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and
Faculty of Biological and Environmental Sciences
Department of Biosciences
Division of Physiology and Neuroscience

Doctoral School of Health Sciences
Doctoral Programme in Integrative Life Sciences
University of Helsinki

THE IMPACT OF MEMBRANE PHOSPHOLIPID
COMPOSITION AND EXTRACELLULAR VESICLES ON
THE IMMUNOREGULATIVE PROPERTIES OF HUMAN
MESENCHYMAL STROMAL CELLS

Lotta Kilpinen

ACADEMIC DISSERTATION

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- Supervisors: Saara Laitinen, PhD
Finnish Red Cross Blood Service
Helsinki, Finland
- Adj. prof Reijo Käkälä, PhD
University of Helsinki
Helsinki, Finland
- Thesis committee: Professor Vesa Olkkonen, PhD
Minerva Foundation Institute for Medical Research
Helsinki, Finland
- Adj. prof Pentti Somerharju, PhD
University of Helsinki
Helsinki, Finland
- Reviewers: Juan Falcón-Pérez, PhD
Center for Cooperative Research in Biosciences
Bizkaia, Spain
- Luc Sensebé, MD, PhD
Université de Toulouse
Toulouse, France
- Opponent: Lorenza Lazzari, PhD
Fondazione IRCCS Ca'Granada Ospedale Maggiore
Policlinico
Milan, Italy
- Custos: Professor Juha Voipio, PhD
University of Helsinki
Helsinki, Finland

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It always seems impossible until it's done
-Nelson Mandela

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LIST OF ORIGINAL PUBLICATIONS

This thesis is based on the following publications:

- I ¹Kilpinen L*, Tigistu-Sahle F*, Oja S, Greco D, Parmar A, Saavalainen P, Nikkilä J, Lehenkari P, Korhonen M, Käkälä R, Laitinen S (2013) Aging bone marrow mesenchymal stromal cells have altered membrane glycerophospholipid composition and functionality. *J Lipid Res* 54:622-635
- II ²Kilpinen L, Parmar A, Greco D, Lehenkari P, Saavalainen P, Laitinen S (2016) Expansion induced microRNA changes in bone marrow mesenchymal stromal cells reveals interplay between immune regulation and cell cycle. *Aging (Albany NY)* 8:2799-2813
- III ³Kilpinen L*, Impola U*, Sankkila L, Ritamo I, Aatonen M, Kilpinen S, Tuimala J, Valmu L, Levijoki J, Finckenberg P, Siljander P, Kankuri E, Mervaala E, Laitinen S (2013) Extracellular membrane vesicles from umbilical cord blood-derived MSC protect against ischemic acute kidney injury, a feature that is lost after inflammatory conditioning. *J Extracell Vesicles* 2: 10.3402/jev.v2i0.21927. eCollection 2013

The publications are referred to in the text by their roman numerals I-III. The original publications are reproduced with the permission of their copyright holders. In addition, some unpublished results are presented.

* The authors have equally contributed to the study. The publication has been included in the thesis of Feven Tigistu-Sahle.

1 Author designed the experiments, performed cell culture and functionality experiments, analyzed the data and wrote the manuscript.

2 Author designed the experiments, performed cell culture experiments, analyzed the data and wrote the manuscript

3 Author designed the experiments, performed co-culture assays, analyzed the data and wrote the manuscript

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Laitinen A, Lampinen M, Liedtke S, **Kilpinen L**, Kerkelä E, Sarkanen JR, Heinonen T, Kögler G, Laitinen S (2016) The effects of culture conditions on the functionality of efficiently obtained mesenchymal stromal cells from human cord blood. *Cytotherapy* 18:423-437

Laitinen, A, Oja S, **Kilpinen L**, Kaartinen T, Moller J, Laitinen S, Korhonen M, Nystedt J (2016) A robust and reproducible animal serum-free culture method for clinical-grade bone marrow-derived mesenchymal stromal cells. *Cytotechnology* 68:891-906

Kerkelä E, Hakkarainen T, Mäkelä T, Raki M, Kambur O, **Kilpinen L**, Nikkilä J, Lehtonen Siri, Ritamo I, Pernu R, Pietilä M, Takalo R, Juvonen T, Bergström K, Kalso E, Valmu L, Laitinen S, Lehenkari P, Nystedt J (2013) Transient Proteolytic Modification of Mesenchymal Stromal Cells Decreases Lung Entrapment and Increases Targeting to Injured Tissue. *Stem Cells Transl Med* 2:510-520

ABBREVIATIONS

AKI	Acute kidney injury
α MEM	Minimum essential medium alpha
AT-MSC	Adipose tissue derived mesenchymal stromal cells
ATN	Acute tubular necrosis
ATP	Adenosine triphosphate
BM-MSC	Bone marrow derived mesenchymal stromal cells
CB-MSC	Cord blood derived mesenchymal stromal cells
CFSE	Carboxyfluorescein diacetate N-succinimidyl ester
COX	Cyclooxygenase
DC	Dendritic cell
DHA	Docosahexaenoic acid
FA	Fatty acid
FAME	Fatty acid methyl ester
FBS	Fetal bovine serum
GPL	Glycerophospholipid
EPA	Eicosapentaenoic acid
ESI-MS	Electrospray ionization mass spectrometry
EVs	Extracellular vesicles
IDO	Indoleamine 2,3-dioxygenase
IFN γ	Interferon gamma
IRI	Ischemia-reperfusion injury
HLA	Human leukocyte antigen
HO	Hemoxygenase
HSC	Hematopoietic stem cell
MHC	Major Histocompatibility Complex
mRNA	Messenger RNA
miRNA	MicroRNA
MSC	Mesenchymal stromal/stem cells
NTA	Nanoparticle tracking analysis
PBMC	Peripheral blood mononuclear cell
PUFA	Polyunsaturated fatty acid
SDF-1	Stem cell derived factor-1
SASP	Senescence associated secretory phenotype
SPM	Specialized pro-resolving mediators
TNF α	Tumor necrosis factor alpha
Treg	Regulatory T-cell

ABSTRACT

Human mesenchymal stem/stromal cells (hMSCs) are currently used in many advanced cellular therapies. The clinical use of hMSCs requires extensive cell expansion, but the consequences of expansion, especially at the molecular level, are not fully understood. The therapeutic effect of MSCs is mediated at least partially via paracrine interactions with immune cells modulating both innate and adaptive immune response. Membrane glycerophospholipids (GPLs) provide precursors for signaling lipids, which modulate cellular functions, including immunological effects via eicosanoids and docosanoids.

The aim of this study was to investigate the effect of the donor's age and cell doublings on the GPLs, gene expression and microRNA (miRNA) profiles of human bone marrow MSCs (hBM-MSC). In order to gain more insight into the functional mechanisms of MSCs, we investigated the extracellular vesicle (EV) secretion from human umbilical cord blood derived MSCs (hCB-MSC), and evaluated their immunosuppressive capacity *in vitro* as well as their possible immunomodulative and protective effect in kidney ischemia-reperfusion injury (IRI) *in vivo*. We were able to demonstrate that the hBM-MSCs, harvested from 5 young adults and 5 old donors, showed clear compositional changes in their GPL profiles during expansion. Most strikingly, the molar ratio of prostaglandin E2 precursor arachidonic acid (20:4n-6) containing species of phosphatidylcholine and phosphatidylethanolamine accumulated, while the species containing monounsaturated fatty acids decreased during passaging. The lipid changes correlated with the decreased immunosuppressive capacity of hBM-MSCs during expansion, suggesting a connection between lipid signaling and immunomodulatory functions. The existence of such a connection was further supported by gene expression results for several enzymes involved in lipid metabolism and immunomodulation. Our results show that extensive expansion of hBM-MSCs harmfully modulates membrane GPLs, affecting lipid signaling, and eventually impairing functionality.

Although we were able to see clear alterations in gene expression levels and lipid profiles, the miRNA expression was more stable. To summarize, the expression levels of 37 miRNAs were changed in the old donors group and 36 miRNAs were changed in the young donors group. Of these, only 12 were differentially expressed in both young and old donor BM-MSCs and their predicted target mRNAs, the expression of which was changed, were mainly linked to cell proliferation and senescence. Interestingly, members of the well-studied miR-17/92 cluster, which is involved in cell cycle regulation, aging and the development of immune system, were down-regulated especially in the old donors group. The role of this cluster in MSC

functionality is worth future studies since it links expansion, aging and immune system together.

When we studied the immunological effect of EVs derived from CB-MSC, we were able to demonstrate their immunological potential both *in vitro* and *in vivo*. Interestingly, these properties were weakened especially in the animal model when MSCs were preconditioned with interferon gamma. A comparative mass spectrometric analysis revealed a clear distinction in the protein content of the IFN γ stimulated EVs. We discovered that two differently produced EV pools contained specific Rab proteins suggesting that, depending on external signals, the same cells produce vesicles originating from different intracellular locations, which also influences their functional properties.

In conclusion, these studies provide a detailed analysis of molecular changes during MSC expansion. The present study demonstrates that the combination of *in vitro* and *in vivo* models accompanied with a detailed analysis of molecular characteristics is essential to a profound understanding of the complexity of the MSC paracrine regulation.

1 INTRODUCTION

Mesenchymal stem/stromal cells (MSCs) were first described as non-hematopoietic progenitor cells from the bone marrow in the 1960's by Friedenstein and co-workers (Friedenstein et al. 1968). Traditionally minimal criteria of International Society for Cellular Therapies (ISCT) defines MSCs as plastic adherent fibroblast like cells that are capable of differentiating into adipocytes, osteoblasts and chondrocytes and that express certain cell surface markers (CD73, CD90 and CD105) but not hematopoietic markers (CD14, CD19, CD34, CD45, and HLA-DR) (Dominici et al. 2006). One of the most fascinating properties of MSCs is their versatile ability to modulate immune cells and enhance the repair of injured tissue. The immunomodulative capacity has made MSCs one of the most attractive cell types for advanced cellular therapies and therefore ISCT suggests that an immunosuppression assay should be included in the releasing criteria for a clinical-grade MSC product (Galipeau et al. 2016).

After the initial discovery in the bone marrow, MSCs have been isolated from several other adult and fetal tissues. It has been suggested that MSCs reside inside all tissues nearby perivascular space (da Silva Meirelles et al. 2008). However, the identification of MSCs' *in vivo* location and physiological role has been extremely challenging, and little is known about their true identity and role in the tissue homeostasis. Several molecular mechanisms have been described, but many open questions still remain. How do these cells perform their function and how many different types of MSCs are there in the body?

After establishment, MSCs are expanded *in vitro*. MSCs, like other primary cells, are not able to divide infinitely, but reach cellular senescence. In recent years, the use of autologous MSCs in several indications impacting aged patients has increased. Donor age introduces another dimension to the puzzle of MSC therapy. The effects of donor age and extensive expansion on the characteristics and functionality of hBM-MSCs are worth studying, in order to develop more efficient MSC therapies.

2 REVIEW OF THE LITERATURE

2.1 Mesenchymal stromal cell niche

Niches are local tissue microenvironments that maintain and regulate stem cells. Hematopoietic stem cell (HSC) niches are present in diverse tissues throughout the development, beginning with the yolk sac, followed by placenta, fetal liver and finally bone marrow (Mikkola and Orkin 2006). In the adult human body, bone marrow has many crucial functions. Most importantly bone marrow is the scene of hematopoiesis, a process that leads to formation of all blood cells. Hematopoietic stem cells (HSC) are self-renewing and multipotent cells giving rise to all blood cells of the myeloid and lymphoid lineages (**Figure 1**). The HSC pool comprises actively self-renewing HSCs (ST-HSC) and quiescent long-term HSCs (LT-HSC). The bone marrow microenvironment seems to be adapted to support these HSC properties. Using mouse as the animal model, it has been suggested that these two types of HSCs are located in different places: LT-HSCs near the endosteum (endosteal niche) and ST-HSC in connection with sinusoidal endothelium (perivascular niche) (Wilson et al. 2008). HSCs are located in the bone marrow in accordance with their differentiation state, and it is the blood flow rate rather than the actual distance from the endosteum that defines the niche (Winkler et al. 2010a). The development of more specific labels to identify HSCs *in vivo* has shown that most of the HSCs are found near sinusoids in the highly vascular endosteal region (Nombela-Arrieta et al. 2013).

In addition to HSCs, a heterogeneous population of stromal cells is found in the bone marrow. A small proportion of these MSCs exhibit stem cell characteristics, such as self-renewing capacity and differentiation potential into adipocytes, osteoblasts and chondrocytes (**Figure 1**). The identification of MSCs *in vivo* is challenging and therefore MSCs are defined according to their characteristics *in vitro*. In mice, several mesenchymal progenitors, such as CXC chemokine ligand (CXCL) 12 abundant reticular (CAR) cells (Omatsu et al. 2010, Sugiyama et al. 2006), stem cell factor expressing cells (Ding et al. 2012), nestin expressing cells (Mendez-Ferrer et al. 2010) and platelet derived growth factor receptor α (PDGFR- α)⁺, Sca-1⁺, CD45⁻ and Ter119⁻ cells (Ding and Morrison 2013, Greenbaum et al. 2013), have been described. All these cells possess highly similar properties, indicating that bone marrow may contain several different pools of MSCs with different roles in the regulation of HSCs. In human bone marrow, CD146⁺ osteoprogenitors with self-renewing capacity have been described, indicating that stromal cells are necessary for maintaining HSC niche also in the human bone marrow (Sacchetti et al. 2007).

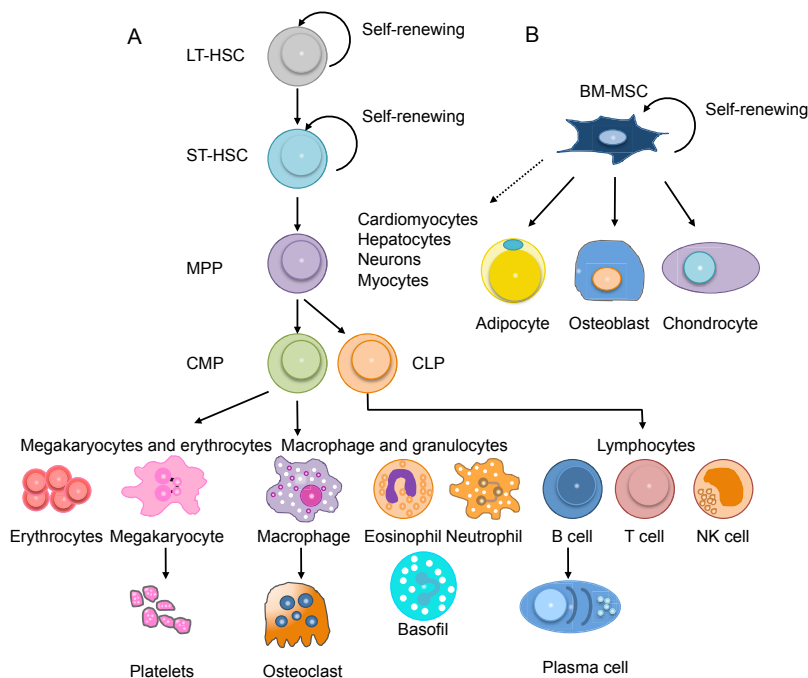


Figure 1 The regenerative cells of the bone marrow niche. A. Hematopoietic stem cells (HSC) are precursors of all mature blood cells. A proportion of these self-renewing cells remain undifferentiated to maintain a pool of long-term reconstituting HSCs (LT-HSC) and short term reconstituting HSCs (ST-HSC). **B.** Bone marrow mesenchymal stromal cells (BM-MSCs) are multipotent, self-renewing progenitor cells that can differentiate into other cell types. Abbreviations: CLP, common lymphoid progenitor cell; CMP, common myeloid progenitor; MPP, multipotent progenitor; NK cell, natural killer cell. Adapted by permission from Macmillan Publishers Ltd: Nature Reviews Rheumatology 12:154:168, copyright 2015.

Recent advances in imaging techniques have elucidated the location and role of MSCs in the microenvironment of bone marrow. Similar findings in fetal human bone marrow are available, (Pinho et al. 2013) but a more detailed analysis of the HSC niche in humans is required. According to the animal studies, MSCs reside mostly perivascularly together with HSCs, but traffic to the endosteal surface to differentiate into osteoblasts (Morrison and Scadden 2014). Recently, a new pool of progenitor cells was described and called bone lining cells. These cells are located on the endosteal surface and act as precursors for osteoblasts and osteoclasts (Matic et al. 2016). The adipogenic potential of these cells has yet to be investigated, but these results reinforce the possibility of secondary pool of MSCs in the bone marrow. One of the major tasks of MSCs is to create a supportive microenvironment for HSCs self-renewal and quiescence in the bone marrow (Mendez-Ferrer et al. 2010, Omatsu et al. 2010). MSCs produce stem cell factor (SCF) and stromal derived factor (SDF1_α) also called CXCL12, and other cytokines that promote the maintenance of HSCs (Sacchetti et al. 2007). In addition to the soluble molecules, miRNAs, delivered in extracellular vesicles, may act as one

mechanism for the maintenance of HSCs (De Luca et al. 2016). The interaction between MSCs and HSCs is far more complex and studies have shown that also HSCs secrete cytokines relevant to the proliferation and differentiation of MSCs as well as to the inhibition of their senescence (Zhou 2015).

Besides HSCs and MSCs, there are several other cell types residing in the niche that are essential for its function. These include osteoblasts, osteoclasts endothelial cells, bone marrow adipocytes, megakaryocytes, tissue resident macrophages, immune cells, and neurons (**Figure 2**). Osteoblasts were the first cell population shown to have an influence on HSCs. Two groups showed with animal models that osteolineage cell activation increased HSC number *in vivo* (Calvi et al. 2003, Zhang et al. 2003). The interaction of angiopoietin-1, expressed by osteoblasts, with its receptor Tie-2, expressed by HSCs, is shown to be essential for HSC quiescence (Arai et al. 2004). Also, local calcium ion concentration has been shown to recruit HSCs to endosteum via calcium sensing receptors (Adams et al. 2006). Osteoclasts are derived from the HSCs in the bone marrow. There is evidence that in addition to participating in the remodeling of the bone, osteoclasts also regulate the HSC niche through the degradation of CXCL12 and SCF (Kollet et al. 2006). Currently, the roles of endosteum, as a regulatory region, and osteoprogenitor cells in the maintenance of HSCs are acknowledged, but mature osteoblasts and osteoclast contribute to the HSC maintenance most likely indirectly through the modulation of the microenvironment (Morrison and Scadden 2014).

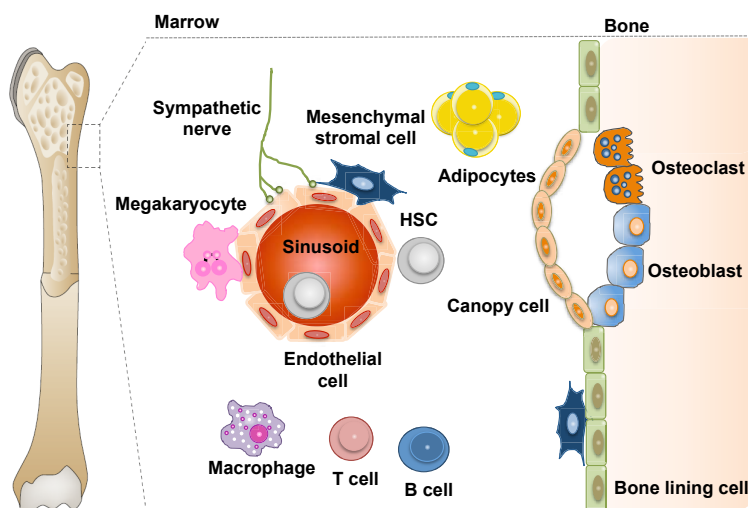


Figure 2 Structure and cellular components of bone marrow niche. Bone marrow is a complex organ containing hematopoietic and non-hematopoietic cell types. The interface of bone marrow is called endosteum, which is covered by bone lining cells, osteoblasts and osteoclasts. Sinusoids are specialized blood vessels that allow trafficking of cells into circulation. Adapted by permission from Macmillan Publishers Ltd: Nature Reviews Rheumatology 12:154-168, copyright 2015.

Sinusoidal endothelial cells participate in the maintenance of HSCs by expressing SDF-1 (Greenbaum et al. 2013), SCF (Ding et al. 2012) vascular endothelial growth factor (VEGF) receptor 2 (Hooper et al. 2009) and e-selectin (Winkler et al. 2012). Megakaryocytes contribute to the niche by supporting HSC quiescence through the production of CXCL4 and transforming growth factor (TGF)- β (Bruns et al. 2014, Zhao et al. 2014b). Marrow adipocytes residing near the endosteal surface do not only act as a filler in the bone marrow, but are also necessary for the maintenance of HSC quiescence through endocrine and paracrine effects (Naveiras et al. 2009). Bone marrow resident macrophages are distributed throughout the bone marrow and are necessary for the endosteal bone marrow niche. Macrophages regulate HSC dormancy by keeping them in their stem-cell state while supporting bone formation via the regulation of MSC osteogenic differentiation (Chang et al. 2008, Winkler et al. 2010b). Finally, the sympathetic nervous system regulates CXCL12-expression in the bone marrow and further HSC mobilization to the circulation (Katayama et al. 2006). HSC mobilization follows physiologically regulated circadian rhythms. Cyclic release of HSCs and downregulation of CXCL12 are regulated by molecular clock genes mediated by circadian release of noradrenaline from sympathetic nerves. The signal is mediated through β 3 adrenoreceptor that is expressed by MSCs (Mendez-Ferrer et al. 2008).

If the bone marrow is the scene of hematopoiesis in the adult human body, placenta is a unique hematopoietic organ during the development (Gekas et al. 2005). In contrast to the bone marrow, HSCs are not maintained in dormancy during the development but expand actively without differentiation. HSCs are formed in the large vessels of chorionallantoic mesenchyme and expand in the placental vascular labyrinth. In humans, HSCs seems to be present in the placenta throughout the development. Similar to the bone marrow, the placenta contains stromal cells that support HSCs *in vitro* (Robin et al. 2009). In the human placenta, MSCs are located particularly in the chorionic villi of the placenta residing near blood vessels and regulate vessel maturation and stabilization (Castrechini et al. 2010). The regulation of the HSC niche is complex and involves the activity of several cell types including MSCs, trophoblasts and endothelial cells. One of the key mechanisms for regulating HSCs in the placenta is PDGF-B signaling (Chhabra et al. 2012). Compared to the bone marrow, cellular components and molecular signals maintaining the microenvironment in the placenta are not well understood.

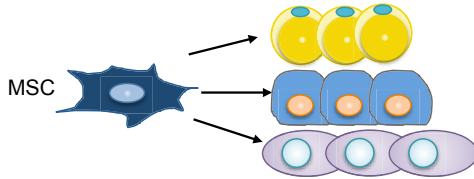
2.2 Mesenchymal stromal cells in cell therapy

MSCs have several properties that make them an intriguing tool for cellular therapy. They have been considered immune privileged since they express low levels of major histocompatibility complex class 1 (MHCI) and they do not constitutively express MHC class II or costimulatory molecules such as CD40, CD80, and CD86 (Tse et al. 2003). These features could protect them from alloreactive natural killer (NK) cell lysis and promote their survival and growth in an allogenic environment (Sotiropoulou et al. 2006). Later studies have shown that MSCs are rejected by NK cells and therefore they should be considered immune evasive rather than immune privileged (Ankrum et al. 2014). MSCs have the ability to home to the sites of inflammation (Spaeth et al. 2008) and perform immunomodulatory functions in the injured tissue. MSCs use both direct cell-to-cell contact as well as secreted soluble immunosuppressive molecules to interact with a wide range of immune cells, including T cells, B cells, NK cells, dendritic cells, and macrophages.

Although MSCs are able to differentiate into various cell types, many of their favorable effects are mediated through cell-to-cell communication, which inhibits inflammation and stimulates the recovery of injured tissue (**Figure 3**). MSCs communicate with target cells either via paracrine signaling or direct cell-to-cell contact. In addition to soluble molecules like bioactive lipids, growth factors and cytokines, paracrine mechanisms of MSCs include secreted extracellular vesicles (EVs). EVs encompass different types of vesicles that differ by their route of origin. Shedding vesicles or microvesicles are produced by outward budding and fission of plasma membrane. Exosomes originate inside cellular multivesicular endosome (MVE) and apoptotic bodies originating from the shedding cells during programmed cell death (Raposo and Stoorvogel 2013). Most studies have not clearly defined the origin of EVs since the development of methods to discriminate between exosomes and microvesicles constitutes a major challenge. Differences in properties such as size, morphology, buoyant density, and protein composition seem insufficient for a definitive distinction (Bobrie et al. 2011). EVs participate in cell-to-cell communication by transferring functionally relevant biomolecules such as proteins, mRNA, and miRNA (Ragni et al. 2017, Tomasoni et al. 2013, Valadi et al. 2007).

MSC mediated immunomodulative and angiogenesis promoting effects are decreased when transwell systems are used, indicating that at least some of the MSC functions are mediated via contact dependent signaling. Besides direct protein-interaction mediated intercellular signaling, MSCs have also been shown to utilize tunneling nanotubes to transfer molecules and even cell organelles such as mitochondria to the target cells such as macrophages and T-cells (Jackson et al. 2016, Liu et al. 2014, Matula et al. 2016).

A. Differentiation of MSCs to replace cells



B. Cell-to cell communication

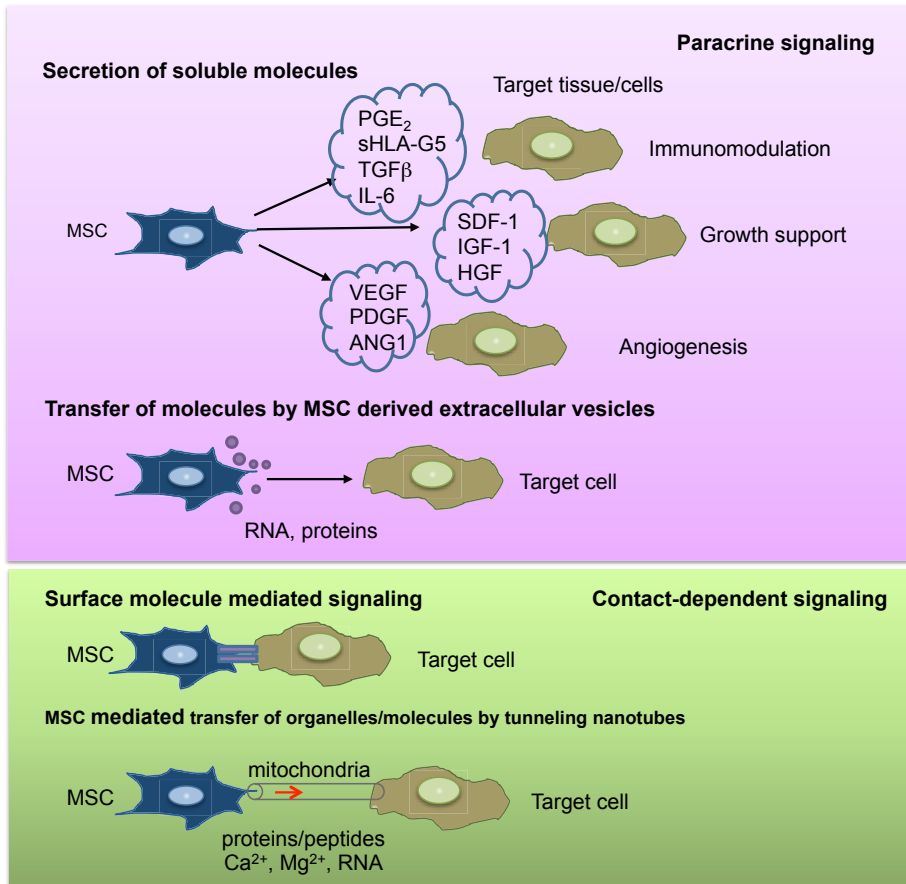


Figure 3 MSCs repair injured or damaged tissues by diverse mechanisms. A. Differentiation into different cell types to replace cells in the damaged tissue. **B.** Intercellular signaling includes paracrine and contact-dependent mechanisms. Paracrine mechanisms include secretion of soluble molecules such as growth factors, hormones and cytokines and secretion of extracellular vesicles to transfer protein/peptides, RNA or other molecules. Contact-dependent signaling is mediated by surface proteins or tunneling nanotubes. Abbreviations: PGE₂, prostaglandin E₂; sHLA-G5, soluble human leukocyte antigen G5; TGFβ, transforming growth factor beta; IL-6, interleukin-6; SDF-1, stromal-derived factor-1; IGF-1, insulin-like growth factor-1; HGF, hepatocyte growth factor; VEGF, vascular endothelial growth factor; PDGF, platelet-derived growth factor; ANG1, angiopoietin-1. Figure is adapted from (Spees *et al.* 2016) under license <http://creativecommons.org/licenses/by/4.0/>

The beneficial properties of MSCs are utilized for various indications in clinical trials and the number of ongoing trial is continuously increasing. As of August 2016, the clinical trials database (<http://www.clinicaltrials.gov>) showed 418 clinical trials using MSCs for various indications (**Figure 4**). Bone marrow is still the most commonly used source of MSCs (n=204), but other tissues, especially adipose tissue (n=79) and umbilical cord (n=53), are also often used. In particular, interest in adipose tissue as autologous source of MSCs is increasing.

Most of the clinical trials are in Phase I (safety studies, n=147) or in combined Phase I and II (n=151). A total of 84 studies have reached phase II (proof of concept for human patients). Only 18 studies are currently in phase III (comparison of new treatment with standard treatment) and 13 studies are in combined Phase II and Phase III. In general, MSCs appear to be well tolerated and safe. In meta-analysis, a significant association between MSC administration and transient fever was reported (Lalu et al. 2012).

Fetal bovine serum (FBS) has historically been considered essential for obtaining MSCs of high quantity and quality. However, FBS carries the risk of transmitting immunogenic xenoproteins or infectious agents. The development of human supplements, such as platelet rich plasma or platelet lysate, has led supplements to produce high-quality clinical-grade MSCs for therapeutic applications (Bieback et al. 2009, Juhl et al. 2016, Laitinen et al. 2016a). Also, the actual composition of nutrients in FBS has not been optimized and especially the fatty acid composition may not be optimal in terms of the best possible therapeutic outcome (Tigistu-Sahle et al. 2017). Despite the availability of animal serum-free culture methods, FBS is still the most commonly used medium supplement in expansion of MSCs since only seven clinical trials reported the usage of a human medium supplement.

The most significant results on the immunosuppressive effects of MSCs so far have been observed in the treatment of acute graft versus host diseases (GVHD) after allogenic hematopoietic stem cell transplantation (Le Blanc et al. 2008). After the first trials, MSCs have been shown to be a promising new therapy for both acute and chronic steroid resistant GVHD (Chen et al. 2015). Recently, the use of MSCs has been expanded to other hematological disorders (Cle et al. 2015) and co-transplantation in allogenic HSC transplantation to prevent GVHD or improve the engraftment (Liu et al. 2011a). Based on their ability to modulate T-cell proliferation and function, MSCs have also been proposed as a therapeutic tool for Chron's disease (Forbes et al. 2014), autoimmune diseases (Wang et al. 2014), diabetes (Carlsson et al. 2015), renal transplantation rejections (Reinders et al. 2015), and in the treatment of various immune-mediated neurodegenerative disorders such as amyotrophic lateral sclerosis (Oh et al. 2015, Petrou et al. 2016) and multiple sclerosis (Karussis et al. 2010, Llufriu et al. 2014). Osteoarthritis is a disorder that leads to cartilage damage associated with synovial inflammation. The immunomodulatory capacity of AT-MSCs is used to alleviate osteoarthritis in the knee and other sites (Pers et al. 2016).

The regenerative potential and particularly the differentiation capacity into osteoblasts exhibited by MSCs have given rise to studies investigating their therapeutic use in osteogenesis imperfecta (Gotherstrom et al. 2014). Even though the majority of the experimental evidence on differentiation capacity of MSCs comes from *in vitro* experiments, there are also results indicating that engrafted MSCs can promote tissue regeneration by differentiating into tissue-specific cells *in vivo* such as cardiomyocytes needed for repair of injured tissues (Gojo et al. 2003). Later it has been shown that the trophic effects of MSCs are of great significance in tissue regeneration. After engraftment, MSCs produce a number of molecules that can not only reduce inflammation but also stimulate tissue generation by promoting cell-to-cell connections (Plotnikov et al. 2008). The regenerative potential of MSCs is nowadays harnessed to treat various conditions such as, ischemic cardiomyopathy (Hare et al. 2009), liver diseases (Shi et al. 2012, Zhang et al. 2012), spinal cord injury (Mendonca et al. 2014, Satti et al. 2016), and stroke (Honmou et al. 2011, Lee et al. 2010).

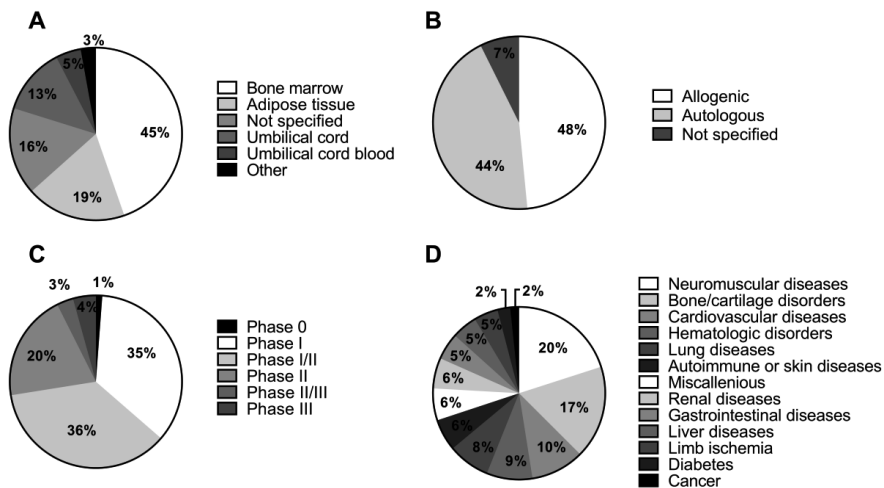


Figure 4 Summary of clinical trials using MSCs. The data were derived from ClinicalTrials.gov (<http://www.clinicaltrials.gov>) on August 8, 2016. Keywords “mesenchymal stromal cells OR mesenchymal stem cells” were used. Trials with unknown status or terminated before enrolment were excluded from the analysis, n=418 **A.** Tissue sources of MSCs currently used. “Not specified” category includes trials that did not clearly state their cell sources including trademark products. “Other” includes tissue sources such as menstrual blood or skin. **B.** Donor type of MSCs used in clinical trials **C.** Current phases of clinical trials **D.** Clinical indications that are targeted with MSC therapy. Disorders are divided in larger categories.

MSC therapy in acute kidney injury

Acute kidney injury (AKI) is a common clinical syndrome in hospitalized patients, particularly those with chronic kidney disease, diabetes, and vascular diseases. Furthermore, 30-40% of all cases of AKI observed during hospitalization occur in the context of surgical operations and especially after cardiovascular surgery. AKI is currently defined as a rapid decrease in kidney function as measured by an increase in serum creatinine and/or urine output (Erpicum et al. 2014, Tögel and Westenfelder 2012). AKI commonly involves tubular damage called acute tubular necrosis (ATN) and a reduced glomerular filtration rate caused by transient ischemia and reperfusion (I/R) (Schrier et al. 2004). Pathophysiology of I/R consists of diverse metabolic and inflammatory events. A rapid drop in oxygen and nutrition concentrations leads to vasoconstriction, separation of tubular cells and obstruction of tubules. Even though oxygen supply limits oxidative phosphorylation, anaerobic glycolysis allows a residual production of ATP. However, the formation of lactate results in the acidification of cell cytosol, finally leading to the disruption of mitochondrion and cell functions. In addition, the lack of energy delivery induces morphologic changes, including disruption of the cytoskeleton and intercellular tight junctions, loss of cell polarity and the translocation of the Na⁺/K⁺ATPase transporter from the basolateral membrane to the cytoplasm causing apoptosis of tubular cells (Schrier et al. 2004, Seo-Mayer et al. 2011).

Both innate and adaptive immune responses are important in the pathology of ischemic kidney injury. Injured tubular epithelium releases pro-inflammatory cytokines and chemokines, which aid in recruiting immune cells. Epithelial cells also express adhesion molecules, toll-like receptors (TLRs), complement and complement receptors, and T cell costimulatory molecules, which activate the immune cells (Bonventre and Yang 2011). T cells are key mediators in the renal IRI (Ascon et al. 2006). The recruitment of regulatory T cells is one of the anti-inflammatory mechanisms in the recovery of an injured kidney (Gandolfo et al. 2009, Kinsey et al. 2010). Recently, the importance of TLR9 in Treg recruitment in AKI was demonstrated (Alikhan et al. 2016).

Currently, available treatments are largely supportive, including fluid maintenance, vasoactive drugs, cytoprotective therapy, and dialysis (Thakar 2013). There is a clear need for novel therapeutic approaches to increase the survival rate in AKI. Even when injured, the kidney has a great regeneration potential. MSCs could offer an innovative approach to the promotion of proliferation and differentiation of progenitor cells inside the kidney and inhibition of inflammation. Previous studies based on animal models have shown the effectiveness of MSCs derived from bone marrow (Alfarano et al. 2012, Morigi et al. 2008, Wise et al. 2014), adipose tissue (Furuichi et al. 2012), and umbilical cord blood (Jang et al. 2014) in the treatment of IRI. In addition, other models using glycerol (Herrera et al. 2004, Qian et al. 2008)

or cisplatin (Qi and Wu 2013) to induce kidney injury have been used to study the therapeutic effect of MSCs. In the initial clinical trials, the safety and feasibility of MSC therapy were assessed in patients with a high risk of developing AKI after cardiac surgery (Gooch et al. 2008, Tögel and Westenfelder 2012). Two phase II trials aimed at showing the efficacy of MSC treatment in AKI patients are on-going (NCT01275612 and NCT01602328), but no results have been reported so far for these trials.

The mechanisms of MSCs-mediated renoprotective functions are divided into differentiation-dependent and differentiation-independent mechanisms. Although studies in both animals and humans have shown that MSCs are able to differentiate into tubular epithelial cells (Herrera et al. 2004, Morigi et al. 2004), the primary modes of action are considered to be paracrine and also endocrine since only very limited engraftment and differentiation into target cells have been observed *in vivo* (Morigi et al. 2008). More recently, Zhao *et al.* (2014a) showed that an intrarenal injection of MSCs resulted in differentiation into vascular endothelial cells indicating that at least part of the regenerative potential could after all be differentiation-dependent.

The paracrine action of MSCs involves the delivery of trophic factors and anti-inflammatory soluble molecules to the kidney. AKI causes a significant up-regulation of SDF-1 and hyaluronic acid in the kidney, thus resembling the microenvironment in the bone marrow niche. Infused MSCs are able to home to the injured kidney through the use of homing receptors CXCR4 (SDF-1 receptor) and CD44 (the hyaluronic acid receptor) (Herrera et al. 2007, Tögel et al. 2005b). The expression of CXCR4, however, decreases during *in vitro* cell culture, thus reducing the homing ability of transfused MSCs. There is an elevated expression of transforming growth factor β (TGF β) in I/R injured kidneys, which induces the expression of CXCR4 on cell membranes, resulting in enhanced homing of MSCs (Si et al. 2015). Also, *in vitro* hypoxic preconditioning is shown to increase the expression of CXCR4, further enhancing the homing and therapeutic effects in AKI (Liu et al. 2012a).

MSCs *in situ* adapt their gene expression profile in response to extracellular signals and, via cross-talk, regulate the gene expression of renal epithelial, endothelial, and immune cells. MSCs down-regulate the expression of pro-inflammatory TNF- α , IL-1 β , and IFN- γ , and significantly up-regulate gene expression of anti-inflammatory cytokine IL-10, antiapoptotic BCL-2, basic fibroblast growth factor (bFGF), and transforming growth factor α (TGF α) in order to accelerate the repair process in the injured kidney (Tögel et al. 2005a).

MSCs release vascular endothelial growth factor (VEGF), insulin-like growth factor 1 (IGF-1), hepatocyte growth factor (HGF), and SDF-1, which exert anti-apoptotic, mitogenic, and angiogenic functions in AKI (Imberti et al. 2007, Tögel et al. 2009, Zarjou et al. 2011). The secretion of anti-inflammatory factors, such as prostaglandin E2 (PGE2), TGF β , HLA-G5, and HGF, can down-regulate several types of immune cells, such as T cells (both

CD4⁺ and CD8⁺), NK cells, B cells, dendritic cells, and macrophages. The relevance of these factors in IRI has yet to be fully studied. In addition to soluble molecules, MSCs release extracellular vesicles as part of their paracrine mechanisms to transfer mRNA, miRNA, and other molecules to the injured cells to protect against AKI or to induce recovery (Bruno et al. 2009, Collino et al. 2015, Tomasoni et al. 2013). In contrast, Xing *et al.* (2014) used MSC conditioned medium to show no effect in AKI.

In IRI induced AKI, the lack of oxygen causes one of the most immediate effects by depressing the oxidative phosphorylation in mitochondria. Recently, MSCs have been shown to fully restore mitochondrial respiration, resulting in enhanced ATP synthesis in kidney mitochondrion after I/R (Beiral et al. 2014).

2.3 Immunomodulative mechanisms of MSCs

MSCs affect both innate and adaptive immune systems by suppressing the proliferation of T cells, maturation and antigen presentation of dendritic cells, and the proliferation and antibody production of B cells, by inhibiting the cytokine production and cytotoxicity of NK cells, and by promoting the generation of regulatory T cells. The full picture of how MSCs regulate different immune systems remains unclear. A number of mechanisms have been reported, involving cell-to-cell contact, secretion of soluble factors and extracellular vesicles, and induction of anergy, apoptosis, and regulatory cells (**Figure 5**). In the immune system, immune cells and non-immune cells are linked together in a complex network of cytokine production and responses. MSCs are not considered to be immune cells, but should be regarded as coordinators of immune system (Hoogduijn 2015).

When lymphocytes are activated, they proliferate and differentiate to execute their effector functions. Various stimulants can be used to activate T cell proliferation. MSCs are shown to inhibit dose dependently T-cell proliferation induced by alloantigens (Krampera et al. 2006, Meisel et al. 2004, Ryan et al. 2007), polyclonal activators such as PHA (Aggarwal and Pittenger 2005) and antiCD3/CD28 (Castro-Manreza et al. 2014, Melief et al. 2013). This immunosuppressive capacity has been demonstrated by using both peripheral blood mononuclear cells and populations enriched in CD3⁺, CD4⁺, and CD8⁺ T cells. Besides proliferation, MSCs can modulate T cell differentiation into subtypes characterized by the secretion of a set of cytokines. For instance, MSCs inhibit the production of proinflammatory cytokines IL-17, IL-22, IFN γ , and TNF α and the differentiation of naïve CD4⁺ lymphocytes to Th17 cells. Additionally, MSCs promote the production of IL10 and the expression of transcription factor Foxp3, indicating differentiation toward Treg phenotype (Ghannam et al. 2010). Recently, it has been suggested that these phenomena are not independent; instead,

MSCs are able to convert Th17 cells into cells with a Treg phenotype (Obermajer et al. 2014).

B lymphocytes are involved in the adaptive immune response. These cells are responsible for humoral immunity and are specialized in antibody production. MSCs from healthy human donors can inhibit normal B cell proliferation, differentiation, and antibody secretion (Corcione et al. 2006). When purified mouse B cells were used, MSCs seemed to induce the proliferation and differentiation of B cells (Traggiari et al. 2008). This phenomenon can be explained by cross-talk between T and B cells. The signals arising from T cells are required for MSCs to apply their immunomodulatory effects on B cells (Rosado et al. 2015).

Dendritic cells (DC) are the most important antigen presenting cells in the body. DCs must undergo maturation to initiate an appropriate immune response and during this process, DCs increase their expression of HLA class II molecules and costimulatory molecules CD80 and CD86. MSCs have an effect on the recruitment, maturation, and function of DCs. MSCs can significantly reduce monocyte differentiation into DCs, affecting the upregulation of costimulatory molecules and other dendritic cell markers (Spaggiari et al. 2009, Jiang et al. 2005).

Within the innate immune system, macrophages are key players in initiating and controlling inflammation. Monocytes arriving at the site of inflammation can differentiate into activated pro-inflammatory M1 macrophages or convert into alternatively activated anti-inflammatory M2 macrophages (Mantovani et al. 2013). The production of proinflammatory M1 macrophages or T cells may activate MSCs and trigger the release of mediators that skew the differentiation of monocyte toward M2 profile (Le Blanc and Mougiakakos 2012). Together with macrophages, NK cells are important in innate immunity and participate in the body's defenses against infections and cancer. MSCs affect the phenotype, proliferation, cytotoxicity, and cytokine production of NK cells (Sotiropoulou et al. 2006, Spaggiari et al. 2008). Neutrophils act as first line defense in the innate immunity against pathogens. MSCs' interaction with macrophages and NK cells has been described in detail, but neutrophils have been studied to a lesser extent. Recently, Jiang *et al.* (2016) showed that MSCs suppress respiratory burst, apoptosis, peroxidase, and protease release in neutrophils *in vitro*.

Currently, several mechanisms involving both cell-cell contact-dependent and contact-independent mechanisms for MSC immunoregulation have been described. However, the results are derived from co-culture *in vitro* assays, and only little is known about MSCs' immunoregulative capacity and functions *in vivo* (Consentius et al. 2015).

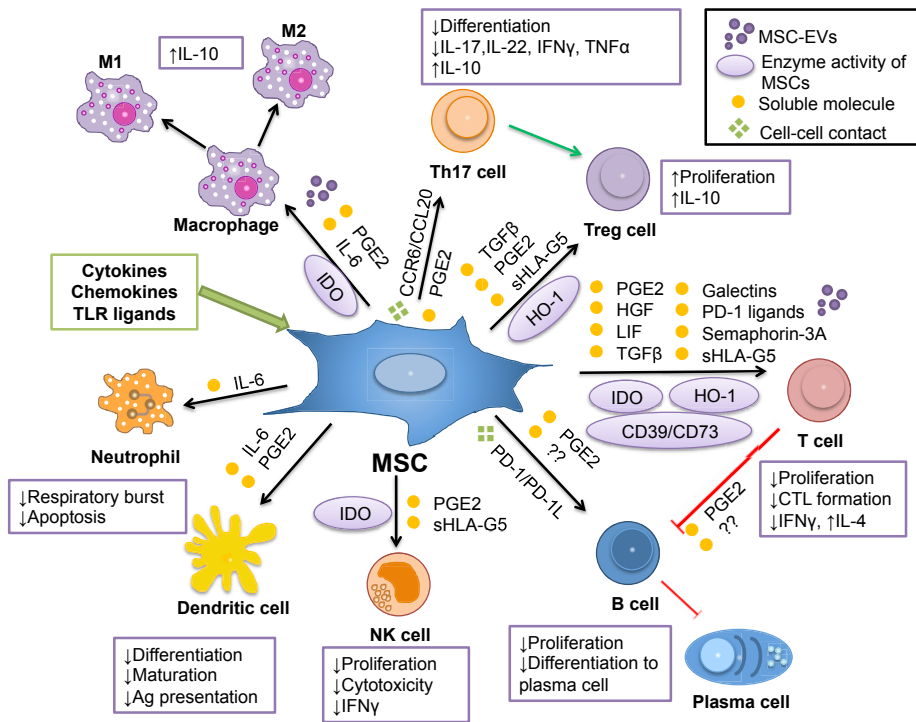


Figure 5 Immunomodulatory effects of MSCs and potential mechanisms in response to inflammatory signals. CTL, Cytotoxic T lymphocyte; HGF, hepatocyte growth factor; HLA, HO, hemioxygenase; human leukocyte antigen; IFN γ , interferon, IL, interleukin; IDO, indoleamine 2,3-dioxygenase; LIF, Leukocyte inhibitory factor; NK, natural killer; PGE2, prostaglandin E2; PD-1, Programmed death-1; TLR, Toll-like receptor

2.3.1 Soluble factors

MSCs regulate immune cells via both cellular contact-dependent and independent mechanisms. The first molecules described in MSC-mediated immunoregulation of alloantigen-activated T-lymphocytes were TGF β 1 and HGF (Di Nicola et al. 2002). MSCs constitutively express TGF β 1 and HGF, which seem to act synergistically (Ryan et al. 2007). TGF β 1 is involved in MSC-mediated generation of CD4 $^{+}$, CD25 $^{+}$ Foxp3 $^{+}$ Tregs (English et al. 2009) and in decreased proliferation of NK cells (Spaggiari et al. 2008).

HLA-G molecules are non-classic HLA molecules that have a limited number of allelic polymorphisms and are expressed in specific tissues. MSCs express the soluble isoform sHLA-G5, which expression is increased by IL-10. The secretion of HLA-G5, which requires direct cell-to-cell contact, has been demonstrated to suppress T-cell proliferation, probably via Treg induction. In addition to adaptive immunity, HLA-G5 regulates innate immunity by decreasing the cytotoxicity and IFN γ production of NK cells (Selmani et al. 2008).

Several other soluble molecules are identified as modulators of MSC-mediated T-cell proliferation including Galectins 1, -3, -9, (Gieseke et al. 2013, Lepelletier et al. 2010, Sioud et al. 2011), Semaphorin 3A, (Lepelletier et al. 2010), LIF1 (Nasef et al. 2008), and PD1 ligands (Davies et al. 2017). Despite several molecules and factors having been described so far, MSCs' immunodulative mechanisms are not yet fully understood. Most of these molecules were identified in *in vitro* blocking assays, and their relevance *in vivo* remains to be investigated.

Prostaglandin E2

Membrane lipids not only are structural components of cell membranes but also mediate biological signals through G-protein activators, second messengers, and nuclear receptors. The structures of glycerophospholipids (GPL), an important group of membrane lipids, are extensively varied. As a consequence of the combination of different polar head groups assembled together with various acyl, alkyl, or alkenyl chains, a single cell can contain more than a thousand different GPL molecular species. Cellular mediators such as inositol phosphates, diacylglycerols, lysophospholipids, ceramides, cleaved fatty acids, or their derivatives are released from membrane lipids. These mediators have been shown to have a crucial role in many physiological processes, including the regulation of immune system and inflammation. The essential polyunsaturated fatty acid (PUFA) arachidonic acid (20:4n-6, AA) is found primarily at the sn-2 position of most membrane phospholipids. It is a precursor for the synthesis of prostaglandins, thromboxanes, and leukotrienes (Funk 2001). PGE₂ is one of the lipid mediators produced from 20:4n-6 in a reaction catalyzed by COX1 and COX2 enzymes. These enzymes are constitutively expressed in MSCs, although COX2 expression increases dramatically in an inflammatory environment. Similarly, the production of PGE₂ is induced by IFN γ and TNF α (Aggarwal and Pittenger 2005). PGE₂ has been shown to have pleiotropic effects on immune cells. PGE₂ inhibits the proliferation of T lymphocytes (Aggarwal and Pittenger 2005) and B lymphocytes (Hermankova et al. 2016) and promotes Treg differentiation (English et al. 2009). PGE₂ is involved in a decrease in differentiation of DCs from monocytes (Spaggiari et al. 2009) and a decrease in proliferation and cytotoxic activity of IL2 activated NK cells (Spaggiari et al. 2008).

Extracellular vesicles

Besides soluble molecules, MSCs secrete EVs that have been demonstrated to possess immunoregulative properties. EVs collected from MSC-conditioned medium suppressed the production of pro-inflammatory cytokines TNF α and IL1 β but increased the concentration of TGF β during *in vitro* culture. In addition, EVs reduced the differentiation of Th17 cells while promoting Treg

differentiation (Chen et al. 2016). Del Fattore *et al.* (2015) reported similar results showing that MSC-EVs promote Treg induction and IL-10 production but do not inhibit the proliferation of CD3⁺ T-cells. As IDO seems to be one of the main mechanisms in MSC mediated immunoregulation, MSC-EVs mediate their functions through IDO-independent mechanisms (Chen et al. 2016, Del Fattore et al. 2015). One possible mechanism might involve CD73 and CD39 enzymatic activity. Kerkelä *et al.* (2016) showed that both MSCs and MSC-derived EVs produce adenosine from adenosine monophosphate. Recently, Di Trapani *et al.* (2016) elegantly demonstrated the uptake of MSC-derived EVs into T, B and NK cells and that the uptake on the effector cells was enhanced by cytokine priming. Most interestingly, only the inhibition of endocytic vesicle production pathway influenced immunomodulation. In addition to regulation of lymphocytes, MSC-EVs have been shown to promote the macrophage polarization toward M2 phenotype (Lo Sicco et al. 2017).

2.3.2 Contact dependent mechanisms

The immunosuppressive capacity of MSCs can only partially be explained by soluble factors. However, in human MSCs only few contact-dependent mechanisms have been identified so far. MSCs express notch ligand Jagged-1, and with the addition of Jagged-1 neutralizing antibody, MSCs recovered their ability to suppress the proliferation of CD4⁺ T cells (Liotta et al. 2008). In inflammatory conditions, MSCs inhibit the differentiation and function of Th17 cells through cell-cell contact, mediated by joint participation of CCR6 and CD11a/CD18, expressed by T-cells, and their respective ligands CCL20 and CD54 (Ghannam et al. 2010).

Instead, in mouse models contact dependent mechanisms have been studied more extensively. In addition to PD1/PD-L1 pathway, which participates in the inhibition of T and B cell activation (Augello et al. 2005, Hermankova et al. 2016), other membrane proteins, such as Fas-FasL and adhesion molecules intercellular adhesion molecule 1 (ICAM1), and vascular cell adhesion molecule 1 (VCAM1), have been suggested to mediate MSC immunoregulation (Akiyama et al. 2012, Ren et al. 2010).

2.3.3 Enzymatic activity of MSCs

In human MSCs, tryptophan degrading enzyme indoleamine 2,3-dioxygenase (IDO) represents the main pathway of immunosuppression. Tryptophan starvation is the primary reason for T-cell inactivation, but tryptophan metabolites, such as kynurenine, also regulate the proliferation and survival of T-cells (Mellor and Munn 2004). IDO has been reported to have an immunosuppressive role in many other settings including cancer (Katz et al. 2008). Meisel *et al.* (2004) were the first to show that MSCs express IDO in an IFN γ -dependent manner and thus identified IDO-mediated tryptophan

catabolism as a novel T-cell inhibitory mechanism of MSCs. Recently IDO-independent mechanisms induced by IFN γ using P7H1 and B7DC/PD1 pathways were demonstrated (Chinnadurai et al. 2014).

Extracellular adenosine triphosphate (ATP) and adenosine (Ado) are involved in inflammatory processes. ATP is a mostly pro-inflammatory molecule and is released during hypoxic conditions and by necrotic cells, as well as by activated immune cells and endothelial cells. Extracellular ATP can be hydrolyzed into Ado by a two-step enzymatic process catalyzed by two ectonucleotidases, CD39 and CD73, which are expressed in many tissues. Regulatory T-cells (Tregs) are shown to utilize CD39 CD73 machinery to inhibit T-cell proliferation and cytokine production (Deaglio et al. 2007, Schuler et al. 2014). Human MSCs express constitutively CD73, but CD39 expression levels vary according to the tissue source (Kerkelä et al. 2016). It has been demonstrated that this pathway is at least partially responsible for T-cell suppression of MSCs (Huang et al. 2017, Huang et al. 2017, Kerkelä et al. 2016, Saldanha-Araujo et al. 2011).

Hemoxygenases (HOs) are intercellular enzymes that catabolize heme into biliverdin, CO, and divalent iron. HO-1 is constitutively expressed in MSCs and has been described as immunoregulative molecule (Najar et al. 2012). Later studies have demonstrated that HO-1 may act as one mediator of suppression of alloactivated T-cells (Chabannes et al. 2007) and induction of Tregs (Mougiakakos et al. 2011).

2.3.4 Extracellular signals and immunomodulation

In any site of inflammation, there are several cytokines in abundant quantities. It has been suggested that MSCs monitor the inflammatory environment and switch between pro-inflammatory and anti-inflammatory modes of action (Bernardo and Fibbe 2013). There is extensive evidence showing that MSCs need to be activated by cytokines produced by T cells, macrophages, and NK cells, indicating that communication between MSCs and immune cells is reciprocal. At least IFN γ on its own is needed for MSC activation but it can be accompanied by TNF α , IL-1 α , or IL-1 β (Aggarwal and Pittenger 2005, Ryan et al. 2007, Ryan et al. 2007). Pro-inflammatory cytokines induce the expression of HLA II molecules as well as the expression or production of several other molecules, such as IDO, galectin-9, HO-1, and PGE $_2$ mediating the immunomodulative functions of MSCs (Le Blanc et al. 2003, Aggarwal and Pittenger 2005, Gieseke et al. 2013, Mougiakakos et al. 2011). Pro-inflammatory preconditioning affects also the functionality of MSC-derived EVs (Di Trapani et al. 2016). Interestingly, pro-inflammatory cytokines alter the phospholipid profile of MSCs, indicating that the composition of their membrane lipids is relevant to their function (Campos et al. 2016). MSCs express several TLRs, including TLR3 and TLR4, and it has been shown that the *in vitro* activation of specific TLRs affects the immunoregulative properties of MSCs. For instance, MSCs induce the

formation of Tregs after TLR3 and TLR4 activation in a contact dependent manner (Rashedi et al. 2017). Interestingly, it has been suggested that MSCs may polarize into either pro-inflammatory or immunosuppressive phenotypes depending on the received signals. MSCs primed with TLR3 ligand poly (I:C) suppressed T-cell proliferation, while the expression of IDO and PGE2 production was enhanced. TLR4 activation with lipopolysaccharide on the other hand did not induce the production of immunosuppressive factors, but TLR3-primed MSCs were in fact pro-inflammatory (Waterman et al. 2010). Recently, it was demonstrated that direct cell-to-cell contact with M1 or M2 macrophages through CD54 also changes the immunosuppressive capacity of MSCs (Espagnolle et al. 2017).

2.3.5 Tissue source

Bone marrow was the first established source of MSCs. Since this discovery, it has remained the most widely investigated and used MSC source in therapeutic applications. After being initially found in the bone marrow, MSCs have been isolated from various adult and neonatal tissues, of which adipose tissue (AT) and birth associated tissues (placenta, umbilical cord UC and cord blood CB) are well characterized and commonly used. The collection of bone marrow is always an invasive procedure containing a risk of infection, thus making alternative sources very attractive. Both birth associated tissues, as well as excess adipose tissue removed by liposuction can be regarded as biological waste and available for MSC isolation and production.

According to the minimal criteria defining MSCs issued by the ISCT, all MSCs should be plastic-adherent spindle-shaped cells with certain immunophenotype and tri-lineage differentiation potential (Dominici et al. 2006). Although MSCs from different sources in general fulfill these criteria, there is some variation in the expression of cell surface antigens, differentiation potential, and especially in the functional properties of MSCs. When initial capacity for colony formation was compared, AT turned out to be superior in comparison to CB or BM (Kern et al. 2006). Even though CB contains a low number of MSCs and the success rate for isolating MSCs is lower, the proliferation rate and capacity of CB and other birth associated tissues-derived MSCs are higher (Barlow et al. 2008, Jin et al. 2013, Kern et al. 2006). The expression of cell surface antigens seems relatively invariable since in most comparative studies no differences in immunophenotype were reported. The only observed deviation to the minimal criteria is moderate expression of hematopoietic marker CD34 in AT-derived MSCs at least at the beginning of *in vitro* culture (Gronthos et al. 2001, Maumus et al. 2011, Mitchell et al. 2006, Pachon-Pena et al. 2011, Traktuev et al. 2008). In contrast to immunophenotype, differentiation potential shows more variation among MSCs from different sources. In several studies MSCs derived from CB and other birth associated tissues show poor or decreased

adipogenic potential (Barlow et al. 2008, Castro-Manrreza et al. 2014, Kern et al. 2006).

The origin of MSCs seems to affect more dramatically the epigenetics (Reinisch et al. 2015), gene expression (Al-Nbaheen et al. 2013, Kang et al. 2016, Roson-Burgo et al. 2014, Wagner et al. 2005, Wegmeyer et al. 2013), miRNA expression (Ragni et al. 2013), proteomics (Jeon et al. 2016), secreted molecules (Pires et al. 2016), and even the content of extracellular vesicles (Baglio et al. 2015), but the functional consequences of these differences are not yet known. The ability to modulate immune responses is one of the most important properties of MSCs. In many comparative studies, MSCs collected from different tissues showed very similar immunomodulatory properties when a T-cell proliferation assay or a mixed lymphocyte reaction was used (**Table 1**). When cytokine secretion, TLR expression, or MSCs' responses for the inflammatory milieu were studied, some differences between MSC from different sources were observed (Prasanna et al. 2010, Raicevic et al. 2011b, Roemeling-van Rhijn et al. 2013b). This indicates that MSCs of different origins may have slightly different roles *in vivo* and more importantly their mechanisms of action may be different.

The comparison of functional properties of MSCs from different sources is challenging as the same culture conditions may not be optimal for all the MSC types, which may explain some of the differences observed in the standardized culture conditions (Fazzina et al. 2016). Furthermore, MSC donors show high heterogeneity, which has an impact on MSC functionality (Ketterl et al. 2015). When BM-MSCs and AT-MSCs derived from the same donor were compared, there was no difference in the inhibition of T-cell or NK cell proliferation. However, only BM-derived MSCs were able to inhibit NK cell cytotoxicity, and correspondingly AT-MSCs were more potent in inhibiting dendritic cell differentiation (Valencia et al. 2016). On the other hand, when placenta-derived MSCs were compared with umbilical cord-derived MSCs from the same donor, placenta-derived MSCs were shown to be more efficient in the T cell suppression and also in supporting the growth of Treg population (Talwadekar et al. 2015).

Table 1 Summary of comparative studies of hMSCs from different tissue sources

<i>Cell types</i>	<i>Parameters</i>	<i>Outcome</i>	<i>Reference</i>
AT, BM, PL, UC	Angiogenesis	BM, PL>AT, UC	(Du et al. 2016)
AT, BM, UC	Proliferation	CB=AT>BM	(Fazzina et al. 2016)
	Differentiation	BM=AT>CB	
	T-cell proliferation	BM>UC>AT	
AT, BM, CB, PL	Proliferation	PL>AT=BM=CB	(Heo et al. 2016)
	Differentiation	BM=AT (CB,PL	
	T-cell proliferation	none)	
		BM>AT>CB>PL	
BM, CB	Intestinal ischemic injury model	BM=CB	(Jensen et al. 2016)
BM, WJ, UC	T-cell proliferation	No differences	(Mennan et al. 2016)
AT, BM	T/NK proliferation	BM=AT	(Valencia et al. 2016)
	NK cytotoxicity	BM>AT	
	Dendritic cell differentiation	AT>BM	
BM, UC	Immunogenicity	BM>UC	(Barcia et al. 2015)
	Lymphocyte proliferation	BM<UC	
PL, UC	T-cell proliferation	PL>UC	(Talwadekar et al. 2015)
BM, CB, PL	Adipogenic differentiation	BM=PL (CB none)	(Castro-Manreza et al. 2014)
	Osteogenic differentiation	BM=CB=PL	
	T-cell proliferation	BM=CB>PL	
AT, BM, PL, WJ	Proliferation	WJ>AT>PL>BM	(Li et al. 2014)
	Adipogenic differentiation	AT>WJ>BM>PL	
	Osteogenic differentiation	WJ>PL>AT>BM	
	T-cell proliferation	WJ>PL>AT>BM	
AT, BM	Lymphocyte proliferation	AT>BM (at low doses)	(Montespan et al. 2014)
AT, BM, CB	Proliferation	CB>BM>AT	(Jin et al. 2013)
	Senescence	CB<BM=AT	
	Immunosuppression	CB>BM=AT	
BM, PL	T-cell proliferation	BM=PL	(Luan et al. 2013)
AT, BM	Lymphocyte proliferation	AT>BM	(Melief et al. 2013)
	Dendritic cell differentiation	AT>BM	
AT, BM	T-cell proliferation	AT>BM	(Menard 2013)
AT, BM, WJ	T-cell proliferation	AT>BM=WJ	(Najar et al. 2013)
AT, BM, UC	T/NK cell proliferation	AT>BM=UC	(Ribeiro et al. 2013)
	B cell proliferation	AT=BM (UC none)	
AT, BM	T-cell proliferation	AT=BM	(Roemeling-van Rhijn et al. 2013a)
CB, PL, CL, WJ	Proliferation	CL, CB>PL, WJ	(Stubbendorff et al. 2013)
	Migration	CL, CB, PL, WJ	
	Adipogenic differentiation	only CL	
	Immunogenicity	CB, WJ>CL,PL	
	T-cell proliferation	CL>CB=PL=WJ	
AT, BM	Proliferation	AT>BM	(Xishan et al. 2013)

	T-cell proliferation	BM>AT	
AT, BM, PL	T-cell proliferation	AT=BM=PL	(Lee et al. 2012)
AT, BM, WJ	TLR expression	BM=AT, WJ lack	(Raicevic et al. 2011a)
	T-cell proliferation	TLR4	
		BM=AT=WT,	
BM, WJ	Lymphocyte proliferation	WJ>BM	(Prasanna et al. 2010)
AT, BM	Dendritic cell differentiation	AT>BM	(Ivanova-Todorova et al. 2009)
AT, BM, CB, WJ	T-cell proliferation	no differences	(Yoo et al. 2009)
BM, PL	Proliferation	PL>BM	(Barlow et al. 2008)
	Adipogenic differentiation	BM>PL	
	Osteogenic differentiation	BM=PL	
	<i>in vivo</i> toxicity	BM=PL	
AT, BM, CB	Isolation success rate	AT=BM>CB	(Kern et al. 2006)
	Proliferation	UCB>AT>BM	
	Osteogenic differentiation	No differences	
	Adipogenic differentiation	BM=AT (CB none)	
AT, BM	Immunogenicity	BM=AT	(Puissant et al. 2005)
	Lymphocyte proliferation	BM=AT	

Abbreviations: AT, adipose tissue; BM, bone marrow, CB, cord blood; CL, umbilical cord lining cells; PL, placenta; UC, umbilical cord; WJ, Wharton's jelly

2.4 Replicative senescence of MSCs

Although MSCs are present in almost all tissues, they are rare in the human body. The frequency of MSCs is approximately 0.01-0.001% and their number has been shown to decline with age (Caplan 2009). The decline in the numbers or potential of stem cell population in adult organs may contribute to human aging and even affect the life span of an individual (Van Zant and Liang 2003). The effect of donor age on the characteristics of hMSCs has yet to be thoroughly studied. Zhou *et al.* (2008) showed an age-dependent decrease in proliferation and osteoblast differentiation, and an increase in senescence-associated β -galactosidase-positive cells and apoptosis in hMSCs. Wagner *et al.* (2009) show that donor age influences the gene expression of MSCs. In rodents, donor age is shown to have a negative effect on the growth kinetics as well as capacity to suppress the proliferation of CD3+CD4+ T cells (Wu et al. 2014).

MSCs, like other cultured primary cells, do not grow infinitely, instead the cells can undergo a limited number of divisions before reaching senescence (Hayflick 1965). At a molecular level, telomere-dependent replicative senescence or stress-induced premature senescence is triggered by retinoblastoma protein (Rb) or p53 pathways, which activate cyclin-dependent kinase inhibitors p16 and p21, respectively. These pathways can induce each other and work cooperatively (Collado et al. 2007). Senescent

cells undergo irreversible growth arrest, but stay metabolically active and develop large, flat morphology and typically exhibit a senescence-associated β -galactosidase (β -gal) activity. In addition, senescent cells secrete growth factors, proteases, and cytokines called senescence associated secreted phenotype (SASP) (**Figure 6**).

Cell therapy protocols usually require hundreds of thousands hMSCs per treatment and because they are so rare in the human body, extensive *in vitro* expansion is required to obtain sufficient numbers of MSCs for cell therapy. Long-term expansion may cause continuous changes in gene expression, miRNA expression, and DNA methylation patterns of MSCs (Bork et al. 2010, Hackl et al. 2010, Schellenberg et al. 2011, Wagner et al. 2008, Wagner et al. 2009, Yoo et al. 2014). However, these studies were not able to identify specific markers for senescent MSCs. Cellular senescence induced by gamma radiation affects hMSCs' immunoregulatory properties both *in vitro* and *in vivo* (Sepulveda et al. 2014).

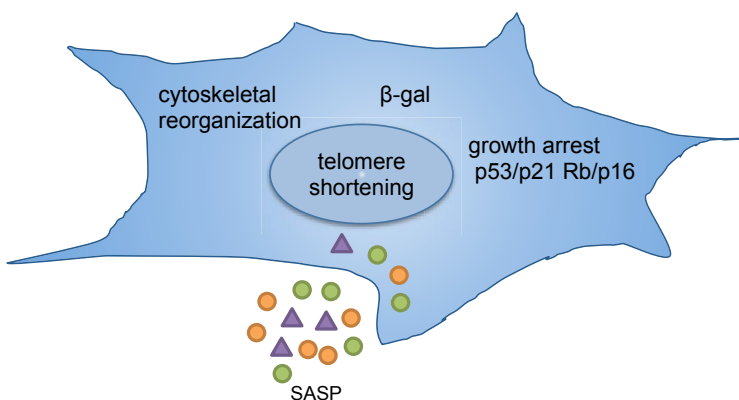


Figure 6 The phenotype of senescent MSCs Abbreviation: SASP, Senescence associated secretory phenotype. Figure is adapted from (Turinetto et al. 2016) under license <http://creativecommons.org/licenses/by/4.0/>.

2.5 MicroRNA regulation in MSCs

MiRNAs are small non-coding RNAs (20-22 nucleotides) targeting messenger RNA (mRNA) for degradation or direct translational repression, thus suppressing protein synthesis. To date 2588 distinct miRNA molecules have been identified (Griffiths-Jones et al. 2006) (<http://www.mirbase.org/index.shtml>, accessed February 25, 2017), and it was estimated that miRNAs regulate 30% of protein coding genes (Lewis et al. 2005). One miRNA can target several dozen or even hundreds of mRNAs and conversely a single gene has binding sites for several miRNAs in their 3' untranslated regions (Selbach et al. 2008). Development of computational and bioinformatics prediction methods has accelerated the research on

miRNA function and possible targets, revealing the full complexity of the miRNA regulation network (Bartel 2009, Lu et al. 2012, Maragkakis et al. 2009). Currently, there are numerous different prediction tools and softwares available, but the high rate of false positive interactions hampers the research (Pinzon et al. 2017). MiRNAs have been shown to have a crucial role in regulating almost all cellular processes, including cell growth, proliferation, and differentiation (Ameres and Zamore 2013, Bartel 2009). The role of miRNA regulation in both embryonic and somatic stem cell fate and differentiation has been studied extensively during the past few years (Ivey et al. 2008, Ong et al. 2015). Most studies investigating the role of miRNA regulation in MSCs have focused on osteogenic or adipogenic differentiation (**Table 2**). In hBM-MSCs silencing, Dicer or Drosha inhibits both adipogenic and osteogenic differentiation, indicating that miRNAs are important regulators of the MSC differentiation (Oskowitz et al. 2008).

Several miRNAs have been shown to either promote or inhibit the osteogenic differentiation of hBM-MSCs. MiR-20a, miR-21, miR-29, miR-489b, and miR-196 have been shown to promote the osteogenic differentiation, whereas miR-27a, miR-31, miR-34a, miR-138, miR-204, miR-489, and miR-541 have been shown to have an inhibitory effect (Baglio et al. 2013, Candini et al. 2015, Chen et al. 2014, Eguchi et al. 2013, Huang et al. 2010, Kapinas et al. 2010, Schoolmeesters et al. 2009, Yang et al. 2013b, Zhang et al. 2011). Adipogenesis and osteogenesis are usually presented as reciprocally regulated events. Several miRNAs regulate the balance between osteogenesis and adipogenesis. MiRNAs, including miR-17-5p and miR-106, have been shown to promote adipogenesis and inhibit osteogenesis (Li et al. 2013a), whereas miR-22 inhibits adipogenesis and stimulates osteogenesis in human adipose tissue derived MSCs by repressing its target *HDAC6* (Huang et al. 2012). MiRNA-mediated regulation of adipogenic differentiation of hBM-MSCs is less studied, but it has been shown that miR-369-5p inhibits adipogenic differentiation, whereas miR-371 has a strong enhancing effect (Bork et al. 2011).

MiR-21, miR-155, and miRNA family 17~92 are called immunomirs and they regulate T-cell differentiation, function, and aging (Kroesen et al. 2015). Of these miRNAs, miR-21 is highly expressed in MSCs and its expression has been shown to be induced by an anti-inflammatory lipid molecule, resolvin D1, which participates in the attenuation of the inflammatory response (Recchiuti et al. 2011). MiR-155, on the other hand, inhibits the immunosuppressive capacity of MSCs by reducing iNOS expression in mice (Xu et al. 2013). MiR-181 is not included in immunomirs, but it has been shown to be involved in T- and B-cell development (Ebert et al. 2009). In MSCs, elevated miR-181 expression enhances IL-6 and IDO expression, and the capability of MSCs to suppress mitogen activated T-cell proliferation was also attenuated by miR-181 in, at least partly, IL-6-dependent manner (Liu et al. 2012b).

MSCs can be isolated from virtually any tissue (Meirelles et al. 2006). In therapeutic applications, BM, AT and CB are the most relevant sources. The different origins have been shown to produce MSCs with different immunomodulatory properties (Di Trapani et al. 2013), but the results from different studies are contradictory (Mattar and Bieback 2015). Since miRNA regulation is thought to be one of the key players in MSC differentiation and functionality, MSCs have been proposed to have a typical miRNA expression pattern, which varies only slightly according to the tissue origin (Ragni et al. 2013).

The age of MSC donors and the required *in vitro* culture of the therapeutic MSCs are considered to be a potential factor that may affect the properties and the functionality of MSCs and eventually deteriorate the therapeutic outcome. The age-dependent changes in miRNA expression may be one possible explanation for the observed differences between the aged and younger donors. Despite miRNA expression being relatively stable in MSCs, some age-dependent miRNA expression changes have been previously identified (Candini et al. 2015). Interestingly, the miRNA expression of hBM-MSCs and hAT-MSCs is differently affected by the donor age (Pandey et al. 2011). Replicative senescence has also been described to be at least partly driven by miRNA regulation (Wagner et al. 2008, Yoo et al. 2014). The results are, however, contradictory and the influence of donor age on senescence has not yet been thoroughly studied.

Table 2 MiRNAs in regulation of hMSCs

<i>miRNA</i>	<i>MSC source</i>	<i>Target gene</i>	<i>Effects</i>	<i>Reference</i>
<i>Differentiation</i>				
miR-10a	BM	KLF4	Promote differentiation	(Li et al. 2013b)
miR-22	AT	HDAC6	Inhibit adipogenesis Promote osteogenesis	(Huang et al. 2012)
miR-21	AT	SPRY2, TGFBR2	Promote adipogenesis	(Kim et al. 2009a, Mei et al. 2013)
miR-30	AT	RUNX2	Promote adipogenesis	(Zaragosi et al. 2011)
let-7	BM	IL-6	Inhibit adipogenesis	(Sung et al. 2013)
miR-27	AT	PPAR γ , PHB	Inhibit adipogenesis	(Kang et al. 2013, Karbiener et al. 2009)
miR-23b	BM	PRKACB	Promote chondrogenesis	(Ham et al. 2012)
let-7, miR-24, miR-125b, miR-138	BM	n.d	Promote osteogenesis through PDGF pathway	(Goff et al. 2008)
miR-148b	BM	n.d	Promote osteogenesis	(Schoolmeesters et

miR-17	PO	SMURF-1	Promote osteogenesis	al. 2009) (Liu et al. 2011b)
miR-196a	AT	HOXC8	Promote osteogenesis	(Kim et al. 2009b)
miR-20a	BM	PPAR γ , BAMBI, CRIM1	Promote osteogenesis	(Zhang et al. 2011)
miR-21	AT, BM	SPRY1/2, SPRY2	Promote osteogenesis	(Mei et al. 2013, Yang et al. 2013a)
miR-218	AT	SFRP2, DKK2	Promote osteogenesis	(Zhang et al. 2014)
miR-29a	BM	DKK1, KREMEN2, SFRP2	Promote osteogenesis	(Kapinas et al. 2010)
miR-346	BM	GSK-3 β	Promote osteogenesis	(Wang et al. 2013)
miR-26a	AT	SMAD1	Inhibit osteogenesis	(Luzi et al. 2008)
miR-27a	BM	SATB2	Inhibit osteogenesis	(Schoolmeesters et al. 2009)
miR-31	BM	OSTERIX	Inhibit osteogenesis	(Baglio et al. 2013, Gao et al. 2011)
miR-100	AT	BMPR2	Inhibit osteogenesis	(Zeng et al. 2012)
miR-138	BM	FAK	Inhibit osteogenesis	(Eskildsen et al. 2011)
<i>Proliferation/senescence</i>				
miR-10a	BM	KLF4	Inhibit senescence	(Li et al. 2013b)
miR-16	PL	CCNE1	Inhibit proliferation	(Wang et al. 2012)
miR-196a	BM	HOXB7	Inhibit proliferation	(Candini et al. 2015)
<i>Immune regulation</i>				
miR-181	BM	TGFBR1, TGFBRAP1	Inhibit immune suppression	(Liu et al. 2012b)
<i>Angiogenesis</i>				
miR-16	PL	CCNE1	Inhibit angiogenic potential	(Wang et al. 2012)

3 AIMS OF THE STUDY

In general, the aim of this study was to investigate the regulatory network between cell cycle, immunosuppression, and membrane lipids of MSCs by analyzing immunosuppressive capacity, phospholipid composition, and gene expression changes related to expansion and donor age.

The specific aims of this study were:

1. To investigate the immunosuppressive capacity of BM-MSCs and CB-MSCs
2. To investigate the role of membrane lipid composition in the functionality of MSCs
3. To investigate the effect of IFN γ stimulus on the secretion and function of CB-MSC derived extracellular vesicles
4. To analyze age- and expansion-induced changes in phospholipid composition, mRNA, or miRNA expression

4 MATERIALS AND METHODS

Materials and methods used in this study are summarized in **Table 3**. More detailed information can be found in the original publications.

Table 3 Summary of methods used in the study. The original publications are referred to using their Roman numerals I-III

Experimental procedure	Publication
Cell culture	I, II and III
Co-culture assays	I and III
Isolation and size determination of extracellular vesicles	III
Experimental animal procedures	III
Gas chromatographic analysis of fatty acids	I
Mass spectrometric lipidomics	I
Mass spectrometric proteomics	III
Gene expression analysis	I and II
Senescence indicators	I
Bioinformatics and Statistical analysis	I, II and III

4.1 Cell culture

Bone marrow derived MSCs (I,II)

Human bone marrow derived MSCs (hBM-MSCs) were obtained from bone marrow aspirates taken from the iliac crest or upper femur metaphysis of adult patients after written informed consent. All patient protocols were approved by the Ethical Committee of Northern Ostrobothnia Hospital District or the Ethical Committee of Hospital District of Helsinki and Uusimaa. The BM-MSCs collected from donors of different ages (anonymous coding) used in this thesis are summarized in **Table 4**.

Cells were cultured in minimum essential medium alpha (α MEM), supplemented with 20mM HEPES, 10% heat inactivated fetal bovine serum (FBS), 2mM L-glutamine, and 100 U/mL penicillin and 100 μ g/mL streptomycin. The same serum lot was used throughout the study. The cells were plated at a density of 1000 cells/cm², medium was renewed twice a week, and the cells were harvested when 70-80% confluent.

Cord blood derived MSCs (III)

Cord blood units were collected at the Helsinki University Central Hospital, Department of Obstetrics and Gynaecology, and Helsinki Maternity Hospital. All donors gave informed consent and the study protocol was approved by

the ethical review board of the Helsinki University Central Hospital and the Finnish Red Cross Blood Service.

Cord blood mononuclear cells were isolated by gradient centrifugation and 1×10^6 / cm^2 mononuclear cells were plated on fibronectin-coated tissue culture plates. The initial CB-MSC establishment was performed under hypoxic conditions (5% CO_2 , 3% O_2 at 37°C) in medium containing α -MEM with Glutamax™, 10% FBS, 10ng/mL epidermal growth factor, 10ng/mL recombinant platelet-derived growth factor, 50nM dexamethasone, 100U/mL penicillin, and 100 μg /mL streptomycin. The cells were allowed to adhere overnight, and non-adherent cells were washed with medium changes. For further experiments, CB-MSCs were cultured in normoxic conditions (5% CO_2 and 20% O_2 at 37°C) and media was renewed twice a week. For flow cytometric analysis, CB-MSCs were trypsinized and 1×10^5 cells were suspended in a staining buffer (0.3% bovine serum albumin in 2 mM EDTA-PBS). Fluorescein isothiocyanate (FITC) and allophycocyanin (APC) conjugated antibodies against HLA-DR and HLA-ABC were used for direct labeling. Appropriate isotype controls were used.

Table 4 Age and gender of BM-MSCs from young and old donors used in the thesis.

<i>BM-MSC donor</i>	<i>Age (year)</i>	<i>Gender</i>
<i>young donors</i>	<i>mean age 22.2</i>	
081	20	male
088	21	male
089	23	female
091	23	female
092	23	male
<i>old donors</i>	<i>mean age 74.6</i>	
164	75	male
172	72	female
194	82	male
271	75	male

Co-culture assays (I, III)

PBMCs were isolated from buffy coats from healthy anonymous blood donors (Finnish Red Cross Blood Service) by density gradient centrifugation (Ficoll-Paque plus, GE Healthcare) and cryo-preserved for later use. PBMCs were chosen over purified T-cells for practical reasons. Isolation of PBMCs is less time-consuming and they provide co-stimulation for T-cells. MSCs or EVs were co-cultured with CFSE (5(6)-Carboxyfluorescein diacetate N-succinimidyl ester) labeled PBMCs. To activate the T-cell proliferation, 100ng/ml of the anti CD3 antibody clone Hit3a was added to the co-culture. T-cell proliferation was recorded after four days of incubation as a dilution of

fluorescent dye by flow cytometry. The proliferation of PBMCs without MSCs was designated as 100%.

PBMCs were co-cultured with EVs or CB-MSCs in order to analyze the impact on Treg induction. After 7 days of incubation, non-adherent PBMCs were harvested and labeled with fluorogenic antibodies, CD4-APC-Cy7, CD25-AlexaFluor®647, FOXP3-PerCP5.5) to evaluate the proportion of CD4+CD25+FOXP3+ Tregs. Cells were fixed and permeabilized with FOXP3 Staining Buffer Set (eBioscience) according to the manufacturer's instructions and including the blocking step with 2% rat serum. PBMCs cultured without MSCs or EVs were used as a control. Appropriate isotype controls were used.

Isolation and size determination of extracellular vesicles (III)

Cell culture medium (80-160 ml) was centrifuged at 2,000g for 20 minutes in +4 °C, succeeded by a further ultracentrifugation step at 100,000g for 1-2 h at +4 °C. The pellet was washed with phosphate buffered saline (PBS) and submitted to a second 1-2h ultracentrifugation in the same conditions. EVs were suspended in 50-150µl of PBS and stored at -80 °C.

After centrifugation, EVs were resuspended with PBS, and analyzed with the nanoparticle tracking analysis (NTA) instrument LM14C with blue laser (405 nm, 60 mW) and a CMOS camera to determine the vesicle size distribution and concentration. The data were analyzed with NTA 2.3 software.

4.2 Experimental animal procedures

Eighteen 6- to 7-week-old male Sprague Dawley rats were purchased from Charles River Laboratories (Research Models and Services, Sulzfeld, Germany). The protocols were approved by the Animal Experimentation Committee of the University of Helsinki, Finland, and the Provincial State Office of Southern Finland (approval number STH059A), whose standards correspond to those of the American Physiological Society. The rats were divided into three groups: 1) I/R group (n=8), 2) I/R group + control EV (n=5), 3) I/R group + IFN γ -treated EV (n=5). An established model of kidney I/R injury was used (Lempiäinen et al. 2012). Twenty-four hours after the operation, blood samples were collected from the tail vein under short isoflurane anesthesia. Terminal samples were harvested 48 hours after the operation; the rats were anesthetized with isoflurane, and blood samples were collected from inferior vena cava with a 5ml syringe and 22G needle for biochemical measurements. The kidneys were excised, washed with ice-cold saline, blotted dry, and weighed. The left kidney was used for histological examinations. Tissue samples for histology were fixed in 10% formaline and processed to paraffin with routine methodology.

4.3 Gas chromatographic analysis of fatty acids

Total lipids of the BM-MSCs or FBS were extracted according to Folch *et al.* (1957) and converted into FA methyl esters (FAME) by heating with methylation reagent (1% H₂SO₄ in methanol). The dried and concentrated FAME solutions were analyzed by gas-liquid chromatography (6890N network GC) using flame ionization detection and DB-wax capillary columns (30 m, ID 0.25 mm, film 0.25 μm). Agilent Chemstation software was used for peak area integration. The identification of the FAMES was based on retention time, mass spectra acquired earlier for similar samples, and comparisons with standards of known composition. The FA composition was calculated as mol%, and the FAs were marked by using the abbreviations: [carbon number]:[number of double bonds] n-[position of the first double bond calculated from the methyl end] (e.g. 22:6n-3).

4.4 Mass spectrometric analysis

ESI-MS analysis of cellular phospholipids (I)

Total lipids of BM-MSCs were dissolved in chloroform/methanol 1:2 for a direct infusion experiment. Several internal standards were used to correct for the effects of the polar head group and acyl chain length on the instrument response according to previously reported procedures (Hermansson *et al.* 2005, Käkälä *et al.* 2003, Koivusalo *et al.* 2001). Immediately prior to the mass spectrometry, 1% NH₄OH was added and the lipid extracts, with the internal standards, were infused to the electrospray source of a Quattro Micro triple quadrupole mass spectrometer) at the flow rate of 8 μl/min. The collision energy of the instrument was set to 25–65 eV, depending on the detection mode, and both negative and positive ion modes were used. Argon was used as the collision gas. The PC and lysoPC (precursor of 184), PE (neutral loss of 141), PS (neutral loss of 87), and PI (precursor of 241) species were selectively detected using head-group specific MS/MS scanning modes (Brügger *et al.* 1997, Sullards and Merrill 2001). The acyl chain assembly of the major lipid species was confirmed with MS/MS techniques. The mass spectra were processed by MassLynx software and the individual lipid species quantified by using the internal standards and LIMSA software (Haimi *et al.* 2006). The lipid species were abbreviated: [total carbon number in the chains]:[total number of double bonds in the chains]. The relative concentrations of the lipid classes were obtained by summing up the concentrations of the individual molecular species in a class.

Proteomic analysis of EVs (III)

Gel-based proteome analysis of EVs was performed with the liquid chromatography-mass spectrometry (LC-MS) of tryptic peptides. Proteins from collected EVs were run in a 4-20% sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) gel. The gel was silver stained and sliced into pieces. Each gel piece was processed using an in-gel reduction, alkylation and trypsin digestion protocol as previously described (Shevchenko et al. 2006). Peptides were loaded to precolumn (Protecol Guard C18, 150µm, 10mm, 3µm) and separated in a reversed-phase analytical column (Acclaim PepMap100 C18, 75µm, 150mm, 3µm) with a linear gradient of acetonitrile. Ultimate 3000 LC instrument was operated in nano scale with the flow rate of 0.3 µl/min. Eluted peptides were introduced to LTQ Orbitrap XL mass spectrometer via ESI Chip interface (in a positive ion mode). Data files from MS were processed with Mascot Distiller. The processed data was searched with Mascot Server against human proteins in UniProtKBdatabase (release 2012_08).

4.5 Gene expression analysis

RNA was extracted using Qiagen AllPrep DNA/RNA Mini Kit (Cat. no. 80204, Qiagen, CA, USA) and a Qiagen supplementary protocol “Purification of total RNA containing miRNA from animal cells using the RNAeasy Plus Mini Kit “according to the vendor’s instructions.

Labeled RNAs (800 ng/sample) were hybridized onto Agilent SurePrint G3 Human GE 8x60K or Agilent Human miRNA 8x60K microarray (release 16.0) and then the slides were washed and scanned according to the manufacturer’s recommendations. The raw data files (.txt files) were imported into the R v. 2.13 software (R Core Team 2015) and preprocessed by the BioConductor package limma v.3.4.5 (Smyth 2005). After quality control of the data, the median probe intensities were log₂ transformed and normalized according to the method of the quantiles (Bolstad et al. 2003). The probes for the same Entrez Genes or lincRNAs (as of 1st January 2012) were averaged. A linear model including the AGE*PASSAGE + SUBJECT + DYE terms followed by a moderated t-test was utilized for finding the differentially expressed genes (log₂ Fold Change >0.58) in the comparisons of interest (nominal p-value < 0.01).

For miRNA expression analyzes, 100 ng of total RNA was reverse-transcribed and amplified with real-time PCR using miScript-System including miScript II RT-Kit, miScript SYBR-Green PCR-Kit, and miScript Primer Assay according to the manufacturer's protocol. For endogenous control, RNU6 was used. All PCR reactions were performed in triplicate in 384-well plates and measured by ABI 7900HT detection system. Mean

values and standard deviations were calculated and fold changes were determined using the $\Delta\Delta\text{CT}$ method.

4.6 Senescence indicators

Telomere length analysis

Telomere lengths were analyzed by the southern blot analysis of terminal restriction fragment (TRF) lengths (Kimura et al. 2010). Genomic DNA from snap-frozen cell pellets was purified using the Qiagen DNeasy Blood and Tissue Kit and extracted with ethanol. Quality of purified DNA was evaluated with 1% agarose gel electrophoresis. Telomere length analysis was performed using TeloTAGGG Telomere Length Assay Kit. DNA was digested using *RsaI* and *HinfI* enzymes and electrophoresed on a 0.8% agarose gel 5V/cm. Southern blotting was performed using 20X salium sodium citrate buffer. The blot was hybridized overnight using a digoxigenin (DIG)-labeled telomere specific probe (TTAGGG) and incubated with an alkaline phosphatase-labeled anti-DIG antibody. The blot was then incubated with CDP-Star chemiluminescent substrate and exposed to an autoradiography film. The autoradiogram was scanned by densitometry and TRF length was calculated using ImageJ analysis software (Schneider et al. 2012) according to $\text{TRF} = \Sigma \text{OD}_i / \Sigma (\text{OD}_i / L_i)$, where OD_i is optical density and L_i is the length of the TRF at position i . TRF signals between 3 and 20 kb were used for telomere length measurements (Kimura et al. 2010).

Western blotting

Snap-frozen cell pellets were lysed using RIPA-buffer (containing Protease Inhibitor Cocktail). 20 μg of total protein was run on a 12% SDS-PAGE gel and electrotransferred to Hybond ECL Nitrocellulose membrane. The membrane was then blocked with 5% milk in PBS containing 0.1% Tween-20 and immunoblotted using anti-p16^{INK4A} (1: 800, clone DCS-50) and anti-p21 (1:250, Clone SXM30). β -actin (1: 8000, monoclonal anti- β -actin, clone AC-74) was used as a loading control. Polyclonal anti-mouse horseradish peroxidase (HRP) conjugated antibody was used as a secondary antibody (1:1000). Detection was performed using an enhanced chemiluminescent detection system. Quantification of band intensities was performed using GS 800 densitometer and Quantity One software.

4.7 Bioinformatic and statistical analysis

In study I, the differentially expressed genes were analyzed for significant enrichments of GO-BP classes by using R library GOSim v. 1.2.5 using default parameters (Frohlich et al. 2007). Enrichments with a p-value <0.01 were considered significant.

In study II, the prediction and functional analysis of putative targets for selected miRNAs were performed through the use of QIAGEN's Ingenuity Pathway Analysis (IPA QIAGEN Redwood City, www.qiagen.com/ingenuity).

In study III, subcellular locations for identified EV proteins were collected from UniProt database (as is 23.11.2016). Gene ontology (GO) enrichment analysis of identified proteins was performed using the Database for Annotation, Visualization and Integrated Discovery (DAVID, version 6.7) (Huang da et al. 2009) using default settings.

In all studies results are represented as mean+standard deviation or standard error of the mean. In study I statistical significances for the differences between BM-MSCs from the young and old donors or early and late passages were calculated using student's paired t-test (* p-value <0.05, ** p-value < 0.01, *** p-value <0.001). In study II, non-parametric Spearman correlation was used to calculate correlation between miRNA expression and proliferation of MSCs. In study III, statistically significant differences in mean values were tested by one-way analysis of variance (ANOVA) and the Tukey's post-hoc test. Analyses were performed with GraphPad Prism 7.00 software or using statistical programming software R.

5 RESULTS

5.1 Immunosuppressive properties of MSCs

In this study, the immunosuppressive properties of both BM-MSCs and CB-MSC were assessed. MSCs were characterized and they fulfilled the established minimal criteria for MSCs (data not shown). One of the key functions of MSCs is their capability to suppress T-cell proliferation. The immunosuppressive capacity of both MSC types was ascertained by T-cell proliferation assay. MSCs were co-cultured with CFSE-labeled PBMCs and T-cells were activated by CD3 antibody. Proliferation of CFSE labeled cells was seen as dilution of CFSE dye measured by flow cytometry. We were able to demonstrate that both CB-MSCs and BM-MSCs have strong capacity to suppress T-cell proliferation in a dose-dependent manner (**Figure 7**).

Umbilical cord blood is an attractive MSC source since it is easily available and the collection is non-invasive procedure. The establishment and culturing of CB-MSCs are more complicated than that of BM-MSCs. In our laboratory, CB-MSC culture medium is supplemented with growth factors (EGF, PDGF and dexamethasone (DX)), whereas BM-MSCs are cultured with FBS. Since the different culture conditions have modulating effects on cell functions, it is impossible to separate the effect of the cell source on cell functionality from that of the culture conditions (Laitinen et al. 2016b). Therefore, direct comparison of the immunosuppressive capacity of CB-MSCs and BM-MSCs was not possible. However, the immunomodulative properties of MSCs derived from different tissue sources have been compared in previous studies (summarized in **Table 1**), although with contradictory results. Heo *et al.* (2016) reported that BM-MSCs are more immunosuppressive than CB-MSCs. On the other hand, Castro-Manreza *et al.* (2014) were not able to see any difference in the immunosuppressive capacities. In contrast, Jin *et al.* (2013) showed that CB-MSCs are actually more immunosuppressive than BM-MSCs. While CB-MSCs and BM-MSCs were cultured in similar culture conditions in these studies, T-cell proliferation was assessed by different methods, rendering a comparison of the results difficult.

In addition to CB, AT, umbilical cord, and placenta are commonly used sources of MSCs. Similarly, the results are contradictory and it is impossible to prioritize different tissue sources according to their immunosuppressive capacity. Notably, in all studies MSCs showed clear capacity to suppress T-cell proliferation regardless of tissue source and it is therefore other characteristics such as availability and proliferative capacity that are more important to consider when tissue source is selected.

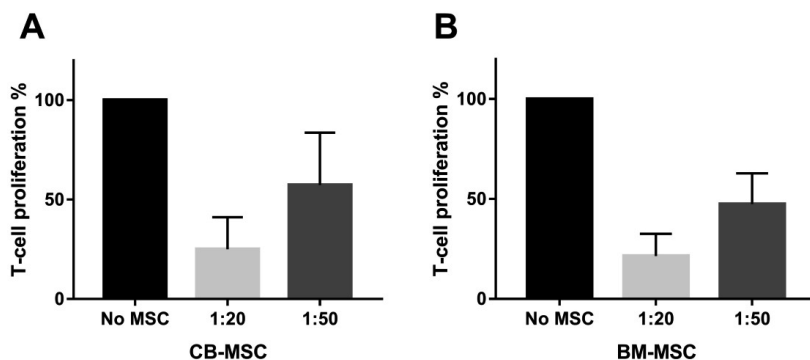


Figure 7 The immunosuppressive capacity of MSCs. A. CB-MSC (n=12) B. BM-MSC (n=16). MSCs between passages 4-5 were used. The proliferation of activated PBMCs in absence of MSCs was set as 100%. PBMC:MSC ratios 1:20 and 1:50 were used. Results are expressed as mean±SD. Unpublished data.

5.1.1 MSCs have dual role in the regulation of T-cell proliferation

The possible immunogenicity of MSCs has been one of the concerns in MSC therapy. According to our results, MSCs do not activate T cell proliferation in co-culture. Since MSCs lack the expression of MHCII molecules as well as costimulatory molecules, CD80 and CD86, on their surface, they are considered to be non-immunogenic, which makes them an excellent candidate for cell therapy (Tse et al. 2003).

In our studies of the immunosuppressive capacity of MSCs, we have used PBMCs as responders and activated them with CD3 antibody alone without the costimulatory CD28 antibody. We have observed inter-experimental variation in the response, and in some experiments T cells do not proliferate at all. When T cells are activated to proliferate, MSCs are highly suppressive. However, in the absence of T-cell response MSCs have the opposite, stimulatory effect on proliferation (**Figure 8**). It is noteworthy that in the absence of CD3 antibody MSCs do not induce T-cell proliferation. This may be due to the inadequate number of antigen presenting cells with co-stimulatory molecules. Further, this leads to inadequate proliferation and cytokine production by T-cells. In these situations, MSCs may act as pro-inflammatory factors, stimulating T-cell proliferation as previously described in mice (Li et al 2012).

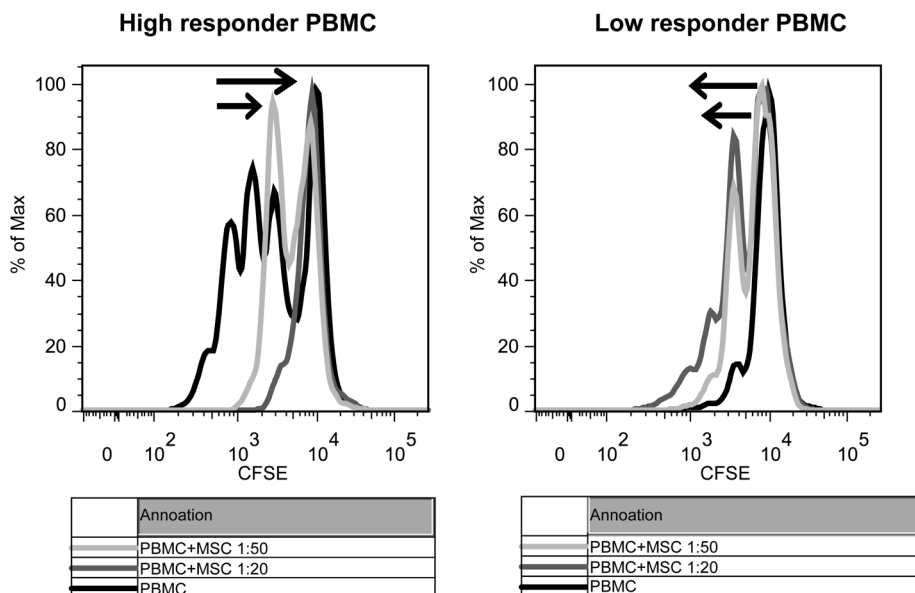


Figure 8 MSCs have an inhibitory and stimulatory effect. BM-MSCs were co-cultured together with either high responder PBMCs (left) or low responder (right). PBMCs were labeled with CFSE and stimulated with antiCD3 antibody. If PBMCs responded poorly to the stimulant (low responder), MSCs boosted the T-cell proliferation. When PBMCs responded efficiently (high responder), MSCs had an inhibitory effect on the T-cell proliferation. Unpublished data.

5.1.2 Effect of IFN γ preconditioning on MSC immunosuppressive potential

The surrounding microenvironment is one of the key regulators of MSC functionality. MSCs have been shown to have the ability to react differently according to the external stimuli. On the site of inflammation in the injured tissue, there are large numbers of different cytokine molecules in concentrations that fluctuate depending on the phase of the on-going inflammation. Several studies have demonstrated that cytokines, such as IFN γ and TNF α , regulate the mRNA expression of IDO and production of MSC-derived soluble molecules such as PGE $_2$ (Aggarwal and Pittenger 2005). For this reason, it has been suggested that priming of MSCs may enhance their immunosuppressive capacity and improve the therapeutic outcome in clinical application. In our study, we were not able to see any influence of IFN γ priming on the immune suppressive capacity of BM-MSCs (**Figure 9**). In the literature, the stimulation times, cytokine concentrations, and cytokine cocktails vary greatly. We were able to show that even though the immunosuppressive capacity measured by T-cell proliferation was not affected, the IFN γ stimulation did increase the expression of HLA I and HLA II molecules after 48 hours of stimulation with 100ng/ml IFN γ . This effect was not seen after 24 hours of stimulation (Publication III, Fig. S2). Stubbendorf *et al.* (2013) showed that the same effect could be obtained

using only 25ng/ml IFN γ . We also used a combination of IFN γ and TNF α to stimulate CB-MSC and BM-MSCs. We were not able to see any difference in the immunosuppressive capacity of stimulated or control MSCs (data not shown).

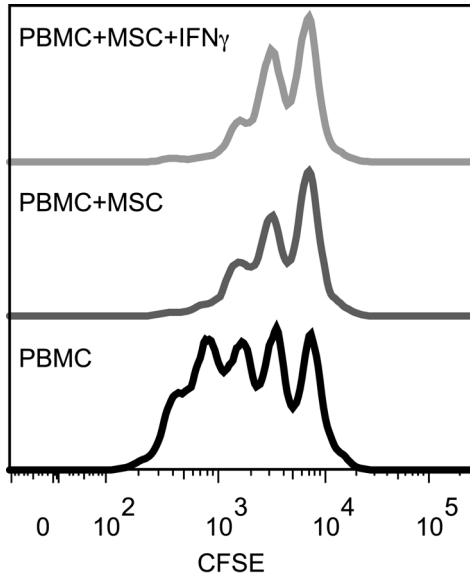


Figure 9 Interferon gamma priming does not improve the immunosuppressive capacity of BM-MSCs. Representative result using BM-MSC: MNC ratio 1:50 is shown.

5.1.3 Membrane lipid composition of MSCs is related to functionality

Instead of being passive structural components of the cell membrane, lipids are actively involved in cellular signaling events employed in immune functions. Membrane lipids act as precursors for lipid mediators that regulate immunological events. PGE₂, which is produced from 20:4n-6, has been shown to have a significant role in MSC-mediated immunosuppression (Aggarwal and Pittenger 2005, Chen et al. 2010, Duffy et al. 2011, English et al. 2009). The other important FAs, eicosapentaenoic acid (20:5n-3, EPA) and docosahexaenoic acid (22:6n-3, DHA), serve as precursor for specialized proresolving mediators (SPM). SPMs have been shown to modulate the innate immune system and their role in regulating the resolution phase of inflammation has recently been described (Serhan et al. 2015). SPMs, such as 22:6n-3-derived resolvins, not only regulate the innate immunity, as previously described, but are also important regulators of adaptive immunity. These mediators reduce cytokine production of activated CD4⁺ and CD8⁺ T cells and inhibit the differentiation of Th17 cells (Chiurchiu et al. 2016). The immunomodulatory function of MSCs resembles the active resolution of inflammation (English 2013) and there is a possibility that

SPMs have a role in MSC immunoregulation, which remains to be elucidated in future.

Modern mass spectrometric methods enable researchers to use a lipidomic approach to the analysis of cellular lipids as a whole to get a broader view of the cellular functions. The lipidomic approach has been used to study membrane lipidomes of hematopoietic progenitors and embryonic stem cells (Fuchs et al. 2007, Park et al. 2010), but lipidomics studies on MSCs are lacking. In this study, we report correlation between membrane lipid composition and the immunosuppressive capacity of MSCs. Molecular percentage of 20:4n-6 containing phosphatidylcholine (PC) species PC38:4 and PC38:5 and 20:4n-6 itself correlates negatively (correlation coefficients PC38:4, $R=-0.91$; PC38:5, $R=-0.82$ and 20:4n-6, $R=-0.71$) with the immunosuppressive capacity of BM-MSCs. (Publication I, Table II) Interestingly, a particular n-3 PUFA, 22:6n-3 correlated positively with immunosuppressive capacity ($R=+0.75$). Our result indicates that variation in the membrane lipid composition and especially changes in the ratio of certain molecular species may have consequences on the MSC functionality. The role of composition of lipid mediator precursors in the cell membrane in the actual production of the novel SPM mediators needs to be confirmed and elucidated in more detail.

5.1.4 MSC-EVs are immunosuppressive

To investigate the potential immunomodulative properties of MSC-EVs, we co-cultured PBMCs together with isolated CB-MSC-EVs. We showed that CB-MSC-EVs suppress T-cell proliferation, but the effect is milder (Publication III, Fig. 1). In addition to direct suppression of T-cell proliferation, MSCs induce the production of regulatory T-cells. When T-cells were co-cultured with MSCs or MSC-EVs, the proportion of CD4⁺CD25⁺FOXP3⁺ increased (Publication III, Fig. 1). These results indicate that the immunosuppression of MSCs may be at least partially mediated by secreted EVs. Gouveia de Andrade *et al.* (2015) showed that BM-MSC and AT-MSC derived EVs failed to suppress lymphocyte proliferation. These contradictory results emphasize the need for standardization of EV collection and purification methods.

Di Trapani *et al.* (2016) have shown that the inhibition of exosomes restores T- and B- cell proliferation in the presence of MSCs. This phenomenon is more evident in primed MSCs compared to resting MSCs. Inhibition of microvesicle shedding and apoptotic body release had no effects on effector cell proliferation. In the proteomic analysis, we observed that primed MSCs produce EVs that contain different set of Rab proteins compared to resting MSCs, indicating that priming induces exosome production through MVEs (Publication III, Fig. 7). Taken together, these results suggest that MSCs produce immunosuppressive EVs that are transferred to effector cells, a phenomenon that is enhanced by priming MSCs with TNF α and IFN γ .

One of the proposed mechanisms of MSCs is mediated through purinergic signaling. CB-MSCs and also CB-MSC-EVs contain CD73 (Publication III, Fig. 4). Previously, it has been shown that MSC-EVs exhibit similar activity to MSCs in the production of adenosine from adenosine monophosphate (Kerkelä et al. 2016).

5.1.5 Interferon gamma stimulation deteriorates the *in vivo* functionality of MSC-EVs

MSC-derived EVs have been shown to have a therapeutic effect in AKI. In this study, we used an IRI rat model to investigate the protective capacity of CB-MSC-EVs. In line with previous studies using glycerol or cisplatin induced AKI models, we were able to show that EV-treated rats developed less severe AKI. Kidney damage was measured as elevated serum creatinine and urea levels at time points 24h and 48h after operation. In rats that were treated with MSC-EVs, the dramatic elevation of serum creatinine and urea was significantly reduced (Publication III, Fig. 5). The protective effect of MSC-EVs was also seen in histopathological analysis of the kidney after 48 hours. The signs of injured kidney, vast necrosis of tubular cells, tubular dilatation, and cast formation, were almost absent in the MSC-EV treated rats in comparison to control rats (Publication III, Fig. 6). Our results are thus in line with previous studies, demonstrating that MSC-EVs have renoprotective effects during the early phase of AKI. In our AKI model, EVs were injected to the rats immediately after reperfusion, thus protecting kidneys from injury.

There is convincing evidence that MSCs require extracellular cytokine stimulus for complete immunomodulation. MSCs have been shown to produce EVs constitutively, but we hypothesized that their quantities and/or functionality could be improved with external IFN γ stimulus. We were not able to see any difference in the morphology, particle number, or size distribution between stimulated and nonstimulated MSCs. (Publication III, Fig. 1) Surprisingly, stimulated CB-MSC-EVs did not prevent the development of AKI (Publication III, Fig. 5 and 6).

5.1.6 Proteomic analysis of EVs

Mass spectrometric proteomic analysis was applied to the analysis of the protein content of IFN γ stimulated and nonstimulated CB-MSC-EVs. The identified proteins originated from different cellular compartments as illustrated in **Figure 10**. The distributions of stimulated and nonstimulated EVs were highly similar, while the protein compositions were different. First of all, we were able to identify almost 700 different proteins from stimulated MSC-EVs, whereas from control EVs, only 446 proteins were identified (Publication III, Fig. 2).

According to MS data, only EVstim contained exosome markers CD9, CD63, and CD81. MSC markers CD73 and CD90 were found in both EVs. Of immunomodulative factors (proteins) shown to mediate MSCs immunomodulative functions (see **Figure 5**), only galectins 1 and 3 were identified from the EVs (both stimulated and nonstimulated). On a protein family level, we noticed that members of Rab proteins were present in both stimulated and nonstimulated EVs. However, the individual proteins were mostly different. EVs secreted from stimulated CB-MSCs were linked to exocytosis and deeper endosomal pathway (Rab 1, 2, 6, 8). In contrast, EVs from nonstimulated MSCs contained Rabs (3, 5, 14, 34) that were more related to the early endosomal recycling, near plasma membrane (Publication III, Fig. 7).

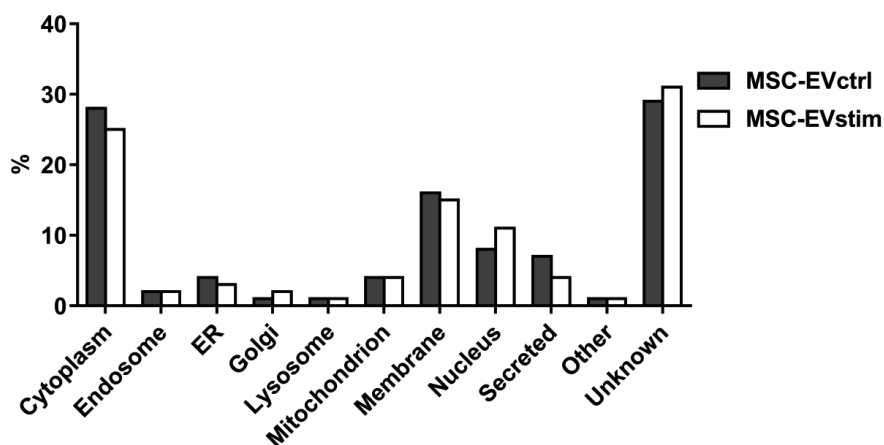


Figure 10 Subcellular locations of MSC-EV proteins. CB-MSC proteome was used as reference. Retrieved from Uniprot as is 23.11.2016. Obsolete protein entries were removed from the analysis.

5.2 Age-induced changes in MSCs

Prior to clinical use, MSCs need extensive *in vitro* expansion. In order to investigate the effects of long-term cell culture on the functional properties of MSCs, we isolated BM-MSCs from five young (20-24 years of age, mean 22.2 years) and five old donors (62-82 years of age, mean 74.6 years) (see **Table 4** for details). BM-MSCs were cultured until senescence was reached and samples for further analysis were collected from every other passage. The proliferation capacity of young and old donors was similar, but considerably more interindividual variation was seen in the old donors group (**Figure 11A** and Publication I, Fig. 1).

Replicative senescence was studied from selected cells and samples. We used morphology, telomere lengths, and protein expression of cell cycle components as indicators for replicative senescence. Late passage BM-MSCs gradually adopted the typical flattened morphology accompanied by increased cell size. Telomere length measurements showed that in passage 11 cells telomeres were 1.0 ± 0.5 kbp shorter than in passage 4 cells (**Figure 11B**).

The expression of cell cycle components p16^{INK4A} and p21^{CIP/WAF1} were also increased in passage 11 cells in comparison to passage 4 cells as analyzed by western blot (**Figure 11C**). These results indicate that among the three selected cell donors, the degree of senescence and the proportion of senescent cells were not equally high.

The immunosuppressive capacity of early and late passage cells was measured using CFSE staining and anti CD3 stimulated PBMCs. The early passage cells suppressed T-cell proliferation almost completely, but later passage cells were less immunosuppressive (Publication I, Fig. 1).

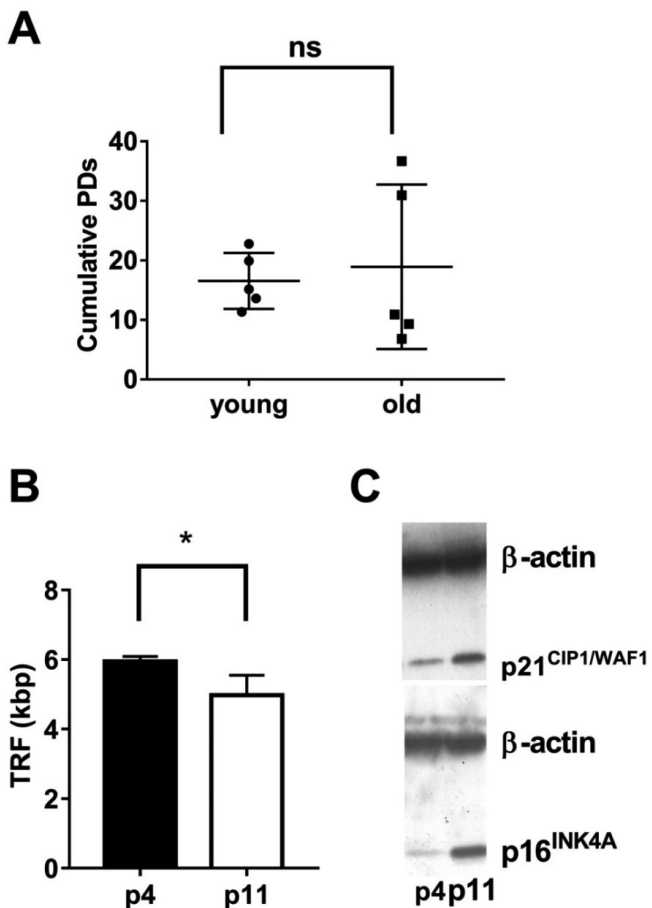


Figure 11 Proliferation and senescence of BM-MSCs. **A.** Cumulative population doublings at the end of the cell culture. The proliferation capacity between young (n=5) and old donors (n=5) is similar, but there is more individual variation among the old donors group. Non-parametric Mann-Whitney test was used to test the difference between groups (ns= non significant) **B.** Telomere lengths (TRF, Terminal restriction factor) were determined in early and late passage cells. Results are mean+SD of three BM-MSC donors. Paired one-tailed t-test was used to test the difference between the means. * P<0.05. **C.** Representative result of western blot analysis of cell cycle components p16 and p21. β-actin was used as a loading control.

5.2.1 MSC lipid profile changes during *in vitro* expansion

Prior to use in therapy, MSCs need to be extensively expanded. While the effect of expansion on the DNA integrity, miRNA profiles, and gene expression has been previously studied, other molecular level changes are less well-studied. We had very little knowledge about membrane GPL composition of MSCs, along with the kind of changes that might take place in membrane composition during expansion. We used lipidomic approach to analyze cellular GPLs and total FA profiles from young and old donors. GPLs were analyzed with ESI-MS/MS techniques and the FA composition of total lipids was measured with gas chromatography. All results are shown as mol % per total lipids in that class or per total FAs.

The GPL class profiles demonstrated that PC and phosphatidylethanolamines (PE) are the most abundant types of phospholipids in MSCs. This result is in line with other reports, apart from the MSCs having a higher proportion of PE than the previously described, otherwise very similar, fibroblasts (Blom et al. 2001)(Publication I, Table 1). When young and old donors were compared, the GPL profiles were highly similar.

During expansion, phosphatidylinositol (PI) totals increased. This phenomenon was more evident when PI totals were compared to phosphatidylserine (PS) totals. The increase of PI was more evident in the BM-MSCs from young donors, since in the BM-MSCs from old donors the PI/PS ratio was already high in the early passage cells (Publication I, Fig. 3).

Expansion of BM-MSCs induced alterations in the mol percentages of numerous phospholipid species especially in the PC and PE classes-. In general, long and unsaturated PL species were increased at the expense of shorter and monounsaturated species. The molar percentage of PC38:4, PC36:4, PC36:1, PE38:4, PE38:1, and PE36:4 increased towards late passages while PC34:1, PC34:2, PE36:1, and PE34:1 decreased. Most noticeable increase was observed in PC38:4 and PE38:4, which happened at the expense of the monounsaturated species PC34:1 and PE36:1 (**Figure 12**).

The FA profiles measured by GC supported the clearest finding in PC and PE phospholipid species. The increases in PC38:4 and PE38:4 were accompanied by a clear increase in 20:4n-6 in FA profiles. At the same time, the two most prominent n-3 PUFAs, 22:5n-3 and 22:6n-3, decreased, the effect being clearer for 22:6n-3 (**Figure 13**). In addition to measuring the relative quantities of different FAs in the BM-MSCs and FBS, we also measured the total quantity of FAs available for BM-MSCs on the culture dish. These results demonstrated that there is an excessive quantity of essential FAs for cells. (Publication I, Fig. 5B).

Results

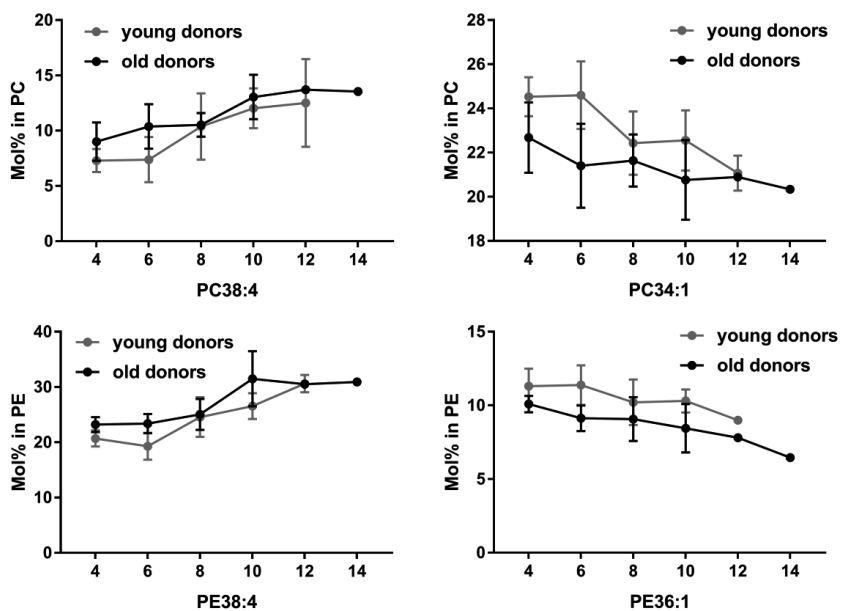


Figure 12 Effect of expansion on selected PC and PE species in hBM-MSCs. Mean values of PC38:4, PC34:1, PE 38:4, and PE 36:1 over different cell passages (x-axis). Error bar represents SD of individual BM donors, n=5

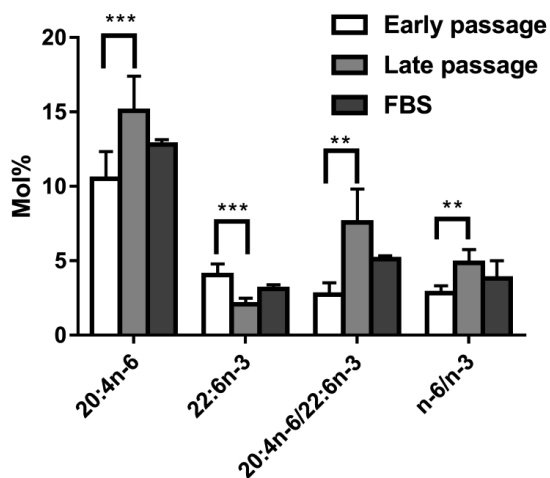


Figure 13 Effect of expansion on selected PUFAs and their ratios in hBM-MSCs. Results are mean+SD of all donors. (n=10). For FBS, three replicates were analysed.

5.2.2 Gene expression changes related to donor age and cell expansion

In order to elucidate the role of gene expression regulation during expansion, we analysed mRNA expression and miRNA expression in passage 4 and passage 8 cells. Previous findings on proliferation kinetics and lipidomic changes had shown that most dramatic changes occur at passage 8. Therefore, p8 was selected as the late passage time point for microarray experiments. Gene expression analysis demonstrated that mRNA expression was remarkably different already in the early passage BM-MSCs of young and old donors (Publication I, Fig. 6). MiRNA expression, on the other hand, was very robust, and only minor changes between young and old donors were observed (*data not shown*). Expansion seems to have a different effect on the BM-MSCs from young and old donors. The expression of only 36 mRNAs and 12 miRNAs was changed during the expansion in both young and old donors' BM-MSCs. Thus, the majority of the observed differences were unique to either the young or old donors (Publication I, Fig. 6; Publication II, Fig. 1).

We selected five common miRNAs for qPCR validation. The qPCR results confirmed our microarray results, and we also showed that while miRNA expression mostly increases gradually, it takes a leap from passage p6 to p8 (**Table 5**, Publication II, Table 1 and Fig. 2). BM-MSCs were passaged when confluency was 80%, resulting in different culture times. At p8, the culture time varied between 31 and 71 days. We noticed that miRNA expression levels measured as dct values showed similar variation. We performed a correlation analysis, which showed that miRNA expression correlates significantly with the expansion time (at passage 8) (**Table 5**).

Table 5. miRNA expression and correlation analysis between miRNA expression and expansion time. BMMSC donors 081 and 271 were removed from FC calculations. Correlation of dct values at passage 8 with expansion time (days) was calculated using spearman's correlation (n=9).

<i>miRNA</i>	<i>FC</i>	<i>p</i>	<i>r</i>	<i>p</i>
miR-1207-5p	1.3	0.004	-0.8	0.007
miR-1915-3p	2.5	<0.001	-0.8	0.01
miR-3665	2.6	0.002	-0.5	0.07
miR-4281	1.42	0.004	-0.7	0.02
miR-762	2.13	0.006	-0.7	0.02

Detailed analysis of differentially expressed genes revealed that the expression of several genes operating in lipid metabolism were decreased in the old donors' cells already at passage 4. These genes included FA desaturases *FADS1*, *FADS2*, *SCD*, lysoPC acyltransferase genes *LPCAT2* and *LPCAT3*, FA elongase 3 (*ELOVL3*), and leukotriene C4 synthase (*LTC4S*). In addition, the *PTGS1* gene coding cyclooxygenase 1 enzyme (COX1), which is

responsible for PGE₂ synthesis, were more highly expressed in passage 8 cells (old donors) than in passage 4 cells (Publication I, Table 3).

As an indicator for the modulation of immune functions, the genes for the suppressors of cytokine signaling (*SOCS1* and *SOCS3*) were expressed at a lower level in the old donor cells (at passage 4). In addition, the expression of *SOCS3* decreased during passaging in the old donors group. Interestingly, *SOCS3* is a predicted target for three miRNAs (miR-181-5p, miR-762, and miR-2861) whose expression increased during expansion (Publication I, Table3, Publication II, and Fig. 2).

A more detailed analysis of miRNA changes demonstrated that the expression of miRNA cluster 17/92 was decreased either in old donors' cells (miR-17, miR-18a, miR-19a, and miR-20a) or in young donors' cells (miR-93, miR-25, and miR-92a-3p) (**Figure 14**). This cluster has been studied extensively, with the results indicating downregulation of miR-17, miR-20a and miR-106a in aging (Hackl et al. 2010). MiRNAs are found as clusters in the chromosomes, with miRNAs belonging to the same cluster most likely expressed together. In addition, miRNA in miR17/92 cluster and its paralogues miR106a/363 and miR106b/25) are divided into four families according to their seed sequences (see **Figure 14**). MiRNAs with similar seed sequences are likely to target the same genes and to share similar functions.

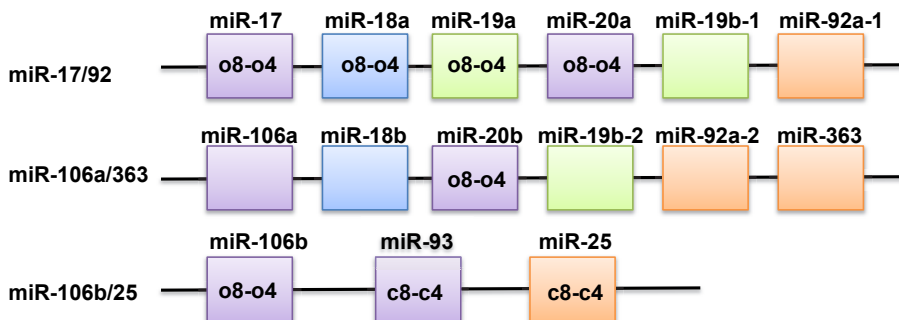


Figure 14 miR17/92 cluster. Differential expression in BM-MSCs of members of the miR-17/92 cluster and its two paralogues miR-106a/363 and miR-106b/25 and their differential expression in BM-MSCs during expansion. o8-o4 old donors group, y8-y4 young donors group, c8-c4 common group. Purple: members of the miR-17 family; blue members of the miR-18 family; green members of the miR-19 family; orange; member of miR-92 family

6 DISCUSSION

Cells are extremely complex, yet organized entities. In a single cell, there are myriad of genes, protein, and lipids, which are all strictly regulated in order to allow the cells to fulfill their tasks and functions. The development of new technologies and bioinformatic tools has led to an era of “omics”, a field where the numerous molecules of a cell are examined as an entity. This approach presents certain challenges: How to comprehend the massive data? How the relevant information is filtered from the irrelevant? What do these results mean in a context of cell biology? In this study, one of the challenges was to utilize omics data and to convert it to applicable information about MSCs functionality.

MSCs contribute to the maintenance of the hematopoietic niche in the bone marrow and placenta. They are rare in the body, and therefore extensive *in vitro* passaging is required before use in therapeutic applications. MSCs, like all other primary cells, do not divide infinitely, but their proliferative capacity is limited. The effects of expansion on MSCs' molecular composition and functionality are poorly understood. Donor age is one factor that is associated with a loss of proliferative capacity and cellular senescence of MSCs. Biological markers for cellular senescence indicate that MSCs from old donors show accelerated senescence (Stenderup et al. 2003). In the field of advanced cell therapy, the use of autologous MSCs also for older patients is continuously increasing.

The aim of this study was to investigate the effects of donor age and extensive expansion on the proliferation, quality, and immunosuppressive capacity of hBM-MSCs. We used the omic approach to analyze the molecular changes in hBM-MSCs during extensive expansion.

6.1 Lipid metabolism is connected to MSCs functionality

In this study, we analyzed the membrane GPL and cellular FA composition of hBM-MSCs. In general, we showed that the GPL composition of membranes is highly similar to that previously reported for fibroblasts: only the PE level is higher in MSCs than in fibroblasts, which in other respects are very similar to MSCs. Next, we studied how expansion changes the GPL species composition of hBM-MSCs. We observed that the proportion of 20:4n-6 containing PC and PE species (38:4 and 36:4) increased, whereas n-3 PUFA containing species (40:5, 40:6 and 40:7) and shorter monounsaturated species decreased. These findings were supported by FA analysis. Aging MSCs accumulated 20:4n-6 and lost 22:6n-3 and other n-3 PUFAs. The 20:4n-6 is a precursor for several pro-and anti-inflammatory lipid

mediators, such as prostaglandins and lipoxins (**Figure 15**) (Stables and Gilroy 2011).

The shift in the balance between n-6 and n-3 PUFAs may influence responsiveness to inflammatory signals and capability for immunomodulation (Schoeniger et al. 2011). This hypothesis was strengthened by the observation that both expansion and a high content of 20:4n-6 resulted in decreased capacity for T-cell proliferation. In addition, our gene expression data revealed that the expression of COX-1 gene *PTGS1* was elevated in late passage cells compared to early passage cells. A similar pattern was seen in the *PTGS2* gene, but the difference was not statistically significant.

A simultaneous decrease in the n-3 PUFA content is of immunological importance as well. Traditional eicosanoids have been found to be accompanied by SPMs, including resolvins, protectins, and maresins, which are derivatives of 22:6n-3 and 20:5n-3 FAs. SPMs are needed in the resolution phase of inflammation (Serhan et al. 2015, Stables and Gilroy 2011). SPMs, which are mainly produced by macrophages and neutrophils, prevent inflammation from spreading and halt the formation of chronic inflammation. SPMs are described as modulators of innate immunity but little is known about their effects on the cellular components of adaptive immunity. Both CD4+ and CD8+ T cell responses are reduced by RvD1, RvD2, and Mar1. Particularly the differentiation of Th17 cells was inhibited (Chiurchiu et al. 2016). Even though MSCs have several properties that suggest a potential role also in the resolution phase of inflammation, little evidence of the secretion of SPMs is available. Human periodontal stem cells with MSC-like characteristics have been shown to produce several 20:4n-6, 20:5n-3, and 22:6n-3-derived mediators, but their role in MSC mediated immune modulation remains to be elucidated (Cianci et al. 2016).

It is important to highlight that same cyclooxygenase and lipoxygenase pathways produce different lipid mediators with completely different, even opposing, functions (**Figure 15**). Different GPL/FA compositions in the cell may cause hBM-MSCs to respond very differently to the same external stimuli. The availability of GPL/FA substrate is reflected also in the produced lipid mediators and ultimately in the functionality of MSCs.

In this study, MSCs were cultured in FBS. Due to the constant excess quantity of FAs in the surrounding medium compared to the cells, we can assume that the observed changes in hBM-MSCs lipidome were due to an active senescence-associated process. However, it is possible that supplementing the culture medium with even more n-3 PUFAs might support hBM-MSCs growth and maintain their physiological functionality. Interestingly, our group has shown that MSCs are not able to synthesize long chain PUFAs from the short chain precursors (18:2n-6 or 18:3n-3). Thus, 22:6n-3 should be added to culture medium in order to increase 22:6n-3 levels in MSCs (Tigistu-Sahle et al. 2017). However, there may be a limit as too high n-3 PUFA contents in membranes may even impair raft-related

functions and signaling events occurring in lipid rafts (Fan et al. 2004, Turk and Chapkin 2013).

In therapeutic applications, FBS is more often replaced by human platelet lysate or other animal-free supplements. These products show more variation between batches, which may be caused by differences in growth factor concentrations, but the FA composition of these products may also vary. It would be interesting to compare the lipid profile and its changes during passaging in xeno-free cultured MSCs and compare the results with MSCs cultured in FBS.

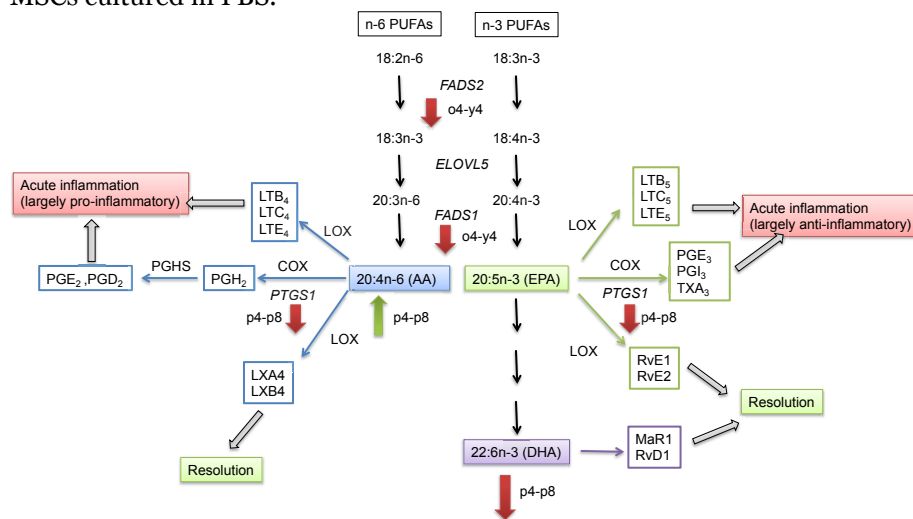


Figure 15 Scheme of n-6 and n3 PUFA metabolism and release of lipid mediators. Green and red arrows indicate either increase or decrease, respectively of FA or mRNA levels observed in this study. p4-p8 refers to change during expansion and o4-y4 refers to difference between young and old donors at passage 4. Abbreviations: AA, arachidonic acid; COX cyclooxygenase; DHA, Docosahexaenoic acid, ELOVL, fatty acid elongase; EPA eicosapentaenoic acid; FADS fatty acid desaturase, LOX lipoxygenase, LT, leukotriene; MaR, maresin; PG, prostaglandin; PUFA, polyunsaturated fatty acid; Rv, resolvin; TX, thromboxane.

6.2 MicroRNA regulation connects cell cycle and immunoregulation

In the second publication in the thesis, we further investigated expansion-induced changes in hBM-MSCs. We noticed that miRNA levels were relatively robust during expansion. In this study, the most highly expressed miRNAs were generally the same that have previously been described and reviewed by Clark *et al.* (2014). This indicates that MSCs have a particular miRNA expression pattern that is not susceptible to changes.

In this study, we had the opportunity to investigate the possible miRNA-mRNA interactions and their role in the proliferation of MSCs. We used a microarray platform to analyze miRNA and mRNA expression in the same cells. We used an ingenuity pathway analysis tool to predict potential targets

for miRNAs and then combined this information with the actual expression levels in the cells. As expected, we saw that in many cases the expression of miRNA and its potential target changed in opposite directions (Publication II, Fig.4). However, in many cases the expression of miRNA and its target mRNA changed in same direction. There are several possible explanations for this. The most likely one is that our experiment did not catch the direct and short-lived causality of the miRNA and its target mRNA. Also, the expression of miRNA and its target may be regulated by the same factor or mechanism. Further, as miRNA regulation is post-transcriptional, it is not self-explanatory that miRNA regulation is seen automatically as reduced expression of its target mRNA. And again, miRNAs regulate tens to thousands of mRNA molecules. Development of prediction tools offers an excellent starting point for narrowing down the potential targets or signaling routes, but further experimental validation is needed to fully understand the role of specific miRNAs in MSCs functionality.

MiRNAs are involved in many cellular processes, and especially in the development and differentiation of stem cells. In the context of MSCs biology, several miRNAs have been shown to regulate the differentiation, proliferation, and immunosuppression of MSCs. Our analysis revealed that several members of the miR17/92 cluster were down-regulated in old donor cells and in a few members of the young donors group. This miRNA cluster is of a particular interest since miR-17, miR-20a, and miR-106a are down-regulated in aging (Hackl et al. 2010). It is also known that the cell cycle regulator p21, whose expression is increased in senescent cells, is regulated by this cluster (Gomez-Cabello et al. 2013, Ivanovska et al. 2008).

6.3 Extracellular vesicles mediate immunoregulative functions of MSCs

The therapeutic effect of MSCs is currently explained by their capacity to regulate immune cells through paracrine mechanisms. MSCs secrete EVs that are immunosuppressive (Di Trapani et al. 2016) and repair injured tissues in ischemic animal models (Bruno et al. 2009, Collino et al. 2015, He et al. 2012). Although the effects of external cytokine stimulus in the MSC-mediated immunosuppressive mechanisms have been widely studied, the effect on EV production is less well-known. In this study, we show that hCB-MSCs secrete constitutively (in serum deprived culture media) EVs that remarkably attenuate IRI in a rat model. Our results are thus in line with previous reports demonstrating that BM-MSC-derived EVs are renoprotective in the early phase of AKI. Innate immunity plays a major role in regulating the early phase of AKI. MSCs are known to interact with innate immune cells regulating, for instance, the macrophage polarization toward an anti-inflammatory M2 phenotype. Recently, the role of MSC-derived EVs in macrophage polarization was also demonstrated (Lo Sicco 2017). In

literature, the IFN γ concentration used to stimulate MSCs ranges from a few ng/ml up to 100 ng/ml. In this study, we used the highest concentration, 100 ng/ml, to stimulate CB-MSCs to produce EVs. We noticed that when MSCs were stimulated with a high quantity of IFN γ , the protective effect of EVs was not seen.

The proteomics analysis of stimulated and non-stimulated CB-MSC EVs showed clear differences between these two groups. In stimulated CB-MSC EVs, the presence of MHC I was observed, which at least partly may explain why they were not protective in the AKI model. Therefore, it is highly possible that innate immune cells recognize these EVs as foreign and consequently they are lysed. Further, we identified larger number of proteins from stimulated EVs compared to non-stimulated EVs. The further analysis of individual proteins gave us some candidates that could explain the differences observed in the functionality of EVs. Strikingly, our proteomic data imply that IFN γ stimulation induces EV production via a secretory route, whereas constitutively produced EVs were produced by either membrane blebbing or by rapid recycling route. This could explain the observed differences in protein content, such as exosomal markers that were found only from stimulated EVs. EVs also contain other molecules in addition to proteins, such as lipids, miRNAs, and mRNAs, whose role in EV-mediated immunosuppression requires further studies.

6.4 Conclusions and future perspectives

In this study, we provide new insight into the importance of the membrane lipid composition and lipid metabolism for the functionality of MSCs. We show for the first time that major changes take place in the composition of GPL species and total FAs during expansion of therapeutically important hBM-MSCs. We demonstrate that the cellular relative content of 20:4n-6 increases while that of n-3 PUFAs decrease. The PUFA alterations reported here presumably affect the production of pro- or anti-inflammatory eicosanoids, as well as SPMs needed for resolution of inflammation. Thus, our results will serve as a basis for further studies aimed at understanding the role of lipid mediators in MSC-mediated immunosuppression. Modification of culture conditions may serve as one way of preventing the harmful effects of long-term cell culture. On the other hand, we show that the immunosuppressive capacity of BM-MSCs shows variation that correlates with the PUFA composition of the cells. Therefore, selected lipid or FA molecules may serve as biomarkers for the good quality and functionality of MSCs.

In addition to changes in lipid molecules, we investigated gene expression changes in hBM-MSCs. We demonstrated that gene expression of MSCs from young and old donors differed already at passage 4, but the expansion

induced changes were minor. In general, the changes observed in both miRNA and mRNA expression levels were moderate. This may be because MSCs are an extremely heterogeneous cell population and a given cell culture probably contains many different types of MSCs. Gene expression of single cells should be studied using single cell analytics to gain a more profound understanding of different populations and their characteristics in this heterogeneous pool of MSCs. This new analytics method will most likely help us to understand the puzzling question of whether all MSCs are equally multipotent or whether we need to admit that MSCs are actually a collection of cells with different abilities

We further investigated the role of miRNA regulation of BM-MSCs. MiRNAs have been shown to have a role in many aspects of MSC biology. In this study, we report comparative analysis of miRNA expression in young and old donors at the early and late passages. We demonstrate the regulative network that connects the regulation of the cell cycle and immune regulation. This observation needs further validation. We also report that MSCs secrete EVs that are immunosuppressive *in vitro* and protect against acute kidney injury *in vivo*. In this study, we used CB-MSCs instead of BM-MSCs since they seemed to be more active in producing EVs, critical study material for many different experimental steps. Research should next be extended to BM-MSCs, since BM is still the most frequently used MSC source in cell therapy. In future experiments, the mRNA and miRNA content of EVs should be investigated. Since EVs are membranous structures it is plausible that they transport also lipid mediators, or enzymes that may catalyze the production of these mediators from the lipids of EVs *in situ*. Whether the lipid composition of EVs resembles the cell membrane of the mother MSCs and what role EVs play in the immunosuppression of MSCs are questions that require further investigations.

ACKNOWLEDGEMENTS

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A handwritten signature in black ink, appearing to read 'Lotta', written in a cursive style.

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