

## Original Paper

# Rapid Induction of Osteogenic Markers in Mesenchymal Stem Cells by Adipose-Derived Stromal Vascular Fraction Cells

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## Key Words

Adipose-derived stromal vascular fraction cells • Bone marrow-derived mesenchymal stem cells • Osteogenesis • Transforming growth factor beta • Bone morphogenetic protein 2 • Co-culture system

## Abstract

**Background/Aims:** Stromal vascular fraction (SVF) cells are a mixed cell population, and their regenerative capacity has been validated in various therapeutic models. The purpose of this study was to investigate the regenerative mechanisms utilized by implanted SVF cells. Using an *in vitro* co-culture system, we sought to determine whether SVF implantation into impaired tissue affects endogenous mesenchymal stem cell (MSC) differentiation; MSCs can differentiate into a variety of cell types, and they have a strong regenerative capacity despite their low numbers in impaired tissue. **Methods:** Adipose-derived SVF cells obtained from four donors were co-cultured with bone marrow-derived MSCs, and the differential expression of osteogenic markers and osteogenic differentiation inducers over time was analyzed in mono-cultured MSCs and MSCs co-cultured with SVF cells. **Results:** The co-cultivation of MSCs with SVF cells significantly and mutually induced the expression of osteogenic-specific markers via paracrine and/or autocrine regulation but did not induce adipocyte, chondrocyte or myoblast marker expression. More surprisingly, subsequent osteogenesis and/or comparable effects were rapidly induced within 48 h. **Conclusion:** To the best of our knowledge, this is the first study in which osteogenesis and/or comparable effects were rapidly induced in bone marrow-

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derived MSCs and adipose-derived SVF cells through co-cultivation. Our findings suggest that the positive effects of SVF implantation into impaired bone may be attributed to the rapid induction of MSC osteogenesis, and the transplantation of co-cultured and preconditioned SVF cells and/or MSCs may be more effective than the transplantation of untreated cells for the treatment of bone defects.

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## Introduction

Adult mesenchymal stem cells (MSCs) can be isolated from bone marrow [1], skeletal muscles [2], adipose tissues [3], synovial membranes [4], trabecular bone [5] or adenoid tissues [6]. MSCs were first isolated from bone marrow, which is still a commonly used source for MSC isolation because they are easy to harvest and have potent differentiation ability [7-10]. Bone marrow-derived MSCs can differentiate into multiple lineages, including osteoblasts, chondrocytes, adipocytes, tenocytes and vascular smooth muscle cells [7, 11], and they support hematopoiesis *in vivo* upon *de novo* bone formation [12].

Adipose-derived stem cells (ASCs), which are a form of MSCs, have been intensely studied due to their multipotent differentiation capacity, paracrine effects and implications for regenerative medicine [13-15]. A recent shift of focus has directed attention away from the study of ASCs to that of the heterogeneous mixed cell population from which they are derived, the stromal vascular fraction (SVF) [16, 17]. SVF cells, which are traditionally isolated through enzymatic processing, contain MSCs, endothelial (progenitor) cells, immune cells, smooth muscle cells, pericytes and other stromal components [18]. SVF treatment has been shown to provide therapeutic effects similar to those of ASC treatment in osteochondral defects and myocardial infarction [19, 20], and SVF cells have been demonstrated to have similar neuroprotective effects and greater immunomodulatory properties than ASCs in experimental chronic autoimmune encephalitis studies [21]. The regenerative capacity of SVF cells has been validated in various therapeutic models, such as fat grafting, multiple sclerosis, burn injury, diabetes, radiation, Crohn's disease, cardiac disease and bone defect models [13, 14]. When applied to these models, SVF cells have shown angiogenic, immunomodulatory, differentiation, proliferation, and pro-survival properties that are important for regeneration and repair [13]. These regenerative properties of SVF cells can be attributed to the heterogeneity of the cell population, which likely employs numerous mechanisms to facilitate regeneration [13]. Despite these attractive advantages of SVF implantation in clinical interventions, the status of recent clinical studies for many diseases has not been fully evaluated [22].

The final purpose of this study was to investigate some of the regenerative mechanisms utilized by implanted SVF cells. Here, using an *in vitro* co-culture system, we sought to determine whether SVF implantation into impaired tissue affects endogenous MSC differentiation, as MSCs can differentiate into a variety of cell types and have a strong regenerative capacity despite their low numbers in impaired tissue. Furthermore, adipose-derived SVF cells obtained from four donors were co-cultured with bone marrow-derived MSCs, and the differential expression of osteogenic markers and osteogenic differentiation factors over time was examined over time in mono-cultured MSCs and MSCs co-cultured with SVF cells. Surprisingly, we observed that both MSCs and SVF cells significantly and mutually enhanced the expression levels of osteogenic-specific markers via paracrine and/or autocrine regulation but did not enhance adipocyte, chondrocyte or myoblast marker expression. More surprisingly, subsequent osteogenesis and/or comparable effects were rapidly induced within 48 h. This duration is very rapid compared with the typical time required for the *in vitro* osteogenic differentiation of MSCs. To the best of our knowledge, this work is the first to report the rapid induction of osteogenesis and/or comparable effects in bone marrow-derived MSCs through co-cultivation with adipose-derived SVF cells. This finding provides new insights into the potential clinical applications of adipose-derived SVF cells and/or bone marrow-derived MSCs for bone diseases.

## Materials and Methods

**Table 1.** Cell donor information

### *Adipose tissue harvesting and isolation of SVF cells*

Human adipose tissue samples for SVF isolation were obtained from four donors who were recruited at International St. Mary's Hospital of the Catholic Kwandong University, and the donor information is shown in Table 1. The

SVF cell sample number	Age (Years)	Sex	Body mass index
#1	62	Male	25.46
#2	42	Male	27.32
#3	55	Male	25.78
#4	54	Male	26.21

study protocol was approved by the ethics review committee of the Institutional Review Board, College of Medicine, Catholic Kwandong University. Liposuction was performed under general anesthesia and sterile conditions, and the adipose tissue samples were harvested from the abdominal wall using gentle manual techniques. SVF cells were isolated from adipose tissues using a SmartX kit (Dongkoo Bio & Pharma Co., Seoul, South Korea) according to the manufacturer's instructions. Briefly, water, tumescent tissue and oil was removed from the isolated adipose tissue, and then the tissue was digested with 0.075% collagenase type I at 37°C for 30 min. Digested tissue was filtered through a 75- $\mu$ m strainer to remove residual tissue, and the filtered cell suspension was centrifuged at 2,000 $\times$ g for 3 min and washed with phosphate-buffered saline (PBS; HyClone, Logan, UT, USA) three times. Total and live cell counts were performed using a Nucleocounter<sup>®</sup> NC- 200<sup>™</sup> automated cell counter (Chemometec, Denmark).

### *Culture of human adipose-derived SVF cells and bone marrow-derived MSCs*

Isolated SVF cells and MSCs (ATCC, Manassas, Virginia, USA) were cultured in Dulbecco's modified Eagle's medium (DMEM; Gibco, Waltham, Massachusetts, USA) containing 10% fetal bovine serum (FBS) (Gibco) and 1% penicillin/streptomycin in a humidified atmosphere with 5% CO<sub>2</sub> at 37°C. SVF cells (passage 3) and MSCs (passage 8) were used for all experiments.

### *Co-culture of SVF cells and MSCs*

MSCs were plated 24 h prior to co-culture at a density of 5 $\times$ 10<sup>4</sup> cells/cm<sup>2</sup> in 24-well and 6-well plate, and individual SVF cells from four donors were plated on trans-well inserts with a 0.4- $\mu$ m porous translucent PET membrane (FALCON, Pittston, PA, USA) at a cell density identical to that of MSCs. After 12, 24 and 48 h, SVF cells and MSCs were harvested for analysis. Western blot analysis was used to detect secreted proteins in the culture medium (serum-free medium) after up to 48 h of culture.

### *Alkaline phosphatase (ALP) staining*

An ALP Staining Kit (Cosmo Bio, Tokyo, Japan) was used for the ALP staining of MSCs co-cultured with SVF cells. The MSCs in a 24-well plate were fixed in 10% formalin (Sigma-Aldrich, St. Louis, MO, USA) for 20 min at room temperature after being washed with PBS and then deionized water three times each. Chromogenic substrate dissolved in substrate-containing buffer (kit component) was added to each well, and after incubation at 37°C for 20 min, the cells were washed with deionized water to stop the reaction. A digital camera (eXcope T300, Olympus, Tokyo) attached to an inverted phase-contrast microscope (CKX-41, Olympus) was used for microscopic observation.

### *ALP activity*

Co-cultured MSCs with SVF cells in a 24-well plate were fixed with an acetone/ethanol (Sigma-Aldrich) mixture (50:50, v/v) for 20 min at room temperature after being washed with PBS and then deionized water three times each. The MSCs were incubated in a substrate solution (0.1 M diethanolamine (Sigma-Aldrich), 1 mM MgCl<sub>2</sub> (Sigma-Aldrich), and 10 mg/ml p-nitrophenyl phosphate (Sigma-Aldrich)) for 20 min at 37°C, the reaction was stopped by adding 5 M NaOH (Sigma-Aldrich), and absorbance was measured at 405 nm using a microplate reader (Multiskan FC; Thermo Fisher Scientific, Vantaa, Finland).

### *RNA isolation, reverse transcription (RT)-PCR and quantitative real-time PCR (qPCR)*

Total RNA was isolated from MSCs and SVF cells using TRIzol Reagent Solution (Life Technologies, Frederick, Maryland, USA) according to the manufacturer's instructions. Oligo dT-primed cDNA was

synthesized from total RNA using a Maxime RT PreMix kit (iNtRON Biotechnology, Seongnam, Korea). The expression of each gene transcript was quantified by qPCR using an Applied Biosystems StepOnePlus real-time PCR System (Foster City, CA, USA) with a SYBR Green Dye system (SYBR Premix Ex Taq, Tli RNase Plus and ROX reference dye (Takara Bio Inc. Foster City, CA, USA)). All values are shown as the normalized target gene expression level (fold change;  $2^{-\Delta\Delta Ct}$ ) relative to the GAPDH transcript level. Primers were designed using Primer3 and BLAST, and the primer set sequences are listed in Table 2.

#### Western blot analysis

The MSCs and SVF cells were washed with PBS and lysed with RIPA buffer (Cell signaling Technology, Danvers, Massachusetts, USA) containing 1% phosphatase inhibitors (Sigma-Aldrich) and 1% protease inhibitors (Sigma-Aldrich). Conditioned medium (CM) from the cells was centrifuged for 30 min at 1,000 ×g and 4°C to remove cell debris and then concentrated using an Amicon Ultra Centrifugal Filter (Millipore Corporation, Bedford, MA, USA) with a membrane for a nominal molecular weight limit (NMWL) of 3 kDa. The protein content was determined using Bradford protein assays (Bio-Rad, Hercules, CA, USA). The concentrated media were treated with equivalent volumes of lysis buffer (1% Triton X-100, 30 mM Tris (pH 8.0), 137 mM sodium chloride, 15% glycerol and 5 mM EDTA containing 1% phosphatase inhibitors and 1% protease inhibitors) to obtain soluble protein samples. Protein samples were boiled with 0.1% bromophenol blue and 5% β-mercaptoethanol for 1 min at 100°C, subjected to sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and transferred to a polyvinylidene difluoride membrane (Millipore, Billerica, Massachusetts, USA). The membrane was blocked with 5% skim milk in Tris-buffered saline/0.1% Tween 20 buffer (TBS-T) for 30 min at room temperature and incubated with a 1:1000 dilution of primary antibodies in TBS-T buffer containing 5% bovine serum albumin (AMRESCO, Solon, Ohio, USA) and 0.02% sodium azide (Sigma-Aldrich) overnight at 4°C. The membrane was washed five times for 5 min with TBS-T and incubated with horseradish peroxidase-conjugated secondary antibodies (Santa Cruz Biotechnology, Dallas, Texas, USA) for 1 h at room temperature. After five washes, the bands were enhanced with chemiluminescence (ECL; Western Detection Kit, Abclon, Seoul, Korea) and detected using a Western imaging (CAS 400SM) system (Davinch-K, Seoul, South Korea). The band intensities were quantified using ImageJ software.

#### Network analysis

For gene and protein network analyses, changed genes and proteins with altered expression based on qPCR and Western blot analysis in co-cultured MSCs and adipose-derived SVF cells were analyzed using GeneMANIA (<http://www.genemania.org>) [23]. Associations between differentially expressed genes and proteins with broadly defined molecular networks were combined and visualized using Cytoscape\_v3.3.0. Using the web interface, we predicted protein/gene interactions and their interacting partner proteins identified in this study.

#### Statistical analysis

All data were compared via one-way analysis of variance (ANOVA) using the Statistical Package for the Social Sciences (SPSS, version 14.0K) program. The data are expressed as the means ± SEM. Group means were considered significantly different at  $p < 0.05$ , as determined by the protected least-significant difference (LSD) test when ANOVA indicated an overall significant treatment effect ( $p < 0.05$ ).

**Table 2.** Sequences of primers used for qPCR. <sup>a)</sup> F, sequence of sense strands; <sup>b)</sup> R, sequence of anti-sense strands

Genes		Primer sequence (5' - 3')
OSX	F <sup>a)</sup>	TGCTTGAGGAGGAAGTTCACATG
	R <sup>b)</sup>	TGCCAGAGTTGTTGAGTCC
RUNX2	F	AAGGGTCCACTCTGGCTTTG
	R	CTAGGGCGATTTCAGGTGCT
ALPL	F	GACCCCTTGACCCCCACAAT
	R	CGCCTCGTACTGCATGTCCCCT
COL1A1	F	CCGGAACAGACAAGCAACCCAAA
	R	AAAGGAGCAGAAAGGGCAGCATTG
COL2A1	F	TGGTCTTGGTGGAACTTTGCTGC
	R	AGGTTACCAGGTTACCAGGATT
OPN	F	CATATGATGGCCGAGGTGATAG
	R	CATCCAGCTGACTCGTTTCATA
OCN	F	TCACACTCCTCGCCCTATT
	R	TGAAAGCCGATGGTCAG
BMP2	F	GGAACGGACATTGCGTCTT
	R	CACCATGGTTCGACCTTTAGGA
TGFB1	F	TGGCGATACCTCAGCAACC
	R	CTCGTGGATCCACTCCAG
Internal control		
GAPDH	F	GAAAGCCTGCCGGTGACTAA
	R	AGGAAAAGCATCACCCGGAG



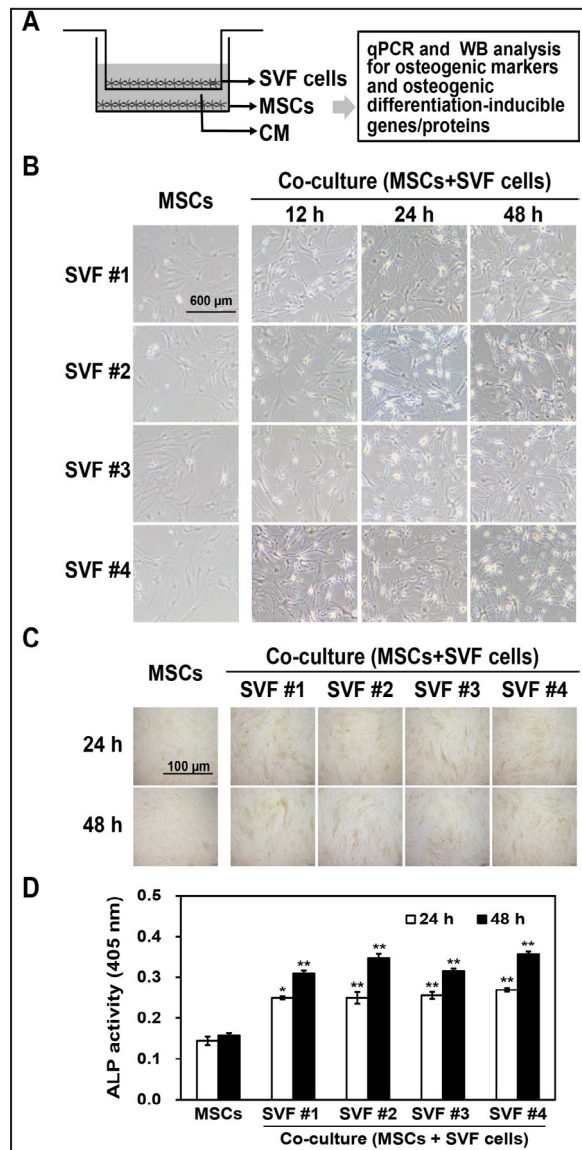
## Results

### Co-culture of SVF cells and MSCs

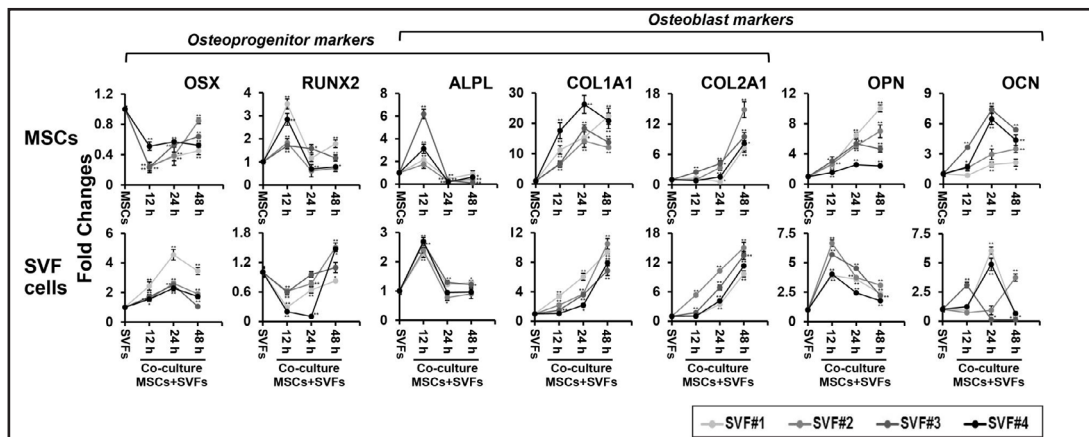
To investigate the effects of adipose-derived SVF cells on bone marrow-derived MSCs, SVF cells were obtained from four donors (Table 1). Isolated SVF cells from human adipose tissues were cultured up to passage 3 when the number of cells had increased sufficiently for co-culturing with MSCs. A previous study using flow cytometry indicated no differences in marker expression in the first three SVF cell passages [24]. Therefore, individual SVF cells at passage 3 were seeded on a trans-well chamber that was inserted into cultured MSCs, and then the differential expression levels of osteogenic genes and protein markers and osteogenic differentiation-inducible genes and proteins were examined over time in mono-cultured MSCs/SVF cells, MSCs co-cultured with SVF cells/SVF cells and CM (Fig. 1A). We first verified that the spindle-shaped morphology of MSCs was altered to an osteoblast-like shape or an increased circular and elongated spindle-shape by SVF cells as time progressed (Fig. 1B). To determine the osteogenic differentiation ability of MSCs co-cultured with SVF cells, MSCs were co-cultivated with SVF cells for up to 48 h and evaluated by ALP staining and activity during *in vitro* osteogenic differentiation. As indicated in Figs. 1C and 1D, co-cultivation with SVF cells slightly promoted osteogenic differentiation in MSCs after 24 h and 48 h. However, the number of ALP-stained MSCs and the ALP activity of MSCs, which represent osteogenic differentiation, were not increased in MSCs co-cultured with SVF cells compared with mono-cultured MSCs after 12 h (data not shown).

### Time-dependent differential regulation of osteogenic genes

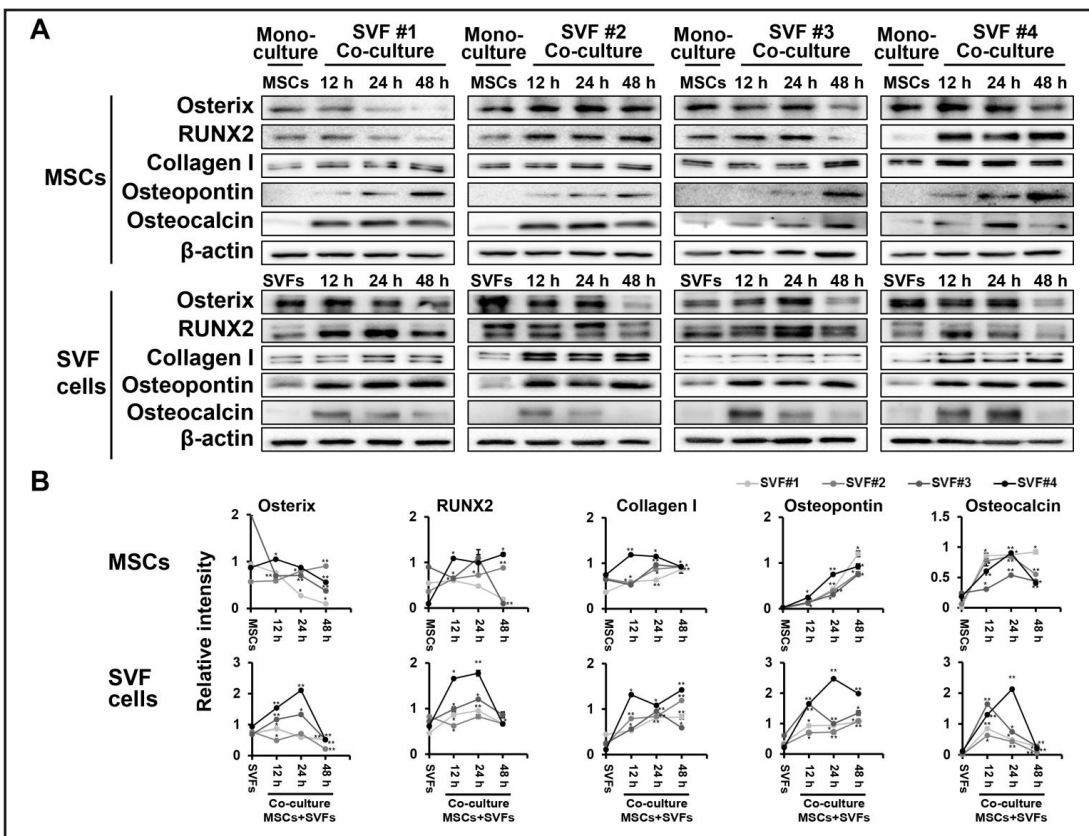
On the basis of morphological changes and ALP activity enhancement in MSCs induced by SVF cell treatments, the expression levels of osteoprogenitor markers (osterix (OSX), runt-related transcription factor 2 (RUNX2), alkaline phosphatase, liver/bone/kidney (ALPL), collagen type I alpha 1 (COL1A1) and COL2A1) and osteoblast markers (ALPL, COL1A1, COL2A2, osteopontin (OPN) and osteocalcin (OCN)) were measured over time using qPCR in mono-cultured MSCs/SVF cells and MSCs co-cultured with SVF cells (Fig. 2). RUNX2/ALPL, COL1A1/OCN, and COL2A1/OPN showed the greatest expression increase at 12, 24 and 48



**Fig. 1.** Experimental scheme of our study (A). Time-dependent morphological changes (B) and ALP staining (C) and ALP activity (D) of MSCs co-cultured with SVF cells. The data are representative of three independent experiments. Significant differences among the co-culture groups and the mono-culture group were determined via ANOVA, with p values indicated as \* $p < 0.001$  and \*\* $p < 0.0001$ .



**Fig. 2.** Time-dependent differential regulation of osteogenic markers in mono-cultured or co-cultured MSCs with SVF cells as determined by qRT-PCR. All values are shown as the normalized target gene expression level (fold change;  $2^{-\Delta\Delta Ct}$ ) relative to GAPDH transcript levels. The data are representative of three independent experiments. Significant differences among the co-culture groups and the mono-culture group were determined via ANOVA, with p values indicated as \* $p < 0.05$  and \*\* $p < 0.01$ .



**Fig. 3.** Time-dependent differential regulation of osteogenic markers in mono-cultured or co-cultured MSCs with SVF cells as determined by Western blot analysis (A). Band intensity was measured as area density and analyzed in ImageJ (B). Relative intensity levels indicate protein levels normalized to  $\beta$ -actin levels. The data are representative of two independent experiments. Significant differences among the co-culture groups and the mono-culture group were determined via ANOVA, with p values indicated as \* $p < 0.05$  and \*\* $p < 0.01$ .

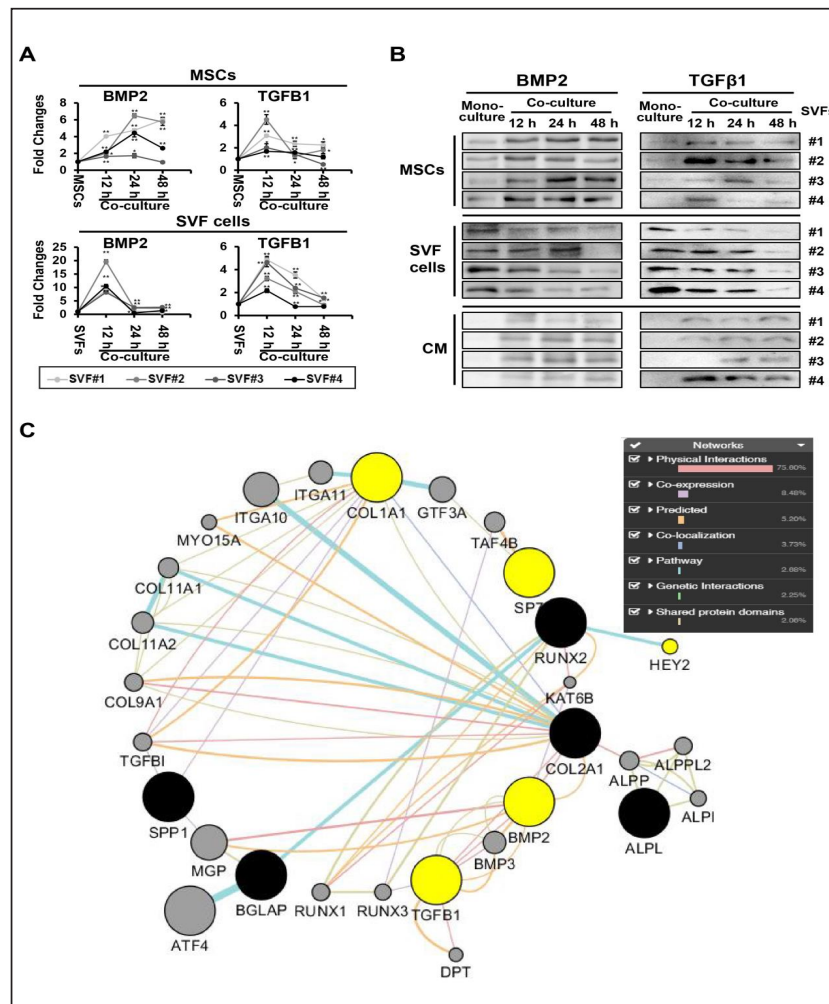
h in MSCs after co-culture (Fig. 2). In contrast, only OSX was down-regulated in MSCs by co-culture with SVF cells (Fig. 2). Meanwhile, ALPL/OPN, OSX/OCN and RUNX2/COL1A1/

COL2A1 showed the largest expression increase at 12, 24 and 48 h in SVF cells after co-culture (Fig. 2). However, at most time points, gene expression levels in MSCs co-cultured with SVF cells were approximately the same or higher than in mono-cultured MSCs, with the exception of OSX or RUNX2 (Fig. 2). In addition, the highest gene expression time points were different between MSCs and co-cultured SVF cells, and the transcript fold changes in MSCs were higher than those in co-cultured SVF cells (Fig. 2). Mono-cultured MSCs, which were used as a control for qPCR analysis, were harvested 24 h after changing the medium because the differential expression of osteogenic genes was not observed between cells harvested 12, 24 and 48 h after changing the medium (data not shown).

*Time-dependent differential regulation of osteogenic proteins*

In addition to osteogenic genes, osteogenic protein expression over time in the upper layer of cells (SVF cells) and the bottom layer of cells (MSCs) in co-culture conditions was investigated using Western blot analysis (Fig. 3). The osteogenic protein expression was dissimilar to gene expression in many aspects (Fig. 3). There were wider individual variations in osteogenic protein expression than in gene expression, and the time points with the highest osteogenic protein expression were distinct from those observed for gene expression in MSCs and SVF cells under co-culture conditions (Fig. 3). Some proteins in certain SVF cells even showed an expression pattern opposite to the gene expression pattern (Fig. 3). However, the protein expression levels at most of the time points in MSCs and SVF cells under co-culture conditions were approximately the same or higher than those in mono-cultured MSCs and SVF cells (Fig. 3).

**Fig. 4.** Time-dependent differential regulation of osteogenic differentiation-inducible genes/proteins in mono-cultured or co-cultured MSCs with SVF cells as determined by qRT-PCR (A), Western blot analysis (B), and network analysis (C). The five yellow circles indicate predicted targets associated with stem cell differentiation. All qPCR values are shown as the normalized target gene expression level (fold change;  $2^{-\Delta\Delta C_t}$ ) relative to GAPDH transcript levels. The data are representative of three independent experiments. Significant differences between the co-culture groups and the mono-culture group were determined via ANOVA, with p values indicated as \* $p < 0.05$  and \*\* $p < 0.01$ .





### *Time-dependent differential regulation of osteogenic differentiation-inducible genes/proteins*

Considering the above results, we predicted that proteins secreted by the co-cultured cells would induce osteogenic differentiation and/or comparable effects in both MSCs and SVF cells via paracrine and/or autocrine regulation. The BMPs and TGF $\beta$  have widely recognized critical roles in osteogenesis [25-27]. Therefore, we investigated the gene/protein expression of BMP2 and TGF $\beta$ 1 in MSCs, SVF cells and CM (Fig. 4). Surprisingly, BMP2 and TGF $\beta$ 1 transcripts were significantly increased in both MSCs and SVF cells under co-culture conditions (Fig. 4A). BMP2 and TGF $\beta$ 1 in MSCs exhibited the highest expression at 24 h and 12 h, respectively, but both transcripts in SVF cells exhibited the largest expression increase at 12 h under co-culture conditions (Fig. 4A). Meanwhile, the protein expression of both BMP2 and TGF $\beta$ 1 was similar to the gene expression pattern in MSCs during co-culture with SVFs (Fig. 4B). However, BMP2 and TGF $\beta$ 1 protein expression was remarkably decreased in SVF cells from the initial co-cultivation stage, in contrast to the gene expression (Fig. 4B). These results were assumed to be attributed to BMP2 and TGF $\beta$ 1 secretion after the induction of cells via co-culture. As expected, both BMP2 and TGF $\beta$ 1 expression levels in CM were significantly up-regulated over time (Fig. 4B). Furthermore, for the prediction of osteogenic differentiation-inducible factors, network analysis using differentially expressed osteogenic markers was performed and, therefore, the relationships between bone morphogenetic proteins (BMP)/transforming growth factor beta (TGF $\beta$ ) and changed osteogenic markers were identified (Fig. 4C). Our data suggest that secreted BMP2 and/or TGF $\beta$ 1 proteins from MSCs and SVF cells under co-culture conditions induce osteogenesis and/or a comparable effect via paracrine and/or autocrine regulation.

### Discussion

SVF cells generally consist of blood-derived cells (CD45<sup>+</sup>), ASCs (CD31<sup>-</sup>, CD34<sup>+</sup>, CD45<sup>-</sup>, CD90<sup>+</sup>, CD105<sup>-</sup> and CD106<sup>+</sup>), MSCs (CD31<sup>-</sup>, CD34<sup>+</sup>, CD45<sup>-</sup>, CD90<sup>+</sup>, CD105<sup>+</sup> and CD106<sup>-</sup>), endothelial (progenitor) cells (CD31<sup>+</sup>, CD34<sup>+</sup>, CD45<sup>-</sup>, CD90<sup>+</sup>, CD105<sup>-</sup> and CD106<sup>+</sup>), vascular smooth muscle cells (CD31<sup>-</sup>, CD34<sup>+</sup>, CD45<sup>-</sup>, CD90<sup>+</sup>, CD105<sup>-</sup> and CD106<sup>-</sup>), pericytes (CD31<sup>-</sup>, CD34<sup>-</sup>, CD45<sup>-</sup>, CD90<sup>+</sup>, CD105<sup>-</sup> and CD106<sup>+</sup>) and others [28, 29], but the composition differs between laboratories according to the SVF isolation procedure, the age of the patients, downstream processing, etc [30]. In the present study, the SVF cells did not express CD31 and CD34 but expressed CD45, CD90, CD105 and CD106, and the differential expression of surface markers in the first three passages of SVF cells was not observed [24]. These data suggest that the cultured SVF cells contained a heterogeneous cell population and that they may affect other cells and/or be influenced by them through various mechanisms. The relationship between the regenerative capacity and the heterogeneity of SVF cells has been verified in diverse human trials and animal experiments [13], and there is evidence of regenerative activity through cross interactions between different cell populations in the SVF cells and their hosts [13, 31, 32].

In a previous study, we investigated whether SVF cells affected epithelial cells or MSCs that are present in heart tissue to examine the potential benefits of SVF transplantation as a therapy for heart disease *in vitro* system. We found that epithelial cells co-cultured with SVF cells exhibited enhanced anti-inflammatory and pro-angiogenic responses under oxidative stress conditions [24], and MSCs co-cultivated with SVF cells ameliorated the apoptosis induced by oxidative stress. Co-culture is a useful and powerful tool to understand cellular interactions and paracrine mechanisms [33], and this method can present a more comprehensive signal for differentiation to a certain lineage; however, it is very difficult to standardize in primary cells due to variation between individual donors [33]. We wondered whether SVF cells also induce the differentiation of MSCs, which are multipotent stromal cells that can differentiate into a variety of cell types. For that reason, we initially examined lineage-specific markers, namely, adipocyte, osteoblast, chondrocyte and myoblast, protein markers, in MSCs co-cultured with SVF cells for 48 h and found that SVF cells induced only



the expression of osteogenic differentiation-specific markers in MSCs without inducing expression of other lineage-specific markers. On the basis of preliminary data, we investigated the differential expression of osteogenic markers over time, not only on MSCs co-cultured with SVF cells but also on SVF cells co-cultivated with MSCs. MSCs and SVF cells significantly and mutually induced the expression of osteogenic-specific markers via paracrine and/or autocrine regulation within 48 h (Figs. 2 and 3). Because this period is very short compared with the typical time required for the *in vitro* osteogenic differentiation of MSCs [33-35], we could not identify a proper positive osteogenic control and used only negative controls such as mono-cultured MSCs or SVF cells in all experiments.

RUNX2 is expressed in cells prior to the formation of the skeleton, as early as E10.5, at which stage cells still have the capacity to differentiate into osteoblasts or chondrocytes [36-38]. RUNX2 is a master transcription factor for osteoblast differentiation, matrix production and mineralization during bone formation [38]. RUNX2 regulates OSX, which is a zinc-finger-containing transcription factor expressed in osteoblasts that is essential for osteoblast differentiation and bone formation, [39] and ALPL, which is translated into a ubiquitous cellular protein that is an early indicator of cellular activity and differentiation [40, 41]. RUNX2 also regulates major osteoblast-specific downstream genes, such as COL1A1, OPN and OCN, which determine the osteoblast phenotype and function in skeletogenesis and are translated into matrix proteins [37]. In other words, RUNX2 controls OSX, which may regulate COL1A1, OPN and OCN [38, 42]. With this connection in mind, in the present study, while RUNX2 and ALPL were significantly increased within 12 h, COL1A1, OPN and OCN were subsequently remarkably up-regulated in MSCs co-cultured with SVF cells isolated from four donors (Fig. 2). Although it was a short period of time, these data closely resembled the expression pattern of osteogenic markers during general osteogenesis. Interestingly, only OSX was significantly decreased in MSCs by SVF cells (Fig. 2). OSX may act downstream and act independently of RUNX2 in osteogenesis [39, 43]. These results suggest that the co-cultivation of MSCs with SVF cells may rapidly induce osteogenesis and/or comparable effects through a RUNX2-dependent and OSX-independent mechanism.

The expression of osteogenic-specific genes and proteins induced by the co-culture of MSCs and SVF cells showed differences, especially in early markers such as RUNX2, osterix and collagen I (Fig. 3). These results were believed to result from differences between gene and protein expression. Gene expression is often interpreted in terms of protein levels, but the correlation can be as little as 40% depending on the system [44]. Therefore, the differences between gene and protein expression were likely due to various causes, including RNA stability and processing and protein stability and modification [44]. Moreover, RUNX2 mRNA levels were constitutively expressed, but a distinct lack of correlation between RUNX2 mRNA and protein levels was observed, indicating that RUNX2 may be regulated at multiple levels, including changes in mRNA and protein levels [45].

BMPs/TGF $\beta$  have widely recognized roles in bone formation during mammalian development and multiple functions in the body [25-27]. Autocrine and paracrine stimulation with TGF $\beta$  is critical in maintenance and expansion of MSCs and osteoblast progenitors [46], and osteoblast-enriched populations are more sensitive to its mitogenic effect than other populations at earlier developmental stages [47]. TGF $\beta$  signaling also promotes osteoprogenitor proliferation, early differentiation, commitment to the osteoblastic lineage and cooperation between BMPs and TGF $\beta$  [26]. The BMP signaling pathway is also involved in various stages of the developmental process, such as osteoblast differentiation, mesoderm patterning and bone formation [27]. BMP is required for MSC differentiation into osteochondroprogenitor cells, which are able to differentiate into chondrocytes and osteoblasts [27], and for the secretion by differentiated osteoblasts of the matrix upon which bone formation occurs [48]. In particular, BMP2 can induce the up-regulation of critical osteogenic regulators [27]. Therefore, we predicted that BMP2 and/or TGF $\beta$  may be osteogenic differentiation-inducible factors of co-cultured MSCs and SVF cells. Surprisingly, BMP2 and TGF $\beta$ 1 were significantly secreted by MSCs and SVF cells during co-cultivation (Fig. 4).

ASCs have been demonstrated to be highly efficient in inducing bone generation and healing in animal studies [17] as well as in human clinical trials [49, 50]. ASCs seeded in a scaffold of beta-tricalcium phosphate ( $\beta$ -TCP) implanted into four patients using a cranioplasty procedure achieved successful ossification without complications [49]. Placing  $\beta$ -TCP, BMP2 and ASCs into an anterior mandibular defect also induced sufficient ossification [50], and ASCs injected into bone defects appeared to accelerate bone healing [51]. In addition, several studies of SVF application for bone generation have been reported [19, 52, 53]. Recombinant BMP2 stimulated osteoblastic differentiation in SVF cells to generate ectopic bone tissue [52], and SVF and ASCs seeded in a scaffold demonstrated a high degree of regeneration in osteochondral defects [19]. SVF supplementation on bone substitutes for maxillary sinus floor elevation (MSFE) showed potential effectiveness for bone formation [53]. The application of SVF cells and/or ASCs is a promising approach for the treatment of bone defects, although it is still in the experimental phase [30].

In summary, we found that bone marrow-derived MSCs and adipose-derived SVF cells significantly and mutually induced the expression of osteogenic-specific markers via paracrine and/or autocrine regulation through BMP2 and/or TGF $\beta$ 1 but did not induce adipocyte, chondrocyte or myoblast marker expression. Osteogenesis and/or comparable effects were rapidly induced within 48 h. Our findings suggest that the positive effects of SVF implantation into impaired bone may be attributed to the rapid induction of MSC osteogenesis and that the transplantation of co-cultivated and preconditioned SVF cells and/or MSCs may be more effective than the transplantation of untreated cells to treat bone defects.

## Abbreviations

ALP (alkaline phosphatase); ASCs (adipose-derived stem cells); CM (conditioned medium); MSCs (mesenchymal stem cells); qPCR (quantitative real-time PCR); SVF (stromal vascular fraction).

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## Disclosure Statement

The authors declare that they have no competing interests to disclose.

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