

الجلسة العلمية الثانية

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قاعة البرامج الخاصة الدور الارضى

1: Epidemiological Investigation of *Helicobacter pylori* as an Emerging Zoonosis in Matrouh Province, North-West Egypt: A Community Based Cross-sectional Study

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Abstract

Helicobacter pylori is newly emerging bacteria and one of the most common infections worldwide with over one-half of the world is infected with this organism. A total of 250 stool samples were collected from farm animals (sheep and Camels) and humans in Matrouh Province, North-West Egypt. Samples were examined using *H. pylori* Stool Antigen Enzyme Immunoassay test and *H. pylori 16S rRNA* PCR. Statistical analysis was applied using Chi^2 and IBM SPSS Statistics 25. The overall prevalence of *H. pylori* infection in the study by HpSA and PCR were 27.6% and 24.4%, respectively. Based on the results of HpSA test, it was found that the prevalence was 12% and 26% in sheep and camels, respectively, with statistically significant association between the prevalence and locality or age of sheep. Moreover, the prevalence of *H. pylori* infection in human was 44% by HpSA test with statistically significant association between the prevalence and gender or locality being higher in males than females with greater rural prevalence than urban. On the other hand, there was a non-statistically significant differences between *H. pylori* prevalence and sex, breed, and health status of examined animals or age, residence, and occupation of enrolled individuals. Conclusively, *H. pylori* was detected in both animal and

human samples is alarming in Matrouh Province where our findings suggest that farm animals could transmit the infection to humans. Therefore, there was an urgent need for implementing a proper control program.

Key words: *Helicobacter pylori*, Sheep, Camels, Humans, Prevalence, HpSA, *16S rRNA* PCR, Zoonosis.

2: Effect of Various Disinfectants on Biofilm-Forming Ability of *E. coli* Isolated from Water Pipes in Broiler Farms of Giza and Dakahlia

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Abstract

In poultry, *Escherichia coli* infections lead to substantial deaths and financial losses for producers each year. This study aimed to investigate the prevalence of *E. coli* from water pipes and drinkers in broiler farms, to characterize the isolated *E. coli* strains in terms of serotypes, biofilm production degree, presence of the *adrA* gene The gene "*adrA*" encodes for the Adhesion Regulating Protein A. AdrA is a protein that plays a role in regulating the adhesion and biofilm formation of Escherichia coli bacteria., and the efficacy of various disinfectants on *E. coli* biofilms. A total of 100 swab samples were collected from drinking water pipes and drinkers from different broiler farms in Giza and Dakahlia governorates in Egypt.18 *E. coli* serogroups were identified in 50 positive samples, and the most predominant serogroup was O91, which showed the highest incidence (20%), followed by serotypes O78 (18%), and O26 (8%). Microtiter-plate test for determination of biofilm production for 50 *E. coli* isolates. PCR was done for the detection of the virulence gene *adrA* in the 13 strong biofilm *E. coli* isolates, and the results revealed that 100% were positive for the virulence gene. We then evaluated the effect of disinfectants on biofilm by using ZnO nanoparticles, acidifiers, and quaternary ammonium dioxide. This study found a high prevalence of *E. coli* in water samples, identified various *E. coli* serotypes, observed biofilm production, and determined the effectiveness of different disinfectants on *E. coli* biofilms.

Keywords: Biofilm production, *E. coli*, AdrA gene, ZnO nanoparticles, Egypt.

3: Detection of extended-spectrum β-lactamases producing *Escherichia coli* from beef in Mansoura, Egypt

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Abstract
Objective: The objective of the current study was to identify extended-spectrum β-lactamase-producing *Escherichia coli* (ESBLs) from beef meat in Mansoura City, Egypt.
Design: Randomly selected 150 buffalo meat samples were obtained from retail butcher shops located in Mansoura City, Egypt. Samples were inoculated into enriched broth media and then directly streaked on *E. coli* selective agar for selective isolation of *E. coli*. A biochemical examination was performed for the preliminary identification of *E. coli*. Suspected *E .coli* isolates were then confirmed by PCR targeting 16S rRNA. Confirmed *E. coli* isolates were tested for their susceptibility to antimicrobials by using Kirby–Bauer disc diffusion method. Additionally. *E. coli* were tested for the presence of β-lactamases (*bla*$_{CTX}$, and *bla*$_{SHV}$ and *bla*$_{TEM}$) using PCR.
Results: *E. coli* was isolated from 37 out of 150 tested samples with a total prevalence of 24.66 %. *E. coli* isolates revealed a high resistant against cefotaxime and ceftazidime, and moderate resistance against amoxyclavulanic acid, while a high sensitivity of *E. coli* was displayed against meropenem and imipenem. Moreover, the tested *E. coli* (n=37) harbored ESBLs genes with percentages of 40.5% for both *bla*$_{CTX,}$ and *bla*$_{SHV}$ and 35% for *bla*$_{TEM}$
Conclusion and clinical relevance: *E. coli* produces extended-spectrum β -lactams that were isolated from meat and contained a substantial level of antibiotic resistance genes. To increase food processing quality and provide safe food for consumers, it is crucial to build food traceability and monitoring systems for meat and meat products.
Keywords: *E. coli*, beef, ESBL, antimicrobials susceptibility

4: Characterization of Vancomycin Resistant Enterococci (VRE) isolated from retail poultry meat

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Abstract

Antimicrobial-resistant bacteria in poultry meat threaten the public health. The present study was designed to detect the presence of *Enterococcus* species in poultry meat

collected from Mansoura retail outlets with characterization of vancomycin-resistant enterococci (VRE). Thus, poultry meat samples (breast and thigh) were collected from separate grocery stores around Mansoura city, Egypt. By conventional and molecular methods, out of the total examined samples (n=120), 44 *E. fecalis* isolates have been recovered with a percentage of 36.66%. All strains were assessed for their antimicrobial susceptibility using disc diffusion method, the highest rate of resistance (100%; 44/44) was displayed to ceftazidime, streptomycin, gentamycin, and clindamycin, while, a resistance rate of 36.3%, 40.9%, 68.1% and 77.2% were displayed against ciprofloxacin, penicillin, erythromycin and vancomycin respectively. Interestingly, all isolates were exhibit multidrug resistance (MDR; Resistance to three or more antimicrobial class). Screening vancomycin -resistant strains (n= 34) by PCR for the presence of vancomycin resistance genes, *van*A was identified in 47.1% *van*B in 33.4%, *van*C1 in 14.7% and *vanC*-2 C-3 in 5.9%. By testing the ability of the isolated strains for the biofilm production by Congo Red Method, 31.8 % of the tested isolates were tested positive. Hence, standard manufacturing procedures and adequate hygiene conditions must be integrated into all phases of poultry meat preparation, production and consuming, and public knowledge should be improved.

Key words: *Enterococcus*, Poultry meat, VRE, Biofilm production

5: Re-shedding Trials of *Toxoplasma gondii* Oocysts from Experimentally Infected Kittens Reference to Strain Types I, II and III; Zoonotic and Histopathological Confirm

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Abstract

Cats are the only definitive host of *Toxoplasma gondii* (*T. gondii*) that shed millions of un-sporulated oocysts. The current study aimed at evaluating the serological and histopathological potential ratio of *T. gondii* oocysts shedding and re-shedding kittens. Blood and fecal samples collected from fifty-seven un-weaned kittens from various districts of Cairo Governorate, Egypt. All kittens serologically screened for *T. gondii* using the Latex agglutination test (LAT), and fecal materials inspected daily for oocysts. Only proven seronegative un-shedding kittens employed in the three experimental re-

shedding studies using the three *T. gondii* strain types II, III, and I with the third trial focusing on the ability of re-shedding with corticosteroid therapy. One kitten corresponding to each type sacrificed for histo-pathological assay and IgM/IgG serum antibodies recorded along the trials course using ELISA. The overall sero-negative percentage was 59.7%, with 35.1 and 24.6% in shedding and un-shedding ones respectively. The shedding number of oocysts /100 mg/feces scored (7, 5 and 3); (30, 15 and 7); (20, 10 and 5) corresponding and sequence to the three *T. gondii* strain types I, II and III respectively. In addition, the average IgM/IgG ELISA titers recorded significance variations sequence to the three strain types. Corticosteroids therapy stimulates re-shedding ability for the third time. The findings concluded that kittens shed oocysts at a high rate; regard shedding and re-shedding qualities as a critical component in developing oocyst-borne human and animal toxoplasmosis effects. Strong protection against vaccinated cats are required, as is close interaction between cats and farm animals.

KEYWORDS
Toxoplasma gondii strains, kittens, Shedding and re-shedding, Histopathology, ELISA.

6: Molecular typing of virulence and antimicrobial resistance genes with mutation tracking of *gyr*A gene of fluoroquinolone-resistant strains of *Campylobacter* isolated from broiler chickens.

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Abstract

Campylobacter is the most common bacterial cause of gastroenteritis globally. A total of 182 fully identified strains of *Campylobacter* species (42 *C.coli* and 140 *C.jejuni*) collected from 6 broiler farms were subjected to studying the antimicrobial resistance pattern and molecular typing of virulence (*cad*F, *ctd*A, *dna*J *waa*C,*iam*, and *fla*) and antimicrobial resistance genes (bla_{OXA-61}, *gyr*A, *tet*A, *tet*O, and IR) with sequencing of *gyr*A region of one strain of fluroquinolones resistant *C.coli* and *C.jejuni*. The identified isolates were highly resistant to erythromycin and sulfamethoxazole-trimethoprim. Furthermore, both meropenem and imipenem were effective against the recovered isolates. The

tested *C.jejuni* and *C.coli* strains had 100%, 83.3%, and 83.3% prevalence of *cad*F, *ctd*A, and *dna*J virulence genes, respectively, while *waa*C, *iam*, and *fla* genes couldn't be detected. The bla_{OXA-61} resistance gene was found in all of the *Campylobacter* spp. examined. Furthermore, *gyr*A, *tet*A, *tet*O, and IR resistance genes were found in 100%, 83.3%, 83.3%, and 66.7% of the retrieved *C. jejuni* strains, respectively. Likewise, resistance genes were found in 83.3%, 83.3%, 83.3%, and 66.7% of the retrieved *C.coli* strains, respectively. Approximately 58% (7/12) of the *Campylobacter* spp. recovered were MDR. Furthermore, 50% (3/6) of the *C. jejuni* strains recovered were MDR, while 66.7% (4/6) of the *C.coli* isolates recovered were MDR with MARI(0.22-0.55). For detection of mutations of the *gyrA* gene, the sequence data of two isolates (*C. jejuni* and *C.coli*) were analyzed against the reference sequence on the gene bank where the *C.jejuni* strain had six mutations, while the *C.coli* strain had twenty-three. The current findings suggest that MDR Campylobacter strains in poultry may be able to transmit highly virulent *Campylobacter* as a foodborne pathogen.

Keywords: Broilers; Resistance genes, Antimicrobials, C. coli, C. jejuni

7: Genetic analysis of *mec*A gene of Methicillin-resistant *Staphylococcus aureus* from human, canine and feline origins

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Abstract

The aim of the present study was to determine the genetic relatedness between Methicillin-resistant *Staphylococcus aureus* (MRSA) isolated from pet animals and human. In that context, 561 swabs were collected from dogs (n=238) and cats (n=323). In addition, 30 MRSA positive isolates from Qasr Elainy hospital, from different patients were also included. The collected samples were subjected for bacteriological examination for isolation of *S. aureus*. The recovered *S. aureus* isolates that were resistant to oxacillin and cefoxitin were tested for the presence of *mec*A, *mec*C, *spa*, and *nuc* genes by PCR, followed by a sequence analysis of the *mec*A gene in seven selected isolates. Out of 238 swab samples collected from dogs and 323 swab samples collected from cats, 13 (5.46%) and 8 (2.48%) isolates respectively were confirmed to be MRSA. In addition, the 30 human isolates were all categorized as MRSA. The *mec*A gene was successfully identified in all isolates from dogs, cats and human, while *spa* was harbored by 13, 4 and 30 isolates from dogs, cats and human respectively. Furthermore 13, 4 and 23 isolates from dogs, cats and human were positive for the *nuc* gene. And, *mec*C was not identified from all

examined isolates. The phylogenetic analysis of the *mec*A gene sequence in seven selected MRSA isolates demonstrated a high degree of similarity among isolates originating from dogs, cats, and humans. This study confirms the zoonotic spread of *S. aureus* and suggests that dogs and cats are probably contributing to the spread of MRSA to human.

Key words: MRSA- *mec*A*, mec*C*, spa, nuc, Staphylococcus aureus*

8: Virulotyping and antibiograms of pathogenic Escherichia coli isolated from calves suffering from diarrhea

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Abstract

Escherichia coli is an important cause of diarrhea in calves and has negative economic effects on the livestock industry worldwide due to high mortality and reduced growth rate. The present study was aimed to investigate the prevalence of E. coli in 120 fecal samples from diarrheic mixed-sex neonatal calves, molecular detection of virulence genes, and antimicrobial resistance testing. The high occurrence of E. coli (90/120; 75%) was detected in diarrheic calves. The molecular detection of virulence genes (*iron, papc, asta, iuta, omp, hyl* and *iuc*) showed that the high occurrence of *ast*A (78.8%), *iucD* (66.6%)*,* and *pap*C (64.4%) genes in examined strains, while only 19 strains devoid of virulence genes. Furthermore, antimicrobial susceptibility testing of *E. coli* isolates showed absolute resistance to ampicillin (100%), followed by streptomycin (95.5%), tetracycline, sulfonamides, gentamycin and chloramphenicol (77.7% each). In the other hand, strains revealed high rates of susceptibility to ciprofloxacin (80%) and enrofloxacin (77.8%). The multidrug-resistant (MDR) E. coli strains were determined as 77.7% (70/90) and the most identified antimicrobial resistance patterns in 31 strains was C, S, CN, N, TET, AM, SXT**.** Also, the identified antibiotypes had MAR index values ranged from 0.1 to 0.9. The results of current study indicate the importance of routine monitoring of E. coli isolated from diarrhetic calves to reduce the transmission to humans and animals as well as to select the most appropriate antibiotics. The antibiograms in our study emphasizes the risks associated with the random use of antibiotics.

Keywords: Antibiograms, Pathogenic E. coli, diarrheic calves, Virulotyping

9: Prevalence, identification and antibiotic susceptibility profiles of *Enterococcus faecium* and *Enterococcus faecalis* isolated from chicken carcasses retailed in Mansoura city

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ABSTRACT

Objective: To detect the prevalence of *Enterococcus faecium* and *Enterococcus faecalis* in investigated chicken carcasses and characterize their antibiotic susceptibility profiles.
Design: Observational study.
Procedure: A total of 65 freshly slaughtered whole chicken carcasses were collected from different poultry shops distributed in Mansoura city. All samples were individually packed in a clean polyethylene bag then transported without delay in an ice box to the laboratory of Meat Hygiene, Safety and Technology, Faculty of Veterinary Medicine, Mansoura University, wherein the microbiological analyses were done.
Results*: Enterococcus* species were isolated from 84.6% of the tested chicken carcasses in counts ranging from 1×10^2 to 8.7×10^4 cfu/cm^2 with a mean count of 9×10^3 cfu/cm^2. Of the *Enterococcus* species identified, *E. faecium* and *E. faecalis* represented 16.7% and 23.1%, respectively. The antibiotic resistance profiles of tested *E. faecium* and *E. faecalis* showed high resistance rates of 100% and 100%, 100% and 84.6% and 72.2% against kanamycin, clindamycin, and colistin, respectively, but conversely, lower resistance rates of 15.4% and 11.1%, 7.7% and 5.6, and 15.4% and 5.6% were detected towards linezolid, vancomycin, and tigecycline, respectively. Of the *E. faecium* and *E. faecalis* isolates tested, 69.2% and 61.1% were multidrug resistant with average MAR index of 0.497 and 0.412, respectively.
Conclusion and clinical relevance: The high incidence of *Enterococcus* spp. contamination detected in tested chicken carcasses can constitute a potential risk for human public health. Therefore, special programs are urgently needed to control the contamination of chicken carcasses in poultry shops with *Enterococcus* spp.
Keywords: Enterococci, Chicken carcasses, Antibiotic resistance.

10: Antimicrobial Resistance of Salmonella Species Isolated from some food products and Human in Alexandria, Egypt

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Abstract :

This study was carried out in Alexandria Province for a period of 12 months from November 2021 to October 2022 in the laboratory of Animal Hygiene and Zoonoses Department, Faculty of Veterinary Medicine, Alexandria University for isolation and molecular identification of Salmonella from some food products of animal origin as well as humans. In addition, the antimicrobial susceptibility testing of the identified bacterial strains was assessed. A total of 450 food samples, comprising chicken paneeh, chicken burger, chicken luncheon, minced meat, beef burger, and kariesh cheese (75 each), were randomly gathered from. In addition, a total of 100 human stool samples have been obtained from 60 diarrheal individuals and 40 apparently healthy ones. Isolation of

Salmonella from food samples on XLD clarified that the recovery rate was 12, 8, 5.3, 13.3, 9.3 and 5.3 % for Chicken paneeh, Chicken burger, Chicken luncheon, Minced meat, Beef burger and Kariesh cheese, respectively (40 isolates) while biochemical identification showed that the detection rate was 9.3, 5.3, 5.3, 8, 5.3 and 4% from the same samples, respectively (28 isolates only). Moreover, the molecular identification revealed the detection of 11 isolates only. Finally, the serological identification of 11Salmonella isolates clarified the presence of S. Enteritidis, S. Haifa, S. Inganda, S. Tamale, S. Typhimurium and S. Shangani with various rates. Antimicrobial susceptibility of Salmonella strains (n=11) isolated from food products revealed that Ciprofloxacin was the most effective antibiotic against the tested isolates (90.9 %) followed by Doxycycline (72.73 %) while Cephalexin was the least effective antibiotics as it was noticed that 100% of isolates were resistant. On the other hand, Isolation of Salmonella from the stool samples on XLD (43 isolates) clarified that the recovery rate was 53.3 and 27.5 % for diarrheic and apparently healthy individuals, respectively while biochemical identification tests showed that the detection rate was 25 and 10 % for diarrheic and apparently healthy individuals, respectively (19 isolates only). In addition, the molecular identification of isolates revealed the detection of 16 isolates only. Finally, the serological identification of Salmonella isolates (n=11) recovered from food products clarified the presence of S. Enteritidis, S. Haifa, S. Inganda, S. Typhimurium, S. Montevideo and S. Tsevie with various rates. Finally, antimicrobial susceptibility of Salmonella strains (n=11) isolated from stool samples revealed that Vancomycin and Doxycycline were the most effective antibiotics against the tested isolates (93.75 %) while it was noticed that 100% of isolates were resistant to the remaining antibiotics (Ampicillin, Cefotaxim, Cephalexin, Ciprofloxacin, Penicillin G, Streptomycin and Tetracycline).

Key words: Antimicrobial Resistance, Salmonella, Food products, Human

11: Prevalence, antibiotic sensitivity testing and molecular characterization of virulence and antimicrobial resistance genes in *Clostridium perfringens* in fish

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Abstract

Fish is one of the most widely advertised foods, and Egypt is now recognized as a significant global fish producer. Human and animal intestinal illnesses and significant histotoxic illnesses are caused by foodborne microorganisms as *Clostridium perfringens*

(*C. perfringens*). This study was directed to monitor the prevalence, antibiotic susceptibility testing, detection of some virulence and antibiotic resistance genes of multidrug-resistant *C. perfringens* recovered from fish. A total of 250 samples were collected from gills and intestine of Catfish, Tilapia and Dennis). Bacteriological examination was conducted, the obtained *C. perfringens* strains were tested for antibiogram, PCR screening of virulence and antibiotic resistance genes. The investigated samples showed *C. perfringens* prevalence of 58%. *C. perfringens* isolates were resistant to several antibiotics as clindamycin (90%), cefprozil (80%), novobiocin (80%), aztreonam (80%) and erythromycin (80%). While, isolates were sensitive to nalidixic acid (90%), ofloxacin (90%), chloramphenicol (90%) and rifampicin (80%). Multidrug-resistant (MDR) *C. perfringens* was detected in 80% of tested strains. PCR proved that the obtained *C. perfringens* strains were carrying the virulence genes: *cpa*, *cpb* and *cpe* in a prevalence of 60%, 40% and 10%, respectively. As well, *bla* and *erm*B antibiotic resistance genes were detected in *C. perfringens* strains in a prevalence of 100% for both genes. In conclusion, *C. perfringens* isolated from fish was multidrug- resistant (MDR) bacteria and was harbored *cpa*, *cpb* and *cpe* virulence genes and *bla* and *erm*B antibiotic resistance genes. The development of MDR *C. perfringens* is conceived as a public health threat.

Key words: *Clostridium perfringens*, antibiotic susceptibility testing, virulence, antibiotic resistance genes, PCR.

12: Enterobacterial repetitive intergenic consensus- PCR of Methicillin-resistant Staphylococcus aureus isolated from pet animals

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Abstract

Methicillin-resistant *Staphylococcus aureus* (MRSA) is one of the potential pathogens in pet animals and has public health hazards worldwide. This project was aimed to investigate the frequency of MRSA in pet animals and to assess the antimicrobial susceptibility of the recovered strains as well as to determine the isolates genetic relatedness using Enterobacterial Repetitive Intergenic Consensus (ERIC)-PCR. Out of the 270 swab (nostril, mouth, and abscess swabs) samples collected from veterinary clinics and shelters in Mansoura city, Egypt, 64 (23.7%) *S. aureus* isolates (49/224; 21.8 % from cats and 15/46; 32.6% from dogs) were identified. Among them, 40.6% (26 /64) were confirmed to be MRSA and 59.4% (38/64) were identified as MSSA. Antimicrobial susceptibility test results showed the highest resistance rates of MRSA isolates to penicillin (100%), oxacillin (100%), followed by amoxicillin-clavulanic acid (92%), cefotaxime (92.4%), kanamycin, streptomycin, tetracycline (84.6%; 22/26 each), and lower resistance to vancomycin (38.5%). Furthermore, MSSA isolates showed moderate resistance to amoxicillin-clavulanic acid (52.6%), followed by sulfamethoxazole trimethoprime (26.3%). Multi drug resistant (MDR) was found in all MRSA isolates (100%; 26/26) and the most identified antimicrobial resistance

patterns was P, AMC, OX, CTX, TE, S, K. A total of 26 identified MRSA strains were divided into 22 ERIC-PCR groupings (A-V) that were categorized into two clusters, ERIC cluster I and ERIC cluster II. Among them, the most common ERIC type (11.5%) was ERIC A. The significance of multidrug resistance MRSA to public health needs continuous testing of antimicrobial medications against MRSA isolates. Also, ERIC PCR demonstrate promising typing that might be conveniently employed on a regular basis to study the genotypic alterations of MRSA, particularly in pets.

13: Detection of extended-spectrum β-lactamases producing *Escherichia coli* from beef in Mansoura, Egypt

Amera Elasyeh, Khaled salam

Abstract

Objective: The objective of the current study was to identify extended-spectrum β-lactamase-producing *Escherichia coli* (ESBLs) from beef meat in Mansoura City, Egypt.

Design: Randomly selected 150 buffalo meat samples were obtained from retail butcher shops located in Mansoura City, Egypt. Samples were inoculated into enriched broth media and then directly streaked on *E. coli* selective agar for selective isolation of *E. coli*. A biochemical examination was performed for the preliminary identification of *E. coli*. Suspected *E .coli* isolates were then confirmed by PCR targeting 16S rRNA. Confirmed *E. coli* isolates were tested for their susceptibility to antimicrobials by using Kirby–Bauer disc diffusion method. Additionally. *E. coli* were tested for the presence of β-lactamases (*bla*$_{CTX}$, and *bla*$_{SHV}$ and *bla*$_{TEM}$) using PCR.

Results: *E. coli* was isolated from 37 out of 150 tested samples with a total prevalence of 24.66 %. *E. coli* isolates revealed a high resistant against cefotaxime and ceftazidime, and moderate resistance against amoxyclavulanic acid, while a high sensitivity of *E. coli* was displayed against meropenem and imipenem. Moreover, the tested *E. coli* (n=37) harbored ESBLs genes with percentages of 40.5% for both *bla*$_{CTX,}$ and *bla*$_{SHV}$ and 35% for *bla*$_{TEM}$

Conclusion and clinical relevance: *E. coli* produces extended-spectrum β -lactams that were isolated from meat and contained a substantial level of antibiotic resistance genes. To increase food processing quality and provide safe food for consumers, it is crucial to build food traceability and monitoring systems for meat and meat products.

Keywords: *E. coli*, beef, ESBL, antimicrobials susceptibility

14: Detection virulence determinants and antimicrobial susceptibility of *Vibrio species* isolated from raw fish markets

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Abstract

Vibriosis is a major cause of death in farmed aquaculture systems around the world caused by an infection with *Vibrio spp*. This study was performed to detect the prevalence of pathogenic *Vibrio species* from various fish species (n=200) collected from Port-Said fish markets as well as to assess the antimicrobial resistance profile and virulence determinants of the isolated *Vibrio*. Fish samples were inoculated onto *Vibrio*-selective medium (TCBS), and phenotypically identified using biochemical tests and the suspected isolates were then confirmed by PCR targeting collagenase gene followed by sequencing of the amplified gene. Disc diffusion method was used to investigate the antimicrobial susceptibility of the isolated strains as well as the virulence determinants were detected by PCR assay. Out of 200 fish samples, 80 *Vibrio* isolates including *V. parahaemolyticus* (22 /80) and *V. alginolyticus* (58 /80) were recovered. While, *V. vulnificus* couldn't be identified. *Vibrio* isolates displayed high resistance to beta-lactams antimicrobials and a lower resistance were displayed against tetracycline, quinolones and carbapenems. Additionally, *tlh* gene was present in all *V. parahaemolyticus* isolates, while the *tdh* gene was present in 27.1% (6/22). In conclusion, the results of this study provide information on the hazards that certain fish and shellfish could bring by transferring virulent and genetic resistance of *V. parahaemolyticus* and *V. alginolyticus* to people through seafood., therefore, consumers should be more alert, prepare seafood properly, and avoid undercooked or cross-contaminated fish.
Key words: *V. parahaemolyticus***,** *V. alginolyticus*, seafood**,** virulence determinants, antimicrobial susceptibility.

15: Assessing the biosecurity measures in broiler farms in Dakaliya Governorate – Egypt in relation to the seasonal prevalence of Salmonellosis and Colibacillosis

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Abstract

Background and Aim: The implementation of biosecurity practices in broiler farms is a must for its success. This study was carried out to score the biosecurity measures in three broiler farms in the Dakahliya – Egypt in relation to the seasonal prevalence of colibacillosis and salmonellosis.

Materials and Methods: A cross-sectional study was conducted on randomly selected three broiler farms of different housing systems from (July 2022- June 2023). A total of 540 litter samples were collected during four successive seasons.

Results: The computed average score for the three broiler farms; A, B, & C was 14, 15 and 26, respectively, out of 39 estimated items. The findings showed that farm C had better levels of commitment and discipline to biosecurity measures than the other two broiler farms. Highly significant increases of *E. coli* ($p<0.0001$**)** in summer compared to other seasons in the broiler farms with the lowest prevalence rate in farm C with the highest biosecurity score. The same pattern was found for *Salmonella* prevalence of ($p<0.0001$) in broiler farms during summer months.

Conclusion: Insufficient biosecurity measures in broiler houses were not enough to prevent the entrance and multiplication of *E. coli* & *Salmonella spp.* Disciplines, commitment, and regulations of biosecurity need to be enforced in broiler houses to prevent the introduction and spread of diseases.

Keywords: biosecurity score, broiler farms, *Salmonella*, *E. coli*, seasonal prevalence