Influence of Phage Transduction on Antimicrobial Resistance Properties of ESKAPEE Bacteria

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The weakening pipeline of the discovery of novel antibiotics and the excessive use of antibiotics have contributed to the recent emergence of antimicrobial resistance. In response to this emergence, the World Health Organization created a list of pathogens that are particularly deleterious and frequent called the ESKAPEE pathogens: Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, Enterobacter spp., and Escherichia coli. Horizontal gene transfer (HGT), the spread of genetic material through non-parent-offspring means, has played a significant role in the spread of antibiotic resistance genes. The purpose of this research is to investigate the extent that bacteriophages contribute to the antimicrobial resistance of ESKAPEE. To address this purpose, 1050 genomes from NCBI databases were scanned for prophage-associated antimicrobial resistance genes (pARGs). The study found that antimicrobial resistance (AMR) genes in ESKAPEE come from prophage regions 53.8% of the time on average. Antimicrobial resistance in E. faecium seems to be influenced by bacteriophages the most as it has the highest average percentage of AMR genes that are within prophage regions as well as the highest percentage of genomes with at least one pARG. Furthermore, genes that confer aminoglycoside, sulfonamide, tetracycline, fosfomycin, and multi-drug resistances are most frequently transmitted by bacteriophages, suggesting that phage transduction plays an important role in the spread of said resistances to ESKAPEE bacteria. The extent that phages transmit antibiotic resistance genes is essential information in phage therapy, as phage transduction can compromise its effectiveness in combatting antimicrobial resistance.

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