

CHARACTERIZATION OF INCREASED VIRULENCE OBSERVED IN CLINICAL ISOLATES OF *Vibrio cholerae*

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Cholera is an important infectious intestinal disease caused by the bacterium *Vibrio cholerae*. Bacterial infection can lead to dehydration and severe diarrhea, and if untreated or not treated properly, can quickly lead to death. Recently, there have been growing concerns as *V. cholerae* has evolved to become more virulent, causing much more severe cases of disease at a much faster rate than previously observed. These increasingly virulent strains continue to be a major focus of research, especially after it was observed in Haiti, where more than 300,000 cases and nearly 8,000 deaths have been reported since the initial outbreak began in October 2010. The *primary research goal* is to identify the genes involved and the mechanism by which these clinical isolates of *V. cholerae* are exhibiting increased virulence. Through next generation deep sequencing data analysis, we identified and hypothesized five genes (*hapR*, *hns*, *vieA*, *luxO* and *frhA*) to be involved in the increased virulence observed. We have demonstrated that point mutations in these five genes found in the clinical isolates of *V. cholerae*, resulted in increased virulence factor production and virulence, but to what capacity each gene is involved and the precise mechanism are the subjects of this study. Identification of this mechanism will greatly enhance our understanding of not only cholera, but also other enteric diarrheal diseases, and help better prepare emergency healthcare professionals to assess and treat the disease in areas where the disease persists, and when natural disasters lead to regional outbreaks.