Comparative Genome Analysis Of Non-toxigenic Non-01 Versus Toxigenic O1 *Vibrio Cholerae*

- Infectious microbes such as *Staphylococcus aureus* and *Vibrio cholerae* are causative agents of serious infectious disease, that have evolved poorly understood virulence factors, such as drug resistances, facilitating pathogenesis in humans.
- Multi-drug resistant bacterial pathogens compromise chemotherapeutic efforts and enhance both morbidity and mortality, the mechanisms of which represent good targets for study towards the efforts in the effective treatment of infectious disease.
- Genomic analyses in which pathogenic bacteria are compared with their non-pathogenic counterparts may identify novel targets for future development of antibacterial therapies.
- Genomic comparison of pathogenic and non-pathogenic *Vibrio cholerae* led to the identification of novel genome elements that encode dormancy, sporulation, ribosome modulation for persistence, lipid metabolism, phage infection, nucleoside metabolism, and sulfur metabolism, which, in turn, is essential for biosynthesis of amino acids, vitamins and prosthetic groups.
- Results set the groundwork for efforts that effectively reduce the conditions which foster virulence and dissemination of *V. cholerae* pathogens.

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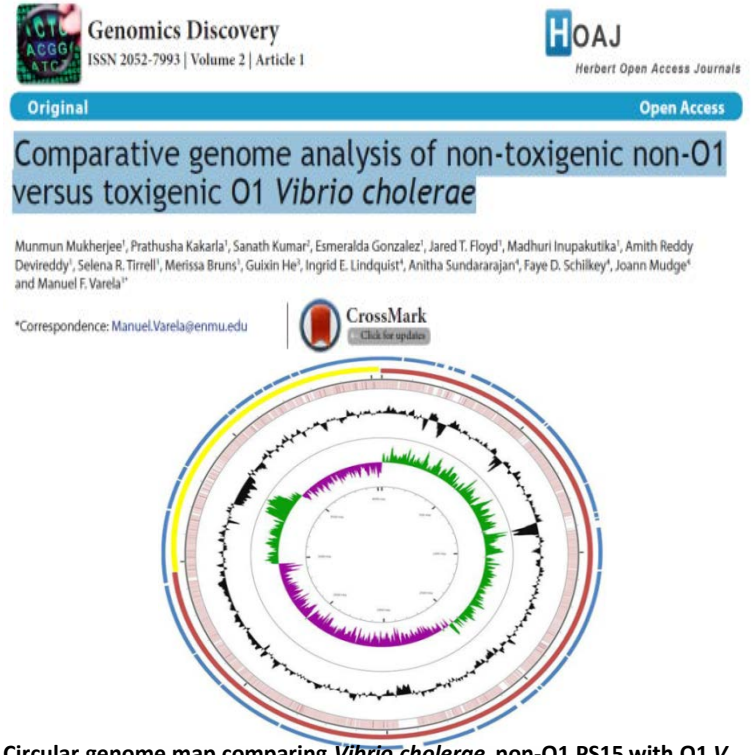

Circular genome map comparing *Vibrio cholerae* non-O1 PS15 with O1 *V. cholerae* N16961.
BLAST was performed on the DNA sequence of the *V. cholerae* non-O1 PS15 (3,910,387 base pairs) with *V. cholerae* El Tor N16961 (4,033,460 base pairs) using CGView server to yield a structural representation of both genomes. The outermost circle in blue represents the entire genome of non-O1 *V. cholerae* PS15, and PS15 gaps in the genome alignment are indicated in white. In the next inner circle, the red and yellow color coded regions represent chromosomes 1 and 2, respectively, of *V. cholerae* N16961. The third inner circle in pink shows matching nucleotide base pairs representing the BLAST analysis for *V. cholerae* N16961 and *V. cholerae* PS15. The fourth inner circle represents the total G+C content color coded in black. In the fifth inner circle, the region in green represents the G+C content of the forward strand, and the region in purple represents the G+C content of the reverse strand. The innermost circle represents the base pair numbers, where kbp stands for kilo base pairs.