Abstract

Both diarrheal diseases caused by bacteria, viruses, and parasites are four leading killers of children in the developing world. In 2004, 3 million deaths in children younger than 5 years due to diarrheal diseases worldwide were reported. In the world's developing countries, Vibrio parahaemolyticus and Vibrio cholerae are two major pathogens that seldom child-related deaths through different mechanisms. The goal of this investigation is to compare the gene expression profile of human intestinal epithelial cells infected with V. cholerae and V. parahaemolyticus using real-time reverse-transcription PCR (RT2 PCR) with appropriate controls for the quantitative PCR for genomic DNA contamination. Additionally, we investigated the inflammatory pathways in both species.

Introduction

Approximately 1 to 2 billion diarrheal illnesses have been attributed to enteric pathogens. Diarrheal diseases caused by bacteria, viruses, and parasites are major causes of diarrheal pneumonia and death in children under the age of five, and have a major impact on developing and industrialized countries. However, V. parahaemolyticus and V. cholerae have been found to cause inflammatory diarrheal diseases. However, V. parahaemolyticus and V. cholerae have been found to cause inflammatory diarrheal diseases. V. parahaemolyticus specifically results from the consumption of contaminated crustaceans, shellfish, and other marine foods, while V. cholerae is caused by consuming raw or undercooked clams, oysters, and other bivalve mollusks. V. parahaemolyticus and V. cholerae both cause a similar type of dysentery also known as ‘cholera diaries’. However, V. parahaemolyticus has a higher prevalence in East Asia and the middle east, while V. cholerae is more commonly found in South America, Asia, and India. V. parahaemolyticus and V. cholerae pathogens remain a vector of diarrhea and cholera related diseases. V. cholerae is known for its pathogenicity specifically through the consumption of oysters, shellfish, and other marine foods. V. parahaemolyticus is known for its pathogenicity through the consumption of contaminated crustaceans, shellfish, and other marine foods.

Methods

The human intestinal epithelial cell line Caco-2 (ATCC, Manassas, VA) was used and each well was grown to 100% confluence and challenged with V. cholerae, V. parahaemolyticus, and challenged with V. cholerae at a multiplicity of infection (MOI) of 100 for 2 hours. Table 1. Primers used for reverse transcriptase PCR. All samples were done in duplicate and standardized against the control using housekeeping genes. Table 2. Fold regulation of similar genes by both Vibrio Species. All results were determined by the manufacturer’s protocol. Table 3. Fold regulation of Caco-2, 2 hour challenge with Vibrio parahaemolyticus. Vibrio cholerae, and Vibrio parahaemolyticus was performed by both pathogens. Table 4. Fold regulation of Caco-2, 2 hour challenge with Vibrio parahaemolyticus. Comparison of Vibrio cholerae and Vibrio parahaemolyticus. Conclusions

Over expression of Tumor Necrosis Factor (TNF) in V. parahaemolyticus and V. cholerae challenge

The results of this investigation are significant because Vibrio cholerae and Vibrio parahaemolyticus have pathogenically distinct infection strategies. V. parahaemolyticus is known for its pathogenicity specifically through the consumption of contaminated crustaceans, shellfish, and other marine foods. V. cholerae is known for its pathogenicity through the consumption of oysters, shellfish, and other marine foods. V. parahaemolyticus has a higher prevalence in East Asia and the middle east, while V. cholerae is more commonly found in South America, Asia, and India. V. parahaemolyticus and V. cholerae pathogens remain a vector of diarrhea and cholera related diseases. V. cholerae is known for its pathogenicity specifically through the consumption of oysters, shellfish, and other marine foods. V. parahaemolyticus is known for its pathogenicity through the consumption of contaminated crustaceans, shellfish, and other marine foods.

Figure 1. Image of vibrio cholerae. Vibrio cholerae has a single polar flagellum and can live as non-hemolytic individuals or form colonial cells.

Figure 2. Response of Vibrio cholerae V. cholerae infection in the United States, incidence of Vibrio cholerae (V. parahaemolyticus) was significantly increased (over 50 fold) whereas IL-7 is not upregulated, but not IL-8. We were surprised and intrigued by the high level (more than 10 fold) of CCL2 overexpressed in Caco-2 cells, 2 hour challenge with V. cholerae. All results were determined by the manufacturer’s protocol. Table 1. Primers used for reverse transcriptase PCR. All samples were done in duplicate and standardized against the control using housekeeping genes. Table 2. Fold regulation of similar genes by both Vibrio Species. All results were determined by the manufacturer’s protocol. Table 3. Fold regulation of Caco-2, 2 hour challenge with Vibrio parahaemolyticus. Vibrio cholerae, and Vibrio parahaemolyticus was performed by both pathogens. Table 4. Fold regulation of Caco-2, 2 hour challenge with Vibrio parahaemolyticus. Comparison of Vibrio cholerae and Vibrio parahaemolyticus. Conclusions

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Over expression of Interleukin 7 (IL-7) in V. parahaemolyticus and V. cholerae

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