#	Research Title	Field	Abstract	Year of Publication Publishing	Publishing Link "URL"
1	Genotypic And Phenotypic Characterization Of Extended-Spectrum B-Lactamase-ProducingKlebsiella Pneumoniae From Clinical Samples in Egypt	Antibiotic Resistance	*Extended-Spectrum β-lactamase Enzymes producing bacteria presents a serious antibiotic management problem. Extended-Spectrum β-lactamase Enzymes producing bacteria can hydrolyze extended-spectrum penicillins, cephalosporins, and aztreonam. They are generally abundant in members of the family Enterobacteriacea such as Klebsiella pneumoniae. This study was conducted to detect ESBL-producion among Klebsiella pneumoniae isolates from Egyptian patients and to determine the prevalence of the β-lactamase resistance genes together with the prevalence of both class 1 and class 2 integrons by molecular and phenotypic methods. One hundred clinical Klebsiella pneumoniae isolates were collected. They were phenotypically characterized by double disk diffusion test (DDDT). Polymerase chain reaction (PCR) analysis was futher carried out to detect the β-lactamase*	2019	N. Egypt. J. Microbiol. Vol. 53, May, 2019

			resistance genes. Phenotypic characterization results indicated that 24 % of the K. pneumoniae isolates were found to be phenotypically positive. Among these 15 of the phenotypically positive isolates were carriers for at least one of the ESBL production genes. The bla SHV gene was the most prevalant (62.5%), followed by blaCTX-M gene (45.83%), and the blaTEM (25%). The int1 gene was highly prevalent among all isolates tested (90%), while only one isolate harbored the int2 gene (1%).The results of the current study indicates the high prevalance of ESBLs as well as integrons. Based on the wide spread distribution of ESBL-producing K. pneumoniae isolates, this study focused mainly on the patterns of antibiotic resistance ESBL producing K. pneumoniae isolates and the prevalence of ESBL resistance genes. Accordingly, clinical laboratories should employ simple rapid tests for identification and confirmation of ESBL production so that beta-lactam antibiotics and beta-lactamase inhibitors should be prescribed only		

			based on antibacterial susceptibility test.		
2	Multidrug Resistance in Integron Bearing Klebsiella pneumoniae isolated from Alexandria University Hospitals, Egypt	Antibiotic Resistance	*Klebsiella pneumoniae* is by far one of the most common Enterobacteriaceae associated with hospital-acquired infections. The dissemination of multi drug resistant *Klebsiella pneumoniae* is causing difficulty to treat infections worldwide. Of additional concern, multi drug resistant *Klebsiella pneumoniae* acquires and transfers antibiotic resistance genes among other bacterial isolates. Integrons have the main role in the acquisition as well as dissemination of resistance genes. Accordingly we aimed to investigate the frequency of resistance genes *sul1*, *sul2*, *tetA*, *tetB* and *aac (3) IIa*, class one (*int1* gene) and class two integrons(*int2* gene) in *Klebsiella pneumoniae* clinical isolates from four major hospitals in Alexandria, Egypt using Polymerase Chain Reaction. In addition we aimed to evaluate the association between multidrug resistance and presence of integrons in hospital-acquired *Klebsiella pneumoniae* in our …	2020	https://doi.org/10.1007/s00284-020-02217-7

3	Comparative Study of ESBL Production Among Uropathogenic Escherichia coli Clinical Isolates from Pre- and Post-menopausal Women in Egypt. Current Microbiology.	Antibiotic Resistance	Urinary tract infection (UTI) is regarded one of the most frequent bacterial infections in women. Accordingly, the aim of the current study was to determine the prevalence of extended-spectrum beta-lactamase (ESBL), as well as the degree of antimicrobial resistance among premenopausal (n=44) and postmenopausal (n=49) women sufering from uncomplicated UTI. Urinary samples (n=93) collected from women with UTI were tested for their antimicrobial sensitivity and assessed for ESBL production by both phenotypic and genotypic methods. Phenotypically, the presence of ESBL was observed in 64 isolates, while polymerase chain reaction detected ESBL-encoding genes in 57 isolates. The CTX-M gene was the most predominant (51.6%), followed by TEM (46.2%), and the SHV gene (17.2%). Surprisingly, all ESBL-producing Escherichia coli isolates were multidrug-resistant (MDR). To the best of our knowledge, this is the frst study conducted in Egypt showing signifcant correlation between ESBL production, multidrug resistance and	2021	https://doi.org/10.1007/s00284-021-02599-2

			menopausal state in women. The results demonstrate alarming signal for the dissemination of ESBL genes among uropathogenic E. coli that are MDR in Egypt		
4	Septic Arthritis: Microbiological Etiology and Molecular Detection of the Most Resistant Etiological Agents	Antibiotic Resistance Antibiotic Resistance			
5	Diabetic Foot Ulcer Infections and Pseudomonas aeruginosa Biofilm Production During the COVID-19 Pandemic	Antibiotic Resistance	During the different waves of the coronavirus (COVID-19) pandemic, there has been an increased incidence of diabetes mellitus and diabetic foot infections. Among gram-negative bacteria, Pseudomonas aeruginosa is the predominant causative agent for diabetic foot ulcer infections in lowresource countries. P. aeruginosa possesses a variety of virulence factors, including biofilm formation. Biofilm formation is an important benchmark characteristic in the pathophysiology of diabetic foot ulceration. The main objective of the current study was to identify the most commonly isolated organisms and their antibiotic susceptibility patterns in diabetic foot patients during the	2021	DOI:10.22207/JPAM.16.1.02

			COVID-19 pandemic. We also determined the genes associated with bacterial persistence and biofilm formation in the predominantly isolated organism. Accordingly, 100 wound swab samples were collected from diabetic foot patients from different hospitals in Alexandria, Egypt. Through phenotypic detection of biofilm formation, 93% (40) of the 43 P. aeruginosa isolates examined were categorized as biofilm producers. Molecular detection of the biofilm-encoding genes among the 43 P. aeruginosa isolates was as follows: algD (100%), pelF (88%) and pslD (49.7%), and this highlights a need for biofilm formation inhibitors to prevent the persistence of bacterial pathogens, and thus achieve better clinical outcomes in diabetic foot ulcer infections.		
6	Emergence of Stenotrophomonas maltophilia co-harboring tetM and smqnr and over-expressing different efflux pumps among clinical isolates from tertiary care hospitals in Alexandria, Egypt	Antibiotic Resistance	Stenotrophomonas maltophilia (S. maltophilia), is a remarkable nosocomial pathogen, packed with different intrinsic mechanisms of resistance to most antimicrobials. Trimethoprim/Sulfamethoxazole (SXT) is the treatment of choice for S. maltophilia infections. However,	2022	DOI: 10.21608/MID.2022.117532.1237

			different acquired factors may render SXT ineffective. Our aim was to investigate the susceptibility pattern to levofloxacin (LEV) and minocycline (MIN) among SXT non-susceptible isolates, as well as the different expression levels of different efflux pumps. Methods Susceptibility pattern to LEV and MIN was investigated as well as the expression level of different efflux pumps SmeABC, SmeDEF and SmrA and the presence of smqnr and tetM. Results Among the 19 SXT non-susceptible isolates, 57.89% were susceptible to LEV and 10.52% were susceptible to MIN. It was found that 68.42%, 15.78% and 36.84% of the isolates showed over-expressed SmeABC, SmeDEF and SmrA, respectively. The results showed no significant correlation between over-expression of efflux pumps and resistance to LEV and MIN. Moreover, smqnr was detected in 4 out of 8 LEV non-susceptible isolates, while tetM was present in 11 out of 17 MIN non-susceptible isolates.		

			Conclusion As far as previously reported, this is the first study dedicated to SXT non-susceptible S. maltophilia isolates, that reported the presence of tetM and smqnr and the over-expression of SmeABC, SmeDEF, and SmrA among clinical isolates in Alexandria, Egypt. The findings emphasize that LEV can be used as a suitable option in managing S. maltophilia infections.		
7	A Novel parC Mutation Potentiating Fluoroquinolone Resistance In Klebsiella Pneumoniae And Escherichia Coli Clinical Isolates	Antibiotic Resistance	Introduction: Resistance to fluoroquinolones is mainly due to point mutations that gave rise to amino acid substitutions in the quinolone resistance-determining regions of either gyrA or parC genes, which may be augmented by plasmid mediated resistance. Accordingly, the main aim of the study was to investigate the mutations in gyrA and parC genes as well as the qnrA and qnrB genes acquisition. Methodology: 193 Klebsiella pneumoniae and Escherichia coli isolates were collected, identified and MICs for ciprofloxacin, levofloxacin and moxifloxacin were determined. Polymerase Chain Reaction to	2022	doi:10.3855/jidc.15142

			investigate qnrA, qnrB, gyrA and parC genes followed by DNA sequencing analysis to identify mutations in gyrA and parC genes. Results: The most prominent mutation in gyrA gene was ser83leu, followed by asp87asn, and lys154arg. Regarding parC mutations, ser80ile was the most detected. Other mutations val141ala and glu84ala were also noted. In addition to a substitution mutation at codon 157 of leucine to tyrosin. To the best of our knowledge this mutation was not previously reported. qnrB was the most detected gene, as 64.7% Klebsiella pneumoniae and 57.1% Escherichia coli were positive. qnrA gene was detected in 11% Klebsiella pneumoniae and 4% of Escherichia coli isolates tested. Conclusions: This study suggests that the indiscriminate use of fluoroquinolones resulted in the increase of development of resistance either through mutations in the quinolone resistance-determining regions of either gyrA or parC genes augmented by plasmid mediated resistance. The irrational use of new fluoroquinolones such as		

			moxifloxacin has created selective pressure for the appearance of new mutation.		
8	*Stenotrophomonas maltophilia*: Genotypic Characterization of Virulence Genes and The Effect of Ascorbic Acid on Biofilm Formation	Antibiotic Resistance	*Stenotrophomonas maltophilia* is an environmental bacterium that has gained a lot of attention, as a nosocomial pathogen associated with significant mortality rates. Biofilm formation is considered the corner stone for establishing infections in many bacteria including *S. maltophilia.* The aim of this study was the genotypic characterization of the different virulence-associated genes and the investigation of the effect of ascorbic acid on *S. maltophilia* biofilm formation. A total of 20 *S. maltophilia* isolates from different sources were included in this study. Genes encoding different virulence factors were investigated genotypically. These included *stmPr1*, *stmPr2*, s*mlt3773 locus*, *smf-1*, *rpfF*, *rmlA* and *spgM*. Biofilm formation was investigated phenotypically. The effect of ascorbic acid on biofilm formation was investigated using MIC as well as sub-inhibitory concentrations. Many of the isolates harbored both serine proteases	05 May 2022	https://doi.org/10.1007/s00284-022-02869-7

			genes *stmPr-1* and *stmPr-2*. Fourteen (70%) of the 20 isolates carried *stmPr-1* and 15 (75%) had *stmPr-2*. Most of the isolates (95%) possessed *smlt-3773 locus*. Genes linked to biofilm formation such as *smf-1*, *rpfF*, *rmlA* and *spgM*, were found in (90%), (45%), (85%) and (30%) of the isolates, respectively. Phenotypically, all *S. maltophilia* isolates (100%) were biofilm producers. Fifteen (75%) were strong biofilm producers and 5 (25%) were moderate biofilm producers. In attempts to seek a non-chemotherapeutic alternative that can hinder biofilm formation without provoking antimicrobial resistance, the results, herein, showed that ascorbic acid inhibits biofilm formation in a dose-dependent manner.		
9	Antibacterial and antibiofilm activities of diclofenac against levofloxacin-resistant *Stenotrophomonas maltophilia* isolates; emphasizing repurposing of diclofenac.	Antibiotic Resistance	Background and Objectives: *Stenotrophomonas maltophilia* is an opportunistic pathogen causing nosocomial infections. Diclofenac is an anti-inflammatory drug that is considered a non-antibiotic drug. This study assessed the antibacterial and antibiofilm effects of diclofenac and	2024	doi: 10.18502/ijm.v16i2.15349

			levofloxacin/diclofenac combination against levofloxacin resistant isolates. Materials and Methods: Minimum inhibitory concentration was determined using broth microdilution method for levofloxacin, diclofenac, and levofloxacin/diclofenac combination. Biofilm forming capacity and biofilm inhibition assay were determined. Relative gene expression was measured for efflux pump genes; *smeB*, and *smeF* genes and biofilm related genes *rmlA*, *spgM*, and *rpfF* without and with diclofenac and the combination. Results: Diclofenac demonstrated MIC of 1 mg/ml. The combination-with ½ MIC diclofenac-showed synergism where levofloxacin MIC undergone 16–32 fold decrease. All the isolates that overexpressed *smeB* and *smeF* showed a significant decrease in gene expression in presence of diclofenac or the combination. The mean percentage inhibition of biofilm formation with diclofenac and the combination was 40.59% and 46.49%, respectively. This agreed with biofilm		

			related genes expression investigations. Conclusion: Diclofenac showed an antibacterial effect against *Stenotrophomonas maltophilia*. The combination showed *in-vitro* synergism, significant reduction in biofilm formation and in the relative level of gene expression. Furthermore, it can potentiate the levofloxacin activity or revert its resistance.		
10	Preparation and evaluation of vaginal suppo-sponges loaded with benzydamine, *in-vitro/in-vivo study*		his study aimed to design a new Benzydamine HCl (BNZ) suppo-sponge for controlled, mucoadhesive dosage form for vaginal candidiasis treatment, offering advantages over traditional creams, ointments, or gels. BNZ-loaded suppo-sponges were fabricated by simple casting / freeze-drying technique utilizing the cross-linking of chitosan (Cs) with vanillin (V). Vaginal suppo-sponges were prepared based on different vanillin cross-linking ratios $(V)_n$), from 0 to 2%w/w. To best of our knowledge, this is the first study that uses Schiff's base between chitosan and vanillin as a drug delivery system to treat fungal	2024	https://doi.org/10.1080/10837450.2024.2306803

			vaginal infections. Schiff's base formation was confirmed by FT-IR. *In-vitro* appraisal showed acceptable physical and mechanical characteristics. Formulations based on cross-linking of Cs with V showed a more pronounced *in-vitro* antifungal activity. *In-vitro* drug release revealed a prolonged release pattern		
11	Phenotypic and genotypic evaluation of Gatifloxacin resistance in staphylococcus aureus and pseudomonas aeruginosa clinical isolates in Egypt	Antibiotic Resistance	Introduction: *Pseudomonas aeruginosa and Staphylococcus aureus* continue to be predominant causes of infection with high resistance to antibiotics resulting in treatment failure. Prevalence of highly resistant strains is potentiated by excessive use of broad-spectrum antibiotics. Gatifloxacin (GAT) is a broad-spectrum 8-methoxy fluoroquinolones, active against Gram-positive and Gram-negative bacteria. This study aimed to determine the prevalence of GAT resistance among *S. aureus* and *P. aeruginosa* isolates collected in Alexandria, Egypt, and to study the phenotypic and genetic elements related to drug resistance with some attempts to reduce this resistance. Methodology: One hundred and eight clinical isolates from different clinical	2015	

			specimens were identification by appropriate biochemical tests and their antibiotic susceptibility pattern was determined. The mutations in the quinolone resistance determining region (QRDR) of *gyrA*, *grlA*, and *par C* genes were investigated as well as the possible involvement of efflux pumps in mediating fluoroquinolones resistance. Moreover, the post antibiotic effect (PAE) and combinations with other compounds were tested in an attempt to reduce the resistance and dosing regimens of GAT. Results: Resistance to GAT among *P. aeruginosa* and *S. aureus* isolates tested were found to be 59.2% and 42.5 %, respectively. The PAE of the *P. aeruginosa* isolates reached 2 h while that for *S. aureus* isolates was 1.6 hr. GAT showed synergistic effect when combined with ciprofloxacin and cefoperazone. Upon sequencing the QRDR of *gyrA*, *grlA* and *parC* genes some point mutations, in addition to silent mutations were detected. Conclusions: GAT has bactericidal activity against *S. aureus* and *P. aeruginosa*. Mutations could be rapidly		

			and reliably detected by DNA sequencing. Resistance to GAT in several bacterial species is due to point mutations in the QRDR of the target enzymes rather than other resistance mechanisms. GAT, like other quinolones, was synergistic with ciprofloxacin and cefoperazone. This synergism was observed against some strains that were non-susceptible to GAT alone.		
12	A Molecular study of Sulphonamides Resistance Among Escherichia coli isolated from urine.	Antibiotic Resistance	The aim of this study was to describe the distribution of the sulfamethoxazole resistance genes and their association with class 1 integrons in uropathogenic *Escherischia coli* isolates. This study included 50 sulphonamide resistant *E. coli isolates* that were collected from 74 clinical specimens.Resistance to sulfamethoxazole was assessed by the disk diffusion method and broth dilution method . Polymerase chain reaction (PCR) with primers specific for *sul1*, *sul2*, *sul3* and *int1* was used to detect the three known sulphonamide resistance genes. The *sul1* gene was found in 15 (30%) isolates, *sul* 2 gene in 16 (32%) isolates, and both genes in	2011	

			8 (16 %) isolates. The *sul3* gene was found in 1 (2%) isolate. The *int1* gene was found in 2 out of 15 (13.3%) of the *sul1* positive isolates.		