

CORRECTION

[View Article Online](#)
[View Journal](#) | [View Issue](#)



Cite this: *Food Funct.*, 2021, **12**, 2336

Correction: The chemopreventive effects of Huangqin-tea against AOM-induced preneoplastic colonic aberrant crypt foci in rats and omics analysis

Jie Shen,^{a,b} Pei Li,^{a,b} Shuangshuang Liu,^{a,b} Qing Liu,^{a,b} Yue Li,^{a,b} Zheng Zhang,^{a,b} Chengmin Yang,^{a,b} Mengying Hu,^c Yuhua Sun,^c Chunnian He^{*a,b} and Peigen Xiao^{a,b}

DOI: 10.1039/d1fo90005f
rsc.li/food-function

Correction for 'The chemopreventive effects of Huangqin-tea against AOM-induced preneoplastic colonic aberrant crypt foci in rats and omics analysis' by Jie Shen *et al.*, *Food Funct.*, 2020, **11**, 9634–9650, DOI: 10.1039/D0FO01731K.

The authors regret that the panels for Fig. 3C–E are missing in the original article. The correct version of Fig. 3 is as shown below.



^aInstitute of Medicinal Plant Development, Chinese Academy of Medical Science, Peking Union Medical College, Beijing 100193, China. E-mail: cnhe@implad.ac.cn;
Fax: +86 10 57833165; Tel: +86 10 57833165

^bLaboratory of Bioactive Substances and Resources Utilization of Chinese Herbal Medicine, Ministry of Education, Beijing 100193, China

^cXinjiang Institute of Materia Medica, Urumqi 830004, China

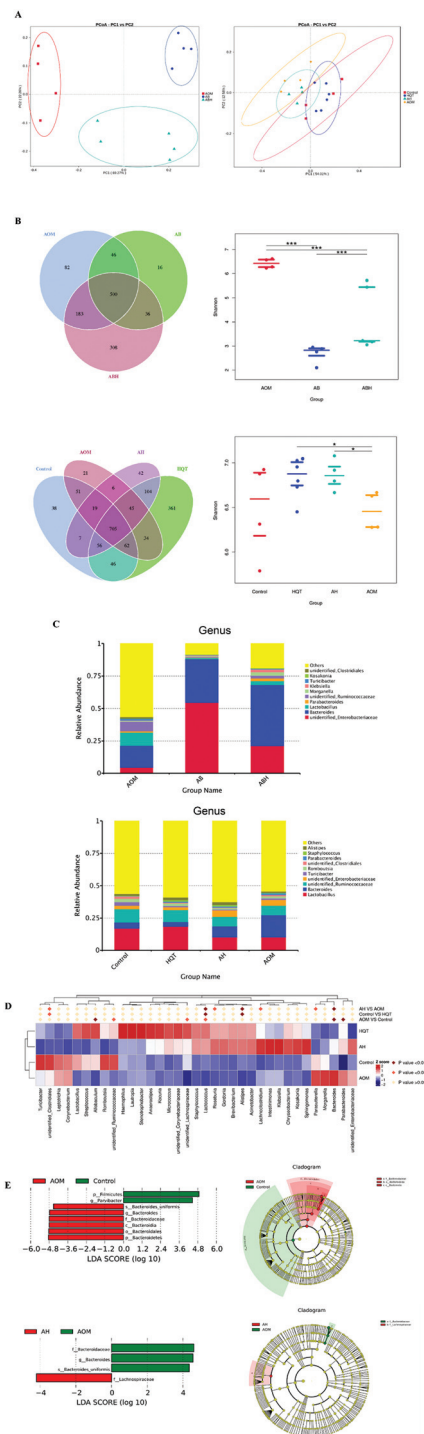


Fig. 3 HQT modulated the gut microbiota community in rats with AOM-induced precancerous colorectal lesions. (A) Principal co-ordinates analysis. (B) Venn diagram showing shared and exclusive bacterial OTUs in the various treatment groups, and alpha diversity was presented by a box plot of the Shannon. (C) The top 10 relative abundances of bacteria at the genus level in different groups. (D) Heatmap: MetaStat analysis of differences in the gut microbiota at the genus level among the groups (control, HQT, AOM, and AH groups). (E) LefSe analysis histogram (left) and biomarker taxa (right).

Consequently, a section of the text in the manuscript should be adjusted as detailed below.

The sentence on page 9640 beginning “In order to find biomarkers between the AOM and AH...” should be correctly given as “In order to find biomarkers between the AOM and AH groups using relative abundances, the LefSe method was used to identify the gut microbiota that was different in abundance in the control, model, and treatment groups (Fig. 3E and Fig. S5†).”

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

