27th ECCMID Vienna, Austria 22 – 25 April 2017

The congress of ESCMID

Session: OS202 MALDI-TOF - diagnostics for the micro lab in the 21st century

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

25 April 2017, 15:18 - 15:28
OS1035

Using MALDI-TOF MS complemented with selected genes (16S rRNA gene, gyrB gene) sequencing to practically identify clinical important Viridans group streptococci

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Background: Clinical significant Viridans Group Streptococci(VGS) identification is important but problematic in particular for the Streptococcus mitis group. MALDI-TOF MS is very practical for clinical identification but for some problematic species, selected gene sequencing is necessary in order to make the identification more reliable. Some studies evaluating the MALDI-TOF MS performance in VGS identification have been done but most are of limited numbers or just evaluate some certain brand of MALDI-TOF MS machines, such as MALDI Biotyper or VITEK MS alone.

Material/methods: We continuously collected 181 clinical VGS isolates. Using 16S rRNA or *gyrB* sequencing as a gold standard, all the isolates were identified to the species level. On the basis of that, the performance of two MALDI-TOF MS instruments: the MALDI Biotyper IVD system and the VITEK MS including the IVD and the RUO system were evaluated.

Results: The MALDI Biotyper identified 88.4%, the VITEK MS IVD 98.9% and the RUO 38.7% of the isolates correctly to the species level, among which most misidentifications were in the Mitis group with 95.5%(21/22) non-pneumococci misidentified as *S.pneumonia*, leading to a low sensitivity and positive predictive value in these species. Accordingly, sensitivity and negative predictive value was 100% for *S.pneumonia*. The VITEK MS IVD, on the other hand, had a better resolution for pneumococci and non-pneumococci despite the inability to distinguish between *S.mitis*/*S.orlis* while the VITEK MS RUO showed a relative low efficiency in whatever VGS species.

Conclusions: Both MALDI-TOF MS IVD systems can provide a good alternative for VGS identification but need further improvements of VGS spectra database for more accurate species-level identification while the VITEK RUO system showed the least significance. So far, gene-based sequencing remains the best way to correctly identify VGS species and 16S rRNA gene plus gyrB gene are good selective targets.