

# In Depth Investigation into Pathophysiology of the Gut Metagenome and Host Response to *VpAHPND* In Madagascar–Malaysia Crossbred Black Tiger Shrimp *Penaeus Monodon* Cohort Stocks

1 Department of Genetics and Molecular Biology, Institute of Biological Sciences, Faculty of Science, University of Malaya, 50603 Kuala Lumpur, Malaysia  
2 Centre for Research in Biotechnology for Agriculture (CEBAR), Research Management and Innovation Complex, University of Malaya, 50603 Kuala Lumpur, Malaysia

Tze Chiew Christie Soo<sup>1\*</sup> and Subha Bhassu<sup>1,2</sup>

Email:  
Tze Chiew Christie Soo- [cstc93@gmail.com](mailto:cstc93@gmail.com)  
Subha Bhassu- [subhabhassu@um.edu.my](mailto:subhabhassu@um.edu.my)

## Introduction

The lethal shrimp bacterial infection known as Acute Hepatopancreatic Necrosis Disease (AHPND) is mainly caused by *Vibrio parahaemolyticus* AHPND strain (*VpAHPND*) bacteria. The *VpAHPND* bacteria mainly colonize the stomach and gut regions and release toxins to damage shrimp hepatopancreas (Figures 1&2). The present study aims to identify the important changes of *Penaeus monodon* gut metagenome and biochemical activities especially in hepatopancreas when infected with *VpAHPND* (Figure 3).

## Materials and Methods

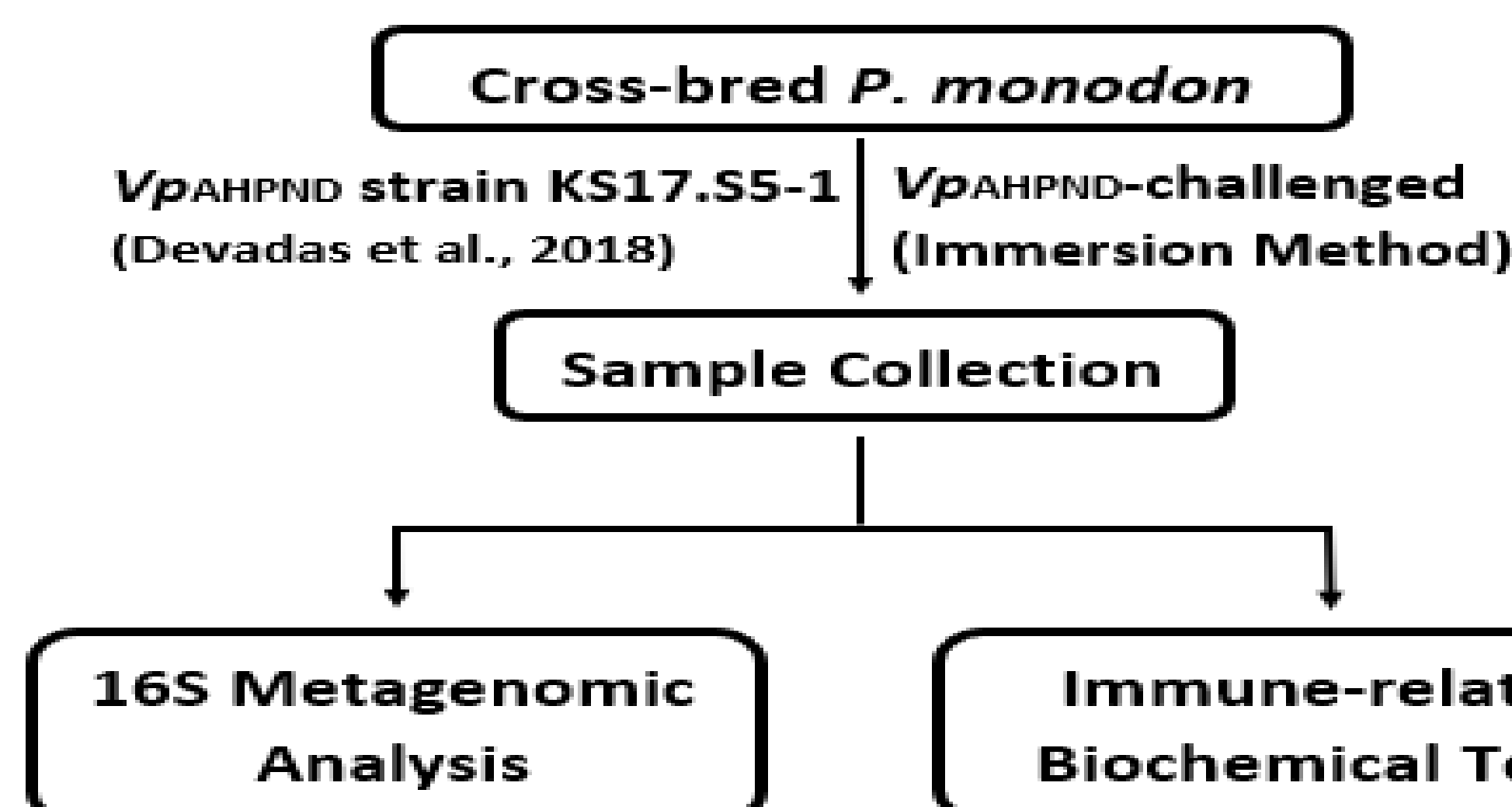


Figure 3. General experimental flow.

- ❖ V3-V4 Hypervariable Region
- ❖ Illumina MiSeq and NGS Data
- ❖ Respiratory Burst (RB) Test (OD 630 nm)
- ❖ Superoxide Dismutase (SOD) Activity Test (OD 560 nm)
- ❖ Phenoloxidase (PO) Activity Test (OD 490 nm)
- ❖ Nitrite (NO<sub>2</sub>-) Concentration Test (OD 540 nm)
- ❖ Total Hemocyte Count (THC)

## Results and Discussion

➤ Significant increments or reductions were identified in the *P. monodon* biochemical activities upon *VpAHPND* infection with respective peaks of (Figure 4):

- ❖ RB- Highest 12 hpi (hours post-infection)
- ❖ SOD activity- Highest 6 hpi
- ❖ PO activity- Highest 12 hpi
- ❖ NO<sub>2</sub>- concentration- Highest 12 hpi
- ❖ THC- Lowest 36 hpi

(Tracey et al., 1995; Huynh et al., 2011; Al-Amin et al., 2015; Al-Amin et al., 2016; Perera et al., 2017; Huynh et al., 2018; Hong et al., 2019; Park et al., 2019)

➤ There is an increment of *Vibrio* spp. and *Bradyrhizobium* spp. relative abundance in *VpAHPND*-challenged *P. monodon* compared to healthy control *P. monodon* (Figure 5).

➤ Interestingly, the highly abundant *Maritimibacter* spp. in control sample is only detected in very less abundance for *VpAHPND*-infected *P. monodon* (Figure 5).

➤ *VpAHPND* infection not only affects the *P. monodon* gut microbiome, but also causes biochemical activity changes.

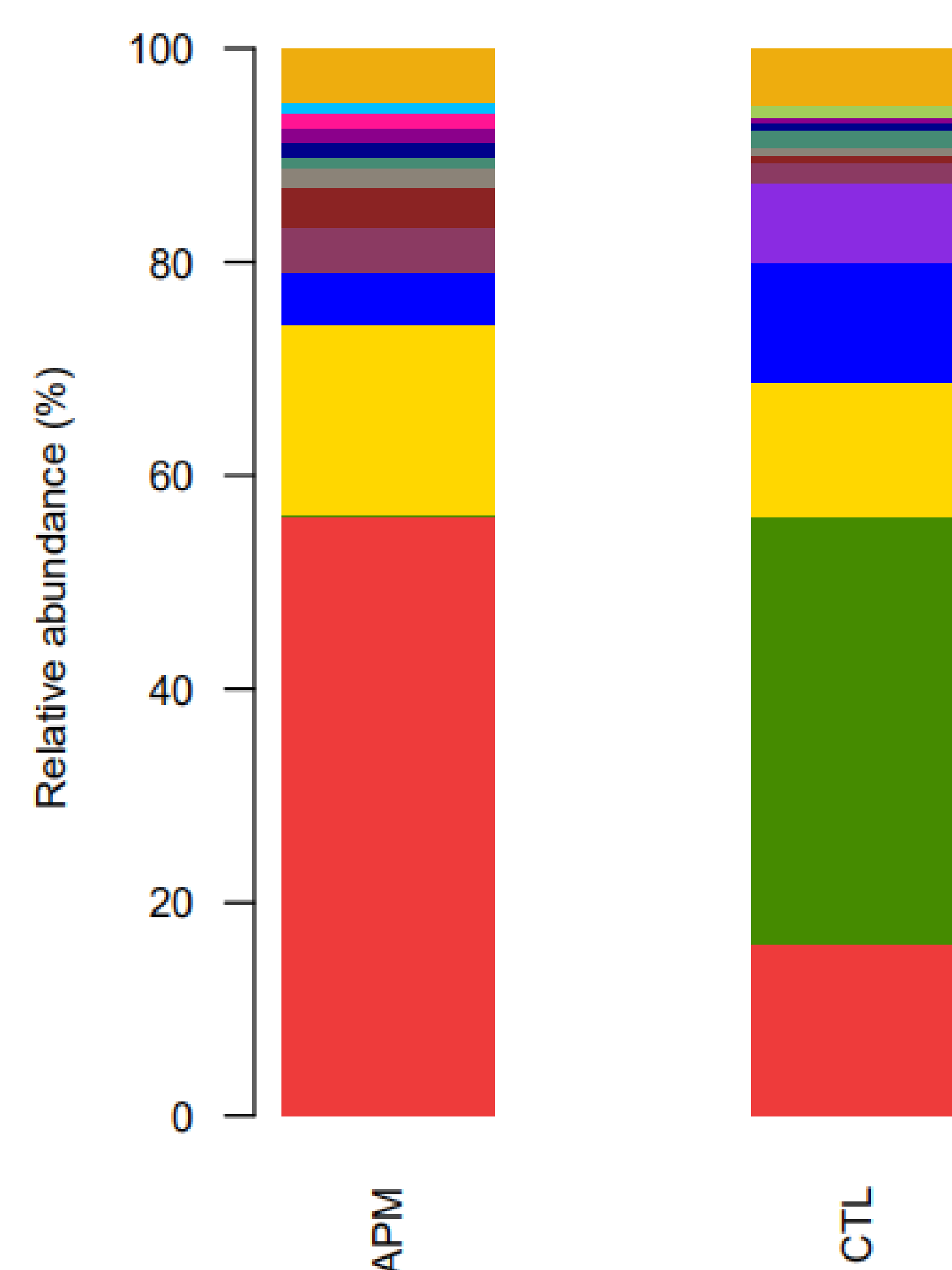


Figure 5. Relative abundance of gut microbiota (genus level) identified in 16S metagenomic analysis (CTL: Healthy control *P. monodon* gut sample, APM: *VpAHPND*-infected *P. monodon* gut sample).

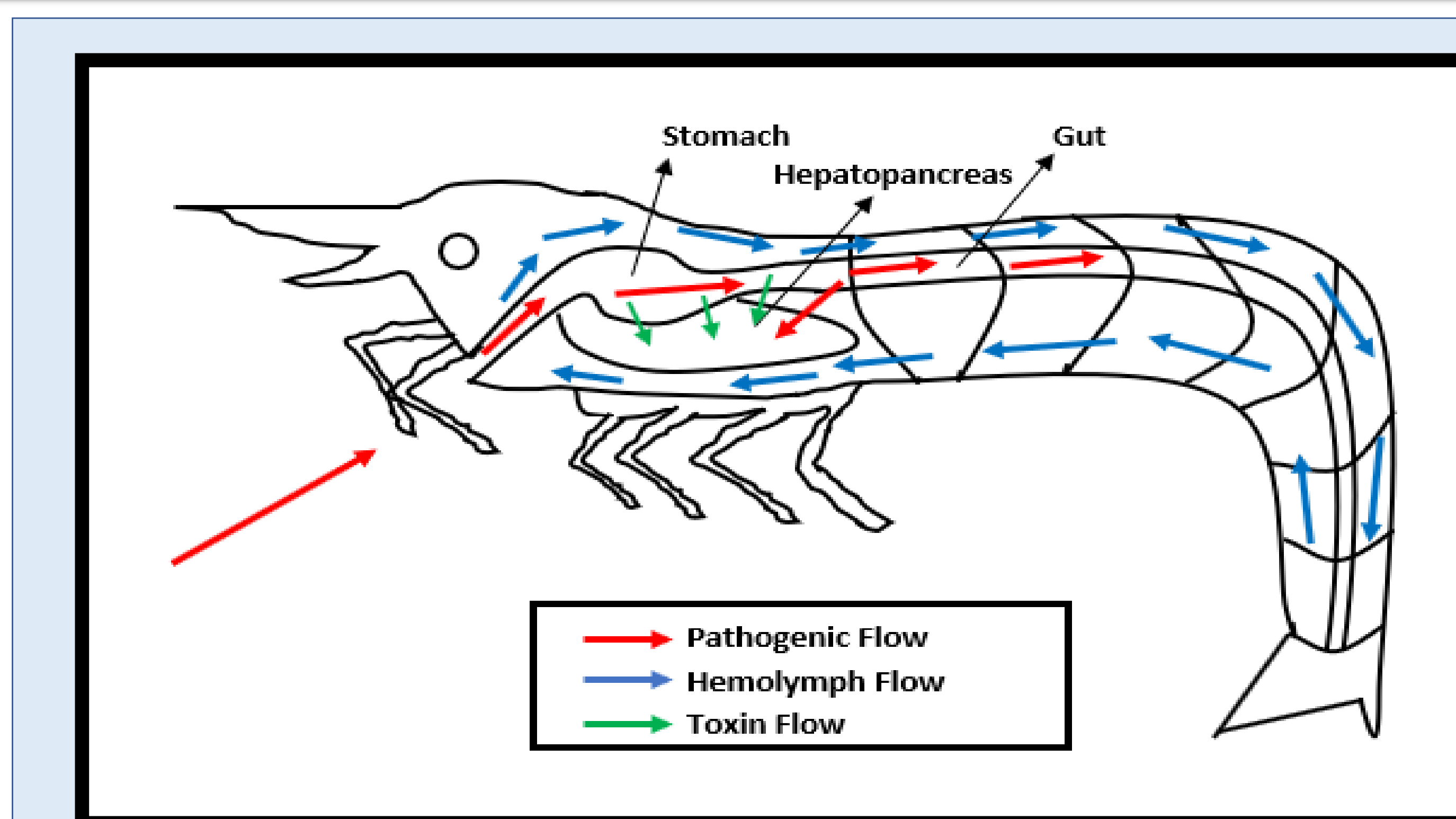


Figure 1. General outline of *VpAHPND* infection in *P. monodon*.

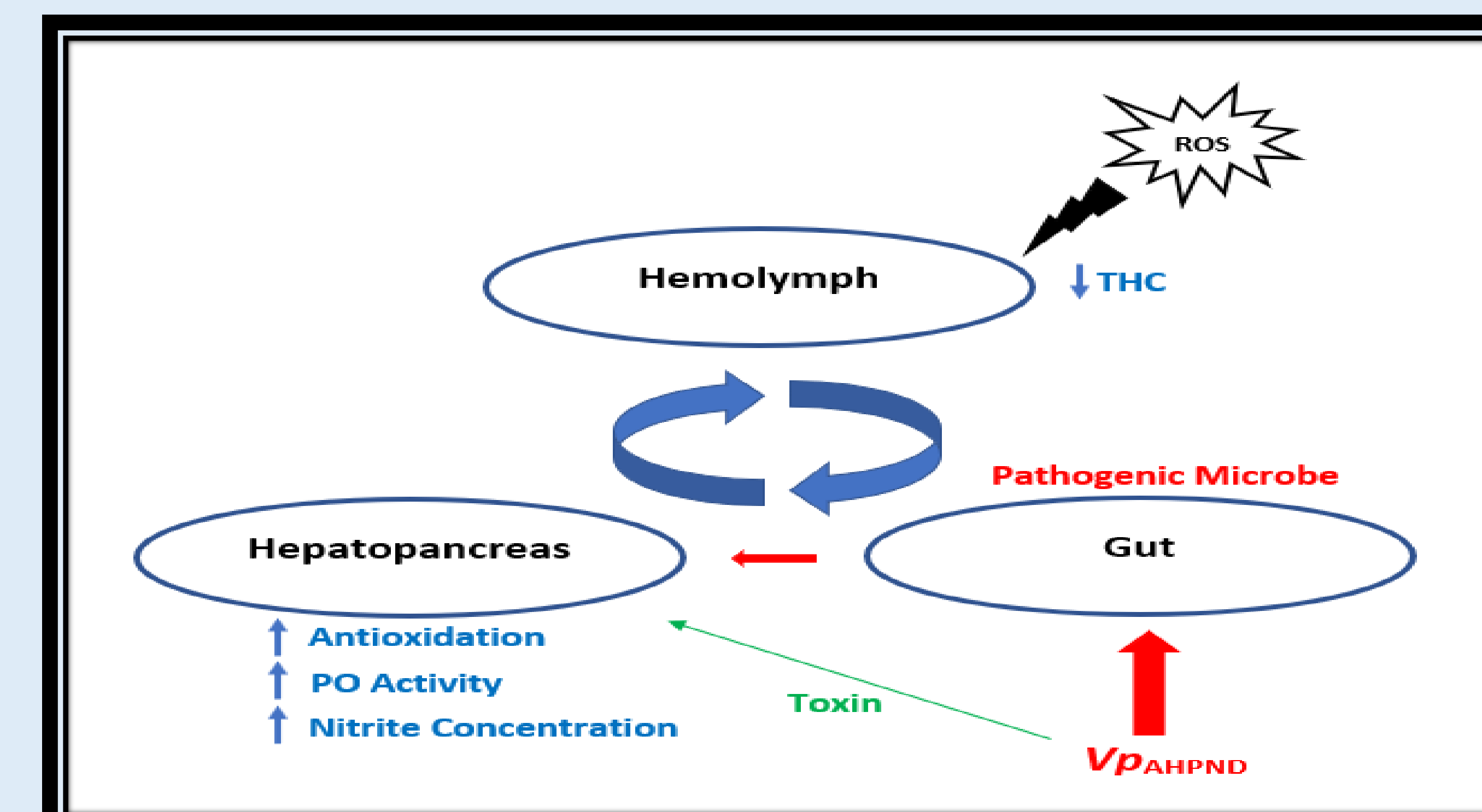


Figure 2. Postulated interactive host response of *P. monodon* towards *VpAHPND* infection.

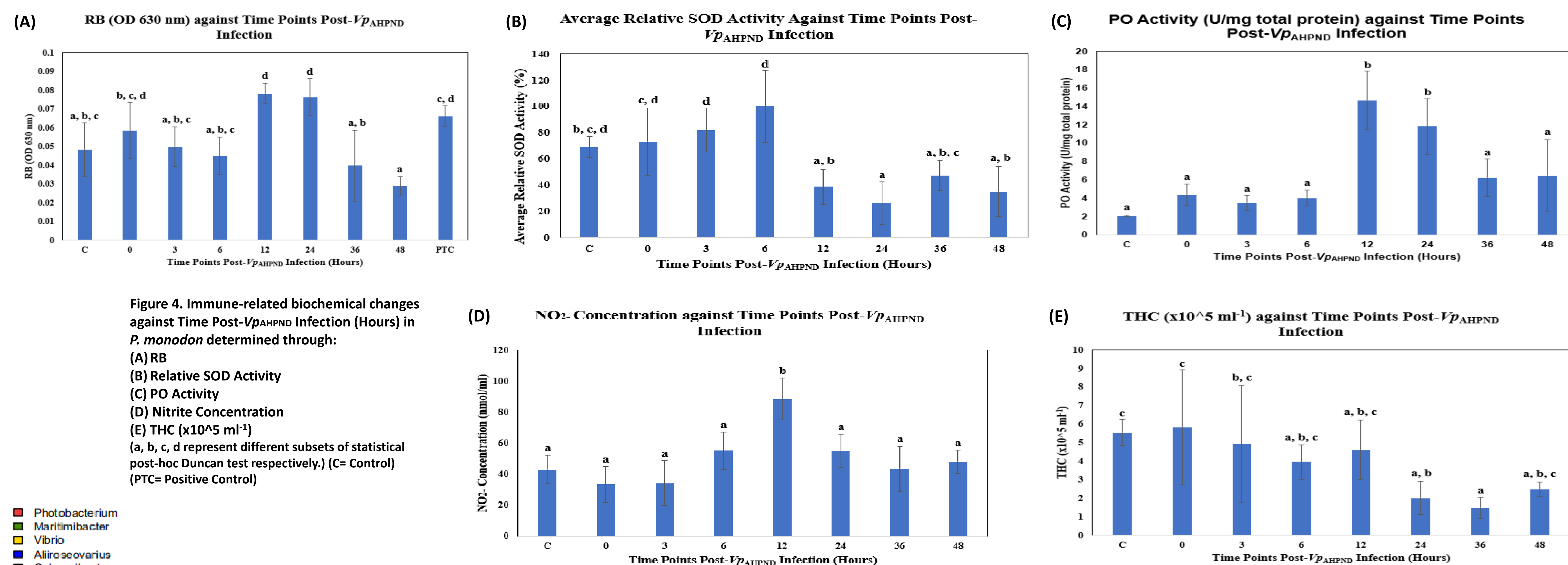


Figure 4. Immune-related biochemical changes against Time Post-*VpAHPND* Infection (Hours) in *P. monodon* determined through:

- (A) RB
  - (B) Relative SOD Activity
  - (C) PO Activity
  - (D) Nitrite Concentration
  - (E) THC ( $\times 10^5 \text{ ml}^{-1}$ )
- (a, b, c, d represent different subsets of statistical post-hoc Duncan test respectively.) (C= Control) (PTC= Positive Control)

## Conclusions

- The 16S metagenomic analysis between *VpAHPND*-infected *P. monodon* and healthy control *P. monodon* samples provided insight into the host-pathogen interaction in the *P. monodon* gut during *VpAHPND* infection.
- The immune-related biochemical changes across different post-infection time points of *VpAHPND*-infected *P. monodon* tissue samples were identified and statistically validated.
- The identified *VpAHPND*-influenced gut microbes or host biochemical properties could potentially be developed as biomarkers for early detection of *VpAHPND* infection in the future with further research.

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