Auburn University

Department on Biological Sciences

101 Rouse Building

Auburn, AL, 36849

Yuanning Li

TEL: (334) 844-3223

FAX: (334) 844-2333

yzl0084@auburn.edu

Dear Editors:

Please consider the manuscript entitled “**Genomic adaptations to chemosymbiosis in the deep-sea seep-dwelling tubeworm *Lamellibrachia luymesi* (Siboglinidae, Annelida)**” for publication in ***Nature Ecology and Evolution.***

We discovered that *Lamellibrachia luymesi*, a common chemosynthetic tubeworm that lives at cold-seeps in the Gulf of Mexico, has several genomic adaptations to facilitate symbiosis. To date, genomic studies of adaptation and evolution in obligate endosymbiosis have focused mainly on modifications found in the endosymbiont (e.g., the bacteria in bacterial-animal symbioses). Herein, we show several genomic adaptions that implicate cellular mechanisms in the host organism. Such host genomic adaptions include loss of essential genes used in amino acid biosynthesis obligating tubeworms to use products provided by endosymbionts and a large expansion of hemoglobin B1 genes which aids transport of H2S to endosymbionts. We also explore the Toll-like receptor pathway involved in host immunity and tolerance to symbionts, and several ­ known to play important roles in longevity are identified. These findings are based on *L. luymesi’*s complete genome (one of the most complete Lophotrochozoan genomes to date) as well as transcriptomes and proteomic data.

These findings help elucidate the genetic mechanisms related to the evolution of holobionts and adaptations to reducing environments. Importantly, our results also hold implications for other symbiotic systems, especially chemosynthetic symbiosis (e.g. deep-sea mussels, shallow water clams, hydrothermal vent shrimp, etc). Thus, ***Nature Ecology and Evolution*** is the best journal for this study given the broad interest to a wide variety of scientific fields (e.g., evolutionary biology, deep-sea biology and symbiosis).

We also attached the current draft of the manuscript in the presubmission system and it is not the final version. We would like to further enhance the manuscript with molecular clock analysis and genes undergone positive selection of the tubeworms.

Your consideration of the manuscript is most appreciated.

Regards,

Yuanning Li

Auburn University