strongly expressing Klf4 were able to differentiate into osteoblasts and form bone nodules. In other words, there is a possibility that Klf4 predicts the osteogenic differentiation of MSCs.

In conclusion, α MEM is more advantageous than DMEM in the primary culture of ABMMSCs. The prediction of differentiation potential by Klf4 might become a useful guide for further improvement of the culture conditions required to culture ABMMSCs derived from older individuals.

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