Acute Hepatopancreatic Necrosis Disease (AHPND): Prevalence, Pathogenesis, Detection, Causative Factors and Mitigating Methods

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Abstract

Since its emergence in 2009, Acute Hepatopancreatic Necrosis Disease (AHPND) has caused substantial economic losses to the shrimp industries. However, presently, there is no 'silver bullet' or effective treatment for this disease. The recent progress in molecular and proteomic techniques has made it possible to obtain information on the AHPND toxins and their characteristics. However, fundamental knowledge gaps remain although some of the key host-pathogen interactions have been well-established via several types of shrimp challenge test, detailed histopathological analysis and development of molecular tools to detect AHPND. Hence, further research is still required to fully understand the mechanisms and mode of infection for this disease. This review provides a state-of-the-art overview of the topic and emphasises the current progress and critique strategies for AHPND treatment.

Importance

Acute hepatopancreatic necrosis disease (AHPND) may be a serious disease that has caused severe damage and significant financial losses to the worldwide shrimp industry. To better understand and stop this shrimp disease, it's essential to thoroughly characterize its causative agent, Vibrio parahaemolyticus. Although the plasmid-encoded binary toxins PirAvp/PirBvp are shown to be the first explanation for AHPND, it remains unknown whether other virulent factors are commonly present in V. parahaemolyticus and might play important roles during shrimp infection. Here, we analyzed the genome sequences of clinical, non-AHPND, and AHPND strains to characterize their repertoires of key virulence determinants. Our studies reveal that an antibacterial type VI secretion system is related to the AHPND strains and differentiates them from non-AHPND strains, almost like what was seen with the PirA/PirB toxins. We propose that T6SS1 provides a selective advantage during shrimp infections

Introduction

Acute hepatopancreatic necrosis disease (AHPND), previously named early mortality syndrome (EMS), may be a newly emerging shrimp disease that's causing serious reductions in shrimp production and financial losses to the global shrimp aquaculture industry. Since the disease outbreak first appeared in China in 2009, it quickly spread to Vietnam in 2010, Malaysia in 2011, Thailand in 2012, Mexico in 2013, the Philippines in 2015, and South America in 2016 .AHPND can cause up to 100% mortality within about 20 to 30 days after a pond gets stocked shrimp postlarvae .Notable symptoms of affected shrimp include an empty gut and an atrophied, pale hepatopancreas. Histopathology analysis shows sloughing of the hepatopancreatic tubule epithelial cells and hemocytic infiltration (1). In 2013, it had been discovered that AHPND was caused by a selected set of Vibrio parahaemolyticus strains (1). Toxic AHPND-causing V. parahaemolyticus strains acquired a 63- to 70-kb plasmid encoding the binary toxins PirAvp/PirBvp, which are homologous to the Photorhabdusluminescens insect-related (Pir) toxins PirA/PirB .PirAvp/PirBvpare secreted toxins that were determined to be the first virulence factors causing AHPND. Based on their structure, theses toxins are almost like Cry insecticidal toxin-like proteins that encode a pore-forming activity wont to kill host cells. This plasmid also encodes a set of conjugative transfer and mobilization genes that could facilitate its spread between different Vibrio species.It is also interesting that this is a "selfish plasmid" that contains a pndA toxin/antitoxin system ensuring the acquisition of this plasmid in bacterial progeny for survival.

In 2015, a strain of Vibrio campbellii isolated from Vietnam and a strain of Vibrio owensii isolated from China were shown to cause AHPND .Both strains contain a plasmid that is highly almost like the one discovered in AHPND-causing V. parahaemolyticus and encodes the binary toxins homologous to PirA/PirB It supports the model that PirAvp/PirBvp are the main virulence factors causing AHPND. This discovery is additionally according to the hypothesis that this plasmid is transmissible and should be shared between different Vibrio species

V. parahaemolyticus may be a Gram-negative, halophilic bacterium that naturally lives in warm marine and estuarine environments found throughout the planet Rising ocean temperatures during recent years have contributed to its global dissemination V. parahaemolyticus is that the world's leading explanation for acute gastroenteritis thanks to the consumption of raw or undercooked seafood (18). It also can cause infection of open wounds through the exposure to contaminated warm seawater (19). In immunocompetent individuals, V. parahaemolyticus infection is generally self-limiting and lasts for about 2 to three days except for individuals with underlying health conditions, the infection can cause severe diarrhea, septicemia, and in some cases subsequent death

Despite the invention of the toxic plasmid and binary toxins PirAvp/PirBvp, no comprehensive studies are done to

characterize the opposite important virulence determinants commonly found in V. parahaemolyticus, such as thermostable direct hemolysin (TDH) and TDH-related hemolysin (TRH) toxins, two type III secretion systems (T3SSs) and two type VI secretion systems (T6SSs) TDH and TRH are pore-forming toxins with hemolytic activities T3SS is a conserved secretory system present in many Gram-negative bacteria that directly delivers bacterial virulence factors, called effectors, into the cytoplasm of host cells to exert various functions V. parahaemolyticus can contain two different T3SSs (T3SS1 and T3SS2) T3SS1 is very conserved and present in both environmental and clinical isolates of V. parahaemolyticus it's activated by low-Ca2+ environments as mimicked by the serum-free Dulbecco's modified Eagle medium (DMEM) and possesses cytotoxicity against various cultured eukaryotic cell lines In contrast, T3SS2 is found only in clinical isolates of V. parahaemolyticus it's activated by bile salts and is that the primary virulence factor for gastroenteritis during human infection T6SS is another protein secretion apparatus present in various Gram-negative bacteria Increasing evidence suggests that the majority of T6SSs play a role in interbacterial competition, as they possess antibacterial activities mediated by delivery of toxic effectors into neighboring cells Importantly, bacteria avoid self-intoxication by these T6SSs with encoded immunity proteins that protect against cognate antibacterial effectors. These T6SS effector/immunity (E/I) pairs are encoded as bicistronic units Two T6SSs have been described in V. parahaemolyticus, T6SS1 and T6SS2 T6SS1 has previously been associated predominantly with clinical isolates of V. parahaemolyticus and was shown to possess antibacterial activities against various bacterial competitors In the clinical isolate RIMD2210633, this antibacterial activity is mediated by at least three delivered toxins, two of which contain an N-terminal MIX (Marker for type sIX effector) domain and are therefore members of the T6SS MIX effector class T6SS2, like T3SS1, is present in all V. parahaemolyticus strains, including both environmental and clinical strains but its role in the V. parahaemolyticus life cycle remains unknown. The two V. parahaemolyticus T6SSs are differentially regulated by external cues like temperature, salinity, and surface sensing.