IN SILICO PHYLOGENETIC ANALYSIS, CHEMORECEPTOR AND SIGNAL TRANSDUCTION OF BACTERIAL CONTAMINATION DENTAL UNIT

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Abstract	The importance of patient safety when carrying out dental and oral care processes is essential. However, the high levels of contamination that have been reported in dental units are of particular concern, so it is necessary to identify and study the patterns of bacterial contaminants and the transduction mechanisms of bacterial responses to their environment. This study investigates the diversity of bacterial contamination in dental units, chemotaxtic signals, and pathways from chemoreceptors through in silico approched. In silico research was carried out using several online and offline software tools utilizing a genomic sequence database from bacteria-contaminated with dental units. Phylogenetic analysis of the tree based on the 16s rRNA gene using MEGA 6 software, protein signaling interactions were analyzed using MiST 3.0 (https://mistdb.com/), signal transduction and protein structure (https://pfam.xfam.org/), the role of chemotaxis using interPro Ebi (https://www.ebi.ac.uk/interpro/structure/), dan biological process using Ebi QuickGo (https://www.ebi.ac.uk/QuickGO/). The analysis showed that 58 species of bacterial contamination showed a similarity test > 95%. Chemosensory pathway analysis of P. aeruginosa with a genome length of 6.538 Mbp through 8 signaling mechanism pathways for a total of 48 MCP. Signaling pathways.MCP signaling analysis classes are 24H, 36H, 40H, and 44H, while the identification of MCP classes is grouped based on chemosensory classes, namely CheW, CheA, CheR, CheB, Chev, CheD, and CheZ. The conclusion of this study, the complexity of the chemoreceptor interaction pathway in adapting quickly to the environment.
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