

Identification of Pho regulon genes and Pho box-like sequences in genomes of clinical and environmental isolates of *Vibrio parahaemolyticus* from Brazil

Leandro de Oliveira Santos, Cristóvão Antunes de Lanna, Paulo Mascarello Bisch,
Wanda Maria Almeida von Krüger

Laboratório de Física-Biológica, Instituto de Biofísica Carlos Chagas Filho - UFRJ

Vibrio parahaemolyticus is a Gram-negative bacteria present mostly in marine and estuarine environments. It is a worldwide cause of food-borne gastroenteritis, associated with raw or undercooked seafood consumption. *V. parahaemolyticus* infection symptoms includes abdominal cramps, diarrhea (in certain cases with presence of blood and mucus), nausea, vomit, low fever and headache. *V. parahaemolyticus* has also been associated with wound infection and septicemia. Several strains of *V. parahaemolyticus* have been isolated in Brazilian territory during outbreaks of gastroenteritis, from oyster farms, fish markets and restaurants, but their genomes have not been sequenced. Aquatic environments are poor in inorganic phosphate (Pi), an essential nutrient for cells. In bacteria the PhoB/PhoR two-component system plays an important role in detecting and responding to the changes of the environmental Pi concentration. PhoR, a transmembrane sensor protein, has a histidine kinase activity and PhoB is a cytoplasmic response regulator that binds to DNA sequences upstream the genes (Pho boxes) and regulates transcription. The set of genes regulated by PhoB/PhoR comprises the Pho regulon. In this work, we searched for Pho regulon genes and upstream Pho box-binding sites on genomes of seven *V. parahaemolyticus* strains from clinical and environmental origins isolated in Brazil. The seven genomes used were sequenced, assembled and annotated by our group. Many putative PhoB/PhoR regulated genes were identified in the genomes of the seven *V. parahaemolyticus* strains among those annotated by the RAST server. Their sequences were then aligned to orthologous gene sequences from *V. parahaemolyticus* strains and other species, to assess sequence diversity, size and arrangement, using Clustal and MEGA7 softwares. For Pho boxes identification we used a consensus (Daniel Costa Leite, personal communication) and MEME/MAST programs. As a result, many Pho regulon gene sequences were identified in all seven genomes, such as *vp2163* for the alkaline phosphatase, *vp0569* for the response regulator PhoB, *vpa0670* for the Pi sensor PhoR, *vpa1461* for the periplasmic Pi transporter PstS, *vp0572* for the exopolyphosphatase PpX, *vp0573* for the polyphosphatase kinase PpK, and *vpa0526* for a putative anionic porin. For most of them, we observed conservation of sequence, size and arrangement in comparison to the reference strains. We also identified Pho box-like sequences upstream those genes in all the seven genomes. These results demonstrate a high conservation of the Pho regulon genes among *V. parahaemolyticus* and other species.