

Bacteriology and Mycology

June 18-19, 2018
Paris, France

Arch Clin Microbiol 2018, Volume: 9
DOI: 10.4172/1989-8436-C1-006

ADAPTIVE IMMUNITY: HORIZONTAL GENE TRANSFER AND PATHOGENICITY IN MULTIDRUG RESISTANT *E. COLI* STRAINS

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Globally drug resistant bacteria are the major problem to treat urinary tract infection(UTI). Five *E. coli* strains were isolated from urine of female patient (60 year old) suffering from severe UTI. Our work shows that 75% genome of these strains is adapted by seven virulent phages that are members of three families of viruses that may follow the adaptation phase of CRISPR (clustered regularly interspaced short palindromic repeats) function by incorporating the spacers to program their activity against invading viruses. Antibiotic resistant genes and their mutated alleles were identified in all *E. coli* strains. Similarly, out of 127 virulent genes 120 genes were shared in common in these strains. The presence of large number of identical genes in five strains may be due to horizontal gene transfer (HGT) by phages. As, all the strains lies in the same cluster of the tree indicates that these strains may evolve from a common ancestor.

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