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Some epidemiological aspects of interepidemic meningococcal infection period in Moscow

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Background: The interepidemic meningococcal infection (MI) period in Moscow has been going since the 1989. Outbreaks of general forms of MI (GFMI) were registered in 1996, 2003, 2008 with their morbidity rates per 100,000 persons (MR) of 4.23, 3.63 and 2.59. In 2012 MR was at 1.56.

Methods & Materials: Meningococcus strains isolated from GFMI patients in Moscow Infectious Diseasaes Clinic were serogrouped, and the specifics of the immunological structure of the population of Moscow were defined.

Results: The predominance of meningococcal serogroup A (MSA) was shown. The highest MSA density was registered in 1996, 2003, 2008 (78.6, 61.5, 76.2%%). MSA density increased in 2009 - 2012 (47.7 - 83.7%%).

The study of the immunological structure of the population using passive hemagglutination test showed, that in 1993-2003 the number of MSA seropositive persons was high (70-90%).

The study conducted in 2004-2012 using enzyme immunoassay allowed both to estimate the state of immunity and indirectly asses the MSA circulation. The presence in the blood serum of IgM antibodies indicates a fresh infection; IgG - a previous infection and the presence of immunity; IgM + IgG - a fresh infection or reinfection.

The years 2004 - 2005 marked significant MSA circulation with a small amount of non-immune individuals. The proportion of adults with IgM, IgM + IgG antibodies was 65%, with IgG - 24%. In the years 2006-2010 the proportion of individuals with IgM, IgM + IgG, IgG decreased and the proportion of seronegative individuals increased.

The year 2011 resumed the tendency for the growth of the proportion of persons with IgM, IgM + IgG antibodies. In 2012 it reached 21.9% in adults and 15.6% in children. Proportion of persons with IgG antibodies decreased to less than 2%. Seronegative were 76.4% of adults and 83.1% of children.

Conclusion: The sporadic incidence of MI in Moscow does not diminish MSA's significance in the structure of GFMI. There is a tendency towards increased MSA circulation with the parallel large amount of non-immune individuals. The studies have to be continued in order to assess changes in the epidemiological situation and at the first sign of trouble to carry out adequate preventive measures.

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Genomic signature of multi-drug resistant *Salmonella typhi* related to the massive outbreak in Zambia year 2010 to 2012

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Background: Retrospectively, we investigated the epidemiology of massive *Salmonella enterica serovar* Typhi outbreak in zambia during 2010 to 2012.

Methods & Materials: Ninety-four isolates were susceptibility tested by MIC determinations. Whole genome sequence typing (WGST) of 33 isolates identified the multilocus sequence (MLST), haplotype, plasmid replicon, antibiotic resistance genes, and the genetic relatedness by Single Nucleotide Polymorphism (SNP) analysis and genomicdeletions.

Results: The outbreak affected 2,040 patients with a fatality rate of 0.5%. Most isolates (83.0%) were mult-idrug resistant(MDR) including 4.3% resistance to fluoroquinolones and 17.0% to azithromycin. WGST revealed the isolates, except one, belonging to MLST ST1 and a new variant of the haplotype; H58B. The isolates were clonal diversified containing 35 deletions, 415 SNPs and 21 bifurcation points in the phylogenetic tree with relation to starins from India and Central Africa. Most isolates contained an incQ-2 plasmid replicon harboring the resistance genes strA, strB, catA 1, bla_{TEM-1},

dfrA7 and sul1/sul2. The remaining isolates contained an incFIB replicon habouring the resistance genes strA, strB, bla_{TEM-1}, dfrA14, and sul2

Conclusion: In contradiction to the common view, that the emerging global S. Typhi haplotype;H58B containing the MDR inc H11 plamid type is responsible for the majority of typhoid infections in Asia and sub-Saharan Africa, we showed that a new variant of haplotype H58B habouring a new MDR plasmid replicon has emerged in Zambia with multiple clones being responsible for the outbreak

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