3. Objectives
3. OBJECTIVES

Cholera, the dreaded diarrheal disease, is caused by *V. cholerae* belonging to O1 and O139 serogroups. *V. cholerae* can survive into two distinct ecological niches *i.e.* human intestine and aquatic environment that differ widely in nutrient availability. To survive within these challenging environments, *V. cholerae* requires switching to appropriate metabolic pathway(s) optimally suited for the utilization of available nutrients to yield sufficient energy for its survival and/or pathogenesis. Evidences suggests that sugar acid metabolism via the ED pathway is important for growth of *E. coli* in both intestinal and aquatic habitats (Peekhaus and Conway, 1998a). In a recent study, obligate involvement of the Entner-Doudoroff (ED) pathway in gluconate utilization and modulating *V. cholerae* pathogenesis has been reported (Patra *et al*., 2012). All these considerations emphasize upon the importance to study the gluconate utilization system and its role pathogenesis of *V. cholerae*.

Emergence of multidrug resistant strains of *V. cholerae* has been also reported (Ghosh and Ramamurthy, 2011). Therefore, development of novel high throughput screening assay (HTS) are thus needed for identification of antimicrobial compounds specific to *V. cholerae*. For this, we collaborated with Helmholtz Center for Infection Research (HZI), Germany, to establish novel high throughput screening assay (HTS) for the identification of *V. cholerae* specific growth suppressing and virulence suppressing compounds.
In two different points of view, the current study has been proposed with the following objectives:

i. Prediction and comparative analysis of *V. cholerae* gluconate utilization system including the ED pathway with different enteric pathogens.

ii. To evaluate and compare expressions/regulation of different virulence factors/genes among pathogenic *V. cholerae* strains grown under different cultural conditions with special emphasis to the role of gluconate utilization system.

iii. To identify and functional analysis of genes of the gluconate utilization system that regulates virulence gene expressions *in vitro* and *in vivo*.

iv. To evaluate preferential involvement, if any, of the metabolic pathway(s) for utilization of sugars like N-acetyl glucosamine, gluconate and glucose etc. and their eventual correlation to *V. cholerae* pathogenesis.