27th ECCMID Vienna, Austria 22 – 25 April 2017
The congress of ESCMID

Session: EV015 Molecular diagnostics and MALDI-TOF

Category: 4b. Diagnostic bacteriology – non-culture based, including molecular and MALDI-TOF

22 April 2017, 08:45 - 15:30
EV0192

Performance of Andromas and Bruker MALDI-TOF MS in the identification of Neisseria

Florence Morel[1], Marine Desroches[2], Herve Jacquier[3], Vincent Fihman[4], Emmanuelle Cambau[5], Jean Winoc Decousser*[6], Beatrice Bercot[7]

[1]*Hôpital Lariboisière, Aphp; Microbiology*

[2]*Inserm Umr1137, Iame Evrest Team, Paris-Diderot University, Faculty of Medicine Xavier Bichat; University Hospital Henri Mondor; Department of Bacteriology and Infection Control (Ap-Hp)*

[3]*Groupe Hospitalier St Louis Lariboisière-Fernand Widal, Aphp; Service de Bactériologie-Virologie*

[4]*Centre Hospitalo-Universitaire Henri Mondor; Département de Microbiologie*

[5]*Hôpital Lariboisière; Service de Bactériologie-Virologie*

[6]*Hopital Henri Mondor; Department of Bacteriology*

[7]*Groupe Hospitalier St Louis Lariboisière-Fernand Widal, Aphp; Servicede Bactériologie-Virologie, Centre National de Référence des Gonocoques*

Background: The reliable identification of *Neisseria* in the genital or oropharyngeal flora is crucial, especially for the management of patients suspected of sexually transmitted infections. Thus, the discrimination between *N. gonorrhoeae, N. meningitidis* and commensal species of *Neisseria* is fundamental in the microbiological diagnosis and management of patients.
In this study, we propose to compare the performances of Andromas and Bruker MALDI-TOF mass spectrometry systems in the identification of *Neisseria* isolates.

Material/methods: A total of 137 *Neisseria* collection strains were used in this study, corresponding to 29 commensal *Neisseria* isolates, 88 *N. gonorrhoeae* (NG) and 20 *N. meningitidis* (NM). The 29 commensal species were all identified by 16S rDNA PCR/sequencing, and included 13 *N.*

subflava/perflava, 6 *N. macacae/mucosa*, 4 *N. elongata*, 1 *N. wearveri*, 1 *N. cinerea,* 1 *N. bacilliformis*, and 1 *N. wadsworthi.* The 88 NG corresponded to 79 isolates collected by the French National Reference Centre for Gonococci, 8 WHO reference isolates and the F89 multidrug resistant isolate; and were typed using *tbp*B and *por*B genes. The 20 *N. meningitidis* consisted of 13 clinical isolates from meningitis and 7 reference strains, and were identified by 16S rDNA PCR/sequencing. All isolates were cultured on chocolate agar plates and incubated 24h under 5 % CO2 atmosphere, and submitted in parallel to Andromas and Bruker MALDI-TOF mass spectrometry systems.

Results: All the NG isolates were correctly identified. Concerning the NM isolates, only one of them, corresponding to a non-capsulated isolate, was not identified by both methods. For commensal species, all *N. macacae/mucosa, N. elongata*, *N. wearveri*, *N. cinerea, N. bacilliformis* were correctly identified by both systems. *N. wadsworthii* lacks in databases and did not yield any identification by both systems. For 12/13 *N. subflava/perflava,* 12 were identified as *N. flavescens*, *N. perflava* and *Neisseria* spp. by Bruker systems and correctly identified by Andromas system. The remaining *N. subflava/perflava* was misidentified as *N. meningitidis* by Bruker system, and did not yield any identification by Andromas.

Conclusions: In our study, the identification of clinical and reference isolates of *N. gonorrhoeae* and *N. meningitidis* was successful for both systems. For commensal species*,* only one major discrepancy (ie between a commensal and pathogenic species) was reported for Bruker system. As a conclusion, Andromas and Bruker MALDI-TOF mass spectrometry systems are reliable tools for identification of commensal and pathogenic species of *Neisseria.*