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## Burden of *Escherichia coli* in poultry production systems in India: A systematic review, meta-analysis, and meta-regression

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### Abstract

*Escherichia coli* is one of the most common bacterial organisms associated with poultry and poultry products and is an important pathogen of economic and public health importance. Numerous studies have reported the prevalence of *E. coli* in poultry in India; however, the overall pooled prevalence and sources of heterogeneity have not been systematically evaluated. This study aimed to estimate the pooled prevalence of *Escherichia coli* in poultry in India using meta-analysis and to evaluate the factors influencing prevalence through subgroup analysis and meta-regression. A meta-analysis was conducted using published studies reporting the prevalence of *E. coli* in poultry in India. Data extracted included author, study year, state, sample type, poultry type, total sample size, and number of positive samples. Meta-analysis was performed in R using random-effects and fixed-effect models. Heterogeneity was assessed using Cochran's Q test,  $\tau^2$ , and Higgins'  $I^2$  statistic. Publication bias was evaluated using funnel plots and Egger's regression test. Subgroup analysis and meta-regression were performed to investigate sources of heterogeneity. Sensitivity analysis and influence diagnostics were conducted to assess the stability of the pooled estimate. A total of 118 studies comprising 6,334 samples were included in the meta-analysis, of which 3,487 were positive for *E. coli*. The pooled prevalence of *Escherichia coli* in poultry in India was 54.36% (95% CI: 47.49-61.06) using the random-effects model. Subgroup and meta-regression analyses indicated that poultry type, sample type, geographic region, and study year contributed to heterogeneity. This meta-analysis demonstrates that *Escherichia coli* is highly prevalent in poultry in India.

**Keywords:** Forest plot, Heterogeneity, Pooled prevalence, Random-effects model, Sensitivity analysis

### 1. Introduction

The poultry industry is one of the fastest-growing agricultural sectors worldwide and plays a significant role in food security, nutrition, and the economy. Poultry meat and eggs are important sources of high-quality protein, and the poultry sector contributes substantially to agricultural income and employment in many developing countries, including India (FAO, 2020; Government of India, 2022) [20, 27]. However, poultry production is associated with various bacterial pathogens that affect poultry health and may also pose risks to public health. Among these, *Escherichia coli* is one of the most important bacterial organisms associated with poultry. It is commonly found that due to the colibacillosis infection results in economic losses in the poultry industry due to mortality, reduced growth, poor feed conversion efficiency, and decreased egg production (Kabir, 2010; Nolan *et al.*, 2013) [2, 5].

The emergence and spread of antimicrobial-resistant *E. coli* in poultry production systems have become major global public health concerns (Van Boeckel *et al.*, 2015; Manyi-Loh *et al.*, 2018) [12, 17].

Several studies have reported the prevalence of *Escherichia coli* in poultry from different regions of India, sample types, and poultry production systems. However, the reported prevalence varies widely across studies due to differences in sampling methods, laboratory detection techniques, geographic regions, farm management practices, and biosecurity

measures. Such variability makes it difficult to estimate the overall burden of *E. coli* in poultry at the national level. Therefore, a systematic synthesis of available data is necessary to estimate the overall prevalence and to identify factors contributing to variability among studies.

The present study was conducted to estimate the pooled prevalence of *Escherichia coli* in poultry in India using systematic review and meta-analysis and to evaluate the effects of study year, sample size, poultry type, sample type, and geographic region on prevalence through meta-regression analysis.

## Materials and Methods

### Study design and data extraction

A meta-analysis was conducted to estimate the pooled prevalence of *Escherichia coli* in poultry in India. Data were compiled in Microsoft Excel and included the following variables: author, study year, state, sample type, poultry type, total sample size, and number of positive samples. Each row represented an independent study or a subgroup within a study.

### Statistical analysis

Meta-analysis was performed in R using the meta and metafor packages. The outcome measure was prevalence (proportion of positive samples). Proportions were logit-transformed to stabilize variance. The pooled prevalence was estimated using a random-effects model with the inverse variance method and the DerSimonian-Laird estimator for between-study variance ( $\tau^2$ ). The Hartung-Knapp adjustment was applied to calculate confidence intervals for the random-effects model. Heterogeneity among studies was assessed using Cochran's Q test,  $\tau^2$ , and Higgins'  $I^2$  statistic. Publication bias was assessed using funnel plot asymmetry and Egger's regression test. Subgroup meta-analyses were conducted based on Poultry type, Sample type and State. Meta-regression analysis was performed to evaluate the effect of Study year, Sample size and State (region). Bubble plots were generated for meta-regression models. Sensitivity analysis was performed using leave-one-out analysis and influence diagnostics to assess the stability of the pooled estimate. All statistical analyses were performed using R software.

## Results and Discussion

### Study characteristics

A total of 118 studies were included in the meta-analysis comprising 6,334 samples, of which 3,487 were positive for *E. coli*.

### Overall pooled prevalence

The pooled prevalence of *Escherichia coli* in poultry was 54.36% (95% CI: 47.49-61.06) using a random-effects model. The fixed-effect model estimated a pooled prevalence of 54.92% (95% CI: 53.48-56.35) (figure.1).

### Heterogeneity

There was high heterogeneity among studies,  $I^2 = 90.8\%$ ;  $\tau^2 = 1.0407$ ; Cochran's  $Q = 1277.13$ ,  $p < 0.0001$ . This indicated substantial variability between studies, justifying the use of a random-effects model.

### Publication bias

Funnel plot analysis showed a symmetrical distribution of studies. Egger's regression test indicated no significant publication bias ( $p = 0.9525$ ).

### Forest plot of pooled prevalence

The forest plot shows the prevalence estimates of *Escherichia coli* reported in individual studies along with their 95% confidence intervals (figure 2). Each study is represented by a square, the size of which is proportional to the weight of the study in the meta-analysis, and horizontal lines represent the confidence intervals. The diamond at the bottom of the plot represents the pooled prevalence estimate obtained from the random-effects model. The forest plot indicates substantial variability in prevalence estimates across studies, which is consistent with the high heterogeneity observed ( $I^2 = 90.8\%$ ). Despite the variability among individual studies, the pooled estimate provides an overall prevalence of *E. coli* in poultry in India.

### Subgroup meta-analysis

Subgroup meta-analysis was performed to investigate the sources of heterogeneity by stratifying studies based on poultry type, sample type, and geographic region (state). The subgroup results table presents the number of studies included in each subgroup, total sample size, pooled prevalence, and heterogeneity statistics ( $I^2$  and  $p$ -value). The subgroup analysis showed variation in prevalence among different poultry production systems, sample types, and regions, suggesting that management practices, environmental conditions, and sampling sources may influence the prevalence of *E. coli*. Some subgroups showed lower heterogeneity compared to the overall analysis, indicating that these factors contributed to between-study variability.

### Meta-regression analysis

Meta-regression bubble plots were generated to examine the effect of study year, sample size, and geographic region on the prevalence of *Escherichia coli*. In the bubble plots, each circle represents an individual study, and the size of the circle is proportional to the study weight or sample size. The meta-regression analysis showed that study year had a significant positive association with prevalence in the multiple meta-regression model, indicating a possible increasing trend in *E. coli* prevalence over time. Sample size did not show a significant association with prevalence. Geographic region (state) significantly influenced prevalence and explained a portion of the between-study heterogeneity. These results suggest that temporal trends and regional differences contribute to the variability in *E. coli* prevalence reported across studies (figure 4 & figure 5).

### Sensitivity analysis

Sensitivity analysis was performed using a leave-one-out approach to evaluate the stability of the pooled prevalence estimate. In this method, the meta-analysis was repeated by removing one study at a time to assess the influence of each individual study on the overall pooled prevalence. The results of the leave-one-out analysis showed that exclusion of any single study did not substantially change the pooled prevalence estimate, indicating that no individual study had a disproportionate influence on the overall results. The pooled prevalence remained relatively stable across all iterations, demonstrating the robustness and reliability of the meta-analysis findings.

### Influence diagnostics

Influence diagnostics were performed to identify studies with a potentially large influence on the pooled effect size and heterogeneity. Several diagnostic measures, including

studentized residuals, Cook's distance, DFFITS, and covariance ratios, were used to detect influential studies.

The influence diagnostic plots indicated that no studies exceeded the critical thresholds for Cook's distance or DFFITS values, and most studies fell within acceptable limits for studentized residuals and covariance ratios. This suggests that no single study unduly influenced the pooled prevalence estimate or the heterogeneity observed in the meta-analysis. Overall, the influence diagnostics confirmed the stability of the meta-analysis results and indicated that the pooled prevalence estimate was not driven by any highly influential studies.

This meta-analysis estimated the pooled prevalence of *Escherichia coli* in poultry in India and evaluated the sources of heterogeneity using subgroup analysis and meta-regression. The overall pooled prevalence of *E. coli* was high, indicating that *E. coli* is widely prevalent in poultry production systems across India. The high prevalence observed in this study is consistent with previous reports indicating that *E. coli* is one of the most common bacterial organisms isolated from poultry environments, faecal samples, and poultry products (Kabir, 2010; Mellata, 2013) [5, 10].

The high heterogeneity observed among studies ( $I^2 > 90\%$ ) suggests substantial variability in prevalence estimates across different studies. This variability may be attributed to differences in poultry production systems, biosecurity practices, environmental conditions, sampling methods, and laboratory detection techniques. Similar high heterogeneity has been reported in other meta-analyses of bacterial prevalence in poultry and livestock populations (Dorado-García *et al.*, 2016; Nhung *et al.*, 2017) [13, 16].

Subgroup analysis indicated that prevalence varied across poultry type, sample type, and geographic region. Differences between broiler and layer production systems may be due to variations in stocking density, management practices, antimicrobial usage, and production cycles. Broiler farms often have higher stocking densities and shorter production cycles, which may facilitate bacterial transmission, whereas layer farms have longer production periods, increasing the

duration of exposure to environmental pathogens. Geographic variation in prevalence observed in this study may be associated with climatic conditions, farm density, regional antimicrobial usage patterns, and differences in farm management practices. Previous studies have reported that environmental temperature, humidity, and farm hygiene play important roles in the survival and transmission of *E. coli* in poultry production systems (Van Boeckel *et al.*, 2015) [12].

Meta-regression analysis showed that study year was significantly associated with prevalence in the multiple meta-regression model, suggesting a possible increasing trend in *E. coli* prevalence over time. This trend may be linked to intensification of poultry production, increased antimicrobial use, and the emergence of antimicrobial-resistant *E. coli* strains. The global increase in antimicrobial resistance in poultry-associated *E. coli* has been widely reported and is considered a major public health concern (Marshall and Levy, 2011; Manyi-Loh *et al.*, 2018) [17].

Sample size was not significantly associated with prevalence, indicating that study size did not influence prevalence estimates in this meta-analysis. However, geographic region explained a portion of the between-study heterogeneity, indicating that regional factors play an important role in determining *E. coli* prevalence in poultry.

Publication bias analysis indicated no significant publication bias, suggesting that the results of this meta-analysis are unlikely to be influenced by selective publication of studies. Sensitivity analysis and influence diagnostics further confirmed the robustness of the pooled prevalence estimate, as no single study significantly influenced the overall results.

The findings of this meta-analysis have important implications for poultry health management and public health. Poultry serves as a major reservoir of *E. coli*, including pathogenic and antimicrobial-resistant strains, which can be transmitted to humans through the food chain, environment, or direct contact. Therefore, improved biosecurity measures, hygienic management practices, rational antimicrobial use, and surveillance programs are essential to reduce the prevalence of *E. coli* in poultry production systems.

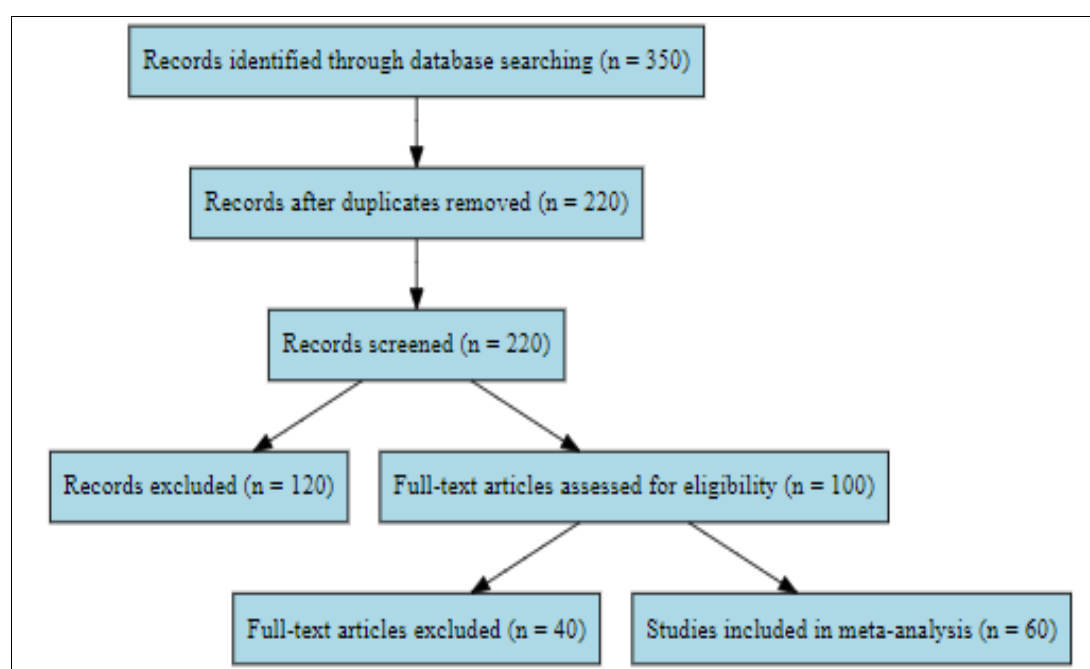
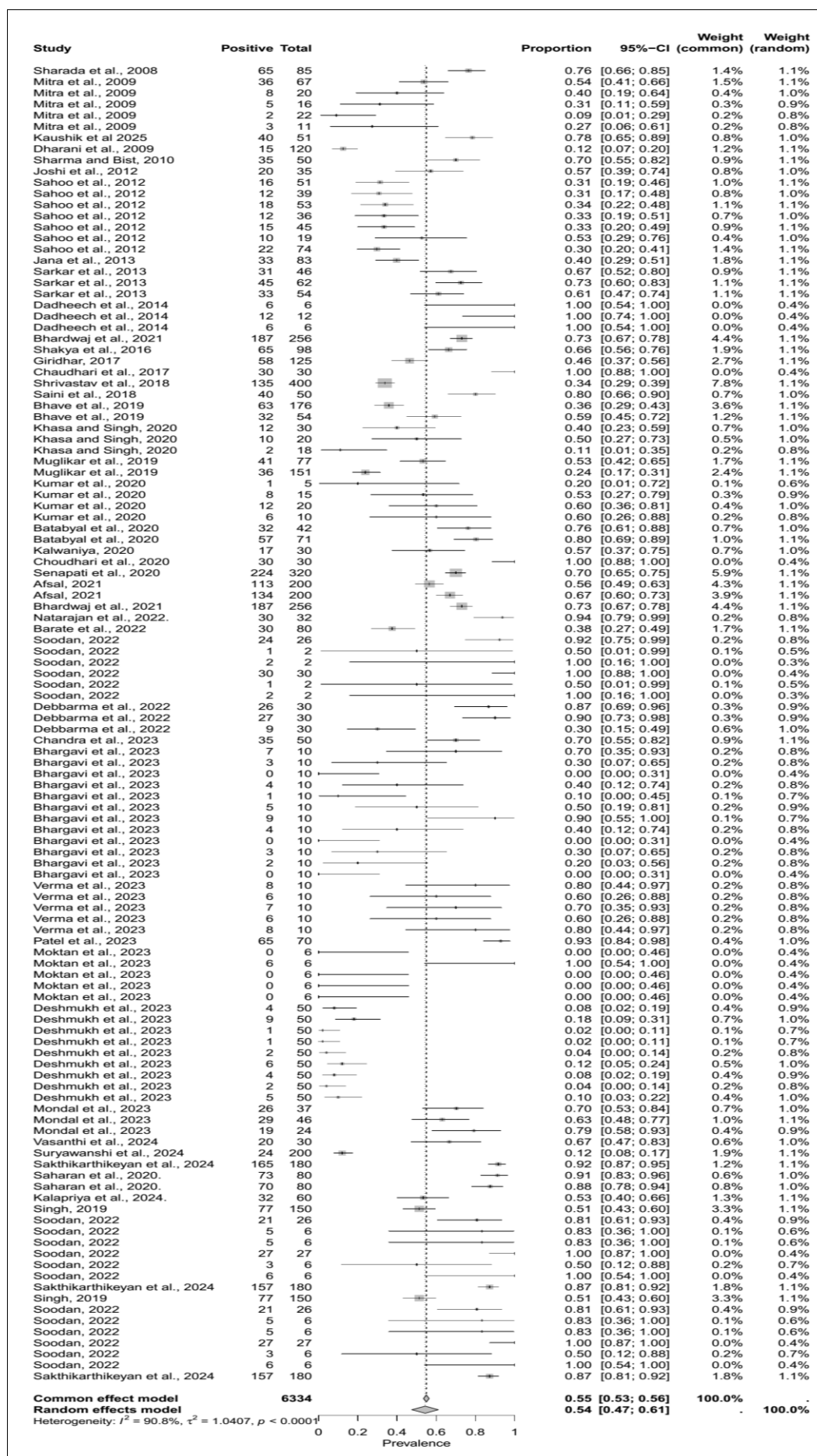


**Fig 1:** PRISMA flow diagram showing study selection process for meta-analysis of *Escherichia coli* prevalence in poultry in India

Fig 2: Forest plot showing pooled prevalence of *Escherichia coli* in poultry in India using a random-effects model.

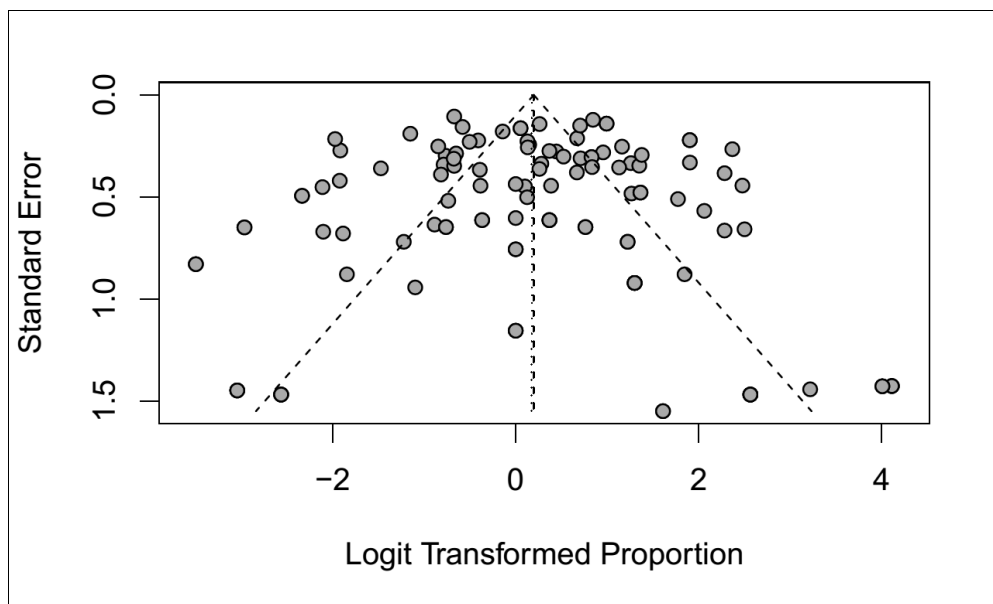


**Fig 3:** Funnel plot for assessment of publication bias in studies reporting prevalence of *Escherichia coli* in poultry in India

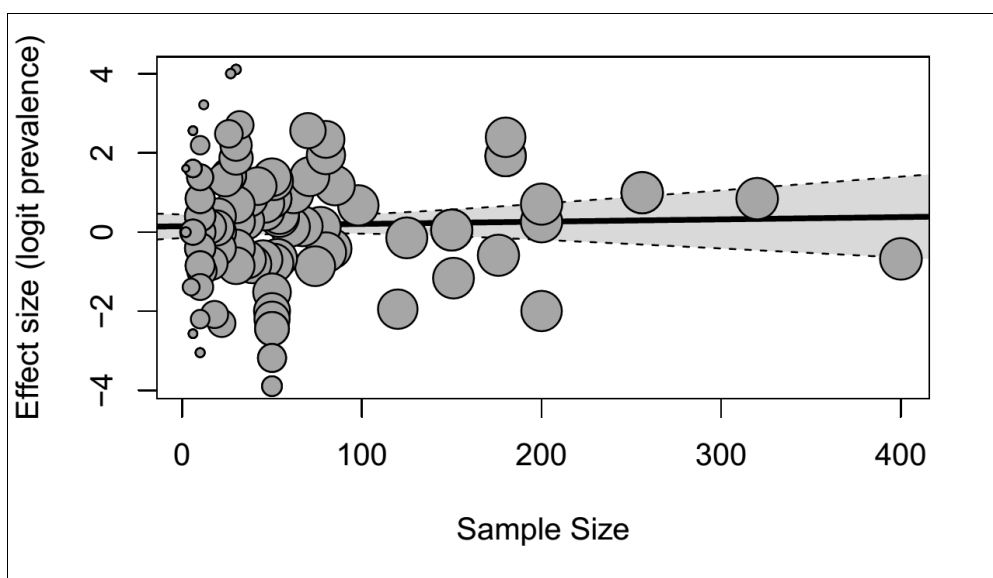


**Fig 4:** Meta-regression bubble plot showing the relationship between sample size and prevalence of *Escherichia coli*

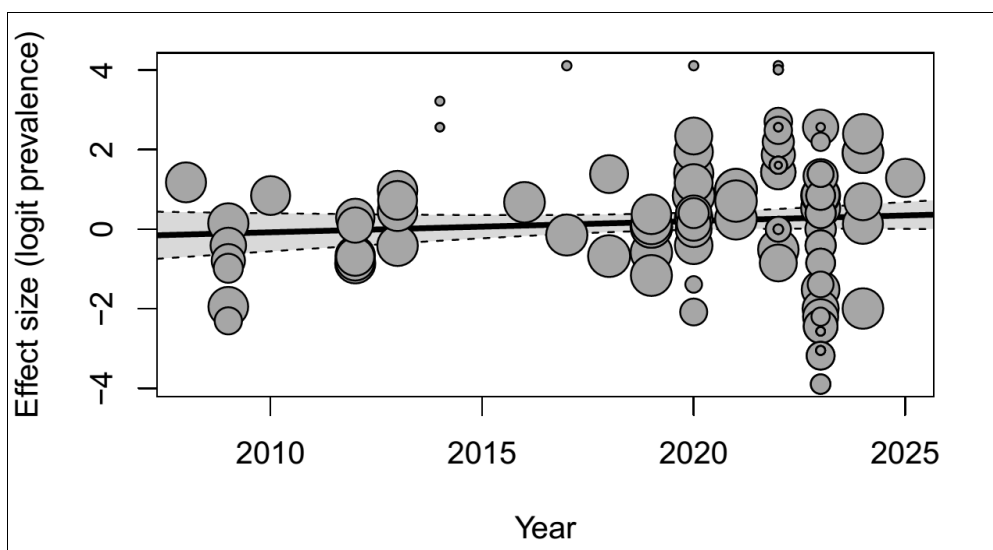


**Fig 5:** Meta-regression bubble plot showing the relationship between study year and prevalence of *Escherichia coli*

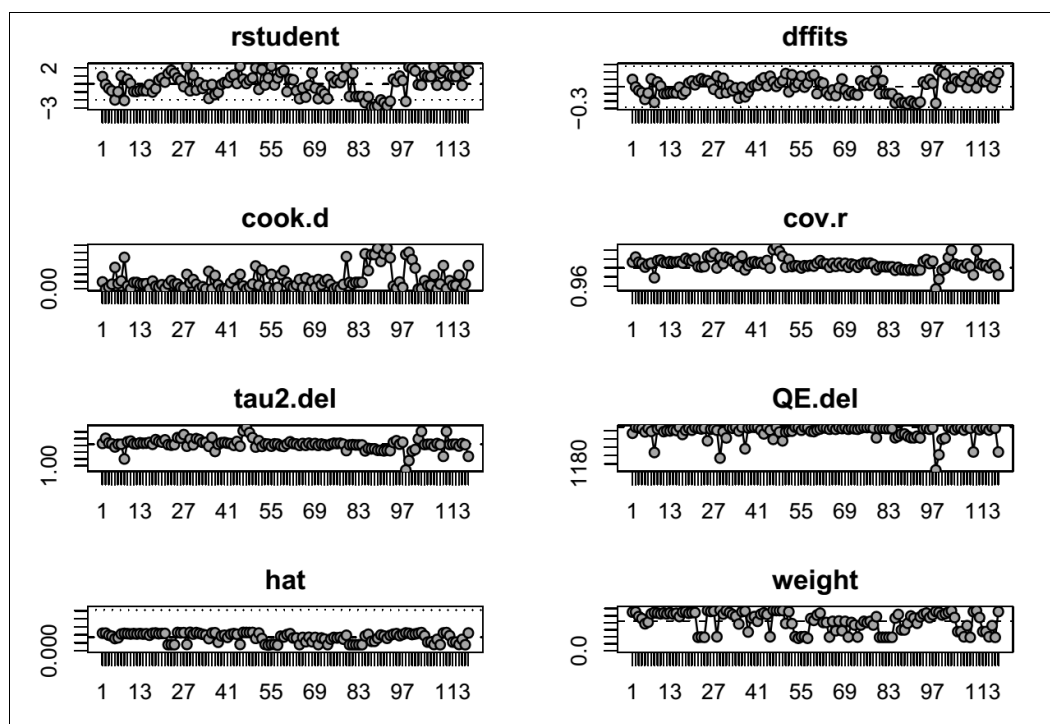


**Fig 6:** Leave-one-out sensitivity analysis plot for pooled prevalence of *Escherichia coli* in poultry in India

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