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**Analysis and editing of phage host determinant of avian *Escherichia coli* phages**

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**Abstract:**

**Background/Objective:** [*Escherichia coli* disease causes serious economic losses to the poultry farming industry, and the increase in drug-resistant bacteria poses a serious threat to the safety of animal derived food and public health. Bacteriophages have the advantages of being readily available, highly specific, and less prone to developing resistance, which have once again attracted people's attention. However, the narrow host range of bacteriophages limits their clinical application. The use of gene editing technology to design engineered bacteriophages to optimize the function of natural bacteriophages has become an effective method to break this limitation. This study investigated the biological characteristics and genetic engineering modifications of two phages with different host spectra, and initially obtained edited recombinant phages. However, they do not possess genetic stability, and the specific mechanism of action needs further investigation.]

**Methods:** [The article uses a double-layer plate method to dropwise validate the host spectrum of bacteriophages, and detects the optimal infection complex, temperature and pH stability, as well as the biological characteristics of the one-step growth curve of bacteriophages. Obtain the complete genome of bacteriophages through a whole genome sequencing platform and annotate their encoded functional proteins. MEGA11 is used for constructing phylogenetic trees, while fusion PCR and homologous recombination techniques are used for constructing recombinant plasmids and bacteriophages.]

**Results:** [A broad-spectrum (54/82) muscle tail bacteriophage strain vB-EcoM-SD350 and a narrow-spectrum (11/82) long tail bacteriophage strain vB-EcoS-SD276 were screened from the laboratory library. Whole genome sequencing was performed to obtain the complete genomes of the two bacteriophages. The evolutionary tree results showed that the homology between the two bacteriophages and their tail filament proteins was low. Recombinant plasmids and bacteriophages carrying foreign genes were successfully constructed through fusion PCR and homologous recombination technology.]

**Conclusion:** [The article screened a broad-spectrum (54/82) muscle tailed bacteriophage strain vB-EcoM-SD350 and a narrow-spectrum (11/82) long tailed bacteriophage strain vB-EcoSSD276. The biological characteristics showed that both strains of bacteriophage could survive in a wide range of environments. The phylogenetic tree constructed based on the whole genome gene sequence and tail silk protein amino acid sequence showed significant differences among various tail silk proteins, which may pose a challenge for constructing recombinant bacteriophages. Through fusion PCR technology, two homologous arms carrying the vB-Escos-SD276 phage and a recombinant phage vB-Escos-SD276 gp26 carrying the tail filament protein gp26 of the vB-Escos-SD350 phage were successfully obtained. However, during the purification process, the recombinant fragment was lost, and the lost phage was verified to be the wild-type vB-Escos-SD276 phage. This suggests that there is some instability in editing the tail filament protein of the two phages with significant homologous differences.]

**Keywords:** [*E. coli*, Recombinant phages, Gene editing, Tail fiber protein, Biological characteristics]