



Corrigendum: Identification of a Novel Small RNA srvg23535 in Vibrio alginolyticus ZJ-T and Its Characterization With Phenotype MicroArray Technology

OPEN ACCESS

Edited and reviewed by:

Eric Altermann, AgResearch, New Zealand

*Correspondence:

Juan Feng juanfeng@scsfri.ac.cn Chang Chen chen.chang@scsio.ac.cn

Specialty section:

This article was submitted to Evolutionary and Genomic Microbiology, a section of the journal Frontiers in Microbiology

Received: 14 December 2018 Accepted: 09 January 2019 Published: 31 January 2019

Citation

Deng Y, Su Y, Liu S, Guo Z, Cheng C, Ma H, Wu J, Feng J and Chen C (2019) Corrigendum: Identification of a Novel Small RNA srvg23535 in Vibrio alginolyticus ZJ-T and Its Characterization With Phenotype MicroArray Technology. Front. Microbiol. 10:21. doi: 10.3389/fmicb.2019.00021 Yiqin Deng ^{1,2}, Youlu Su¹, Songlin Liu³, Zhixun Guo¹, Changhong Cheng ¹, Hongling Ma¹, Jinjun Wu¹, Juan Feng ^{1*} and Chang Chen ^{2,4*}

¹ Key Laboratory of South China Sea Fishery Resources Exploitation and Utilization, Ministry of Agriculture and Rural Affairs, South China Sea Fisheries Research Institute, Chinese Academy of Fishery Sciences, Guangzhou, China, ² Key Laboratory of Tropical Marine Bio-resources and Ecology, Guangdong Provincial Key Laboratory of Applied Marine Biology, South China Sea Institute of Oceanology, Chinese Academy of Sciences, Guangzhou, China, ³ Key Laboratory of Tropical Marine Bio-resources and Ecology, South China Sea Institute of Oceanology, Chinese Academy of Sciences, Guangzhou, China, ⁴ Xisha/Nansha Ocean Observation and Research Station, South China Sea Institute of Oceanology, Chinese Academy of Sciences, Guangzhou, China

Keywords: small non-coding RNAs, srvg23535, Vibrio alginolyticus, identification, Phenotype MicroArray technology

A Corrigendum on

Identification of a Novel Small RNA srvg23535 in Vibrio alginolyticus ZJ-T and Its Characterization With Phenotype MicroArray Technology

by Deng, Y., Su, Y., Liu, S., Guo, Z., Cheng, C., Ma, H., et al. (2018). Front. Microbiol. 9:2394. doi: 10.3389/fmicb.2018.02394

In the published article, there was an error in affiliation 1. Instead of "Ministry of Agriculture" the correct name of the ministry is "Ministry of Agriculture and Rural Affairs".

In Table 1, the references for "53813," "GEB88," and "pSW7848," were incorrectly written as "This lab." It should be "Le Roux et al., 2007," "Nguyen et al., 2018," and "Val et al., 2012," respectively. Additionally, the intermediate host *Escherichia coli* strain was named as "GEB802," but should be "53813."

The corrected Table 1 appears below.

1

TABLE 1 | Strains and plasmids used in this study.

Strains or plasmids	Relevant characteristics	Sources
V. alginolyticus		
ZJ-T	Apr (ampicillin resistant), translucent/smooth variant of wild strain ZJ-51 (Xiaochun et al., 2017); isolated from diseased <i>Epinephelus coioides</i> off the Southern China coast	Chang et al., 2009
ZJ-T-∆srvg23535	Apr; ZJ-T carrying an deletion of srvg23535	This study
E. coli		
П3813	Emr ^r , Tc ^r , lacIQ, thi1, supE44, endA1, recA1, hsdR17, gyrA462, zei298::tn10[Tc], Δ thyA:: (erm-pir116); the intermediate host of suicide vector pSW7848	Le Roux et al., 2007
GEB883	Ery ^r , Tet ^r , WT <i>E. coli</i> K12 Δ dapA::erm pir RP4-2 Δ recA gyrA462, zei298::Tn10; donor strain for conjugation	Nguyen et al., 2018
Plasmids		
pSW7848	Cmr; suicide vector with an R6K origin, requiring the Pir protein for its replication, and the <i>ccdB</i> toxin gene	Val et al., 2012
pSW7848-∆srvg23535	Cmr; pSW848 containing the mutant allele of Δsrvg23535	This study

A correction has also been made to the MATERIALS AND METHODS, Bacterial Strains, Plasmids, and Growth Conditions and Gene Disruption, paragraph one:

"To generate the sRNA disruptant, the sequence from 46 bp before the 5' end to 2 bp after the 3' end was deleted from the chromosome of *V. alginolyticus* ZJ-T. The deletion was constructed by homologous recombination as described before with some modification (Yiqin et al., 2016). Briefly, two flanking fragments of *srvg23535* (Figure 1A) were amplified with two pairs of primers, *srvg23535*-UP-F and -R and *srvg23535*-DOWN-F and -R respectively, and the linearized pSW7848 was amplified with pSW7848-F and -R (Supplementary Table 1). *srvg23535*-UP-F and *srvg23535*-DOWN-R contained overlapping extensions with pSW7848-R and -F, respectively, and *srvg23535*-DOWN-F. The two

flanking fragments were further assembled into the linearized pSW7848 by using a ClonExpress Multis One Step Cloning Kit (Vozyme, China), generating the recombinant plasmid pSW7848- $\Delta srvg23535$ comprising the 1,084 bp upstream and 1,105 bp downstream regions of srvg23535 (Table 1), using *E. coli* П3813 as an intermediate host. The recombinant plasmid was transferred by conjugation from strain GEB883 (Table 1) to *V. alginolyticus* ZJ-T before allelic exchange as described above. The sRNA disruptant was then confirmed by sequencing and the strain was named ZJ-T- $\Delta srvg23535$ (Figure 1 and Table 1)."

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

REFERENCES

Chang, C., Jin, X., and Chaoqun, H. (2009). Phenotypic and genetic differences between opaque and translucent colonies of Vibrio alginolyticus. Biofouling 25, 525–531. doi: 10.1080/08927010902964578

Le Roux, F., Binesse, J., Saulnier, D., and Mazel, D. (2007). Construction of a Vibrio splendidus mutant lacking the metalloprotease gene vsm by use of a novel counterselectable suicide vector. Appl. Environ. Microbiol. 73, 777–784. doi: 10.1128/AEM.02147-06

Nguyen, A. N., Disconzi, E., Charrière, G. M., Destoumieux-Garzón, D., Bouloc, P., Le Roux, F., et al. (2018). csrB gene duplication drives the evolution of redundant regulatory pathways controlling expression of the major toxic secreted metalloproteases in Vibrio tasmaniensis LGP32. mSphere 3:e00582-18. doi: 10.1128/mSphere.00582-18

Val, M. E., Skovgaard, O., Ducos-Galand, M., Bland, M. J., and Mazel, D. (2012). Genome engineering in Vibrio cholerae: a feasible approach to address biological issues. PLoS Genet. 8:e1002472. doi: 10.1371/journal.pgen.1002472

Xiaochun, H., Chang, C., Chunhua, R., Yingying, L., Yiqin, D., Yiying, Y., et al. (2017). Identification and characterization of a locus putatively involved in

colanic acid biosynthesis in Vibrio alginolyticus ZJ-51. Biofouling 34, 1–14. doi: 10.1080/08927014.2017.1400020

Yiqin, D., Chang, C., Zhe, Z., Jingjing, Z., Jacq, A., Xiaochun, H., et al. (2016). The RNA chaperone Hfq is involved in colony morphology, nutrient utilization and oxidative and envelope stress response in *Vibrio* alginolyticus. PLoS ONE 11:e0163689. doi: 10.1371/journal.pone.01 63689

Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Copyright © 2019 Deng, Su, Liu, Guo, Cheng, Ma, Wu, Feng and Chen. 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.