World Academy of Science, Engineering and Technology
International Journal of Bioengineering and Life Sciences
Vol:10, No:07, 2016

Genome-Wide Identification of Genes Resistance to Nitric Oxide in Vibrio parahaemolyticus

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Abstract : Food poison caused by consumption of contaminated food, especially seafood, is one of most serious public health threats worldwide. Vibrio parahaemolyticus is emerging bacterial pathogen and the leading cause of human gastroenteritis associated with food poison, especially in the southern coastal region of China. To successfully cause disease in host, bacterial pathogens need to overcome the host-derived stresses encountered during infection. One of the toxic chemical species elaborated by the host is nitric oxide (NO). NO is generated by acidified nitrite in the stomach and by enzymes of the inducible NO synthase (iNOS) in the host cell, and is toxic to bacteria. Bacterial pathogens have evolved some mechanisms to battle with this toxic stress. Such mechanisms include genes to sense NO produced from immune system and activate others to detoxify NO toxicity, and genes to repair the damage caused by toxic reactive nitrogen species (RNS) generated during NO toxic stress. However, little is known about the NO resistance in V. parahaemolyticus. In this study, a transposon coupled with next generation sequencing (Tn-seq) technology will be utilized to identify genes for NO resistance in V. parahaemolyticus. Our strategy will include construction the saturating transposon insertion library, transposon library challenging with NO, next generation sequencing (NGS), bioinformatics analysis and verification of the identified genes in vitro and in vivo.

Keywords : vibrio parahaemolyticus, nitric oxide, tn-seq, virulence
Conference Title : ICLSBE 2016 : International Conference on Life Science and Biological Engineering
Conference Location : Singapore, Singapore
Conference Dates : July 04-05, 2016