Sequence Analysis and Molecular Modeling of Putative Low Pi Induced Porins of *Vibrio* Species

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Gram-negative bacteria have several strategies to adapt to the various environments. One of those mechanisms is the regulation of expression of outer membrane proteins (OMPs), used by many species to respond to distinct surrounding signals. About 50% of the outer membrane mass is composed of OMPs, and they can be found as integral proteins or anchored via lipids. Environmental signs often regulate expression of OMPs, thus contributing to the bacterial survival and adaptation to different niches. VCA1008 is a *V. cholerae* OMP expressed under Pi starvation conditions. Its expression is induced during infection of infant mice, and its mutation causes a 40-fold attenuation in infectivity. Considering the involvement of VCA1008 in the pathogenicity of *V. cholerae*, we decided to search for homologous genes in *V. vulnificus* LMG 13545T and *V. parahaemolyticus* LMG 2850T, being both human pathogens of the *Vibrionaceae* family. Two OMPs significantly induced under Pi starvation were further investigated. The low Pi-induced OMPs in *V. vulnificus* and *V. parahaemolyticus* were identified by mass spectrometry as the products of VV20580 and VPA0526, respectively. We performed a comprehensive *in silico* analysis and build comparative models for those proteins. V20580 and VPA0526 share with VCA1008 45% sequence identity and several similar structural features, suggesting functional homology. BLASTp and threading search for suitable templates for comparative modeling revealed the phosphoporin phoE from *E. coli* as the best template. The homology models were of good quality. The results indicate that the low-Pi induced OMPs identified are similar to the *E. coli* PhoE phosphoporin and presenting characteristics of classical porins.