Genomic and transmission electron microscopic characterization of coliphage lytic to *Eschericia coli strains*

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Introduction: Avian Pathogenic *Escherichia coli* (APEC) and human Uropathogenic *E. coli* (UPEC) share similar genetic relatedness and causing human and poultry diseases. The two showed great overlap based on their serophylogenetic groups and virulence genotypes. The ability of APEC to spread to human, and its capability to act as human UPEC or its potential to act as reservoir of virulence genes for UPEC has been discerned. Recent reports showed that APEC were incriminated in human Urinary Tract Infections (UTI) which is most common bacterial infections causing significant morbidity and mortality and huge economic burden on the healthcare system worldwide. Also, Extended Spectrum Beta Lactamase (ESBL) producing *E. coli* resistant to third generation cephalosporin has been isolated from poultry products. These pathogens are a great threat to public health and food safety. Poultry is believed to be the source of these pathogens causing diseases in human and avian species.

Objective: To isolate and characterize bacteriophage lytic to susceptible *E. coli* strains.

Methodology: Bacteriophage lytic to *E. coli* strains from chicken was isolated by simple enrichment, soft agar overlay and incubation at 37ºC for 24 hours. The identity of the phage was determined by transmission electron microscopy and partial sequencing of the capsid gene (gp23).

Results: Morphologically the phage possesses icosahedral head and contractile tail, and detection of gp23 gene revealed the phage as T4 like coliphage and a member of the family myooviridae.

Discussion: Due to its lytic activity, the isolated bacteriophage may offer useful application for biocontrolling susceptible *E. coli* strains.