ABSTRACT

Klebsiella pneumoniae is an opportunistic microbe belonging to the Enterobacteriaceae family capable of causing nosocomial and community-acquired infections such as meningitis, bloodstream infections BSI, liver abscesses, urinary tract infections UTI, and surgical site infections SSIs. *Klebsiella pneumoniae* is capable of developing resistance against antimicrobial agents. The extended-spectrum beta-lactamases ESBLs and *Klebsiella pneumoniae* carbapenemases KPC-producing strains significantly mediate high-level resistance against various antibiotic classes. From 2006-2020, year by year the prevalence rate of *Klebsiella pneumoniae* increased from 1.57% to 32.3%. *Klebsiella pneumoniae* exhibit 20.65%-37.4%, 40%-60%, and 30%-40% resistance against carbapenems, third-generation cephalosporins, and fluoroquinolones, 30%-40% resistance against aminoglycoside, respectively. The current study emphasizes multidisciplinary approaches by employing computational biology, bioinformatics, and cheminformatics tools to amplify the understanding of developing novel antimicrobial agents for *Klebsiella pneumoniae.* The current study aims to determine the screening of FDA-approved drugs using *in silico* and *in vitro* strategies against multidrug-resistant *Klebsiella pneumoniae.* This approach explores the novel strategy of drug reprofiling against untreatable diseases. The leading potential candidates selected from *in silico* analysis are subjected to *in vitro* analysis to authenticate their effectiveness against *Klebsiella pneumoniae.*