PROTEOMIC ANALYSIS OF A NON-MOTILE MUTANT OF VIBRIO CHOLERAE O395

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Vibrio cholerae causes cholera, a often fatal human disease. During V. cholerae life cycle, it inhabits aquatic and the human small intestine. In such habitats, locomotion is essential to propel bacteria towards favorable or away of noxious environments, for adhesion and biofilm formation on surfaces. In this work we present a proteomic analysis of a wild type V. cholerae strain (O395) and of a spontaneous motility mutant (WK13), which lacks the single polar flagellum, therefore, is unable to swim or to move in soft-agar medium. Whole cell lysates and periplasmic and outer membrane fractions of cells grown in Luria-Bertani (LB) or minimum media, at 37°C, were analyzed by two-dimensional gel electrophoresis and the effects of the mutation on protein expression was evaluated. For the first dimension, polyacrilamide gel strips of 7 or 11cm and pH range 4-7 or 3-10 were used. Differentially expressed proteins were excised from gels, trypsin digested and the tryptic peptide mixture was analyzed by mass spectrometry (MALDI-TOF); the proteins were identified in the vibrios sp databank entries. Some of the identified proteins are related to iron transport, suggesting a relationship between mechanisms of iron acquisition and motility in V. cholerae and confirming previous microarray analysis data that connected several iron transport systems to many functions, including motility, in the bacterium.

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