



OPEN ACCESS

Edited and reviewed by:
Geert Wiegertjes,
Wageningen University and Research,
Netherlands

*CORRESPONDENCE
Xiaohui Ai
aixh@yfi.ac.cn
Yuhua Chen
510026437@qq.com

[†]These authors share first authorship

SPECIALTY SECTION

This article was submitted to
Comparative Immunology,
a section of the journal
Frontiers in Immunology

RECEIVED 30 June 2022

ACCEPTED 07 July 2022

PUBLISHED 27 July 2022

CITATION

Yang Y, Zhu X, Zhang H, Chen Y, Song Y and Ai X (2022) Corrigendum: Dual RNA-seq of trunk kidneys extracted from channel catfish infected with *Yersinia ruckeri* reveals novel insights into host-pathogen interactions. *Front. Immunol.* 13:982091. doi: 10.3389/fimmu.2022.982091

COPYRIGHT

© 2022 Yang, Zhu, Zhang, Chen, Song and Ai. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) and the copyright owner(s) are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.

Corrigendum: Dual RNA-seq of trunk kidneys extracted from channel catfish infected with *Yersinia ruckeri* reveals novel insights into host-pathogen interactions

Yibin Yang^{1,2†}, Xia Zhu^{1†}, Haixin Zhang^{3†}, Yuhua Chen^{4,5*},
Yi Song² and Xiaohui Ai^{1,2*}

¹Yangtze River Fisheries Research Institute, Chinese Academy of Fishery Sciences, Wuhan, China,

²The Key Laboratory for Quality and Safety Control of Aquatic Products, Ministry of Agriculture, Beijing, China, ³Fish Disease Laboratory, Jiangxi Fisheries Research Institute, Nanchang, China,

⁴Department of Gastroenterology, Zhongnan Hospital of Wuhan University, Wuhan, China, ⁵Hubei Clinical Center & Key Lab of Intestinal & Colorectal Diseases, Zhongnan Hospital of Wuhan University, Wuhan, China

KEYWORDS

channel catfish, *yersinia ruckeri*, dual RNA-seq, host-pathogen interactions, immunity, virulence

A Corrigendum on:

Dual RNA-Seq of Trunk Kidneys Extracted From Channel Catfish Infected With *Yersinia ruckeri* Reveals Novel Insights Into Host-Pathogen Interactions.

Yang Y, Zhu X, Zhang H, Chen Y, Song Y and Ai X (2021) Dual RNA-Seq of Trunk Kidneys Extracted From Channel Catfish Infected With *Yersinia ruckeri* Reveals Novel Insights Into Host-Pathogen Interactions. *Front. Immunol.* 12:775708. doi: 10.3389/fimmu.2021.775708

In the published article, there was an error in Figure 6A as published. Figure 5A was used instead of Figure 6A in the revision of the article. The corrected Figure 6A appears below.

In the published article, there was an error in the legend of Figure 1 as published. There was one mistake in the species names. The corrected legend appears below.

“Figure 1. The gene expression profiles for channel catfish and *Y. ruckeri* during infection. A volcanic plot depicting the differences in the expression profiles of channel catfish and *Y. ruckeri*. The X-axis represents a log2 (fold change) and the Y-axis represents

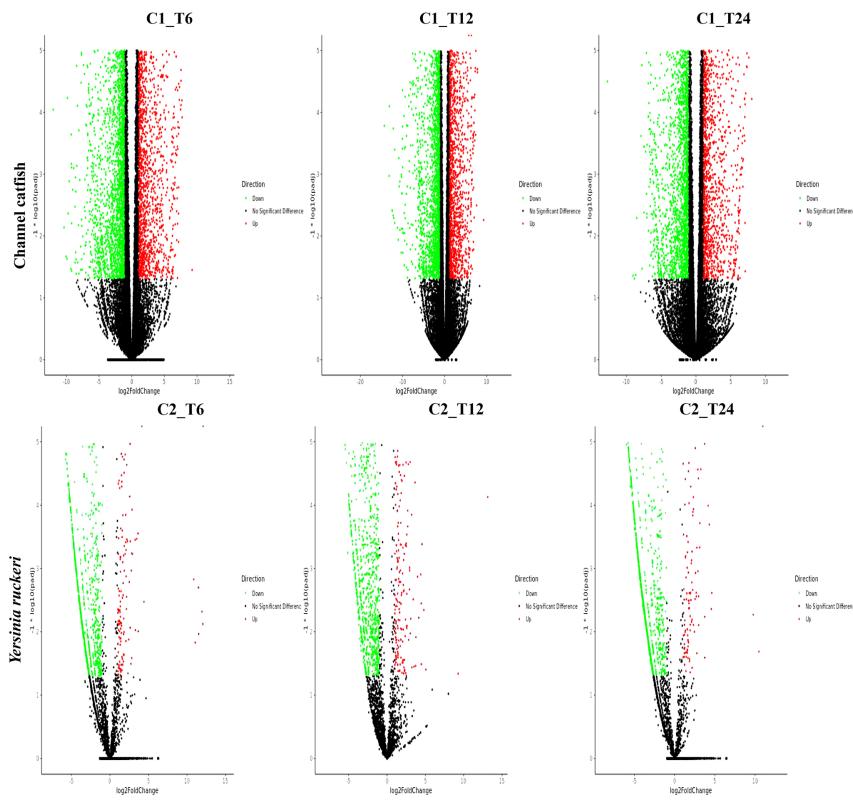


FIGURE 1

The gene expression profiles for channel catfish and *Y. ruckeri* during infection. A volcano plot depicting the differences in the expression profiles of channel catfish and *Y. ruckeri*. The X-axis represents a log₂ (fold change) and the Y-axis represents -log₁₀ (p value). Red represents significantly upregulated genes whereas green represents significantly downregulated genes. Each dot represents a single gene. C1_T6(C2_T6) represents 6 hpi, C1_T12(C2_T12) represents the 12 hpi and C1_T24 (C2_T24) stands for 24 hpi.

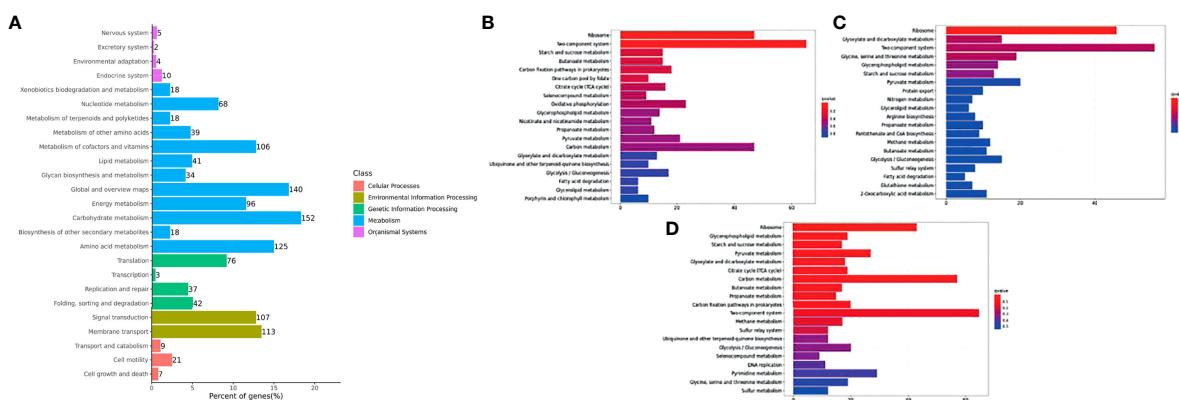


FIGURE 6

Histogram of the top 20 enriched KEGG pathways of DEGs in *Y. ruckeri* at different time points. The Y-axis represents the KEGG pathway categories. The X-axis represents statistical significance of the enrichment. (A) represents the classification of total KEGG, (B) represents the top 20 KEGG pathways in the C2_T6 group, (C) represents the top 20 KEGG pathways in the C2_T12 group and (D) represents the top 20 KEGG pathways in the C2_T24 group.

-log₁₀ (p value). Red represents significantly upregulated genes whereas green represents significantly downregulated genes. Each dot represents a single gene. C1_T6(C2_T6) represents 6 hpi, C1_T12(C2_T12) represents the 12 hpi and C1_T24(C2_T24) stands for 24 hpi.”

In the published article, there was an error. A correction has been made to **DISCUSSION**, Paragraph 7. This sentence previously stated:

“The pathogen HlyA was severely down-regulated by the host, indicating that the pathogen did not rely on hemolysin to cause harm in the host trunk kidney.”

The corrected sentence appears below:

“The pathogen HlyB was up-regulated in the infection, indicating that the pathogen rely on hemolysin to cause harm in the host trunk kidney.”

The authors apologize for these errors and state that they do not change the scientific conclusions of the article in any way. The original article has been updated.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.