• Conclusion
The diversity of disease in poultry is increasing day by day. To control these diseases, antibiotics are considered as the most important tool. But excess used of antibiotics and non medical use of antibiotics create the antibiotic resistance problem in infectious agent. Increasing level of resistance create the great loss in poultry industry so it shows the big demand to find the alternative of antibiotic to control the antibiotic resistant infectious agent. The lytic activity of bacteriophage is very useful to control pathogenic bacteria. Before use such lytic bacteriophage for therapeutic purpose, it is required an extensive study. The successful isolation, enrichment and purification techniques should be developed for the detail research of bacteriophage. Purified lysate of isolated bacteriophage is very useful for the further experiment. The lytic activity of bacteriophage is host specific. But after certain experiment we can conclude that the polyvalent bacteriophage is qualified as an alternative of antimicrobial agent. We can also conclude that if bacteriophage obtains proper environmental condition than it might be infect another host which is near to taxonomically related of their original host.

*E. coli* is an opportunistic pathogen in poultry. With the rapid emergence of antibiotic-resistant bacteria, the use of bacteriophages has regained attention as an efficient alternative method for their control. Virulent phages cause bacterial host cell lysis and not only function to control bacterial populations but also can be used as indicators of bacterial (fecal) contamination and as tools for identifying (typing) specific bacterial strains. Poultry meat is one of the most popular foods. Poultry and poultry meat are often found to be contaminated with potentially pathogenic microorganisms. Improvements in bio security on poultry farms are likely to be very expensive and difficult to maintain so there is a need to find an acceptable, cost-effective way of preventing infection of poultry with coli form bacteria.

Escherichia phage ADB-2 was isolated from a fecal sample of poultry by the double-layer agar plaque method. The Spot test and DAL method were used to determine the host range of the Escherichia phage ADB-2. An antibiogram of the natural host of Escherichia phage ADB-2 showed that the host was sensitive against norfloxacin and gentamicin and that it demonstrated higher resistance against cotrimoxazole and oxytetracycline. Escherichia phage ADB-2 was purified by ultracentrifugation and by the CsCl2 density gradient
purification method. Genomic DNA was extracted from the stock by the alkaline lysis method. The whole-genome sequencing of Escherichia phage ADB-2 was performed using Ion Torrent PGM (Ion 200-bp sequencing kit) (Life Technologies).

The data generated from the genomic library contained 229,781 reads and 45,496,800 nucleotide bases with average read length of 198 bases. The assembly using Newbler version 2.6 generated a 50,552-bp-long single chromosome. The genome annotation and comparative analysis of the genome were done using Rapid Annotation using Subsystem Technology (RAST). The phage has 46% GC with 76 predicted coding regions and 2 RNA genes.

This genome contains functional genes related to phage structure and packaging machinery (major capsid protein, unknown phage structure proteins, and terminase), phage neck protein, tail structure for host interaction (tail fiber protein, tail sheath protein, and tail-associated protein), phage DNA synthesis (helicase, DNA-directed RNA polymerases, endoDNase, and transcription regulator) and host lysis (endolysin without holing). These functional genes are scattered over the genome. The complete genome analysis of this phage provides new insight into its characteristics and interactions with Escherichia coli.

The complete sequence of the Escherichia phage ADB-2 genome can be accessed under the Gen Bank accession number JX912252.1.