

PROJECT SUMMARY

Several genera of bacteria have been implicated in a variety of human diseases, such as sepsis, meningitis, and gastroenteritis. The development of multidrug resistant pathogens has caused great concern for its impact on human health and millions in economic loss. Although numerous reports indicate that antibiotic resistance has an ancient origin, virulence genes responsible for pathogenesis have not been found in environmental microbiota. Virulence genes have been well characterized in clinical settings, and little is known about the impact the environment has on pathogenesis. Environmental samples have shown to contain millions of unknown genes in which could be related to virulence[42]. There is a need to mine genomes of non-clinical isolates in order to discover possible novel virulence and antibiotic resistance genes. Previous reports from our laboratory have demonstrated that persistence of non-clinical E.coli in tropical soils. Also, there is growing evidence supporting the existence of natural populations of these species in tropical soils around the world. However, to date, environmental studies have only focused on the apparent uniqueness of E. coli as part of the environmental microbiota. No studies have been done to understand the molecular tools of survival or the presence of virulence genes in non-clinical isolates from the environment. Therefore, there is the need to elucidate the non-clinical isolate pangenomes and their future impact on human health. We propose that testing our unique non-clinical isolates will reveal novel information, will contribute to understanding the development of virulence mechanisms and identification of prophages for phage therapy uses.