## **Modulating Endothelial Adhesion and Migration impacts Stem Cell Therapies Efficacy**

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- Full Blots

 $\mathbf a$ **MSC** 



**PEI-MSC** 

**PEI-NP-MSC** 



isotype control



 $\mathbf b$ 



## brightfield phase contrast CXCR4 immunofluorescence



merge





#### Supplementary Figure 1 CXCR4 expression pattern on human BM-MSC.

a, The overall expression of CXCR4 was not affected by treatment of MSC with PEI alone and an even distribution of CXCR4 molecules could be observed on the surface of untreated MSCs and MSCs treated with PEI alone. In contrast, the CXCR4 signal was strongly increased on MSCs treated with PEI in combination with NP. In particular, the CXCR4 molecules showed an aggregated distribution pattern on the cellular surface of PEI-NP-MSCs. The absence of green fluorescence in isotype control confirmed specificity of anti-CXCR4 antibodies and excluded unspecific auto-fluorescence of NP. Green: CXCR4; blue: DAPI; scale bar: 50 um. b, PEI-NP-MSC: The increased CXCR4 expression was closely related to the localization of the PEI-NP complexes on the surface of MSC. The PEI-NP complexes in the merged microphotograph were highlighted in grey using Adobe Photoshop CS5.1; scale bar: 50 µm. c, Suggested mechanism of increased CXCR4 expression on PEI-NP-MSC: PEI-NP complexes trigger the inside-out flipping of CXCR4 molecules to the surface of MSC.



**c**









 $\mathsf{d}$ 

**MSC** 



**PEI-MSC** 











**PEI-NP-MSC** 

















**g** 



#### **Supplementary Figure 2 Characterization of treated and untreated human BM-MSC.**

**a,** MSC viability. The viability of MSC was not affected by treatment with PEI alone or in combination with NP. N=5; ANOVA analysis of variance. Error bars: SD. **b,** MSC diameter. The mean diameter of MSC, PEI-MSC and PEI-NP-MSC was not significantly different. N=6; ANOVA analysis of variance. Error bars: SD. **c,** Flow cytometry analyses of MSC phenotype. Treatment with PEI did not affect the percentages of MSC expressing CD10, CD140b (PDGFRb), GD2, or PDPN within the MSC preparation. N=2; two-tailed t-test. Error bars: SD. **d,** *In vitro* differentiation potential of MSC. After treatment with the respective differentiation media, the MSCs differentiated into cells of the adipogenic, osteogenic and chondrogenic lineage *in vitro.* Lipid vacuoles of adipogenic differentiated MSC are stained in red with Red-Oil-O (first row), undifferentiated MSC (second row). Calcium deposits of osteogenic differentiated MSC are stained in red with Alizarin Red (third row), undifferentiated MSC (fourth row). Mucopolysaccharides of chondrogenic differentiated MSC pellets are stained in bluish-green (fifth row). The treatment with PEI alone or in combination with NP did not affect the *in vitro* differentiation potential of the MSC (N=4). Arrows: PEI-NP complexes. Scale bars: 100 μm. e, Immunomodulatory capacities of MSC. The proliferation of 1\*10<sup>5</sup> PBMNC activated by PHA could be significantly suppressed by the addition of 0.1\*10<sup>5</sup> MSC or 0.2\*10<sup>5</sup> MSC, whereas the addition of  $0.05*10^5$  MSC or  $0.025*10^5$  MSC did not show an effect on the proliferation of PBMNC. No differences between the immunomodulatory capacities of untreated MSC, PEI-MSC, or PEI-NP-MSC could be observed within the same MSC-PBMNC ratios. ANOVA analysis of variance; stars indicate statistical comparisons of the respective MSC-PBMNC groups to PBMNCs alone; N=4 (\*\*p <0.01; \*\*\*p <0.001). Error bars: SD. **f,**  Profile of MSC trophic factors. Treatment of MSC with PEI alone resulted in increased secretion and/or production of vascular endothelial growth factor (VEGF)-A, nerve growth factor (NGF)-b, fibroblast growth factor basic (FGFb), and leukemia inhibitory factor (LIF). Notably, accumulated NGF-b could be detected only in the supernatants of untreated and treated MSC but not in the respective cell lysates. Treatment of MSC with PEI with or without NP decreased the secretion and production of hepatocyte growth factor (HGF) and Angiopoietin-1. n.d.: not detectable. N=3; ANOVA analysis of variance (\*p<0.05; \*\*p <0.01; \*\*\*p <0.001). Error bars: SD. **g,** PEI dose effect on CCR4 expression of MSC. Increase of CCR4 expression was clearly dose depending with maximal fold change of CCR4 expression compared to untreated MSC of MSCs treated with 1% PEI (standard dose in this work), followed by 0.5% PEI and 0.25% PEI; ANOVA analysis of variance (\*p <0.05; \*\*p <0.01). Error bars: SD.





#### **Supplementary Figure 3 Nanoparticle tracking analysis of Extracellular Vesicles (EVs)**

Nanoparticle tracking analysis of Extracellular Vesicles (EVs) derived from untreated and PEItreated human BM-MSC (N=3, different donors). PEI-treated MSC released significantly more EVs. EVs were isolated by differential centrifugation. Final 100.000 x g pellets were re-suspended in PBS and size-distribution of EVs was determined by laser based particle tracking. Error bars: SEM. Mean particle size and the total number of particles (area under the curve) collected from each sample type are denoted in the table below the graph.





**b** 



**Phase Object Confluence** 



#### **Effects of PEI treatment on adhesion capacity dynamics of human BM-MSC** *in vitro***.**

Adhesion capacity dynamics of human BM-MSC were assessed by live cell imaging of covered area and confluence in 2 minute-intervals for up to 30 minutes.

**a, b**, Covered area and confluence. Over the recorded time PEI-MSC covered a smaller area hereby reaching a lower degree of confluence. PEI treatment resulted in delayed adhesion capacity of MSC compared to untreated MSC; two-tailed t-test (\*p<0.05; \*\*p<0.01; \*\*\*p<0.001). Error bars: SEM.



#### **Effects of PEI treatment on migration of human BM-MSC subpopulations** *in vitro***.**

Migrated MSC subpopulations were identified by expression of CCR4, CD140b, CD10, or GD2 by flow cytometry under three conditions *in vitro*. Effects of PEI treatment on BM-MSC subpopulations was assessed by analyses of percent migrated antigen positive cells normalized to percent antigen positive cells that were initially seeded.

**a, b** , PEI treatment promoted *in vitro* migration of CCR4+ and CD140b+ human BM-MSC subpopulations; N=2-3 technical replicates out of one experiment per subpopulation marker; two-tailed t-test (\*p < 0.05; \*\*p <0.01; \*\*\*p<0.001). Error bars: SD.

**c, d**, PEI treatment did not promote but appeared to inhibit *in vitro* migration of CD10+ and GD2+ human BM-MSC subpopulations; N=2-3 technical replicates out of one experiment per subpopulation marker; two-tailed t-test (\*p < 0.05; \*\*\*p<0.001). Error bars: SD.



#### *In vivo* **cytokine expressions in the brain after quinolinic acid lesion.**

After unilateral application of quinolinic acid (QA) into the hippocampal region brain lesioned and non-lesioned hemispheres were analyzed separately by multiplex protein quantification assays (a, c-h) or Western blot (b). **a,b**, the lesioned hemispheres contained higher concentrations of the CCR4 ligand MCP-1a (CCL2) as confirmed by two technologies. **c,d**, more MIP-1a and IP-10 protein could be detected in the lesioned hemispheres compared to the non-lesioned hemispheres. **e-h**, no differences in the concentrations of MCP-3, IL-1a, RANTES, and TNF- $\alpha$  were observed.

Two-tailed t-test (\*p <0.05; \*\*p <0.01). N=5; Error bars: SD.

 $\mathsf{a}$ 



 $\mathbf b$ 





**PEI-NP-MSC** 



# **Supplementary Figure 7 Distribution of untreated and treated green fluorescent protein (GFP) positive human BM-MSC in the QA lesioned and non-lesioned hippocampal region.**

Treated and untreated eGFP+MSC could be detected in the brain with relationship to the vasculature, marked by vWF+ endothelial cells.

**a**, In the lesioned hippocampus, we observed more MSC that transmigrated from the vessels into the brain parenchyme (arrowheads) than MSC remaining in intravascular position (arrows). *von Willebrand Factor* (vWF): red; eGFP: green; DAPI: blue; scale bar: 50 m.

**b**, Corresponding to the multiplex analysis more CCL2 protein was detected in the lesioned hippocampus/hemisphere and in particular, PEI-MSC accumulated in areas of high CCL2 protein expression. CCL2: red; eGFP: green; DAPI: blue; scale bar: 100 um.



#### **Supplementary Figure 8 Quantitative analysis of transplanted eGFP positive human**

**BM-MSC and their** *in vivo* **phenotype assessment in the post-ischemic brain.** Mice were exposed to transient focal cerebral ischemia followed by intravenous delivery of untreated MSC or PEI-MSC expressing eGFP for cell tracking as described in materials and methods. Thereafter, mice were sacrificed on day 28 post-stroke and sections for subsequent immunohistochemical GFP staining and immunohistochemical co-stainings against nestin, glial fibrillary acidic protein (GFAP), 2',3'-Cyclic-nucleotide 3'-phosphodiesterase (CNPase), doublercortin (DCX) or NeuN were performed. **a**, **b**, Except for DCX and CNPase, the PEI-MSC group showed a general trend to higher cell numbers but no significant differences between the two groups were observed. Error bars: SD.





#### **Expressions of pro-migratory cytokines in lung and brain** *in vivo***.**

Multiplex analysis of *in vivo* protein expressions of pro-migratory cytokines were quantified in lungs and brains of rats with cerebral QA lesion (N=5 per organ group), stroke-prone spontaneously hypertensive rats (SHRSP) (N=3 [brain], N=2 [lung]) and healthy rats (N=6 per organ group). Except for IL-6 and TNF- $\alpha$ , pro-migratory cytokines could be detected at higher concentrations in the lungs compared to the brains without obvious differences between the animal models; two-tailed t-test (\*p <  $0.05$ ; \*\*\*p< $0.001$ ). Error bars: SD. n.d. = not detactable; a.d.l. = above detection limit.



#### **Supplementary Figure 10 Pro-migratory cytokines in human endothelial cells.**

Analyses of pro-migratory cytokines showed greater expression of CCL2, TGF- $\beta$  and PDGF in endothelial cells derived from human brain (hbMVEC) compared to endothelial cells derived from human lung (hpMEC); N=2-4, each data point represents one biological replicate per group; two-tailed t-test (\*p < 0.05; \*\*\*\*p<0.0001). Error bars: SEM.

### **Supplementary Table 1**



Detection limit: 0.02 ng / mL

#### **Supplementary Table 1 CD44 ELISA analysis of treated and untreated MSC.**

To investigate potential shedding of CD44 molecules from MSC surface after PEI or PEI-NP treatment total MSC protein and supernatants of untreated and treated MSC were analyzed by CD44 ELISA. CD44 protein was detectable only in total MSC protein but not in supernatants indicating that CD44 molecules were not shedded by PEI or PEI-NP treatment.

## **Supplementary Table 2**

Descriptive statistics for comparisons with low sample sizes (N≤4).













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![](_page_35_Picture_72.jpeg)

## **Full Western Blots**

The blue frames indicate the areas shown in the Figures.

![](_page_36_Picture_3.jpeg)

## CD44 Fig.1b

#### **CXC R4 Fig.1 b**

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GAPDH Fig.1b

![](_page_38_Picture_2.jpeg)

### **CCL2 S uppl Fig .6**

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# **GAPDH Suppl Fig.6**

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