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H．知的財産権の出願・登録状況（予定を含む。）

特になし。

Ⅱ．研究成果の刊行に関する一覧表

別紙４

研究成果の刊行に関する一覧表

書籍

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Ⅲ. 研究成果の刊行物・別刷

（主なもの）

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Review

Cell and gene therapy using mesenchymal stem cells (MSCs)

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Abstract

Mesenchymal stem cells (MSCs) are considered to be a promising platform for cell and gene therapy for a variety of diseases. First, in the field of hematopoietic stem cell transplantation, there are two applications of MSCs: 1) the improvement of stem cell engrafting and the acceleration of hematopoietic reconstitution based on the hematopoiesis-supporting ability; and 2) the treatment of severe graft-versus-host disease (GVHD) based on the immunomodulatory ability. Regarding the immunosuppressive ability, we found that nitric oxide (NO) is involved in the MSC-mediated suppression of T cell proliferation. Second, tumor-bearing nude mice were injected with luciferase-expressing MSCs. An in vivo imaging analysis showed the significant accumulation of the MSCs at the site of tumors. The findings suggest that MSCs can be utilized to target metastatic tumors and to deliver anti-cancer molecules locally. As the third application, MSCs may be utilized as a cellular vehicle for protein-supplement gene therapy. When long-term transgene expression is needed, a therapeutic gene should be introduced with a minimal risk of insertional mutagenesis. To this end, site-specific integration into the AAVS1 locus on the chromosome 19 (19q13.4) by using the integration machinery of adeno-associated virus (AAV) would be particularly valuable. There will be wide-ranging applications of MSCs to frontier medical treatments in the near future.

Keywords: Cancer gene therapy; GVHD; Mesenchymal stem cells; Site-specific integration; Tumor targeting

1. Introduction

In bone marrow, there are different types of tissue stem cells (adult stem cells); i.e. hematopoietic stem cells and mesenchymal stem cells (MSCs). MSCs account for a small population of cells in bone marrow as a non-hematopoietic component with the capacity to differentiate into a variety of cell lineages, including adipocytes, osteocytes, chondrocytes, muscles, and stromal cells [1]. Recent studies demonstrated that MSCs are capable of supporting hematopoiesis and of regulating immune response [2]. In addition, since MSCs can be readily isolated and expanded *in vitro*, they are expected to be a source of cell therapy. Interestingly, MSCs have the ability to accumulate at the site of: i) tissue/organ damage; ii) inflammation; and iii) cancer when administered *in vivo*. Therefore, MSCs can be utilized for: i) regenerative therapy; ii) treatment of graft-versus-host disease (GVHD) and Crohn disease; and iii) platform of cancer gene therapy (targeted delivery of anti-cancer agents). Another unique feature of MSCs is little or low immunogenicity due to the lack of expression of co-stimulatory molecules. This phenomenon makes it possible to administer MSCs without HLA matching for cell therapy. A single lot of expanded MSCs from one healthy donor can be utilized for treatment of many patients. Although clinical applications of MSCs have been conducted for the suppression of severe acute GVHD in allogeneic stem cell transplantation [3,4] and for regenerative therapy [5,6], molecular mechanisms underlying the biological effects of

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MSCs remains obscure. Finding key molecules for differentiation, immunosuppression, and hematopoietic support of MSCs would be valuable for further augmenting the efficacy of MSCs in a wide range of clinical applications. In this regard, development of the technology for genetic manipulation of MSCs is also important research project. Site-specific integration of a therapeutic gene into a safe locus in the genome should be investigated from the safety standpoint.

2. Microarray analysis of genes responsible for differentiation of mesenchymal stem cells

Genes regulating the differentiation of MSCs remain obscure and it is technically difficult to do high-throughput analysis using primary MSCs, because such cells contain heterogeneous populations. To overcome the problems related to the heterogeneity of primary MSCs, we utilized MSC-like cell lines. It has been shown that 10T1/2 cells, derived from C3H mouse embryo cells, differentiate into adipocytes, osteocytes, and chondrocytes with a treatment of 5-azacytidine. We previously established two sub-lines from 10T1/2, designated as A54 for a preadipocyte cell line and M1601 for a myoblast cell line [7]. Under appropriate culture conditions, A54 and M1601 cells terminally differentiate into adipocytes and myotubes, respectively, while parental 10T1/2 cells remain undifferentiated under the same culture conditions. Therefore, 10T1/2 cells can be utilized as a model of MSCs, and A54 and M1601 are used as committed mesenchymal progenitors. Gene expression profiles of these cell lines were compared by microarray analysis before and after differentiation.

Each of parent 10T1/2, A54, and M1601 cell lines showed a distinctive and unique gene expression profile despite morphological similarity (Fig. 1) [8]. Parental 10T1/2 cells had 105 elevated genes including ones encoding Activin, Dlk, Nov, Grb10, p15, and many functionally unknown molecules. Dlk and Nov are known to be involved in Notch signaling pathway and were reported to have the ability to inhibit differentiation into adipocytes and osteoblasts [9]. In preadipocyte A54 cells, 201 genes were up-regulated, including genes known to be involved in adipocyte differentiation such as genes encoding C/EBPα, C/EBPδ, PPAR-γ, PAI-I, and Frizzled-1 [10]. Myoblasts M1601 cells showed 137 up-regulated genes, including ones related to skeletal muscle differentiation such as genes encoding MyoD, MLC1F, α-skeletal actin, myosin heavy chain, and myosin light chain [11] as well as genes related to cardiac muscle differentiation such as genes encoding α-cardiac actin, cardiac troponin C, and troponin T2 [12].

Previous studies have shown that preadipocytes have a higher ability to support hematopoiesis than other kinds of stromal cell components *in vitro* [12,13]. Our results of gene expression profile revealed up-regulation of critical cytokines for hematopoiesis such as SCF and SDF-1 in preadipocyte A54 cells. In addition, many chemokines, such as CXCL-1 and CCL-7, were also up-regulated. Since Ang-1 was reported to be indispensable for the self-renewal of hematopoietic stem cells [14], we performed real-time PCR analysis of Ang-1 along with SCF, SDF-1, CEBP-δ, IGF-1, and CXCL-1. The expression of these genes was highest in A54 cells among the three cell lines. Moreover, protein expression of Ang-1 was only detected in A54 among three cell lines and the level of this protein decreased after adipocyte differentiation.

To examine the effects of these three lines on hematopoiesis, we co-cultured mouse hematopoietic stem cell fraction with these three stromal cell lines. The cells in Lin(−)Sca-1(+) fraction were plated on 10T1/2, A54, or M1601 cells.

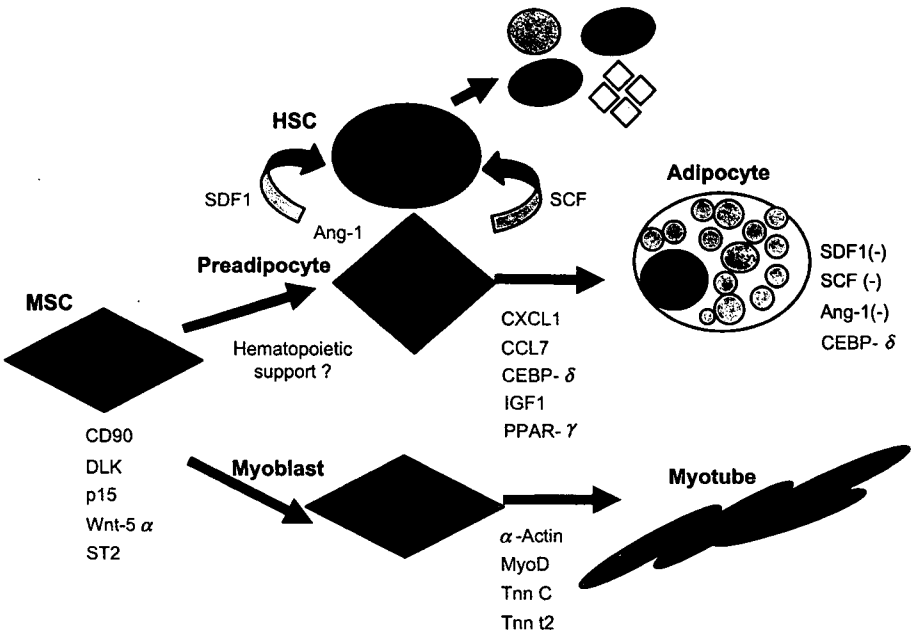

Fig. 1. Proposed model for the hierarchy of the bone marrow stromal system [8].

After 6 days of co-culture, hematopoietic progenitors were detected only on the A54 cells. These results suggest that only A54 cells have the ability to support hematopoietic cell growth among these three cell lines, consistent with the previous report. Hematopoietic cell proliferation was not observed on the layer of the terminally differentiated A54 adipocytes, suggesting that A54 cells lose the ability for hematopoietic cell support after adipocyte differentiation. To understand the molecular mechanisms of this observation, we examined the expression levels of SCF, SDF-1, and Ang-1 during adipocyte differentiation by RT real-time PCR. The expression levels of Ang-1 and SCF decreased immediately after the induction of adipocyte differentiation, and that of SDF-1 decreased gradually. In contrast to this, the level of adipocyte differentiation marker, CEBP-δ, was unchanged.

The analysis of functionally unknown molecules is currently underway. In addition, cell-to-cell contact is also believed to be crucial in the interaction between hematopoietic stem cells and MSCs. We are currently investigating the cellular and molecular events in the interactive communication between hematopoietic stem cells and MSCs.

3. Nitric oxide (NO) plays a critical role in suppression of T-cell proliferation by mesenchymal stem cells

There is a case report of severe steroid-resistant GVHD after bone marrow transplantation, in which intravenous infusion of MSCs greatly improved clinical manifestations [3]. Moreover, multi-institutional clinical trial of MSC-treatment of severe grade III–IV acute GVHD in Europe revealed very high overall response rate (about 70%) (Le Blanc et al., ASH meeting 2006). The molecular mechanisms by which MSCs suppress T-cell proliferation are complicated, and whether a soluble factor plays a major role remains controversial. Transforming growth factor-β (TGF-β), hepatocyte growth factor (HGF), indoleamine 2,3-dioxygenase (IDO), and prostaglandin E_2 (PGE_2) have been reported to mediate T-cell suppression by MSCs [15–17]. In addition, some reports have shown that a soluble factor is the major mediator of suppression, whereas some reports have demonstrated that T-cell-MSC contact is required for this suppression.

We also investigated the molecular mechanisms using primary murine MSCs, and focused on nitric oxide (NO), because it is known to inhibit T-cell proliferation. NO is produced by NO synthases (NOSs), of which there are 3 subtypes; i.e. inducible NOS (iNOS), endothelial NOS, and neuronal NOS. It has been known that macrophages suppress T-cell proliferation, and that this suppression is caused by NO-mediated inhibition of Stat5 phosphorylation [18]. We investigated whether MSCs can also produce NO and whether NO is involved in their ability to suppress T-cell proliferation [19].

T cells proliferated in response to PMA and ionomycin, which act downstream of the T-cell-receptor complex by activating protein kinase C and inducing Ca^{2+} influx, respectively. Such T-cell proliferation was suppressed by the presence of MSC, suggesting that MSCs influence signals downstream of protein kinase C and Ca^{2+} influx. The expression of the activation markers CD25 and CD69 on CD4 or CD8 T cells did not change even in the presence of MSCs. MSCs suppressed the production of IFN-γ but not IL-2.

Although T cells from $Stat5^{-/-}$ mice do not proliferate upon stimulation with anti-CD3, they up-regulate CD25. Because this phenotype is similar to the status of activated T cells in the presence of MSCs, we hypothesized that MSCs suppress Stat5 phosphorylation. Indeed, Stat5 phosphorylation in activated T cells was diminished in the presence of MSCs. We found that MSCs caused a significant and cell-dose-dependent production of NO only when co-cultured with activated T cells. The induction of iNOS was readily detected in MSCs but not in T cells. RT-PCR and Western blot analysis detected iNOS expression in MSCs cocultured with activated splenocytes but not in MSCs or splenocytes when cultured alone. The immunofluorescence studies showed that iNOS was exclusively expressed in $CD45^-$ adherent cells, which correspond to MSCs, but not in $CD45^+$T cells. Next, we investigated the effects of *N*-nitro-L-arginine methyl ester (L-NAME), a specific inhibitor of NOS. As expected, L-NAME dose-dependently inhibited the production of NO by MSCs in the presence of activated T cells. Importantly, L-NAME restored T-cell proliferation and Stat5 phosphorylation, indicating that NO is involved in the inhibition of T-cell proliferation and Stat5 phosphorylation. Moreover, MSCs from inducible $NOS^{-/-}$ mice had a reduced ability to suppress T-cell proliferation.

In the presence of direct interaction between T cells and MSCs, there was a high level of NO production accompanied by a strong suppression of T-cell proliferation. In contrast, both NO production and T-cell suppression were reduced in a transwell system, in which T cells were separated from MSCs by a 1-μm-pore membrane. There are two possible explanations for the difference in T-cell suppression between the presence and absence of the transwell system. First, the amount of NO produced in the transwell system was lower than that in the presence of direct interaction. This finding suggests that direct interaction is critical for efficient production of NO as well as for strong suppression of T-cell proliferation. A second possible explanation is that, because NO is highly unstable, it can lose its activity before it reaches T cells in the transwell system.

Because TGF-β, IDO, and PGE_2 were reported as mediators of T-cell suppression by MSCs, we compared the effects of L-NAME with inhibitors of each mediator. Indomethacin (inhibitor of PGE_2 production) but not 1-methyl-DL-tryptophan (1-MT: inhibitor of IDO) or an anti-TGF-β-neutralizing antibody restored T-cell proliferation as effectively as L-NAME; however, the effects of L-NAME and indomethacin were not additive, suggesting that the NO and PGE_2 share signaling pathways leading to T-cell suppression.

In summary, our hypothesis that NO is produced by MSCs and that it suppresses T-cell proliferation in part through inhibition of Stat5 phosphorylation was supported by the following facts: (1) NO was readily detected in the medium in the co-culture of MSCs and activated T cells; (2) L-NAME restored T-cell proliferation as well as Stat5 phosphorylation; and (3) MSCs from $iNOS^{-/-}$ mice had markedly