



# Corrigendum: Exploring the Mechanism of Total Flavonoids of *Drynariae Rhizoma* to Improve Large Bone Defects by Network Pharmacology and Experimental Assessment

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## A Corrigendum on

### Exploring the Mechanism of Total Flavonoids of *Drynariae Rhizoma* to Improve Large Bone Defects by Network Pharmacology and Experimental Assessment

by Sun, W., Li, M., Xie, L., Mai, Z., Zhang, Y., Luo, L., Yan, Z., Li, Z., Dong, H., Huang, F., Shen, Z., and Jiang, Z. (2021). *Front. Pharmacol.* 12:603734. doi: 10.3389/fphar.2021.603734

In the original article, there was a mistake in the legend for **Figure 8** and **Figure 9** as published. In **Figure 8**, the numbering of figure legends was incorrect. In **Figure 9**, the description of previous **Figure 9** was not detailed enough. The correct legends appear below.

“**FIGURE 8** | Representative images of BMSCs with the alizarin red staining to determine the mineralized nodules. (A) Control group; (B) TFDR low dosage group; (C) TFDR medium dosage group; (D) TFDR high dosage group; (E) The mineralized nodules at each time point of the control group, TFDR low dosage group, TFDR medium dosage group, and TFDR high dosage group were evaluated. The data are expressed as the mean  $\pm$  SEM of three independent experiments. <sup>#</sup> $p < 0.05$  vs. control group,  <sup>$\Delta$</sup>  $p < 0.05$  vs. TFDR low dosage group,  <sup>$\blacktriangle$</sup>  $p < 0.05$  vs. TFDR high dosage group.”

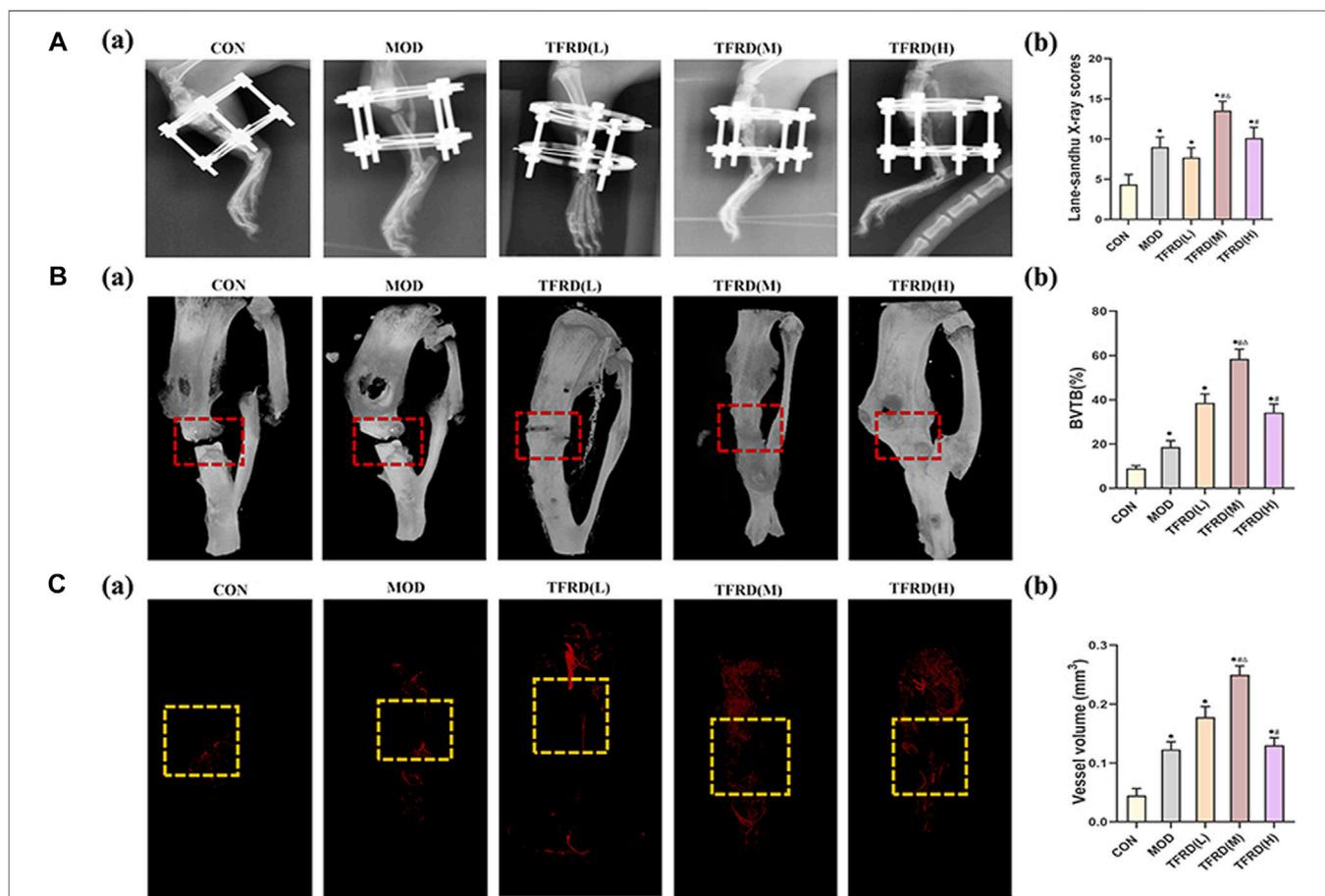
“**FIGURE 9** | The expressions of p38 MAPK, BMP-2, VEGF, HIF-1 $\alpha$ , and RUNX-2 mRNA on BMSCs by quantitative real-time PCR. The data are expressed as the mean  $\pm$  SEM of three independent experiments. <sup>\*</sup> $p < 0.05$  vs. control group, <sup>#</sup> $p < 0.05$  vs. the TFDR low dosage group, TFDR high dosage group. (B) (a) p38 MAPK, p-p38 MAPK, BMP-2, RUNX-2, VEGF, and HIF-1 $\alpha$  protein expression on BMSCs detected by western blot analysis. (b)–(g) were statistical analysis of (a). The data are expressed as the mean  $\pm$  SEM of three independent experiments. <sup>\*</sup> $p < 0.01$  vs. the Control group; <sup>#</sup> $p < 0.01$  vs. the TFDR low dosage group.”

In addition, there was a mistake in **Figure 3**, **Figure 7** and **Figure 9** as published. The authors uploaded the wrong version of **Figure 3** and **Figure 7**, and uploaded the previous version of **Figure 9** by mistake. The corrected **Figure 3**, **Figure 7** and **Figure 9** appear below.

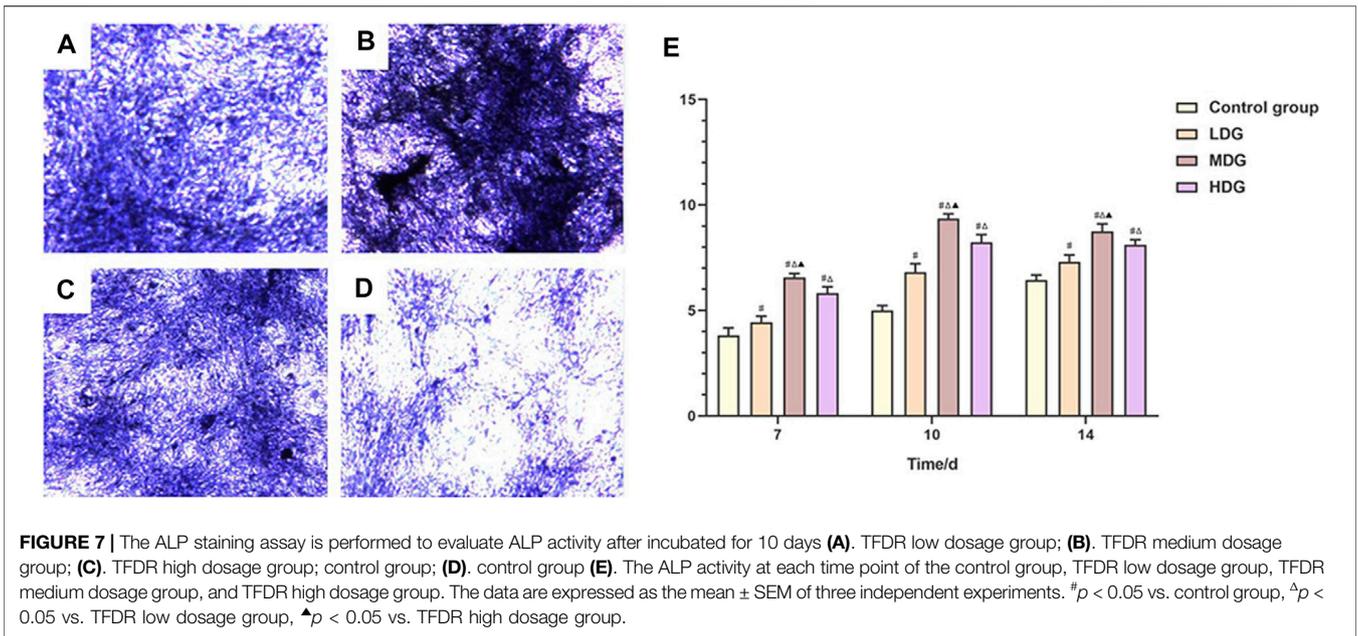
The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

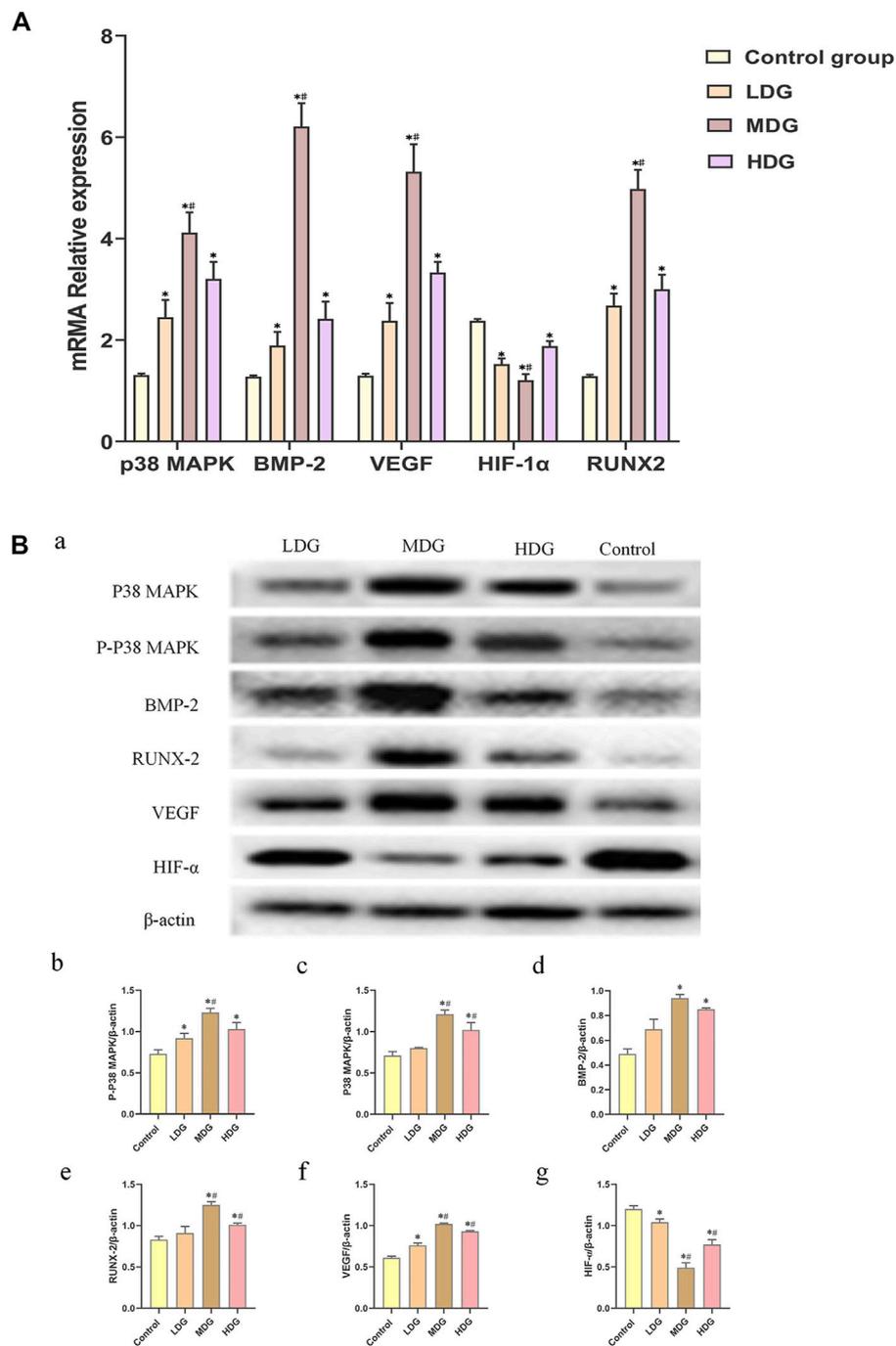
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**FIGURE 3 |** Evaluation of radiological, micro-CT images, angiogenesis of tibial bone repair of five groups **(A)**. Radiological evaluation of bone repair **(A)** (a). Representative radiographs of bone repair of the five groups at 12 weeks after surgery ( $n = 3$  per group); **(A)** (b). Quantitative analysis of radiographic scores **(B)**. Representative micro-CT images of bone repair **(B)** (a). Three-dimensional reconstructed images of bone defects at 12 weeks after surgical dotted boxes indicate region of interest (ROI), representing bone distracted gaps ( $n = 3$  per group); **(B)** (b). Quantification of bone tissue volume/total tissue volume and (BV/TV) inside bone distracted regions **(C)**. Evaluation of angiogenesis within the distracted gaps at 4 weeks after surgery **(C)** (a). Representative angiograms of the distracted gaps in the five groups ( $n = 3$  per group) **(C)** (b). Quantification of vessel volume within the distracted regions (yellow dotted boxes indicate region of interest (ROI), representing bone distracted gaps). The data are expressed as the mean  $\pm$  SEM of three independent experiments. \* $p < 0.05$ , compared with the control group; \*\* $p < 0.05$ , compared with the model group; \*\*\* $p < 0.05$ , compared the difference of the medium dose with the low and high doses in the TFDR group.





**FIGURE 9 |** The expressions of p38 MAPK, BMP-2, VEGF, HIF-1 $\alpha$ , and RUNX-2 mRNA on BMSCs by quantitative real-time PCR. The data are expressed as the mean  $\pm$  SEM of three independent experiments. \* $p < 0.05$  vs. control group, # $p < 0.05$  vs. the TFDR low dosage group, TFDR high dosage group. **(B)** (a) p38 MAPK, p-p38 MAPK, BMP-2, RUNX-2, VEGF, and HIF-1 $\alpha$  protein expression on BMSCs detected by western blot analysis. (b)–(g) were statistical analysis of (a). The data are expressed as the mean  $\pm$  SEM of three independent experiments. \* $p < 0.01$  vs. the Control group; # $p < 0.01$  vs. the TFDR low dosage group.