

OPEN

Author Correction: Metabolomic Changes of Human Proximal Tubular Cell Line in High Glucose Environment

Pascal Zhongping Wei, Winston Wing-Shing Fung, Jack Kit-Chung Ng, Ka-Bik Lai, Cathy Choi-Wan Luk, Kai Ming Chow, Philip Kam-Tao Li & Cheuk Chun Szeto 

Correction to: *Scientific Reports* <https://doi.org/10.1038/s41598-019-53214-1>, published online 12 November 2019

The Authors missed out a previous study on a similar topic. The additional reference is listed below as Reference 1, and should appear in the text as below.

In the Discussion section,

“In contrast, Zhang *et al.*²⁰ reviewed 12 studies published before March 2015, and note that products of lipid and amino acids metabolisms were frequently affected in DKD. More importantly, there were substantial differences in the results between individual metabolomic studies, which may be related to differences in patient population and selection, as well as the technique being used²⁰. Taken together, available data in this area are fragmented, and our present study contribute to the understanding of this difficult subject.”

should read:

“In contrast, Zhang *et al.*²⁰ reviewed 12 studies published before March 2015, and note that products of lipid and amino acids metabolisms were frequently affected in DKD. More recently, Bernardo-Bermejo *et al.*¹ used untargeted liquid chromatography-mass spectrometry to study the metabolomic changes of HK-2 cells induced by hyperglycemia and revealed substantial alterations in the concentration of several metabolites, including hippuric acid, sorbitol, N-steaoryl valine, pyridoxine, 5'-methylthioadenosine, phenylacetyl glycine, and pyroglutamic acid, which are not included in the panel of metabolite in our own study. On the other hand, we examined numerous metabolites in the Krebs cycle, amino acids synthesis, pentose phosphate pathway, glutathione synthesis, and DNA methylation machinery, which were not explored in the study of Bernardo-Bermejo *et al.*¹ More importantly, there were substantial differences in the results between individual metabolomic studies, which may be related to differences in patient population and selection, as well as the technique being used. Taken together, available data in this area are fragmented, and our present study contributes to the understanding of this difficult subject.”

Reference

1. Bernardo-Bermejo, S. *et al.* An untargeted metabolomic strategy based on liquid chromatography-mass spectrometry to study high glucose-induced changes in HK-2 cells. *J Chromatogr A*. **1596**, 124–133 (2019).



Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons license, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons license and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this license, visit <http://creativecommons.org/licenses/by/4.0/>.

© The Author(s) 2020