World Academy of Science, Engineering and Technology
International Journal of Mathematical and Computational Sciences
Vol:14, No:12, 2020

In silico Subtractive Genomics Approach for Identification of Strain-Specific Putative Drug Targets among Hypothetical Proteins of Drug-Resistant Klebsiella pneumoniae Strain 825795-1

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Abstract : Klebsiella pneumoniae, a Gram-negative enteric bacterium that causes nosocomial and urinary tract infections. Particular concern is the global emergence of multidrug-resistant (MDR) strains of Klebsiella pneumoniae. Characterization of antibiotic resistance determinants at the genomic level plays a critical role in understanding, and potentially controlling, the spread of multidrug-resistant (MDR) pathogens. In this study, drug-resistant Klebsiella pneumoniae strain 825795-1 was investigated with extensive computational approaches aimed at identifying novel drug targets among hypothetical proteins. We have analyzed 1099 hypothetical proteins available in genome. We have used in-silico genome subtraction methodology to design potential and pathogen-specific drug targets against Klebsiella pneumoniae. We employed bioinformatics tools to subtract the strain-specific paralogous and host-specific homologous sequences from the bacterial proteome. The sorted 645 proteins were further refined to identify the essential genes in the pathogenic bacterium using the database of essential genes (DEG). We found 135 unique essential proteins in the target proteome that could be utilized as novel targets to design newer drugs. Further, we identified 49 cytoplasmic protein as potential drug targets through sub-cellular localization prediction. Further, we investigated these proteins in the DrugBank databases, and 11 of the unique essential proteins showed druggability according to the FDA approved drug bank databases with diverse broad-spectrum property. The results of this study will facilitate discovery of new drugs against Klebsiella pneumoniae.

Keywords : pneumonia, drug target, hypothetical protein, subtractive genomics
Conference Title : ICSRD 2020 : International Conference on Scientific Research and Development
Conference Location : Chicago, United States
Conference Dates : December 12-13, 2020