CORRECTION

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Correction: Micro/nano-net guides M2-pattern macrophage cytoskeleton distribution via Src–ROCK signalling for enhanced angiogenesis

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Correction for 'Micro/nano-net guides M2-pattern macrophage cytoskeleton distribution via Src–ROCK signalling for enhanced angiogenesis' by Yang Yang *et al.*, *Biomater. Sci.*, 2021, DOI: 10.1039/d1bm00116g.

The authors regret several errors with figures presented in their published manuscript. The following corrections make no difference to the scientific outcomes presented in the published manuscript.

1. In Fig. 2D and E the GAPDH was not displayed correctly. The correct Fig. 2 is shown below. The counting results from the correct Fig. 2D and E still support the conclusions presented in the published manuscript.

2. In Fig. 3D the GAPDH and JNK were not displayed correctly. The correct Fig. 3 is shown below. The counting results from the correct Fig. 3D still support the conclusions presented in the published manuscript.

The authors also regret an error in the counting process used to create Fig. 4B. The correct Fig. 4 is shown below, whilst an incorrect summary of the data is corrected as follows. In the results section "Effect of macrophage CM on angiogenic and osteogenic behaviour", the sentence "However, the SAM-CM group had slight but not significant differences compared with the SLA-CM group except in IGF1R expression" should be corrected to "However, the SAM-CM group had slight but not significant differences compared with the SLA-CM group except in VEGFR expression". This correction does not affect the scientific outcomes presented.

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Fig. 2 Analysis of macrophage adhesion and metabolic activity. (A) Fluorescent staining for macrophage morphology on Ti surfaces or LPS treatment as observed by LSCM. Macrophages were elongated in SAH and SAM, and rounded or polygonal in SLA and LPS groups. (B) Macrophage metabolic activity of four groups tested by CCK-8 at 1 and 3 days. (C) SEM observation for macrophage cytoskeleton arrangement. The whole cell and the pseudopod at cell ridges of SLA (a and b), SAM (c and d) and SAH (e and f) at different magnifications. (D and E) Western blotting analysis of p-Src, Src and ROCK in macrophages cultured under different conditions for 4 h and 24 h, the relative intensity of p-Src and ROCK was measured on the right. * $P < 0.05$, ** $P < 0.01$ compared with SLA, # $P < 0.05$, ## $P < 0.01$ compared with LPS.

Fig. 3 Analysis of macrophage inflammation related genes and proteins. (A) Relative mRNA expression of pro-inflammatory genes IL-1 β , IL-6, and TNF- α and anti-inflammatory genes IL-10 and TGF- β relative to housekeeping gene GAPDH in titanium or LPS groups. (B) Flow cytometry results of CD86 (M1 marker) and CD206 (M2 marker). (C) ELISA assay of IL-1 β and IL-10 concentration in different macrophage CM. (D) Western blotting analysis of p-JNK/JNK and p-ERK/ERK at 24 h. (E) The relative expression of p-ERK to ERK and p-JNK to JNK, respectively, was measured. * $P < 0.05$, ** $P < 0.01$ compared with SLA, # $P < 0.05$, ## $P < 0.01$ compared with LPS.

Fig. 4 Analysis of bEnd.3 cell angiogenic behaviour influenced by macrophage CM. (A) bEnd.3 cell proliferation at 1 day and 3 days. (B) Relative mRNA expression of angiogenic receptor genes PDGFR, IGF1R, FGFR2, PITPNM3 and VEGFR relative to housekeeping gene GAPDH in bEnd.3 cultured with CM. (C) Migration of bEnd.3 cells after incubation for 24 h and (D) the percentage of wound closure area after 24 h was calculated. (E) Tube formation of bEnd.3 cell cultured with different CM for 6 h and (F) quantitative analysis of capillary tube length and (G) branch points per microscopic field. * $P < 0.05$, ** $P < 0.01$ compared with SLA-CM, NS = not significant.

The Royal Society of Chemistry apologises for these errors and any consequent inconvenience to authors and readers.