The strain *Pseudomonas aeruginosa* PA1, isolated from oil waste, produces high amounts of rhamnolipid, a biodegradable surfactant with applications in several industrial and environmental fields. It was recently shown that rhamnolipid production by PA1 strain is partly dependent on the medium oxygenation. Furthermore, studies suggest that rhamnolipids participate in the protection against oxidative stress, preventing the oxygen molecules entry into the solution by forming a foam layer on the surface. The aim of this study was to identify differentially expressed proteins by *P. aeruginosa* PA1 when it was cultured in bioreactor operating with constant oxygenation of 1mgO₂/L and 6mgO₂/L. Cellular samples were taken at stationary growth phase and proteins extracted from the cellular pellet were analyzed and compared using proteomics techniques. The isoelectric focusing was conducted on strips in the pH range of 4 and 7, followed by separation by SDS-PAGE 12%. After preliminary analysis in mass spectrometer, 14 differentially expressed proteins were identified, among them, 2 with unknown biological function. There were identified 5 proteins related to secretion systems, 4 related to metabolism and 3 proteins associated with adaptation and protection against oxidative stress, potentially related to the rhamnolipid secretion. These results contribute to the better understanding of rhamnolipid metabolism regulation and to the choice of future targets of genetic modifications of *P. aeruginosa* in order to increase its rhamnolipid production.

Word Keys: oxidative stress, proteomic, *Pseudomonas aeruginosa*, rhamnolipid

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