Virulence profiling to differentiate avian pathogenic and avian fecal *Escherichia coli* in poultry

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Hypothesis

- Virulence genes present in the *E. coli* can serve as marker to differentiate avian pathogenic and fecal strains of *E. coli*

Introduction

- Emergence of Avian Pathogenic *Escherichia coli* (APEC) among genetically diverse commensal population could be driven by intensification of poultry farming
- Prevalence of virulent genes among APEC considerably varies with geographic region, environment, feed, management practices and gut microbiome
- Due to high genomic plasticity, no single virulence marker is available to distinguish all APEC from all commensal strains

Methods

- Heart blood (n=285) – colibacillosis suspected birds and Cloacal samples (n=15) healthy birds of chick, grower and layer age groups
- Virulence gene profiling was carried out for 13 genes identified by genome wide association study *viz*. *wzzB, fimD, eygS, papD, wcaJ, gnd, gltS, hisB, hokA, hokC, ompT, wcaJ* and *gspO* followed by antimicrobial susceptibility testing

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Results

- 73 APEC- 73 & Avian Fecal *E. coli* (AFEC) - 15 were isolated and confirmed by PCR - *Adk* gene
- Variation in prevalence of *ompT, gspO, fimD* and *hokA* found among the isolates for APEC & AFEC obtained from different age groups
- All isolates were resistant to two or more antimicrobials tested
- Resistance of isolates to tetracycline showed increased trend as age increases
- 23.9 % isolates showed Extended Spectrum Beta Lactamases (ESBL) phenotype by double disc diffusion test

Discussion

- Our results are in agreement with other studies that fimbriae associated genes and outer-membrane proteins may serve as markers for differentiation of APEC and AFEC
- Considering vast genetic variations among *E. coli*, choice of virulence genes to differentiate APEC and AFEC become more intricate
- Presence of multidrug resistance and ESBL isolates in poultry could be a potential threat in one health perspective