1- 
**Nosocomial Infections Caused by Klebsiellae species with Plasmids Carrying bla SHV-5 Extended-Spectrum ?-Lactamase gene in Mansoura University Hospitals**

SHV-5 is a variant of SHV-1 and it is considered now one of the most important ESBL enzymes produced by Klebsiellae species. In this study we aimed to detect the prevalence of plasmid encoded SHV-5 among Klebsiellae strains causing nosocomial infections in Mansoura University Hospitals (MUH). One hundred and seventy four Klebsiellae strains were isolated from overall 680 cases of nosocomial infections (25.59 %) acquired within MUH over 4 months period from July to November 2004. One hundred and thirty six isolates (78.16 %) of them were K. pneumoniae and 38 isolates (21.84 %) were K. oxytoca. MICs (?g/ml) of the isolated strains was done for augmentin, cefoperazone and ceftazidime using E test. One hundred and forty one (81.03 %) of them were ?-lactamase producer as detected by nitrocefin discs, where 77 isolates from ?-lactamase producing strains were ESBL producers constituting 44.25 % of Klebsiellae isolates. Sixty six ESBL producing strains of total 77 were isolated from cases of blood stream infections (85.71 %). Sixty five ESBL producing strains were isolated from neonatal intensive care unit (NICU) (84.42%). All ESBL producing strains (n=77) posses at least one large plasmid > 23 kbp. SHV-5 gene was amplified by PCR after plasmid isolation from ESBL producing Klebsiellae isolates, reveal that 68 isolates (88.31 %) were harbored SHV-5 gene on their large plasmids.

In conclusion we found that the SHV-5-producing K. pneumoniae isolates were recovered from different wards of Mansoura University Hospital during the studied period. Thus, it was hypothesized that one clone may have persisted in that hospital. We recommend that infection control measure of endemic ESBL producers should include : the consumption of the broad-spectrum cephalosporins needs to be restricted to reduce the selection pressure which enables the proliferation of ESBL producers in hospital, continuous application of infection control program as; surveillance, hand washing and contact isolation procedure

2- 
**Bacterial translocation in an experimental intestinal obstruction model. C-reactive protein reliability?1**

Background: Bacterial translocation occurs in preseptic conditions such as intestinal obstruction through unclear mechanism. The C-reactive protein is an acute phase reactant and a marker of ischaemia.

Material & Methods: 45 albino male rats were divided into 3 groups each 15 rats. GI control, GII simple intestinal-obstruction and GIII strangulated obstruction. Outcome measures were: (1) Bacteriologic count & typing for intestinal contents, intestinal wall, liver, mesenteric lymph nodes and blood (cardiac & portal) (2) Histopathologic: mucosal injury score, inflammatory cell infiltrate in the wall, MLN, liver, (3) Biochemical: serum CRP, IL-10, mucosal stress pattern (glutathione peroxidase-malonyldialdhyde tissue levels).

Results: (1) Intestinal obstruction associates with BT precursors (Bact-overgrowth, mucosal-acidosis, immuno-incomptence), (2) Bacterial translocation (frequency & density) was found higher in strangulated I.O, that was mainly enteric (aerobic & anaerobic) and mostly E.coli, (3) The pathogen commonality supports the gut origin
hypothesis but the systemic inflammatory response goes with the cytokine generating one. (4) The CRP median values for GI, II, III were 0.5, 6.9, 8.5 mg/L, for BT +ve 8 mg/L and 0.75 mg/L for BT -ve rats.

Conclusion: Bacterial translocation occurs bi-directional (systemic-portal) in intestinal obstruction and the resultant inflammatory response pathogenesis is mostly 3 hit model. The CRP is a non selective marker of suspected I.O cases. However, it is a reliable marker of BT, BT density and vascular compromise during I.O.

3-

**Human Papillomavirus Types 16, 18 DNA, Chlamydia Antigen and Tumour Necrosis Factor Alpha in Cervical Cancer in Women from Dakahlia, Egypt**

Infection with human papillomavirus (HPV) and Chlamydia trachomatis are associated with cervical intraepithelial neoplasia. The recognition of HPV infection as a factor that is necessary, but not sufficient, for the development of cervical cancer has resulted in the initiation of several longitudinal studies and randomized clinical trials designed to examine the predictive value of HPV DNA testing. Forty two women were enrolled in this study (patients group) together with 20 apparently normal women (control). For all patients and control groups, cervical swabs were taken, examined for HPV, HPV 16, HPV18 DNA by 2 sequential PCR reactions, Chlamydia antigen and TNF-? by ELISA. Among 42 cases diagnosed pathologically as cervical carcinoma, HPV DNA was detected in 37 cases (88.09%). HPV16 DNA was more common than HPV18 DNA as it was detected in 28 cases (66.7%) while HPV18 DNA was detected in 4 cases (9.5%). There is a statistically significant difference between HPV and control cases, also HPV16 and control cases. Regarding Chlamydia antigen, 10 cases were detected out of 42 cases (23.8%) while, only 3 cases were detected in control group (15%) indicating that there is non statistically significant difference between the two groups. Regarding the pathological types of cervical carcinoma, in adenocarcinoma, HPV DNA was detected in 4 cases (80%), while in Squamous cell carcinoma (SCC), it was detected in 33 cases (89.19%). In adenocarcinoma, HPV 16 DNA was detected in 2 cases (40%), while in SCC, it was detected in 26 cases (70.27%). In adenocarcinoma, HPV 18 DNA was detected in 1 case (20%), while in SCC, it was detected in 3 cases (8.11%). Regarding Chlamydia antigen, in adenocarcinoma, the antigen was detected in 1 case (20%) and in SCC, it was detected in 9 cases (24.32%). Our results emphasized that HPV 16 was more predominant in squamous cell carcinoma, whereas type 18 was relatively high in adenocarcinoma. The level of TNF-? (pg/ml) was 33.81 ± 9.38 in cancer cervix cases, which was statistically significant compared to control cases [1.33 ± 0.74 (P=0.001)]. There is none statistically significant difference between adenocarcinoma (34.12 ± 12.31) and SCC [33.76 ± 9.13 (P=0.970)]. There was no significant difference regarding TNF-? level between HPV positive cases (34.23 ± 9.39) and HPV negative [30.66 ± 9.68 (P = 0.342)]. There was a significant difference between HPV16 (32.88 ± 8.44) and HPV18 (41.98 ± 4.32). Also, there was no significant difference between Chlamydia positive cases (36.62 ± 8.79) and Chlamydia negative cases [32.93 ± 9.52 (P=0.260)]. We conclude that cervical infection with HPV but not with Chlamydia may be an important risk factor for the development of cervical cancer and TNF-? levels increased significantly in cervical carcinoma without special reference to the pathological type of the tumor.
The First Two Vancomycin Resistant Staphylococcus aureus isolates in Mansoura University Hospital; Epidemiology and Antimicrobial Study

Staphylococcus aureus, a major cause of potentially life threatening infections acquired in health care and community settings, has developed resistance to most classes of antimicrobial agents with dramatic increase in the number of health care associated infections due to methicillin resistant S. aureus (MRSA). During the period of our study 974 S. aureus strains were isolated from different types of infections in different wards of Mansoura University Hospitals (MUH), 530 (54.4%) isolates were methicillin sensitive S. aureus (MSSA) and 444 (45.6%) isolates were MRSA. Simplified population analysis of MRSA strains revealed, 27 (6.08%) heterogeneous vancomycin intermediate sensitive S. aureus (hVISA), 12 (2.70%) vancomycin intermediate sensitive S. aureus (VISA), while 2 (0.45%) isolates were vancomycin resistant S. aureus (VRSA). hVISA strains were isolated from different infections, mainly from blood stream infections (29.63%) and infected skin ulcers and bedsores (29.63%), where the 12 VISA strains were isolated from infected skin ulcers and bedsores (41.66%), infected surgical wounds (41.66%) and lower respiratory tract infections (16.67). The 2 VRSA isolates were isolated from blood stream infection (one case) and an infected bedsore (the other case). One of the 2 VRSA cases was isolated from children hospital and the other one was isolated from medical wards. Minimal inhibitory concentration (MIC) of different antimicrobial agents for S. aureus with diminished sensitivity to vancomycin was done by microdilution method revealing a significant difference in resistance among VISA, hVISA and VRSA with vancomycin, linzolide, meropenem. Time kill study of different antibiotics for VRSA isolates showed that, vancomycin exhibited no kill activity at 1X MIC, but killing activity was achieved only at 2X and 4X. Other tested antibiotics were significantly had killing activity more than vancomycin at concentration of 1X MIC. Daptomycin, quinupristin/dalfopristin, tigecyclin, meropenem, ciprofloxacin, and erythromycin were significantly had killing activity more than linezolide at concentration of 1X MIC. In conclusion, the first two identified VRSA isolates from children hospital and medical wards still susceptible to some antibiotics which are not used widely such as, daptomycin, quinupristin/dalfopristin and tigecyclin, also hVISA and VISA had antimicrobial susceptibility pattern similar to VRSA isolates.

Bacterial DNA and its consequences in patients with cirrhosis and culture-negative, non-neutrocytic ascites

The detection of bacterial DNA in serum and ascitic fluid (AF) from patients with liver cirrhosis and ascites is interpreted as molecular evidence of intestinal bacterial translocation (BT) and considered sufficient to activate the cellular immune response leading to greater cytokine synthesis. We studied 34 patients with liver cirrhosis and culture-negative, non-neutrocytic ascites [22 patients without bacterial DNA (group I) and 12 patients with bacterial DNA (group II)]. History and clinical examination were done with the following investigations at first admission and followed up for 24 weeks: serum and AF tumour necrosis factor-alpha (TNF-alpha), AF polymorphonuclear leukocytes, AF cultivation and detection of blood and AF bacterial DNA. Serum and AF TNF-alpha were significantly higher in patients with bacterial DNA compared to those
without bacterial DNA at first admission [54.5+/−22.56 vs 35.2+/−17.97 pg ml(−1) (P=0.02) and 123.2+/−49.32 vs 82.6+/−29.58 pg ml(−1) (P <0.005), respectively]. These changes became highly significant at the end of follow-up of both groups [119.3+/−27.19 vs 40.2+/−16.08 pg ml(−1) (P <0.001) and 518.8+/−91.11 vs 97.6+/−17.81 pg ml(−1) (P <0.001), respectively]. In group II, there was a significant increase in serum and AFTNF-alpha at the end of follow-up compared to at first admission (P <0.001). The relative risk of death, hepatorenal syndrome (HRS) and spontaneous bacterial peritonitis (SBP) was higher in patients with bacterial DNA compared to those without bacterial DNA. We conclude that cirrhotic patients with culture-negative, non-neutrocytic ascites and bacterial DNA have a significantly higher level of serum and AF TNF-alpha and higher risk of HRS, SBP and mortality compared to those without bacterial DNA, suggesting that bacterial DNA and TNF-alpha are implicated in these complications of liver cirrhosis.

6-
**Effect of allergen-specific immunotherapy on interleukin-4, interleukin-5 and interferon-gamma mRNA expression in the nasal mucosa of rats with allergic rhinitis.**

To elucidate the mechanism of immunotherapy, we tested the effect of ovalbumin and ovalbumin-pullulan conjugate immunotherapy on the expression of interleukin (IL)-4, IL-5 and interferon-gamma (IFN-gamma) mRNA in the nasal mucosa of sensitized rats. Forty-five rats were injected with ovalbumin intraperitoneally on three consecutive days and later were exposed to ovalbumin aerosol. The rats were injected intradermally, on six consecutive days, with saline, ovalbumin or ovalbumin-pullulan conjugate. Later, nasal mucosa was obtained and reverse transcription-polymerase chain reaction (RT-PCR) was performed. Nasal responses and specific immunoglobulin E (IgE) were measured. Although the immunotherapy significantly decreased nasal airway resistance, dye leakage and histamine content in nasal irrigation after allergen challenge, no significant difference was found in IL-4 and IL-5 mRNA expression or in specific IgE level among the three groups. We conclude that in this allergic model, the improvement of nasal responses after immunotherapy was the result of a mechanism other than decrease of T-helper 2 (Th2) cytokines.

7-
**Expression of interferon-gamma, interleukin-4 and interleukin-5 mRNA in the nasal mucosal membrane of rats with allergic rhinitis.**

The production of immunoglobulin E (IgE) antibody is largely dependent on the ratio between interleukin-4 (IL-4) (a T helper 2 (Th2)-type cytokine) and interferon-gamma (IFN-gamma) (a T helper 1 (Th1)-type cytokine). Interleukin-5 (IL-5) (also a Th2-type cytokine) is an important eosinophil differentiation factor and also co-stimulates B-cell growth and differentiation. The present study was designed to evaluate and compare the expression of IFN-gamma, IL-4 and IL-5 mRNA in the nasal mucosal membrane of sensitized Brown-Norway (BN) rats. Fourteen BN rats were divided into two groups: non-sensitized (control) and sensitized. The sensitized group was injected with ovalbumin (OA) intraperitoneally on three consecutive days. Twenty-one days later, rats were exposed to 1% OA aerosol. Twenty-four hours after exposure to aerosol, nasal mucosa was extracted from both groups and reverse transcriptase-polymerase chain
reaction (RT-PCR) was performed. The densities of the bands of IL-4, IL-5 and IFN-gamma mRNA were expressed as percentages against beta-actin mRNA. Our results showed that the mean values for IL-4 and IL-5 mRNA were increased significantly in sensitized rats compared with control rats. In contrast, the mean value for IFN-gamma mRNA was significantly lower in sensitized rats compared with those of the control group. Our data therefore suggest that sensitization of rat nasal mucous membranes results in the predominant expression of Th2-type cytokines.

8-

**Allergic fungal rhinosinusitis: detection of fungal DNA in sinus aspirate using polymerase chain reaction**

Abstract

Objective: This study investigated allergic fungal rhinosinusitis cases, and aimed to compare the detection of fungi in sinus aspirate by culture and by polymerase chain reaction assay, and to relate the presence of fungi in the nasal sinuses to the type of fungal allergen causing disease.

Methods: Sixty-eight cases of allergic fungal rhinosinusitis underwent fungal culture and polymerase chain reaction assay for universal fungal, aspergillus and bipolaris DNA. Aspergillus-specific immunoglobulin E levels were measured in sinus aspirate, and total serum immunoglobulin E levels were calculated. A control group of 10 cases was included in the study.

Results: Of the 68 allergic fungal rhinosinusitis cases, only 42 (61.7 per cent) had positive fungal cultures; of the 10 controls, only three (30 per cent) had positive cultures. Species from the dematiaceous family were most commonly grown, being isolated in 30 cases (71.4 per cent). Bipolaris was the most commonly isolated species (18 cases) followed by curvularia (11 cases) and alternaria (one case).

Polymerase chain reaction assay detected fungal DNA in all the allergic fungal rhinosinusitis cases and also in four controls (40 per cent). Ten patients (of 68; 14.7 per cent) were positive for Aspergillus fumigatus specific immunoglobulin E. The mean concentration of this immunoglobulin was 11.32±4.12 IU/ml in patients and 0 IU/ml in controls, a statistically significant difference.

Conclusion: Detection of fungal DNA in nasal aspirate by polymerase chain reaction was superior to fungal cultures as a method of detecting fungal growth. In allergic fungal rhinosinusitis, fungal growth is not always accompanied by an allergic reaction.

9-

**Sinus aspirates in chronic rhinosinusitis: fungal colonization of paranasal sinuses,**
evaluation of ICAM-1 and IL-8 and studying of immunological effect of long-term macrolide therapy*

Purpose: In patients with chronic fungal sinusitis, concentrations of interleukin-8 (IL-8), immunoglobulin E (IgE), and soluble intercellular adhesion molecule-1 (sICAM-1) were compared in paranasal sinus aspirates and serum. Furthermore, immunological effects of macrolide treatment of our patients with chronic fungal rhinosinusitis were also studied.

Materials and Methods: In our cohort study, 108 patients with chronic rhinosinusitis undergoing sinus surgery were selected. Sinus aspirates were collected, and used for immunological assays and cultured for fungal studies. All patients were examined for the presence of characteristic allergic mucin of chronic allergic fungal rhinosinusitis, which was confirmed by measurement of total serum IgE.

Results: Our cases were classified into 3 groups: chronic rhinosinusitis with positive fungal culture and negative allergic mucin, chronic rhinosinusitis with positive fungal culture and positive allergic mucin and chronic rhinosinusitis without fungal growth. A control group was included.

We found 57.4% of the patient cultures positive for fungus and 36.4% of the control subjects. Aspergillus ssp. were the most prevalent followed by Bipolaris ssp., and Curvularia. IgE levels were increased in group II compared to group I, III and IV. ICAM-1 and IL-8 levels were increased in groups I, II and III compared to the control group. Erythromycin given in group II decreased the levels of IL-8 and ICAM-1.

Conclusion: Aspergillus species was the most common. These results confirm the role of ICAM-1 and IL-8 in all types of rhinosinusitis. Erythromycin modulated the immune status of the patients.

Association Between Helicobacter pylori and Hepatitis C Virus-Related Chronic Liver Diseases: Serological and Molecular Study

Recent studies have suggested that bacterial co-infection with Helicobacter pylori (H. pylori) in patients already infected with hepatitis C virus (HCV) could be involved in the development of cirrhosis and hepatocellular carcinoma (HCC). This study planned to suggest the association between H. pylori and HCV in chronic liver diseases. The presence of H. pylori was tested by quantitative measurements of IgG and IgA in the patients sera and by polymerase chain reaction (PCR) using liver samples from three groups of patients. Group A with gastro duodenal problems (n= 14), Group B with cancers (n= 12), and Group C other pathological cases (n= 6). H. pylori DNA (cag-A gene) was found in 18 liver samples out of 26 tested patients (69.2 %) . H. pylori DNA was found in 14 liver samples from patients HCV positive (Group I), 5 liver samples...
from patients HCV negative (Group II), and 8 samples were found negative for H. pylori PCR in spite of the patients were HCV positive (Group III). Six cases were considered as a control since they were negative for both HCV and H. pylori PCR (Group IV).

Association between H. pylori and HCV was detected in our patients in significant value ( P = 0.02), since we found 13 positive liver samples by H. pylori PCR out of 21 Positive HCV patients. This association was reflected on the pathology of the liver (metavaire and activity), and liver enzymes (P = 0.017, 0.04, and 0.01 respectively) by comparing results of Group I and Group II, III, and IV. There was no significant difference among Group II, III, and IV regarding the pathology and liver enzymes. It was found that, no statistical differences among the three clinical groups regarding, metavaire score but Knodell score of activity there was significant difference between Group A and C (P = 0.011). Significant difference was found regarding, H. pylori serology and PCR between Group A and Group B and C (P = 0.012 and 0.004 respectively for H. pylori PCR). Also a significant difference was found between Group A and C regarding liver enzymes (P = 0.042). The overall prevalence of antibodies to H. pylori was 52.6 % (20/38), with the prevalence of 61.9 % (13/21) in the patients reactive to HCV. The value of quantitative measurement of H. pylori IgG & IgA in comparison to PCR was significant since 17 of 18 were positive specially with IgG. From our study, we can suggest that there is an association between the presence of H. pylori DNA in the liver and hepatitis C pathological effect. The presence of these bacteria could resulted in structural changes in the liver or/and H. pylori could be a co-risk factor in HCV chronic liver diseases. This result in highly need for prospective studies to determine the possible role of H. pylori to affect the pathogenesis of HCV by synergistic way and to give trial triple therapy for this bacterium and follow the progression of chronic hepatitis.

11-

Certain severity-related parameters in atopic dermatitis: Possible Candida role and its therapeutic response

Objective: To evaluate certain severity-related markers of atopic dermatitis in relation to Severity Scoring (SCORAD) and to clarify the relationship between Candida albicans colonization and severity of atopic dermatitis with the effect of antifungal treatment on previous markers.

Design: A prospective study included 82 atopic dermatitis (AD) patients and 20 healthy controls. Patients were grouped into two groups according to the severity of the disease. Full history & clinical examination were done to evaluate SCORAD index for each. Blood samples were taken for detection of total eosinophilic count, total IgE, Candida albicans specific IgE, intercellular adhesion molecule-1 (ICAM-1) and eosinophil cationic protein (ECP). Isolation and identification of Candida albicans was done, then an oral antifungal drug (Fluconazole) was given for 4 weeks with monitoring changes in these parameters.

Results: There was significant increase in ECP, ICAM-1, total eosinophilic count, total IgE levels in AD patients as compared with control especially the severe group (P<.001). Serum levels of ECP, ICAM-1 represented high significant positive correlation with SCORAD. Significant high incidence of C. albicans isolates were detected in both AD groups (Severe group 40%, mild-moderate group 36.7%) with significant increase in C. albicans specific IgE that could be correlated with SCORAD (P<.001). With Fluconazole, there was mild to moderate significant improvement of SCORAD, decrease of ECP &
ICAM-1 with high significant decrease in C. albicans specific IgE.
Conclusions: Eosinophils are important effector cells in atopic dermatitis. The serum levels of ECP and ICAM-1 have been proven to be high significant predictors of disease severity. Isolation of Candida albicans and high level of its specific IgE especially in severe AD group that could be correlated with SCORAD confirms a possible role of antifungal treatment of atopic dermatitis with positive C. albicans isolation.

12-

Effect of allergen-specific immunotherapy with high dosage on the expression of Interferon-gamma and Interleukin-4 mRNA in sensitized rats.

Virulence factors including urease, flagella, haemolysin, various fimbriae, IgA protease and a deaminase have been characterized for Proteus mirabilis. The most characteristic attribute of Proteus, swarming growth, enabling them to colonize and survive in higher organisms. In this study we aimed to evaluate the proteolytic activity of Proteus mirabilis and correlate this activity with swarming. The broth culture of the
organism was used to detect the proteolytic activity and the units of proteases were measured for 46 strains. Among 46 strains of Proteus mirabilis, 4 strains were non-proteolytic and 42 strains were proteolytic. The mean value of the amount of proteases was 0.074±0.023 units. The 4 non-proteolytic strains of Proteus mirabilis were unable to form swarming growth on blood agar whereas all the 46 proteolytic strains were able to form swarming growth and this finding suggests that there is a clear association between the ability of the strains to swarm and their ability to form a proteolytic enzyme. Studies of the proteolytic activity of Proteus mirabilis on SDS-PAGE showed that in most isolates except that non-swarming strains, 3 to 4 bands appeared in the same lane of each individual isolate, at least 2 bands of similar or slightly different mobility appeared for all strains. Some strains showed a extra one or two bands and this may be explained by presence of internal proteases in the supernates which appeared due to lysis of some bacterial cells during incubation.

14-

Tinea Capitis in a Locality of EGYPT and its Susceptibility to Certain Antifungal Regimens: An In-Vivo and In-Vitro Study

Tinea capitis is a relatively common fungal infection of childhood. Its epidemiology varies considerably with respect to geography and specific patient populations. Although griseofulvin has been the mainstay of management, the newer antifungal agents have revolutionized treatment with shorter courses of therapy. The objective was to detect the causative fungal strains of tinea capitis in Dakahlia (Egypt) and its in-vitro susceptibility (MIC, MFC) to griseofulvin, itraconazole and terbinafine. Also, to evaluate the clinical and mycological response to certain antifungal regimens with its cost effectiveness. This prospective study included 73 age-matched children with tinea capitis. Clinical scoring was done. Start mycological diagnosis & detection of MIC & MFC of drugs for each strain was done using Broth microdilution Susceptibility testing (NCCLS M27-A). The therapeutic regimens were Griseofulvin (8Ws); Itraconazole (continuous, 4Ws), (pulse 1W, 2-3 pulses, 3Ws interval) and Terbinafine (Short 2Ws & Long 4Ws). Clinical and mycological cure were evaluated at 4Ws & 8Ws with final evaluation at 12 Ws. Trichophyton violaceum and Microsporum canis represented the highest incidence (47.95% & 23.29% respectively). All strains mostly showed the lowest median values of MIC & MFC with terbinafine that was followed by itraconazole with high significant difference (P<0.001) and variability in-between different strains for the same drug. At 12 Ws, Terbinafine (4WS) & griseofulvin (8Ws) represented the highest clinical cure rate (100%). Terbinafine (4Ws) and itraconazole (Pulse regimen) represented the highest mycological cure (93.8 & 88.9% respectively). Some regimens showed mycological recurrence. Griseofulvin (8ws) was the lowest value for cost/mycological cure & relative cost effectiveness followed by terbinafine (4Ws). Non significant correlation was detected between MIC, MFC and clinical or mycological cure. In conclusion, for treatment of tinea capitis in this locality, griseofulvin is found to be to some extent, close similar to terbinafine (4Ws) as regards the clinical cure with lower cost/mycological cure, although it represented the maximal value of MIC & MFC and longer duration therapy. For combined reasons of efficacy & cost, griseofulvin still may represent the treatment of choice for low-income populations.

15-
Local production of IgE in nasal polyps of allergic rhinitis patients.

The mechanism of development of the nasal polyp is still unclear. Up to 1970s, allergy was known as a main cause of nasal polyp. The generation of total IgE and specific IgE in nasal polyp was found to suggest the existence of localized nasal allergy which is assumed to play a some role for the development of nasal polyp. The presence of specific IgE on skin mast cell (skin test) and/or the existence of specific IgE in serum (RAST) indicates sensitization, but not necessarily clinical allergy, in the target organ. Discrepancies between sensitization and disease could be explained by local IgE production. In this study, we aimed to confirm the local production of IgE antibody from nasal polyp and to evaluate the difference between atopics and non-atopics.

Patients were classified into test group which included 16 allergic rhinitis patients with nasal polyps and control group which included 16 non atopic patients with nasal polyps. The diagnosis of allergic rhinitis was confirmed by clinical history, clinical examination, positive skin test for a certain inhalant allergen and elevated total serum IgE. Serum and polyp fluid IgE were measured by ELISA. The amount of serum and polyp tissue albumin was determined by spectrophotometric analysis. The polyp tissue total IgE/albumin and serum total IgE/albumin were significantly higher in 16 atopics (33.1) than in the 16 non-atopics (14.1) with no significant difference in the albumin level between the two groups. The ratio of polyp total IgE/albumin to serum total IgE was greater than 1 in 10 cases of 16 atopics with nasal polyposis and 6 cases of 16 non atopics suggesting that IgE antibody could be locally produced from the nasal polyp tissue of non atopics as well as atopic subjects.

Evaluation of IL-6 and IL-13 levels in nasal polyps of allergic rhinitis patients.

Nasal polyposis is a chronic inflammatory disease of the paranasal sinuses, with a prevalence of 1-4% in the general population. The pathogenesis of nasal polyps is far from clear. Predisposing factors for development of polyps of the nose and paranasal sinuses are chronic inflammation, cystic fibrosis, allergies, production of cytokines and genetic influences. Several cytokines have been identified that may support the development of these benign neoplasms. In a previous study, we indicated that IgE antibody could be locally produced from the nasal polyp tissue of non atopics as well as atopic subjects. In this work, we aimed to evaluate cytokines IL-6 and IL-13 in nasal polyposis. Patients were classified into allergic group with nasal polyposis and non allergic group with nasal polyposis. Serum and polyp fluid IgE, IL-6 and IL-13 were measured by ELISA. The amount of serum and polyp tissue albumin was determined. Our results indicated that the mean value of IgE in polyp fluid in allergic group is statistically significantly higher compared to that in non allergic (control group). Regarding cytokines assay, the mean values of both IL-6 and IL-13 in polyp fluid of allergic group are statistically significantly higher than that in non allergic group. The important observation in our results is there is synchronous relationship between the increase in levels of IgE and IL-13 in polyp fluid of allergic group indicating that IL-13 (not IL-6) has a leading role in IgE formation at the local site of allergic inflammation. The results show that in allergic group, the mean value in serum IgE expressed as percentage to serum albumin is statistically significantly higher than that of non allergic group. There is no significant difference regarding IL-6 concentration in sera of both.
There is a statistically significant increase in the amount of IL-13 in sera of allergic group compared to control group.

**Molecular characterization and virulence properties of Candida parapsilosis isolated from immunosuppressed dermatologic patients.**

Candida parapsilosis (CP) is a very common saprophytic fungus, its pathogenic role has been reported in immunocompromised patients. Over the last few years, its incidence has progressively increased relative to other Candida species in the settings of malignant hemopathic patients to become the most prevalent cause of candidemia. Genetic finger printing has emerged as indispensable tool for studying the incidence, distribution and origin of fungal diseases in human population. This study was conducted in 103 immunosuppressed dermatologic patients, 35 patients with pemphigus vulgaris (PV) & 27 with systemic lupus erethematosis (SLE) & 41 from oncology unit and 61 as control. Patients with PV were subjected to immunosuppressive therapy with corticosteroid +/- immuran. Patients with SLE were treated with corticosteroid +/- (cyclophosphamide, cholorambucil, methotrexate, cyclosporin). Over 6 months, we examined patients and control every 2 weeks for detection of cutaneous candidiasis or oral candidiasis (mucous membrane candidiasis) or even onychomycosis. To all CP isolates, antifungal susceptibility testing was done. The ability to secrete asparatyl proteinase in bovine serum albumin (BSP) was assessed in solid media. Total genomic DNA of the CP isolates was isolated and further digested with the restriction enzymes HindIII and EcoR1. In the present study, mucous membrane candidiasis due to CP were identified in 4/19 (21.5%) of PV patients, 3/12 (25%) in SLE patients, 8/25 (32%) of oncology patients and in the control group 1/6 (16.6%). Only strains of C. parapsilosis isolated from skin produced Sap in moderate amounts while strains from mucous membrane and blood failed to produce this enzyme under our study conditions. Most patients responded to fluconazole 150 mg per day. Some patients needed to increase the dose to 300 mg per day, also some patients showed fluconazole resistance. Regarding EcoR1 There were 11 major chromosomal bands in all isolates (0.8 – 20 Kbp). These bands showed some differences in intensities. Some minor bands with faint intensity appeared and showed some differences among different C. parapsilosis strains, however, it was difficult to use these minor bands to differentiate C. parapsilosis into different groups. HindIII typing showed 12 major bands in C. parapsilosis isolates (0.8 -14 Kbp. The characters of these bands resembled that of EcoR1 restriction cutting. These results indicated that C parapsilosis is genetically heterogeneous and because of many minor bands, it was difficult to differentiate the strains into different groups.

**Nosocomial Urinary Tract Infection And The Importance Of Infection Control Practices In Mansoura University Hospital.**

OBJECTIVES: The purpose of this study was to determine the prevalence of nosocomial urinary tract infection (NUTI), associated risk factors, microbial etiology, and a measure of the quality of care provided to patients in Mansoura University Hospital (MUH). DESIGN: The study design was a retrospective study over a period of 2 years, during that period, patients among different clinical departments at Mansoura University Hospital were surveyed for nosocomial urinary tract infection, and a task force was
formed to design interventions to reduce NUTI.

METHODS: Patients admitted to MUH were subjected to complete clinical examination and investigation, urine samples were collected under complete aseptic precaution from non catheterized, and catheterized patients, urine cultures were done using conventional media for aerobic organisms, biochemical tests for identification, and antibiotic sensitivity tests were done. Policies and procedures were standardized at MUH for catheter insertion and care using CDC guidelines. Educational interventions for catheterized and non catheterized patients involved which included fact sheets, posters, lectures and a study module.

RESULTS: From a total of 11,800 admissions to the MUH wards, 2551 (21%) nosocomial infection were detected, among them 565 (22%) nosocomial urinary tract infections (NUTI) were identified during a 2-year retrospective microbiological review. The ages ranged from 3 days to 70 years, with 68% women and 47% men had positive results. The highest rates of NUTI per service per admissions were seen in the general medicine (21%) followed by oncology (18%) and neurology (17.5%), Emergency (9.3%), Neonate, and Tropical Dept. (5.6%), Dermatology, Cardiothoracic, and Surgery Dept. (6.8%), and lastly Gynecological, and Chest Dept. (0.6%). One hundred and sixty isolates were detected. The incidence of the isolated strains were reported as follow: E.coli (35%), Klebsiella pneumoniae (19%), Candida (16%), Pseudomonas aeruginosa (9%), Proteus mirabilis, Staph.epidermidis & serratia marcescens (5%), G D Streptococci & Staph. aureus (3%) and lastly Acintobacter baumannii (12%). Risk factors include: transurethral and repeated intermittent catheterization (87%), female sex (68%), increased length of stay (57%), diabetes mellitus (31%). The most effective antibiotics were nalidixic acid, gentamicin and amoxicillin-clavulanic acid. Instillation of 1% chlorhexidine through catheter bag, proper hand washing, meatal care minimize the prevalence of NUTI to 4%.

CONCLUSIONS: Given the clinical and economic burden of urinary catheter-related infection, infection control professionals should use the most recent infection control principles and technology to reduce this common complication.

19-

IL-8 levels in nasopharyngeal aspirate and blood of infants with respiratory syncytial virus bronchiolitis: Relation to severity of the disease.
Antibiotic-Resistant Propionibacterium Acnes: Prevalence among Acne Vulgaris patients and possible clinical significance.
Virulence factors of E.coli strains isolated from diabetic women with asymptomatic bacteriuria.

Role of Helicobacter Pylori and Cytomegalovirus Infections in Human Atherosclerotic Plaques.
Detection of Bordetella Pertussis by PCR in Infants with Respiratory Failure.
Bacterial Translocation in an Experimental Intestinal Obstruction Model. C-Reactive Protein Reliability.
Detection of Bordetella Pertussis by PCR in Infants with Respiratory Failure

BACKGROUND: Despite being under-reported, Bordetella pertussis infection remains a severe disease of high incidence world-wide. No cases were reported in Egypt since 2001. Different immunization protocols exist in different countries with variable vaccination coverage ratios.

DESIGN AND SETTINGS: This prospective investigational study was conducted in the PICU of Mansoura University Children Hospital, Mansoura, Egypt

AIM OF WORK: identifying cases of B. pertussis infection among mechanically ventilated infants presenting with respiratory failure and features compatible with pertussis (bronchopneumonia, apnoea, acute life threatening event).

PATIENTS AND METHODS: Infants less than one year of age were enrolled over a period of 12 months. Sixty one specimens of endotracheal secretions were examined by PCR for the presence of a 262-bp target sequence from IS481 specific for B. pertussis.

RESULTS: Nine specimens were positive for B. pertussis, five infants in this group did not survive. All non survivors were younger than 6 months of age. Infants in the PCR-positive group had a younger age (p = 0.038), a longer duration of illness prior to PICU admission (p < 0.01) and a higher mortality rate (p = 0.045) compared to the PCR â€“ negative infants.

CONCLUSION: It is crucial to raise awareness, among medical professionals, of clinical picture and complications and treatment of pertussis. If immunization program of Egypt was to be reviewed, there may be a need for a more accelerated primary immunization program against pertussis with booster doses for young adults.

Genetic polymorphisms of IL-6-174 and IL-10-1082 in full term neonates with late onset blood stream infections

Genetically determined variation in the magnitude of inflammatory response may play a role in determining the risk of developing neonatal sepsis, as well as its outcome. To test the hypothesis that interleukin-6 (IL)-6-174, IL-10-1082 genetic polymorphisms are associated with the risk of sepsis and clinical outcomes in full-term neonates with blood stream infections (BSIs). A total of 54 full-term neonates with BSIs and 70 matched controls were included in this case/control study. DNA amplification using polymerase chain reaction with sequence-specific primers followed by NlaIII restriction enzyme digestion was done for detection of promoter single nucleotide polymorphism of IL-6-174 G/C, amplification refractory mutation system polymerase chain reaction assay was done for IL-10-1082 G/A polymorphism in blood samples from
all infants enrolled in the study. The IL-6 -174 and IL-10-1082 genotypes were not significantly different in neonates with BSIs compared to controls. whereas, IL-6-174CC and IL-10-1082GG genotypes were associated with increased risk for mortality [Odds ratio (95% confidence intervals): 6.2 (1.3â€“28.4), P = 0.02 and 25.0 (2.0â€“74.3), P < 0.01, respectively]. Moreover, IL-6 174CC and IL-10-1082GG genotypes were significantly higher in neonates who required inotropic support and those who developed disseminated intravascular coagulopathy. The IL-6 -174 CC and IL-10 -1082 GG genotypes were associated with increased risk for mortality, need for inotropic support and development of disseminated intravascular coagulopathy in full-term neonates with BSIs. These findings suggest that the genetic composition of the IL-6 and IL-10 promoter areas play a significant role in the pathogenesis of neonatal BSIs.

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The Role of IL-8 in Different Types of Otitis Media and Bacteriological Correlation
Objective: To isolate and identify the different bacterial pathogens causing acute otitis media (AOM), Chronic suppurative otitis media (CSOM) and secretory otitis media (OME). Also to evaluate the role of IL-8 in different type of otitis media (OM).
Study design: Middle ear fluids were collected from 103 patients suffering from different types of OM. Patients separated into 3 groups: group I (AOM), group II (CSOM) and group III (OME). Middle ear fluid was collected and subjected to bacteriological study and assessment of IL-8.
Results: Positive cultures were detected in 68.7% in group I, 88.1% in group II while no bacterial growth was detected in group III. IL-8 was detected in the 3 groups with statistical significance between the 3 groups, it was evident between group I and III and between group II and III. There was significant correlation between the results of bacterial culture and the level of IL-8.
Conclusions: IL-8 plays a role in the development of chronicity of OM. It has intimate relation to the bacterial growth; it acts as a chemo-attractant to neutrophils into the middle ear fluid.

28-
Eotaxin, RANTES and tumor necrosis factor alpha levels in allergic rhinitis
Abstract Objectives: The objectives of this study were to estimate the levels of eotaxin, RANTES and tumor necrosing factor-1 in allergic rhinitis and their relation to disease severity.
Study design: Prospective study.
Setting: Mansoura University Hospital.
Patients and methods: Twenty nine patients suffering from allergic rhinitis were included in this
study (19 patients with allergic rhinitis and 10 patients control group). The patients underwent estimation of eotaxin, RANTES, TNF-1 in the nasal wash using Elisa technique. The patients were divided according to the disease severity into mild allergic rhinitis, severe allergic rhinitis and control groups.

Results: The mean values of eotaxin, RANTES, TNF-1 in severe allergic rhinitis (33.6 11.07±1 pg/ml, 72.17 87.61±1 pg/ml, 25.47 4.04 ±1 pg/ml) were statistically higher than in mild allergic rhinitis (9.80 6.79 ±1 pg/ml, 10.50 6.90±1 pg/ml, 12.993.27 ±1 pg/ml) and the mean values of all these parameters were higher in both groups compared to control group (0.6 0.69 ±1 pg/ml, 0.65 0.74 ±1 pg/ml, 0.63 0.54 ±1 pg/ml).