

method. For this purpose, ten clinically healthy volunteers, aged from 26 to 76 years, were studied. The data showed that age was not a statistically significant factor for glutathione peroxidase activity. At the same time, women demonstrated significantly lower glutathione peroxidase activity than men ($p=0.032$). Future in-depth studies of the blood antioxidant status with a larger number of carefully selected individuals in well-defined age groups are needed to achieve highly reliable experimental results.

Key words: antioxidants, blood, reactive oxygen species, glutathione peroxidase, activity

MICROBIOLOGY, INFECTIOUS DISEASES, EPIDEMIOLOGY AND PARASITOLOGY

PLENARY LECTURES

ANTIMICROBIAL STEWARDSHIP – A HEALTHCARE PRIORITY. NEW ANTIBIOTICS

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Summary

Antimicrobial resistance (AR) currently reaches huge dimensions all over the world. The WHO has recognized it as a global threat requiring priority actions. Medical societies, countries governments and the pharmaceutical industry work together to overcome the increase of AR. This work aims to introduce the Antimicrobial stewardship principles and their implementation in Bulgaria, as well as to overview the new antibiotics. Recently published international literature, together with last-year national developments, were analyzed. There are two main ways to contain AR. The first one – antimicrobial stewardship (AS), aims at better prescribing for patients through rapid clinical and microbiological diagnosis, making an optimal choice of an antibiotic, dose, and duration of treatment. Important pillars in AS are education, control of infection and political engagement. AS will decrease patient morbidity,

mortality, and AR. In 2019, a multidisciplinary committee of experts with the Ministry of Health was set up to prepare the Bulgarian Action plan to contain AR. The draft plan is based on the One Health concept of WHO. First, hospital stewardship requires new guidelines for prescribing antibiotics; a stewardship team to audit; rules to every prescriber, including written basics for bacterial infection and further evaluation of antibiotic therapy, e.g. tailored therapy. Second is the introduction of new antibiotics. In conclusion, the government-supported antimicrobial stewardship programme with prudent use of new antibiotics will contain further development of resistance, preserve antimicrobial agents for future generations and significantly improve patient care.

Key words: antimicrobial resistance, antibiotic policy, Bulgarian action plan

DIAGNOSIS AND ANTIMICROBIAL THERAPY OF BACTERIAL MENINGITIS

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Summary

The aim was to review the recommendations for diagnosing and treatment of bacterial meningitis. We reviewed the literature on management, diagnostic algorithm and antimicrobial therapy of bacterial meningitis. In general, successful treatment of patients with acute bacterial meningitis depends on early recognition of the meningitis syndrome, timely diagnosis and emergent antimicrobial therapy. In the case of suspected acute bacterial meningitis, blood

samples for culture must be obtained, and a lumbar puncture performed immediately to establish the diagnosis of bacterial meningitis. The specific CSF diagnostic tests used to determine the bacterial aetiology include Gram stain, Latex agglutination, biochemical tests for identification, and PCR. The recommendations for empirical and specific antimicrobial therapy, based on the isolated pathogen and susceptibility testing were summarized. The outcome and prognosis for patients with bacterial meningitis depend on the exact etiological diagnosis and early antimicrobial therapy.

ORAL PRESENTATIONS

DRUG SUSCEPTIBILITY AND CHARACTERISTICS OF PENICILLINASE PLASMIDS AND BETA LACTAMASE GENES IN *NEISSERIA GONORRHOEAE* STRAINS

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Summary

Neisseria gonorrhoeae has developed many resistance mechanisms, which are associated with the history of the new antibiotics introduced in the treatment of gonorrhoea. Currently, the most critical problem is the mechanisms which are determining resistance to the beta-lactam antibiotics. The work aims to describe the phenotypic and genotypic characteristics of the resistance of penicillinase-producing *N. gonorrhoeae* (PPNG) Materials and methods 333 *N. gonorrhoeae* strains obtained from the Department of Diagnostic Sexually Transmitted Diseases, Medical University of Warsaw were subject of our study. The tested strains were assessed in phenotypic terms for penicillin and ceftriaxone sensitivity. The mutations within

the *blaTEM* gene were detected and analyzed in the beta-lactamase producing strains (PPNG). Among the tested strains, 49 showed resistance only to penicillin. Beta-lactamase was detected in 21 penicillin-resistant strains. In all of these strains was found the *blaTEM* gene. In 13 (62%) PPNG strains were detected the Africa type plasmid, Toronto/Rio type – in 6 (28%) strains, and the Asia type was detected in 1 strain (5%). One tested strain (5%) had a plasmid with a size close to the 3500 bp standard. With a new generation sequencing technique, this strain was found to contain an Australia-type of plasmid variant. The obtained results allow concluding that among the PPNG strains, there was a change in the prevalence of the TEM-1 beta-lactamase with the TEM-135 dominating in the years of study.

Key words: penicillinase-producing *Neisseria gonorrhoeae*, TEM-1, TEM-135

ANTI-VACCINATION MOVEMENTS: AN OLD MYTH WITH A REAL IMPACT ON THE EPIDEMIOLOGICAL PROCESS OF VACCINE-PREVENTABLE INFECTIONS

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Summary

The achievements of applied epidemiology in controlling the epidemiological process (EP) in many severe and socially relevant infections are indisputable. However, resistance to immunization is an increasingly pressing issue today. This report aims to present the development of anti-vaccine movements and the unfavorable consequences for the EP in contemporary conditions because of their influence. We used the documentary and historical methods, and the

data was obtained from medical literature and referenced legislation database. The analyses and conclusions were based on objective scientific evidence. Anti-vaccine movements first appeared in the late Middle Ages. Historically, there was an early stage characterized by religious and mystic arguments, followed by a period of confrontation based on legal arguments and a new phase with a sophisticated use of legal standards and tendentiously distorted interpretation of official statistical and scientific data. We analysed several major epidemic events in the recent past that occurred because of the low immunization rates. It has been demonstrated that in case of a complicated epidemic situation, immunization is considered as a necessary measure. Vaccination of risk groups leads to curbing the spread of infection, worries fade away, and memories of past tragedies fade away. The circulation of opinions on unwanted post-vaccination complications becomes active again. The need for vaccination is challenged, and the results achieved are denied. This leads to compromising the immunization program and reduces the efficacy of anti-epidemic activities. Anti-vaccine movements of the past and present contest the importance of immunoprophylaxis in protecting the health of an individual, and completely deny the vital role it plays in public health. They have become increasingly aggressive, and their main targets being post-vaccination complications. During the last few decades, the decrease of immunization coverage below the critical minimum level has resulted in epidemics and fatal outcomes from diseases that have been under control. Such a situation enhances the responsibility of all health professionals to vindicate the adopted immunisation strategy convincingly and oppose to attempts for neglecting epidemiologic control and immunoprophylaxis.

Key words: anti-immunization movements, history, meaning, last epidemic situations

PREVALENCE OF ANTIMICROBIAL RESISTANCE-MEDIATING MUTATIONS IN *NEISSERIA GONORRHOEAE* AND *MYCOPLASMA GENITALIUM*

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Summary

The emergence of antimicrobial resistance in *Neisseria gonorrhoeae* and *Mycoplasma genitalium* present a great threat to effective treatment. This study aimed to determine the prevalence of antimicrobial resistance-mediating mutations in *N. gonorrhoeae* and *M. genitalium* infections in Sofia, 2018-2019. *N. gonorrhoeae* positive samples were analyzed for antimicrobial resistance to cephalosporins and fluoroquinolones by detecting the presence of a mosaic *penA* gene and mutations in the *gyrA* gene by real-time PCR. *M. genitalium* positive samples were examined for mutations associated with resistance to macrolides and fluoroquinolones – by DNA sequencing of the 23S rRNA and *parC* genes. For 2018-2019, samples of a total of 18 *N. gonorrhoeae*-positive patients were analyzed, whereas mutations associated with fluoroquinolone resistance in the *gyrA* gene were detected in 61.11% (n=11/18) of the cases. No mosaic *penA* gene was detected in any of the samples. Out of a total of 11 *M. genitalium*-positive patients, mutations associated with macrolide resistance were found in 45.5% (n=5/11) of the cases. The detected mutations were A2059G (n=4) and A2058G

(n=1), respectively. No mutations associated with fluoroquinolone resistance were detected. The results of this study show for the first time the emergence of macrolide resistance in *M. genitalium* infections in Bulgaria. In gonococcal infections, resistance to cephalosporins was not demonstrated, but the high prevalence of fluoroquinolone resistance was confirmed. In conclusion, it is highly advisable to implement antimicrobial surveillance in *N. gonorrhoeae* and *M. genitalium*, whereas microbiological diagnosis should be done with contemporary laboratory methods and supplemented with antimicrobial sensitivity testing.

Key words: *Neisseria gonorrhoeae*, *Mycoplasma genitalium*, antimicrobial resistance, antimicrobial resistance-mediating mutations

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INEVITABLE LETHAL OUTCOME OF SEVERE MENINGOCOCCAL SEPSIS: CASE REPORTS

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Summary

The aim of this report is to present two clinical cases of fulminant meningococcal sepsis. The effect of the gram-negative bacteria *Neisseria meningitidis* could vary from asymptomatic infection to severe clinical presentation, directly endangering a patient's life. Such conditions present serious problems, especially in pediatric pathology. The fulminant development of these diseases acquires a careful follow up of the diagnostic and treatment guidelines and detailed discussion of clinical cases. We made a retrospective research based on detailed medical documentation and pathological expert reports on two clinical cases of children admitted to the ER in critical general conditions, presenting with fever and a petechial rash. Despite all diagnostic and resuscitation efforts few hours after hospitalization, both children developed severe septic shock accompanied by purpura fulminans, which led to a lethal outcome. Samples of cerebral spinal fluid were examined by PCR-real time. The causing agent found was C serotype of *Neisseria meningitidis*. These cases demonstrate the worst development of the meningococcal disease – developing of Waterhouse-Friderichsen syndrome, which is well-known to be strongly irreversible and leads to multiple organ dysfunction. However, the most surprising of all is the lack of a severe prior symptom, and also the fulminant beginning and extremely rush development of a fatal end. The most significant problem is the absence of response to a maximum of treatment. Therefore, the primary attention should be focused on constructing a future strategy for managing such cases, preventing the inevitable from happening.

Key words: *Neisseria meningitidis*, meningococcal sepsis, Purpura fulminans, Waterhouse-Friderichsen

VIRAL HEPATITIS E – CLINICAL, LABORATORY AND EPIDEMIOLOGICAL CHARACTERISTICS

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Summary

Viral hepatitis E (VHE) is endemic in most countries nowadays and is mostly a zoonotic infection. Our objective was to analyze the characteristics of VHE during the last years. We performed a retrospective analysis of clinical, laboratory and epidemiological data of 33 consecutive serologically confirmed cases of VHE, treated in Clinic of Infectious Diseases at the University Hospital – Pleven (2016-2019) (18 males – 56%, mean age 59±15 years). Statistical methods – t-test and χ^2 test (for parametric and non-parametric distributions, respectively; $p < 0.05$ was considered to be significant). A total of 283 cases of hepatitis were treated in the Clinic (2016-2019). Of these, the cases of VHE accounted for 12%. Fifty-five per cent of VHE cases were older than sixty years, 79% were urban residents; 39% acquired the disease in March – April. Only two cases had contacts with pigs. The most prevalent symptoms were hepatomegaly (100%), adynamia (94%), the darkness of urine (92%), jaundice (79%), anorexia (76%), splenomegaly (67%), nausea and vomiting (58%). Laboratory investigations revealed mild leukocytosis (21%), thrombocytopenia (18%), increased serum bilirubin with prevalence of direct fraction (82%; mean \pm SD 94±91 μ mol/L; 95% CI – 63÷125), increased aminotransferases in 100% (ASAT mean \pm SD 812±629 IU/L; 95% CI – 598÷1027; ALAT mean \pm SD 1327± 790 IU/L; 95% CI – 1058÷1597), mild to moderate increased alkaline phosphatase and GGT (90% and 100%, respectively). All patients were

successfully treated with glucose infusions, hepatoprotectors and vitamins (mean ten days). We conclude that clinicians should consider VHE in the diagnostic process and that the disease usually affects older ages and jaundice is protracted.

Key words: viral hepatitis E, serum bilirubin, aminotransferases, treatment

FAECAL COLONIZATION WITH VANCOMYCIN-RESISTANT ENTEROCOCCI AMONG PATIENTS IN INTENSIVE CARE UNITS

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Summary

We screened ICU patients for colonization with vancomycin-resistant enterococci (VRE). Rectal swabs were obtained from 71 patients hospitalized between December 2018 and May 2019 in two ICUs (34 in the surgical ICU and 37 in the oncology ICU) at Dr Georgi Stranski University Hospital, Pleven. Samples were cultured onto Brilliance VRE agar as well as into bile esculin azid broth. The isolates were identified by VITEK 2 compact, and their antimicrobial susceptibility was tested. Species confirmation and detection of vanABCDMN was done by colony multiplex PCR. Faecal colonization with VRE was established in

12 out of the 71 patients (16.9%), and one patient was a carrier of two species. A total of 13 VRE were isolated – 6 VR *E. faecium* and seven enterococci with VanC phenotype (4 *E. casseliflavus* and 3 *E. gallinarum*). In 8.5% of the patients (5 from surgical ICU and 1 from oncology ICU), we detected VR *E. faecium* with the same antibiotic resistance pattern: high-level resistance to vancomycin (MIC \geq 256 μ g/ml), teicoplanin (MICs:48-128 μ g/ml), ampicillin (MIC \geq 256 μ g/ml), gentamicin (MIC \geq 1024 μ g/ml), ciprofloxacin (MIC \geq 32 μ g/ml) and susceptibility to linezolid, daptomycin, tigecycline. All VR *E. faecium* isolates carried *vanA* gene. Enterococci with VanC phenotype expressed low-level resistance to vancomycin (MICs:4-16 μ g/ml), susceptibility to Teicoplanin (MICs:0.5-1 μ g/ml) and the rest of antimicrobial agents. Our results showed a relatively high rate of faecal colonization with VRE in ICU patients. There is a distinct prevalence of VR *E. faecium* among patients with a prolonged hospital stay in the surgical ICU.

Key words: faecal screening, vancomycin-resistant enterococci, drug resistance

POLYMERASE CHAIN REACTION-BASED GENOTYPE DIVERSITY OF BLASTOCYSTIS SPECIES ISOLATES OBTAINED FROM PATIENTS WITH BLASTOCYSTOSIS

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Summary

The genotype of human *Blastocystis sp.* isolates is highly polymorphic, and certain genetic types or demes exhibit higher levels of pathogenicity than others. The pathogenic potential of *Blastocystis sp.* isolates can be demonstrated experimentally by reliable molecular biology techniques. Diagnostic polymerase chain reaction (PCR) primers or restriction fragment length polymorphism (RFLP) analysis can be used to determine the genetic heterogeneity of human *Blastocystis sp.* isolates and to investigate if different genotypes can be linked to clinical variations in blastocystosis. We aimed to find out whether genetic differences exist between isolates of *Blastocystis sp.* obtained from a cohort of Bulgarian patients from the Pleven region with blastocystosis and to investigate the role of different genotypes for the development of blastocystosis. *Blastocystis sp.* isolates were collected from patients with clinically confirmed blastocystosis, and genomic DNA was extracted from cultivated *Blastocystis sp.* samples. The isolated DNA was then used to perform genotype classification using known sequence-tagged site (STS) primers and RFLP analysis of small subunit (SSU) rRNA gene. All samples were found positive for *Blastocystis sp.* PCR positivity was used for selection of optimal growth medium for cultivation of *Blastocystis sp.* Subtyping was successfully performed on 35 samples using STS primers and the PCR method. The most commonly detected subtype was subtype 3. No mixed subtypes were detected. We conclude that genotype analysis based on diagnostic PCR primers and RFLP of small subunit (SSU) rRNA gene is a robust method for subtyping *Blastocystis sp.* isolates and can be used to predict the clinical severity of blastocystosis.

Key words: *Blastocystis sp.*, subtype, classification, PCR, RFLP

POSTERS

CLONAL AND SEROTYPE DYNAMICS OF SEROGROUP 6 *S. PNEUMONIAE* ISOLATES COLLECTED DURING THE PNEUMOCOCCAL CONJUGATE VACCINE ERA IN BULGARIA

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Summary

Investigation of the clonal structure and antimicrobial susceptibility patterns of prevalent serogroup 6 *S. pneumoniae* isolates, collected during pneumococcal conjugate vaccine (PCV10) era in Bulgaria. The antibiotic susceptibilities were assessed by broth microdilution. Strains identified as serogroup 6 with latex agglutination method were subjected to serotype-specific PCR's. Erythromycin-resistant strains were analyzed by PCR for the presence of *ermB* and *mefE* genes. MLST was performed to define the clonal composition of the sequence types (STs). Serogroup 6 was

represented by 40 (13.3%) from 301 invasive and non-invasive *S. pneumoniae* isolates. Molecular serotyping revealed new emerging serotype 6C (6.6%), not detected in the pre-vaccine era. Among unvaccinated patients, we observed mostly serotypes 6A (57.1%) and 6B (28.6%). Serotype 6C was distinctive for vaccinated children (64%), followed by 6A (24%). Penicillin and ceftriaxone non-susceptible serogroup six strains were 65% and 5%; erythromycin and clindamycin resistant were 70.0% and 52.5%, respectively. Multidrug-resistant strains (MDR) were 57.5%. The prevalent genetic determinant for macrolide resistance was the *ermB* gene (75%). MLST revealed 17 STs into 5 (clonal complexes) CCs and 7 singletons. Predominant genetic lineage was CC386, represented only by MDR-6C strains. Serotype switching events were detected in CC395. CC490 was associated with low levels of macrolide resistance. We observed an increase in non-vaccine serotypes after PCV10-introduction. The prevalent ST386 was associated with MDR 6C non-invasive strains. Serotype 6B, principally responsible for invasive diseases in the pre-vaccine era, retreated this position to serotype 6A. Further studies are necessary to clarify the fast-changing serotype characteristics.

Key words: *S. pneumoniae*, serogroup 6, vaccine

APPLICATION OF ANTIMICROBIAL PEPTIDES OF THE FLY MEGASELIA SCALARIS (DIPTERA, PHORIDAE) AGAINST MULTIDRUG- RESISTANT STRAINS OF PSEUDOMONAS AERUGINOSA

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Summary

Pseudomonas aeruginosa is one of the most dangerous human pathogen, which exhibits resistance to almost all conventional antibiotics. Therefore, searching for sources of new drugs has become an urgent task. In 2017, WHO published its first ever list of antibiotic-resistant „priority pathogens“, including *Pseudomonas aeruginosa* as a critical threat and pointing out an urgent need for new antibiotics for its treatment. The aim of this work was to verify the use of antimicrobial peptides (AMPs) from *Megaselia scalaris* as an antimicrobial compound. The study was included a series of experiments based on the assessment (measurement) of the effects of hemolymph, extracted from living larvae *Megaselia scalaris* under stress conditions (high temperature, pricking, immunization) and the influence of the hemolymph on *Pseudomonas aeruginosa*. AMP inhibitory effect of *Megaselia scalaris* larvae hemolymph on the in vitro growth of *P. aeruginosa* cells was evaluated by colony forming units (CFUs). *P. aeruginosa* density inoculum of 10⁻⁵ was used for a testing. There was a significant inhibition of the in vitro growth *Pseudomonas aeruginosa* cells over the tested time. In conclusion, the thermo-adaptive abilities of AMPs of *Megaselia scalaris* larvae could significantly affect the production of endotoxins from *Pseudomonas aeruginosa* under high temperature. AMPs present in the hemolymph of *Megaselia scalaris* larvae inhibit the growth of *Pseudomonas aeruginosa*.

Key words: antimicrobial peptides, larvae, hemolymph

LABORATORY DETECTION OF MEASLES AND RUBELLA VIRUS IN BULGARIA: PHASE OF ELIMINATION

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Summary

The study aimed to present optimizing the combined laboratory diagnosis of measles and rubella virus in Bulgaria. It included 2140 patients tested for measles and rubella virus for the period 2013-2018. The specialized laboratory monitoring at the National Reference Laboratory was performed by testing of at least two types of clinical material of each patient: serum samples, nasopharyngeal swab and/or urine. The serological (indirect ELISA test for detection of specific measles/rubella IgM/IgG antibodies and Avidity IgG test in serum) and molecular (RT-PCR assay for detection of viral RNA) methods were used. All serum samples were ELISA IgM tested for both viruses (measles and rubella), regardless of the results. During the study period, 13 samples in 2013, 1 - in 2016, 74 – in 2017, and 13 – in 2018 were laboratory-confirmed for measles infection. For rubella, zero positive IgM and PCR samples were found. Approximately, in 80% of the samples tested, protective measles and rubella IgG antibodies were found. In 96% of serological and molecular assays conducted, similar results for acute infection were found. The cases were confirmed or rejected, observing at least one criterion for laboratory confirmation, according to WHO requirements. In conclusion, the combined laboratory approach to detect measles and rubella in WHO accredited laboratory (immunoenzymatic and molecular assay of each suspected case) is a requisite for measles and rubella surveillance sensitivity and is crucial for successful elimination.

Key words: measles, rubella, ELISA IgM/IgG, RT-PCR, elimination

PARVOVIRUS B19 IMMUNE STATUS OF PREGNANT WOMEN

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Summary

Viral infections during pregnancy are one of the leading causes of severe complications and maternal and fetal mortality. The study aimed to determine the immune status of pregnant women regarding parvovirus B19. A total of 135 serum samples provided by the Capital Regional Inspection were tested. The samples were collected as part of a program for screening pregnant women for sexually transmitted infections. The serological method was used -

the indirect ELISA test for detection of specific B19V IgG and IgM antibodies. Protective B19V IgG antibodies and previous infection were detected in 61 (45.19%) women. The group of B19V ELISA IgM positive included 26 (19.26%) women. They were patients with a potential risk of developing post B19V clinical complications and/or maternal and fetal infection. A predominantly asymptomatic carrier of parvovirus B19 is possibly infected in the absence of specific pathological manifestations. In such cases, it is crucial to include B19V seroprevalence monitoring of pregnant women and women of childbearing age.

Key words: parvovirus B19, pregnancy, ELISA IgG

COLONIZATION WITH *C. ALBICANS* IN PATIENTS WITH HAEMATOLOGICAL MALIGNANCIES

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Summary

The study aimed to assess colonization with *C. albicans* in patients with haematological malignancies. A total of 41 non-repeated *C. albicans* isolates were obtained by screening for oropharyngeal and intestinal colonization of 103 patients, treated in the Hematology ward, Dr G. Stranski University Hospital - Pleven between May 2018 and January 2019. The yeasts were identified by CHROMagar Candida (BD, UK) and VITEK 2 compact (BioMerieux, France) and MIC values of nine antifungals were determined by Micronaut-AM (MERLIN

Diagnostika GmbH). Colonization with *Candida spp.* was observed in 54 patients (51.4%). The colonized patients suffered predominantly from multiple lymphomas and non-Hodgkin's lymphomas. Overall, 57 non-repeated isolates were recovered, and 41 of them (71.9%) were identified as *C. albicans*. This species was most prevalent in all types of colonization – intestinal, oropharyngeal and both intestinal and oropharyngeal. *C. albicans* isolates were sensitive to amphotericin B (MICs: 0.5-1 µg/ml), 5-fluorocytosine (MIC90: 0.125 µg/ml) and echinocandins with MIC90 of micafungin, anidulafungin and caspofungin 0.015, 0.031 and 0.125 µg/ml, respectively. MICs of azoles varied widely – from <0.0078 to >128 µg/ml of fluconazole, >8 µg/ml of voriconazole and posaconazole, and > 4 µg/ml of itraconazole. Cross-resistance to all azoles was determined in 11 *C. albicans* isolates. A high rate of colonization with *C. albicans* was found in patients with haematological malignancies. These results showed that although all *C. albicans* isolates were susceptible to amphotericin B and echinocandins, detection of cross-resistance to azoles is of great importance for the clinical practice.

Key words: *Candida albicans*, colonization, antifungals, resistance

HOT SPOTS INFESTED WITH IXODID TICKS (ACARI: IXODIDAE) AROUND PLEVEN, BULGARIA AND THEIR ROLE AS VECTORS OF LYME BORRELIOSIS

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Summary

Ticks were the first arthropods established as vectors of pathogens, and currently, they are recognized, along with mosquitoes, as the main arthropod vectors of disease agents to humans and domestic animals globally. The study aimed to identify areas with a high population density of ticks and the risk to public health. During the period 2016-2018 hard ticks were collected through the drag-flag method from areas around Pleven with increased outdoor activities. Species, stage of development and sex were determined of all specimens. Among the collected ticks, *Ixodes ricinus* specimens were examined by darkfield microscopy for the presence of *Borrelia spp.* The density of the tick population in the different areas was determined for all territories as a fraction of the number of collected ticks per area. For the period 2016-2019 during the months of February to June, a total of 959 questing hard ticks were collected. The highest number was that of *Ixodes ricinus* (n=771), of which 368 were examined by darkfield microscopy. *Borrelia spp.* was found in 124 of them. The analysis of the data allowed the identification of 5 areas around the city of Pleven with a high frequency of *Ixodes ricinus* ticks. The degree of infection with *Borrelia spp.* ranged between 15.5% and 40%. Pleven region, with its geographical localization and climate, is an appropriate area for tick abundance. Our results show that during their outdoor activities, people are exposed to tick bites, and there is a potential risk for Lyme borreliosis infection.

Key words: Ixodidae; *Ixodes ricinus*; vectors; hard ticks; *Borrelia*; tick-borne disease; Lyme borreliosis; darkfield microscopy

CORRELATION BETWEEN ANTI-PARVOVIRUS B19 IGG AND DEMOGRAPHIC FACTORS IN CHILDBEARING AGE WOMEN

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Summary

The study aimed to determine the susceptibility to Parvovirus B19 in childbearing age women in Pleven region. We conducted a prospective seroepidemiological study in which 90 healthy women of childbearing age were tested at the Medical Center of the Clinical Institute for Reproductive Medicine – Pleven in 2018. The presence of specific Parvovirus B19 IgG was detected using a standardized anti-Parvovirus B19 (IgG) ELISA kit (EUROIMMUN, Germany). The survey results showed that 37.8% of women were positive for anti-Parvovirus B19 IgG. Immunity to the virus increased from 27.3% to 45% with age groups. There was no significant correlation between the presence of antibody and demographic factors as living area (p=0.159), education (p=0.782) and the average number of household members (p=0.984). The survey results showed that a high percentage of the childbearing age women in Pleven region are susceptible to infection with Parvovirus B19. Therefore, monitoring of anti-Parvovirus B19 status should be considered in this risk group.

Key words: anti-Parvovirus B19 IgG, childbearing age

EPIDEMIOLOGY OF CRYPTOSPORIDIUM SPP. IN HUMAN POPULATION IN PLEVEN REGION

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Summary

During the period 2002-2015, only 0.39% of patients with parasitic infections were *Cryptosporidium* spp. positive. For the Pleven region, this per cent was 0. We aimed to check the hypothesis for the presence of natural outbreaks of cryptosporidiosis and estimate the incidence and careership among risk groups in the Pleven's region. During the period 2016-2018 year, we collected 658 human faecal samples from different risk groups and their families. Five hundred seventy-one of them were tested with ELISA tests. Forty-two of the tested samples were positive for *Cryptosporidium* spp. We distributed them by age, gender, ethnicity, and symptomatic and asymptomatic cryptosporidiosis. The

highest was the per cent of the infected persons in the group of the children (2 to 7 years old) – 8.9 % and (0 to 2 years old) – 7.7 %. Ethnic distribution showed the highest percentage of infected Roma, as compared with the Bulgarian and Turkish population. Despite the absence of information in health records for infected people in the Pleven region, it was established that *Cryptosporidium* spp. parasitosis was present, mostly in children in early childhood and among the Roma population, without a clear distinction by sex. It is, therefore, necessary that professionals address the potential danger of widespread disease in the area, taking into account that age and ethnicity are the risk factors.

Key words: *Cryptosporidium* spp., Pleven region, age distribution, ethnical distribution