## Phylogenetic grouping and virulence gene profiles of Escherichia coli isolated from chicken

## ABSTRACT

Colibacillosis is a disease caused by avian pathogenic E. coli (APEC) and is one of the principle cause of morbidity and mortality in poultry worldwide which is represented by a complex syndrome characterized by multiple organ lesions. This study was carried out to determine phylogenetic grouping and virulence associated genes contained by E. coli isolates which is related in causing disease in chicken. E. coli isolates obtained from clinical cases of Veterinary Research Institute were re-identified by conventional methods. Phylogenetic grouping of the isolates was determined by triplex polymerase chain reaction (PCR), and the presence of eight virulence genes were identified by multiplex PCR. A total of 125 E. coli isolates were subjected to analysis of phylogenetic background and virulence associated genes profiling. Phylogenetic analysis demonstrated that most of the E. coli isolated from chicken in this study belonged to group B1 (36.0%), group D (28.0%), group A (27.2%) and group B2 (8.8%). Multiplex PCR analysis demonstrated that 96 (78.6%) of the E. coli isolates harbored at least one virulence gene, while 29 (23.3%) did not contain any virulence genes tested. The most prevalent virulence genes identified were iss (51.2%), followed by iucD (36.0%), tsh (32.8%), vat (16.0%), astA (13.6%), irp2 (11. 2%), papC (9.6%) and the least is cva/cvi gene (0%). None of the isolates harbored more than four virulence genes. Each of phylogenetic groups presented with different combinations of virulence genes, with no specific combinations of virulence genes found to correlate with E. coli phylogroups. None of the E. coli isolates harbored more than four virulence genes, suggesting that E. coli isolates from chicken in this study appear to be derived from commensal strains and may relate to environmental predispose factors especially stress factors in the host to establish infection.

Keyword: E. coli; Phylogenetic group; Virulence genes; PCR