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Corrigendum

Corrigendum to "Enhancing Clinical Efficacy through the Gut Microbiota: A New Field of Traditional Chinese Medicine" [Engineering 5 (2019) 40–49]



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The authors regret to inform that Figs. 2 and 3 were misplaced. The correct figures and figure captions appear below: The authors would like to apologize for any inconvenience caused.

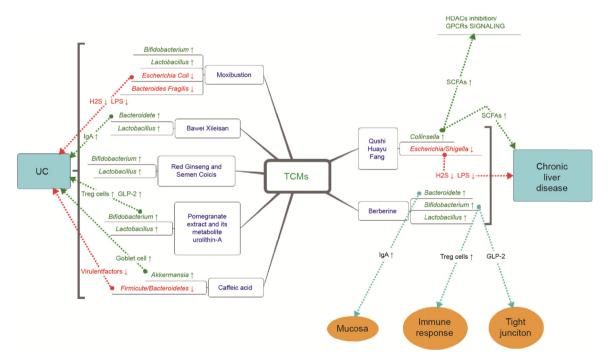


Fig. 2. Changes and potential mechanisms of the major gut microbiota of ulcerative colitis (UC) and chronic liver disease when treated by TCMs. Blue font represents TCM, green font shows increased flora in the experiment, and red font shows decreased flora. The dotted arrow indicates the direction of action, and the text on the dotted line represents the underlying mechanism. Blue dotted lines indicate other potential mechanisms of action. GLP-2: glucagon-like peptide-2; HDAC: histone deacetylases; GPCRS: G protein-coupled receptors.

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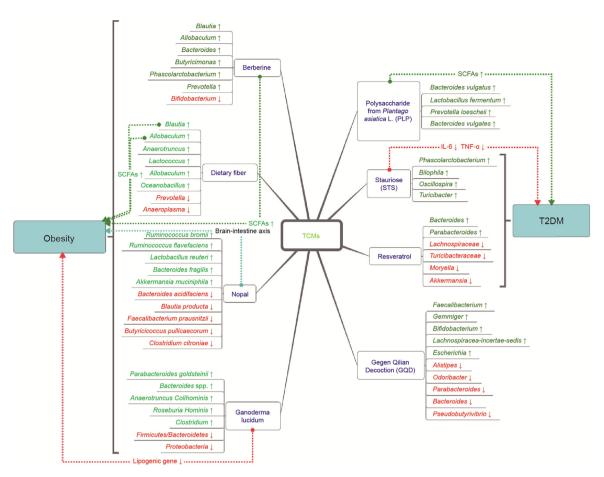


Fig. 3. Changes and potential mechanisms of the major gut microbiota of obesity and Type 2 diabetes (T2DM) when treated by TCMs. Blue font represents TCM, green font shows increased flora in the experiment, and red font shows decreased flora. The dotted arrow indicates the direction of action, and the text on the dotted line represents the underlying mechanism. Blue dotted lines indicate other potential mechanisms of action.