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LIST OF ABBREVIATIONS

AFM	Atomic force microscope
APEC	Avain pathogenic *E. coli*
API	Analytical profile index
BFP	Bundle forming pili
E. coli	*Escherichia coli*
EHEC	Enterohemorragic *E. coli*
EMB	Eosin methylin blue
EPEC	Enteropathogenic *E. coli*
ExPEC	Extra- intestinal pathogenic *E. coli*
F1	Fimbriae
GUD	β- glcoronidase
IMVC	Indole, Methyl red, Voges proskauer, Citrate reactions
IND	Indole
InPEC	Intestinal pathogenic *E. coli*
***iro* N**	Iron acquisition system (siderophores receptor)
iss	Increase serum survival
K	Capsular antigen
LDC	Lysine decarboxylase
***Lux*S**	S-ribosylhomocysteinase
MUG	4-methylum bellifryl-β-D-glucuronide
ODC	Ornithine decarboxylase
***omp* T**	Outer membrane protease T
ONPG	O-Nitrophenyl-beta-D-galactopyranoside
***pap* C**	Pyelonephritis-associated pilli C
PCR	Polymerase chain reaction
PYR	L- Pyrrolidonyl-B naphthylamide

SCFAs	Short chain fatty acids
STEC	Shiga toxin - producing *E. coli*
TBE	Tris borate EDTA
TEM	Transmission electron microscope
Tn21	Transposone 21
TSB	Trypticase soy broth
tsh	Temperature sensation haemagglutination
VTEC	Verotoxin- producing *E. coli*

6. SUMMARY

In recent years, multidrug resistant virulent strains of *E. coli* are circulating in broiler flocks and are implicated in cases of high mortalities causing significant economic losses in poultry industry. Therefore, the goal of the current study was the detection of the most important virulence genes among MDR *E. coli* isolates from different sources with relation to their resistance genes.

In the present work, 242 specimens were collected from different sources (150 broiler organs with a previous history of colibacillosis, 61 chicken by-products and 31 water tank samples) during all seasons of the year from March 2011 to July 2013 in Sharkia province,[Summer (84), autumn (54), winter (38) and spring (66)].

Microbiological analysis of the collected samples revealed that *E. coli* was recovered with a percentage of 20.2%; 22.7% from broiler organs, 14.8% from broiler by-products and 19.4% from water tanks.

Sasso breeds revealed the higher recovery rate of *E. coli* isolates (25.7%). Moreover, the highest isolation rate of *E. coli* was in summer (33.3%).

API 20 E protocol was applied on randomly selected *E. coli* isolates from different sources as a recent standardized and efficient identification protocol. Results of API 20 E confirmed those of the conventional biochemical identification of *E. coli* isolates.

Serotyping of *E. coli* isolates revealed 8 different serotypes from different sources with a dominance O26:K60 and O114:K90

serotypes which was the most prevalent serotypes with a percentage of 20.4% for each one, while the remainder isolates were serotyped as O125:K70, O111:K58, O78:K80, O44:74, O55:K59 and O127:K63 serotypes and 2 isolates were nontypeable by available antisera.

Antimicrobial sensitivity test of all *E. coli* isolates showed that the highest antibiotic resistance pattern was detected against amoxicillin- clavulanic acid, trimethoprime sulfamethoxazole and erythromycin (100%), while the least resistance was detected against doxycycline (51.02%).

Furthermore, the multidrug resistance pattern of *E. coli* isolates revealed that most isolates from different sources were MDR.

PCR was used to test the presence of 5 virulence genes carried on plasmid, those genes had been proven to play an important role in the virulence of *E. coli.* PCR successfully detected *iss, iro*N*, tsh, omp*T and *pap*C genes in the 11 selected *E. coli* isolates with percentages of 100, 90.9, 81.8, 81.8 and 81.8%, respectively. They yielded amplicon sizes of 266, 847, 824, 919 and 501 bp, respectively.

Additionally, uniplex PCR was used for detection of 5 antibiotic resistance genes carried on plasmid that proved to play an important role in the resistance aganist different antimicrobial agents of *E. coli* (*bla*TEM*, aad*A1*, qnr*S*, tet*B and *sul*I genes), It was revealed that *sul*I and *bla*TEM genes were the most prevalent resistance genes, being prevalent in all tested *E. coli* isolates (100%), meanwhile *tet*B gene was the least detected antibiotic resistance gene among the examined isolates (45.5%).

From above mentioned results, it was revealed that MDR *E. coli* isolates from different sources proved to possess several virulence and antibiotic resistance genes carried on the same plasmid. This outcome highlights the risk of spreading of virulence and dissemination of antimicrobial resistance leading to high risk zoonotic importance in human.

7. CONCLUSION

The present study was undertaken to determine the correlation between the multidrug resistance and the occurrence of virulence factors among *E. coli* isolates from different sources in Sharkia province

From the current study, the following points could be concluded:

1. The overall prevalence of *E. coli* isolates from different sources in Sharkia Governorate was 20.2% with a higher prevalence rate in summer season (33.3%).

2. Sasso breed revealed a higher incidence rate of *E. coli* isolates (25.7%).

3. *E. coli* O26:K60 and O114:K90 were the most prevalent serotypes recovered from different sources in Sharkia province.

4. All *E. coli* isolate showed a higher resistance rates against trimethoprim- sulfamethoxazole, amoxicillin-clavulanic acid and erythromycine, while the least resistance rates was shown aganist doxycycline.

5. Most *E. coli* isolates from different sources were highly multidrug resistant. This data suggested the dangerous effect of their strains.

6. There was correlation between phenotypic antimicrobial susceptible profile and genotypic detection of some important virulence genes among different *E. coli* isolates. It was revealed

that MDR *E. coli* isolates possessed at least two virulence genes on the same plasmid with antibiotic resistance genes.

7. There was a good association between multidrug resistance and the occurrence of the most important virulence genes among the selected *E. coli* isolates as most MDR *E. coli* isolates possessed several important virulence and antibiotic resistance genes on their plasmid. These results have important implications with regards to the spread and persistence of resistance and virulence genes in bacterial populations on plasmid. Moreover, *E. coli* can serve as reservoirs of resistance genes for potentially pathogenic bacteria.

8. The unscrupulous use of antibiotics to prevent infections results in emergence of large numbers of multidrug resistant *E. coli.*