



Publications Template

#	Research Title	Field	Abstract	Year of Publication Publishing	Publishing Link "URL"
1	<p>▪ Gaballah, A., Ghazal, A., Metwally, D., Emad, R., Essam, G., Attia, N. M., & Amer, A. N. (2022). Mutation patterns, cross resistance and virological failure among HIV type-1 patients in Alexandria, Egypt. Future Virology, (0).</p>	Virology	<p>Aim: The main purpose of this cross-sectional study was to detect the prevalence of drug resistance mutations related to nonnucleoside/nucleoside reverse transcriptase inhibitors (NNRTIs/NRTIs) and protease inhibitors (PIs). Patients & methods: Patients (n = 45) with HIV type-1 were recruited, 30 of whom were treatment naive and 15 treatment experienced. A partial <i>pol</i> gene covering the protease/reverse transcriptase (PRRT) region was amplified and then sequenced by the Sanger method. Results & conclusion: The most common NNRTI/NRTI-related mutations were 'V179I (24%) and K103N (14.3%)' and 'M41L and V75M' (14.3% each). M36I and H69K were</p>	2021	<p>▪ https://doi.org/10.2217/fvl-2021-0279</p>



			the most prevalent PI-related mutations (86% each). The results of the current study serve as an initial crucial step in defining the overall prevalence of HIV type-1 drug resistance in Egypt.		
2	<ul style="list-style-type: none"> Shawaky, S. M., Al Shammari, M. M. A., Sewelliam, M. S., Ghazal, A. A. E. R., & Amer, A. N. (2022). A study on vaginitis among pregnant and non-pregnant females in Alexandria, Egypt: An unexpected high rate of mixed vaginal infection. <i>AIMS Microbiology</i>, 8(2), 167-177. 	Bacteriology	<p>Background: Many infectious and noninfectious triggers lead to inflammation of the vagina.</p> <p>Aim: We investigated the prevalence of causative vaginitis microorganisms in 516 pregnant and nonpregnant female volunteers. Vaginal samples were examined microscopically, cultured and tested for different pathogens.</p> <p>Results: Of the participants, 310 (60.1%) were pregnant, whereas 206 (39.9%) were nonpregnant. Using Amsel's criteria and Nugent's scores, bacterial vaginosis (BV) was diagnosed in 59.1%, and the prevalence of vulvovaginal candidiasis (VVC) was 50.2% in the population. <i>Candida</i> infections were significantly higher in nonpregnant females</p>	2022	10.3934/microbiol.2022014



			<p>(p value \leq 0.01), and 24% of females had mixed infections. The most common mixed infection was BV and <i>Candida</i> spp., detected in 21% of the cases.</p> <p>Conclusions: Bacterial vaginosis is the most common cause of vaginitis. We observed that 24% of females experienced mixed infections, and <i>Candida albicans</i> was the most common fungal species causing VVC. <i>Trichomonas vaginalis</i> prevalence was underestimated using wet mounts.</p>		
3	<p>▪ Gaballah, Ahmed Hassan, Sherine Shawky, and Ahmed Noby Amer.</p> <p>"Microbiological profiles of neonatal sepsis in northern Egypt." <i>Microbes</i></p>	Bacteriology	<p>Background: This study aimed at analyzing the microbiological profile of neonatal sepsis in Egypt and to determine the antibiotic susceptibility patterns of the isolated microorganisms.</p> <p>Methods: Two thousand and four hundred blood samples were collected from neonates showing symptoms suggestive of septicemia, inoculated into</p>	2022	10.21608/mid.2022.129600.1265



<p><i>and Infectious Diseases (2022).</i></p>		<p>BACT/ALERT culture bottles. Positive blood culture samples were identified and tested for antimicrobial susceptibility. Results: Among the neonates included in our study, 457 (19%) neonates were positively diagnosed with sepsis. early onset neonatal sepsis (EOS) was detected in 181 (39.6%), while late-onset neonatal sepsis (LOS) in 276 (60.4%) cases. <i>Klebsiella pneumoniae</i> was the most commonly isolated microorganism. <i>Staphylococcus aureus</i> and <i>Enterococcus</i> spp. were the most common isolated Gram-positive bacteria. <i>Candida</i> spp. was more encountered in LOS. An alarming feature of the present study is the high incidence of multidrug resistant microorganisms (65%). Among Gram negative isolates (56%) of were extended spectrum beta-lactamase (ESBL) producers and (70.5%) were carbapenem resistant. In Gram positive bacteria, resistance to</p>		
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			<p>methicillin in <i>S. aureus</i> and coagulase negative <i>staphylococci</i> were detected in (50%) and (41%) of isolates respectively. Additionally, 17% of <i>Enterococcus</i> isolates were vancomycin resistant.</p> <p>Cocclusion: Our bacteriological profile of neonatal sepsis showed that Gram negative bacteria represented the majority of isolates. <i>Klebsiella pneumoniae</i> was the predominant isolate. In our study, both EOS & LOS share a nosocomial infection profile, as high antimicrobial resistance was observed among our isolates. The susceptibility profiles of the isolates may urge for the change of the current used empirical therapies.</p>		
4	<p>▪ N. A., Kandil, N. H., & Amer, A. N. (2022). Status of Antimicrobial Stewardship</p>	Bacteriology	<p>Background: Antimicrobial stewardship aims to stop or slow the emergence of antimicrobial-resistant strains. Following the launch of Egypt's National Action Plan</p>	2022	10.21608/ejmm.2022.228828



Implementation in Selected Egyptian Hospitals: A Cross-sectional Study. *Egyptian Journal of Medical Microbiology*, 31(2), 77-83.

on Antimicrobial Resistance, numerous hospitals took steps to adopt ASP, but no formal assessments were conducted. Objectives: The goal of this study is to determine the extent to which ASP is used, as well as stewardship understanding and implementation, in several Egyptian hospitals. Methodology: A cross-sectional study was carried out to measure stewardship knowledge and execution, from June to July 2020, in various Egyptian hospitals. The hospital description, ASP committee, ASP activities, reporting antibiotic use, antibiogram, information technology support, ASP restriction techniques, and future ASP application were all covered in the survey. Results: The study covered a variety of hospitals, the majority of which (61.8%) adopted an ASP program while others (38.2%) did not;



at the time of the study, 71.4 % of the latter were planning to implement an ASP program in the future. Twenty-two institutions (48.5 %) said they routinely use facility-specific antibiograms. Antimicrobial reports were received on a regular basis by thirteen hospitals (37.1%). Fifteen hospitals (42.9%) said they were already using one or more computer applications. Resistance trends, infection rates, duration of stay, mortality rate, and reported adverse drug reactions were all monitored at the hospitals. Only 20% of the hospitals in this study had an ASP training program. Conclusion: Egyptian hospitals have a good ASP implementation; however, IT support programs, cooperation between healthcare members, monitoring outcomes, and infectious disease consultations are still needed.



5	<ul style="list-style-type: none"> AMER, Ahmed Noby, et al. Molecular Epidemiology of HIV-1 virus in Egypt: A major change in the circulating subtypes. Current HIV Research, 2021. 	Virology	<p>Background: Human immunodeficiency virus type 1 (HIV-1) is characterized by high genetic diversity due to its high mutation and recombination rates. Although, there is an increasing prevalence of Circulating Recombinant Forms (CRFs) worldwide, subtype B is still recognized as the predominant subtype in the Middle East and North Africa (MENA) region. There is a limited sampling of HIV in this region due to its low prevalence. The main purpose of this study is to provide a summary of the current status of the resident HIV subtypes and their distribution among Egyptian patients.</p> <p>Methodology: Forty-five HIV-1 patients were included in this study. Partial pol gene covering the protease (PR) and Reverse Transcriptase (RT) was successfully amplified in 21 HIV patients</p>	2021	10.2174/1570162X19666210805091742
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using nested PCR of cDNA of the viral genomic RNA, then sequenced. The sequence data were used for viral HIV-1 subtyping by 5 online subtyping tools: NCBI viral genotyping tool, Stanford University HIV database (HIVDB) subtyping program, REGA tool, Context-Based Modeling for Expeditious Typing (COMET) tool, and Recombinant Identification Program (RIP) tool. The final subtype assignment was based on molecular phylogenetic analysis. **Results:** Unexpectedly, non-B subtypes are dominating, with the most common circulating one is CRF02_AG (57.1%) followed by subtype B (14.3%), subtype BG recombinant (9.5%), CRF35_AD (9.5%), subtype A1 and CRF06_cpx (4.8% each). **Conclusion:** To the best of our knowledge, this is the first study to tackle HIV-1 subtyping among the group



			of HIV-1 patients in Egypt. CRF02_AG is the most prevalent subtype in Egypt.		
6	<ul style="list-style-type: none"> Gaballah, A., Naga, I. S., Zaghloul, M. S., Mostafa, H. M., & Noby, A. (2021). Changes in the co-expressions of interleukin 29 (IL-29), IFN-inducible protein 10 (IP-10) and monokine induced by IFNγ (MIG) genes in chronic hepatitis C Egyptian patients untreated and treated with DAAs. <i>Acta virologica</i>, 65(2), 141-148. 	Virology	<p>Direct acting antiviral agents (DAAs) are a group of antiviral drugs that inhibit specific non-structural proteins of the virus and disrupt viral replication and infection. DAAs regimens for hepatitis C virus (HCV) infection provide a particular event to tackle mechanistic intracellular relationships between the innate immunity and HCV, potentially providing perceptions about the rate of the viral replication and complex decay. Interleukin 29 (IL-29) prevents the replication of HCV. IFN-inducible protein 10 (IP-10) plays a significant role in the pathogenesis of HCV infection. MIG/CXCL9 are produced by inflammatory and stromal cells such as hepatocytes following either stimulation</p>	2021	10.4149/av_2021_209



by interferon lambda (IFN γ) or viral infection. This study aimed to evaluate the co-expression of IL-29, IP-10 and MIG in peripheral blood mononuclear cells (PBMCs) from untreated and treated chronic HCV patients with DAAs. This study included group of twenty naïve HCV patients, group of twenty sustained viral response (SVR) patients and a control group that consisted of 10 healthy subjects. All subjects were tested for liver enzymes, serum albumin level, total serum bilirubin, platelet count, prothrombin activity and viral load. Relative gene expression of IL-29, IP-10, and MIG in PBMCs from all subjects was determined using real time PCR. The mean value of IL-29, IP-10 and MIG gene expression significantly increased in both naïve HCV and SVR groups of patients as compared to normal subjects.



The corresponding value was significantly lower in patients with SVR compared to naïve HCV patients. Infection with HCV significantly triggered the co-expression of IL-29, IP-10, and CXCL9 (MIG) genes in PBMCs of chronic hepatitis C patients and significantly down-regulated in those who achieved SVR after successful DAAs therapy. Keywords: IP10; MIG; IL29; HCV; DAAs; gene expression.