

Exosomes of human adipose stem cells mitigate irradiation injury to salivary glands by inhibiting epithelial-mesenchymal transition through miR-199a-3p targeting Twist1 and regulating the TGF β 1/Smad3 pathway

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Supplementary Figures and Table

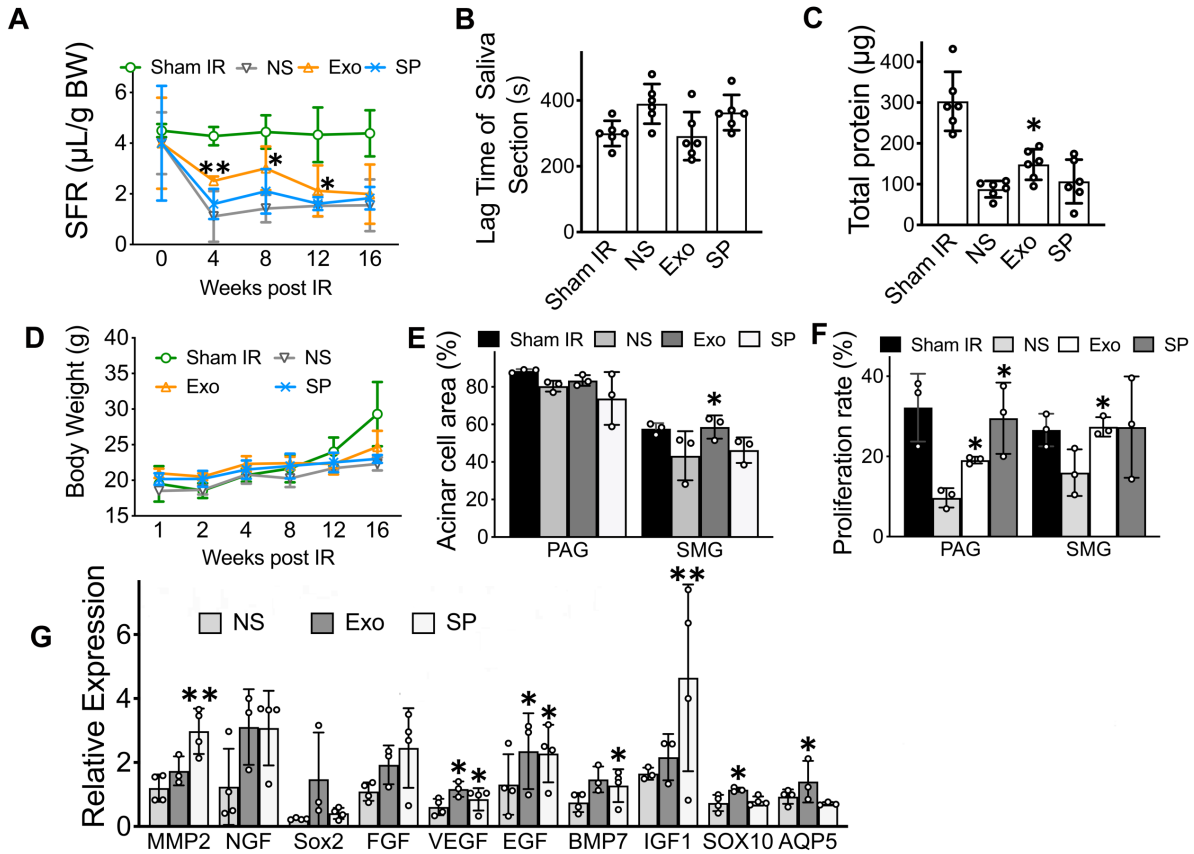


Figure S1. The effect of SP in treating the hypofunction of IR-SG

A) Salivary flow rate (SFR, $\mu\text{L}/10 \text{ min}/\text{g}$ body weight) was measured at week 0 (before IR), 4, 8, 12 and 16 post-IR. B) Time to salivation (lag time) was measured at week 8 post-IR. C) Total protein ($\mu\text{g}/10 \text{ min}$) in saliva was measured by a BCA assay kit at week 8 post-IR. D) Body weight (g) of the mouse. E) Quantification of acinar cells area in PAG and SMG according to the H&E staining. F) Ki67 immunohistochemistry staining was used to calculate the salivary cell proliferation rate at week 8 post-IR. G) Relative expression of genes related to SG repair and regeneration was determined by quantitative real-time PCR. GAPDH was used as the endogenous reference. Three experimental replicates were performed for each sample. All data were presented with mean \pm SD; * $p < 0.05$, ** $p < 0.01$, compared to the NS group (n = 3-6).

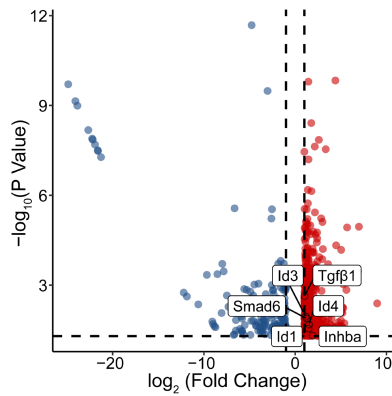


Figure S2.

Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis of TGF β signaling pathway related DEGs in the NS group compared to the Sham IR group.

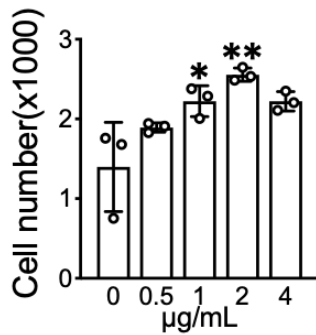


Figure S3. Concentration of Exo treatment in vitro

The number of SMG-C6 cell was measured by using a CCK8 kit. NS or different concentration of ADSC-Exo (0.5, 1, 2 and 4 $\mu\text{g}/\text{mL}$) was added to SMG-C6 cells and observed for 48 h. 2 $\mu\text{g}/\text{mL}$ Exo was chosen for the experiments in vitro. All data were presented with mean \pm SD; * $p < 0.05$, ** $p < 0.01$, compared to the 0 $\mu\text{g}/\text{mL}$ group (n = 3).

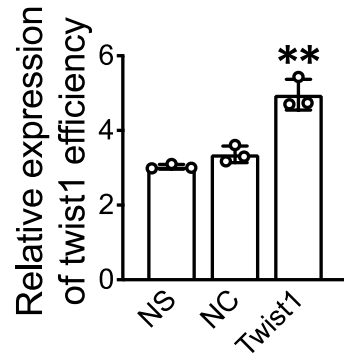


Figure S4. The efficiency of Twist1 infection

Lentivirus infection was used for Twist1 overexpression experiment in SMG-C6 cells. A significant increase of Twist1 expression was detected by qPCR. All data were presented with mean \pm SD; ** $p < 0.01$, compared to the NS group (n = 3).

Table S1. Primer sequences used for qPCR

genes	primer forward (5' -3')	primer reverse (5' -3')
<i>mmu-EGF</i>	AGCATCTCTCGGATTGACCCA	CCTGTCCGGTTAAGGAAAACCTCT
<i>mmu-VEGF</i>	GCACATAGGAGAGATGAGCTTCC	CTCCGCTCTGAACAAGGCT
<i>mmu-IGF1</i>	CTGGACCAGAGACCCCTTTCG	GGACGGGGACTTCTGAGTCTT
<i>mmu-FGF2</i>	GCGACCCACAGTCAAACCTA	TCCCTTGATAGACACAACCTCCTC
<i>mmu-BMP7</i>	ACGGACAGGGCTTCTCCTAC	ATGGTGGTATCGAGGGTGGAA
<i>mmu-NGF</i>	CCAGTGAAATTAGGCTCCCTG	CCTTGGCAAACCTTTATTGGG
<i>mmu-MMP2</i>	CAAGTTCCTCCGCGATGTC	TTCTGGTCAAGGTCACCTGTC
<i>mmu-Sox10</i>	ATCAGCCACGAGGTAATGTCCAAC	ACTGCCACGCCGTAGCC
<i>mmu-AQP5</i>	TCTACTTCTACTGCTTTCCCTCCTC	CGATGGTCTTCTCCGCTCCTCTC
<i>mmu-GAPDH</i>	ACTCCACTCACGGCAAATTCACGGCACAG	GGGTCTCGCTCCTGGAAGATGGTATGGG
<i>mmu-E-Cadherin</i>	CAGCCGGTCTTTGAGGGATT	TGACGATGGTGTAGGCGATG
<i>mmu-Collagen I</i>	AGCACGCTCTGGTTGGAGAG	GACATTAGGCGCAGGAAGGT
<i>mmu-CD44</i>	CATGGAATACACCTGCGTAGC	CTAGATCCCTCCGTTTCATCC
<i>mmu-TGFβ1</i>	TCGACATGGAGCTGGTGAAG	GCAGCTTGGACAGGATCTGG
<i>mmu-Smad3</i>	AGAAGCTCAAGAAGACGGGG	TGACCTGGGGATGGTAATGC
<i>mmu-Twist1</i>	AGCGGGTCATGCTAACG	ATCTTGCTCAGCTGTCCGAG
<i>mmu-GAPDH</i>	CATCACTGCCACCCAGAAGACTG	ATGCCAGTGAGCTTCCGTTCCAG
<i>mmu-AQP5</i>	CTCCCAGCCTTATCCATTG	CCAGAAGACCCAGTGAGAGG
<i>rno-E-Cadherin</i>	ATCCTGGCCCTCCTGATTCT	CGGGTATCGTCATCTGGTGG
<i>rno-Collagen I</i>	GAGCGGAGAGTACTGGATCG	TACTCGAACGGGAATCCATC
<i>rno-CD44</i>	CATGGAATACACCTGCGTAGC	CTAGATCCCTCCGTTTCATCC
<i>rno-TGFβ1</i>	GCAACAACGCAATCTATGAC	GCAGCTTGGACAGGATCTGG
<i>rno-Smad3</i>	AGGAGAAGTGGTGCAGAGAAG	GTGACCTGGGGATGGTAATG
<i>rno-Twist1</i>	CTCGGACAAGCTGAGCAAGAT	CTCGTGGGCCACATAGCTG
<i>rno-GAPDH</i>	ATGCTGGTGCTGAGTATGTC	AGTTGTCATATTTCTCTGGG
<i>rno-AQP5</i>	CTGCATCTTCTCCTCCACCG	CCCTACCCAGAAGACCCAGT
<i>miRNA</i>	Primer (5'-3')	
<i>miR-199a-3p</i>	CGACAGTAGTCTGCACATTGGTTA	
<i>miR-490-5p</i>	CCATTGATCTCCAGTGGGT	
<i>miR-484</i>	GCTCAGTCCCTCCCGAT	
<i>U6</i>	CTCGCTTCGGCAGCACA	