scientific reports

Check for updates

OPEN

Author Correction: Possible roles of Wnt in the shell growth of the pond snail *Lymnaea stagnalis*

Published online: 09 December 2024

Shigeaki Ohta, Koji Noshita, Katsunori Kimoto, Akito Ishikawa, Hideaki Sato, Keisuke Shimizu & Kazuyoshi Endo

Correction to: *Scientific Reports* https://doi.org/10.1038/s41598-024-74794-7, published online 03 November 2024

The original version of this Article contained errors, where the reference citations 48, 49 and 50 were incorrectly cited in the text.

As a result, in the "Materials and methods" section, under the sub-heading "RT-qPCR of the candidate readout genes of the Wnt signaling pathway in *L. stagnalis*",

Total RNA was extracted from four individuals of *L. stagnalis* following the protocol of Isowa *et al.*[19], for each of the BIO-treated (and with the phenotype of shell malformation) and the control samples. The experiments of BIO treatment and subsequent RNA extractions were performed twice independently to serve biological duplicates, which are named Dataset-A and Dataset-B (see Table S4 for details). Complementary DNA was prepared, and quantitative PCR was performed using the StepOne Real-time PCR system (Applied Biosystems, Foster City, USA), based on the protocol of Ishikawa *et al.*[35]. Two sets of primers (20–22 nucleotides in length; Table S5) were designed for each of *Pangolin* and *Frizzled2* genes, using Primer3Plus (https://primer3plus.com/cgi-bin/dev/primer3plus.cgi; last accessed May 3, 2024). A pair of primers designed by Young *et al.*[48] for *L. stagnalis* was used to amplify an *EF1α* gene sequence as the endogenous control. For each combination of the templates (control and BIO-treated of Dataset-A and Dataset-B) and the primer sets (Lst Pangolin-1-F and Lst Pangolin-1-R (Pangolin-1), Lst Pangolin-2-F and Lst Pangolin-2-R (Pangolin-2), Lst Frizzled2-1-F and Lst Frizzled2-1-R (Frizzled2-1), Lst Frizzled2-2-F and Lst Frizzled2-2-R (Frizzled2-2), and the primer set for *EF1α*) (Table S5), three to four technical replicates were included. The qPCR consisted of 95 °C for 30 s; 40 cycles of 95 °C for 15 s, 56 °C for 30 s, and the gene expression levels were quantified using the comparative CT method (Livak and Schmittgen[49]).

Now reads:

Total RNA was extracted from four individuals of *L. stagnalis* following the protocol of Isowa *et al.*[48], for each of the BIO-treated (and with the phenotype of shell malformation) and the control samples. The experiments of BIO treatment and subsequent RNA extractions were performed twice independently to serve biological duplicates, which are named Dataset-A and Dataset-B (see Table S4 for details). Complementary DNA was prepared, and quantitative PCR was performed using the StepOne Real-time PCR system (Applied Biosystems, Foster City, USA), based on the protocol of Ishikawa *et al.*[35]. Two sets of primers (20–22 nucleotides in length; Table S5) were designed for each of *Pangolin* and *Frizzled2* genes, using Primer3Plus (https://primer3plus.com/cgi-bin/dev/primer3plus.cgi; last accessed May 3, 2024). A pair of primers designed by Young *et al.*[49] for *L. stagnalis* was used to amplify an *EF1α* gene sequence as the endogenous control. For each combination of the templates (control and BIO-treated of Dataset-A and Dataset-B) and the primer sets (Lst Pangolin-1-F and Lst Pangolin-1-R (Pangolin-1), Lst Pangolin-2-F and Lst Pangolin-2-R (Pangolin-2), Lst Frizzled2-1-F and Lst Frizzled2-1-R (Frizzled2-1), Lst Frizzled2-2-F and Lst Frizzled2-2-R (Frizzled2-2), and the primer set for *EF1α*) (Table S5), three to four technical replicates were included. The qPCR consisted of 95 °C for 30 s; 40 cycles of 95 °C for 15 s, 56 °C for 30 s, and the gene expression levels were quantified using the comparative CT method (Livak and Schmittgen[50]).

The original Article has been corrected.