ABSTRACT

Industries are fundamental element of our society and they are facing numerous risk factors due to microbial induced corrosion (MIC). Numerous microbes coexist as communities, competing for resources and often linked as biofilms in the surrounding. In this work, effect of proteinase k, trypsin and chymotrypsin on flagellar motility of treated and wild type strains were demonstrated and possible role of involvement of flagellar motility in biofilm formation was studied. Samples were collected from different sites of Lahore. 10 isolated strains were further studied morphologically and biochemically. These isolated bacterial strains were identified by 16S rRNA gene sequencing. Then required motile anaerobic strain was further characterized physiologically and genetically. Genetic analysis revealed that the strain was *Desulfovibrio vulgaris* (DUV) having accession number KY698020. Physiological description demonstrated that the strain indicated optimum growth at 37°C temperature and pH 7. This identified strain was further tested for the quantification of biofilm formation using Congo red assay, Test tube assay and Air- Liquid interface coverslip assay. Significantly high biofilm formation was observed in test tube assay (0.67) compared to air-liquid interface coverslip assay (0.56). Variation in biofilm formation was statistically significant as $0.01^{*}(p < 0.05)$. Treated strains were formed by treating with proteinase k, trypsin and chymotrypsin for about 15 minutes. Motility rate reduced in treated strains than wild strains. This made an effort to classify key characters permitting bacteria to efficiently interrelate flagellar motility and biofilm formation. This indicates the immense role of flagellar motility in biofilm formation. Role of proteinase k, trypsin and chymotrypsin illustrated the low motility and act as inhibitory compounds. Hence, this study suggested that protease treatment induces the protein disruption in flagellar assembly. This led to the reduce rate of biofilm formation.