

Session: P100 Bacterial meningitis: diagnosis and epidemiology

Category: 2e. Skin, soft tissue, bone & joint & central nervous system infections

25 April 2017, 12:30 - 13:30
P2112

Molecular typing and antibiotics sensitivity of *Neisseria meningitidis* strains isolated in Algeria

Tali-Maamar Hassiba^{*1}, Laliem Rym², Badia Guettou³, Kheira Rahal³

¹*Institut Pasteur; Laboratoire de Bactériologie Médicale; Bacteriology*

²*Pasteur Institut; Laboratoire de Bactériologie Médicale; Bacteriology*

³*Institut Pasteur; Laboratoire de Bactériologie Médicale et de Surveillance de la Résistance Aux Antibiotiques*

Background: Invasive meningococcal disease is a public health problem, particularly for the meningitis form that is epidemic. Prevention of meningococcal disease is based on vaccination and chemoprophylaxis. Naturally competent for the transformation, the meningococcus takes a very important genetic variability. The main objective of our work is the determination of MLST profiles isolated *N.meningitidis* strains in Algeria and their sensitivity to antibiotics.

Material/methods: We collected 201 strains of meningococcus from 1992 to 2013. Identification strains is confirmed by PCR (*crgA*, *siaD*, *xcb* and *mynB*). Minimal inhibitory concentration is determined by E test to: penicillin, cefotaxime, chloramphenicol, rifampicin, azithromycin and ciprofloxacin. The determination of sequence type is performed by MLST (www.pubmlst.org/neisseria - Jolley and Maiden 2010, *BMC bioinformatics*, 11: 595), using amplification and sequencing of seven housekeeping genes (*abcZ*, *adK*, *aroE*, *fumC*, *gdh*, *pdhC* and *pgm*), the sequencing of the *penA* locus is performed for penicillin intermediate strains.

Results: Strains are collected from 23 districts, located mainly in the north. The Medea region is the most represented because of the epidemic observed in this district in 1998. Of these strains, 95% were from CSF and 5% of blood cultures. Three serogroups are predominant, A (48%), B (27%), W (14%). The frequency of strains with reduced susceptibility to penicillin was 10.4%, no resistance was found for ciprofloxacin, chloramphenicol, rifampicin, spiramycin and azithromycin. Sequencing the

gene *penA* found a new allele: *penA367*. Analysis of MLST profiles found several clonal complex: ST5 61.25% (n = 49), ST41 / 44 15% (n = 12), ST11 6.25% (n = 5), ST35 5% (n = 4), ST32 2,5% (n=2), ST22 2,5% (n=2), ST23 2,5% (n=2), ST1 1,25% (n=1), ST4 1,25% (n=1), ST167 1,25% (n=1) and ST174 1,25% (n=1).

Conclusions: This study reports for the first time the results of genotyping of *N. meningitidis* isolated in Algeria, it show the clonal diversity among strains. So, the current strategies for management of invasive meningococcal disease in our country, should not be taken to acquired. The clonal diversity justifies increased microbiological monitoring of *Neisseria meningitidis* strains. The revision of the national consensus of management of bacterial meningitis is essential.