Bioinformatic Analysis of CRISPR-Cas System in *Enterobacteriaceae*

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The clustered regularly interspaced palindromic repeats and associated proteins (CRISPR-Cas) is an adaptive and hereditary immune system which can be found in most species of Archaea and Bacteria. This system provides the protection for these prokaryotes from foreign genetic elements such as bacteriophages and plasmids. CRISPR-Cas system is found in many members of *Enterobacteriaceae* family. This study was conducted to analyze the CRISPR-Cas system of selected strains of *Enterobacteriaceae* using bioinformatic tools and to design a KNIME, The Konstanz Information Miner workflow to analyze available CRISPR-Cas data of this family. In this study, one *Enterobacter cloacae* strain and three *E. hormaechei* strains were used. To detect CRISPR sites in the selected strains CRISPRCasFinder, CRISPROne, CRISPR Recognition Tool (CRT) and Piler-CR tools were used. CRISPRCasFinder tool detected CRISPR arrays and their locations in all selected strains and CRISPROne tool detected Cas genes and types of CRISPR-Cas systems present in these strains. CRISPROne tool identified these detected CRISPR-Cas systems as belonging to Type I-A and IV-A systems. Primers for detected CRISPR arrays were designed using the Primer3Plus tool for future analysis. A workflow was designed using KNIME software to analyze available CRISPR-Cas data for the family *Enterobacteriaceae*. Based on the study, CRISPRCasFinder can be recommended as an accurate bioinformatic tool for the detection of CRISPR arrays, while CRISPROne tool can be recommended for the detection of Cas genes. Though type I-E and I-F CRISPR systems are dominant in this family, the study revealed the possibility of having other types and a diversity among CRISPR-Cas systems within the family.

Keywords: CRISPR-Cas, *Enterobacteriaceae, KNIME*

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