Molecular Epidemiology of Avian Pathogenic *Escherichia coli*

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Introduction

❖Avian pathogenic *Escherichia coli* (APEC) are responsible for respiratory tract disease and colisepticaemia in poultry, resulting in considerable economic losses

❖Intestinal tract is believed to be the main source of APEC, whereas faeces and dust preserve the bacteria for further spread (1)

❖Inhalation of contaminated dust is the most important route of entry, and hence the environment is a potential source of infection leading to outbreaks (2)

❖Air sampling and colony blot hybridisation were developed as a rapid diagnostic tool for detecting *E. coli* in the air of poultry sheds

❖**Objectives**

➔to determine the concentration of total *E. coli* and of *E. coli* containing the APEC-specific virulence genes, *iroB*, *iucA* and *hlyF,* at different stages of broiler production and

➔to compare the genotypes of *E. coli* isolated from the air of poultry sheds with that of *E. coli* isolated from lesions in birds

Materials and Methods

❖The M Air T air sampler (Milipore) was used to collect 750 L of air from each of four individual commercial broiler sheds (Little River, Victoria) housing approximately 42,000 to 49,000 chickens per shed at three different time points

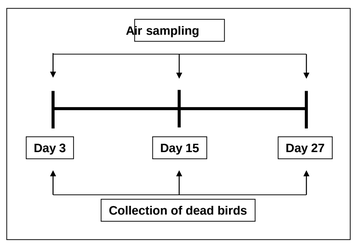
❖Ten recently deceased birds were collected from each shed at each time point, examined at post-mortem and swabs were taken from the liver of each bird

❖The cultures grown from the air samples and liver swabs were screened by colony and array blot hybridisations using digoxigenin (DIG) labeled DNA probes for the presence of *iroB*, *iucA* and *hlyF*

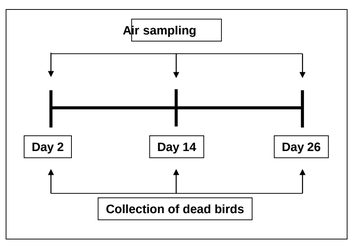
❖Southern blot hybridisation to *Eco*RV and *Bgl*I digests of genomic DNA of selected *E. coli* was performed to compare the genotypes of the *E. coli* populations recovered from the air and livers of dead birds

❖General linear model of ANOVA using Tukey's simultaneous test was conducted to analyse the data in Minitab 16 for Windows

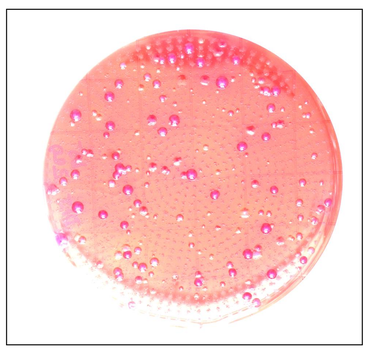
M Air T air sampler (Milipore)



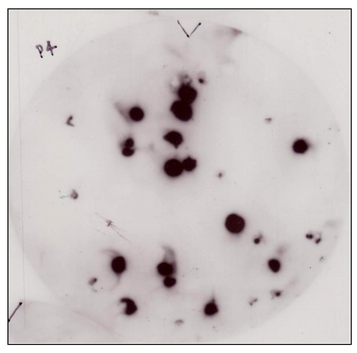
Study design in sheds 2 and 3



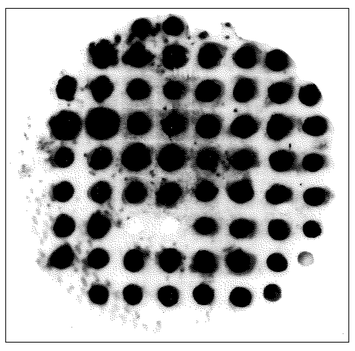
Study design in sheds 4 and 5



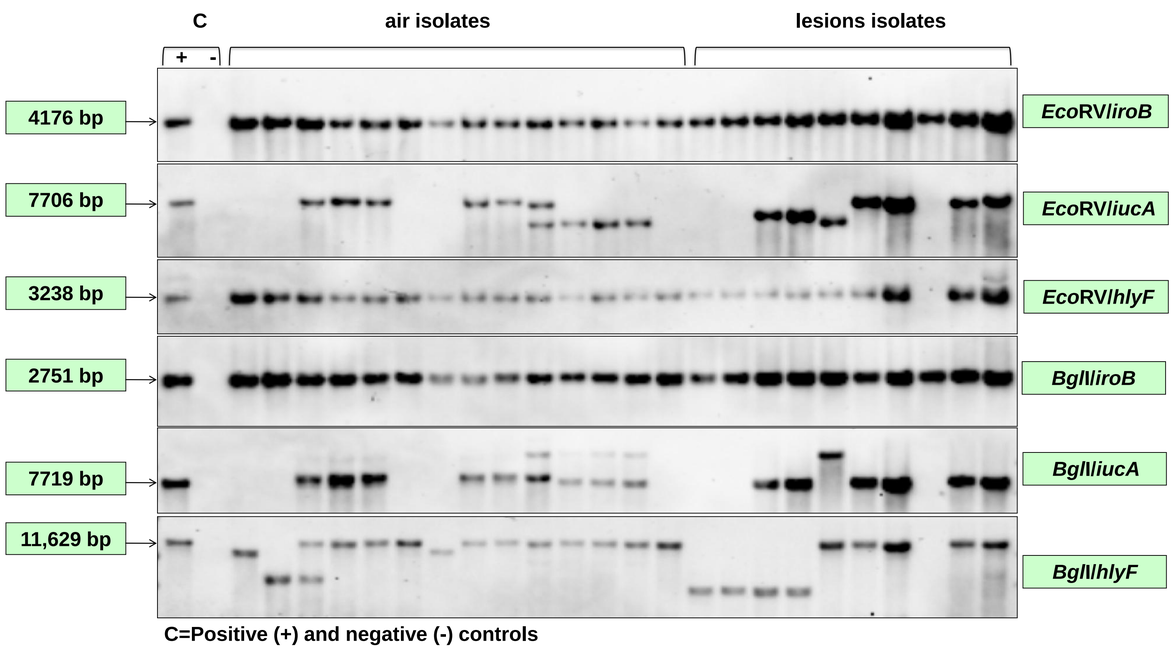
Lactose fermenting *E. coli* grown from the air samples



Chemiluminescent detection of *E. coli* isolates containing the *iroB* gene



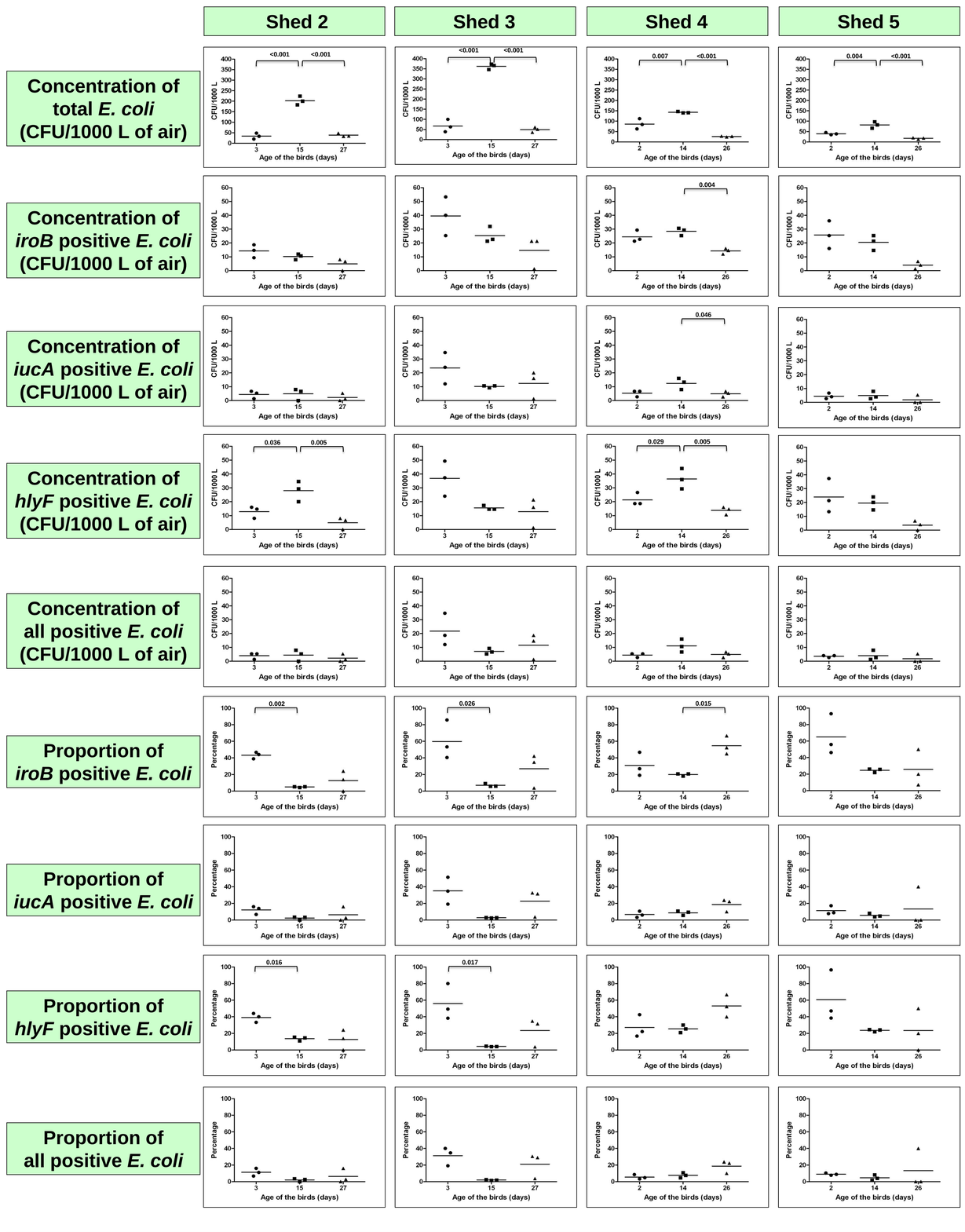
Chemiluminescent detection of an array of *E. coli* isolates containing the *iroB* gene



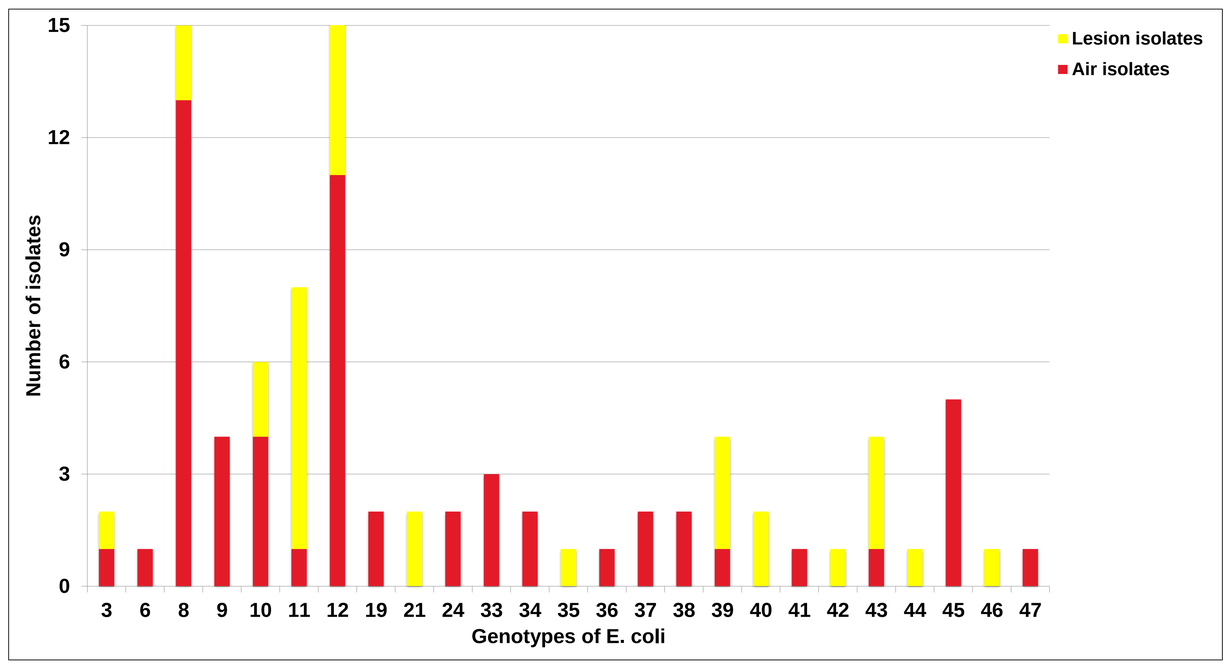
C=Positive (+) and negative (-) controls

Genotypic characterisation of *E. coli* isolates using RFLP and Southern blot hybridisation

Results



Distribution of *E. coli* genotypes



A total of 25 different genotypes were observed amongst 96 *E. coli* isolates from the air and from lesions of birds, with 7 common genotypes

Conclusions

❖The total concentration of *E. coli* (CFU/1000 L) increased significantly from days 2 and 3 to days 14 and 15 and decreased significantly at days 26 and 27 of age ($P<0.05$)

❖In most cases, the concentration of *E. coli* positive for either the *iroB*, *iucA* or *hlyF* probes remained higher up to days 14 and 15 of age, and decreased by days 26 and 27

❖The proportion of *E. coli* positive for the *iroB* and *hlyF* genes remained high at days 2 and 3, whereas the proportion of *E. coli* positive for *iucA* or all three genes remained high either at days 2 and 3 or days 26 and 27

❖Southern blot hybridisation revealed that similar genotypes of *E. coli* were present in the air and the liver lesions in birds

❖Detection of higher concentration of airborne pathogenic *E. coli* early in the production cycle in broiler sheds could be used to guide the introduction of preventive measures to control colibacillosis in chickens

Acknowledgements & References

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