

P2382 Comparison of *Aspergillus* sp. identification using a simplified and rapid extraction procedure coupled with MALDI-TOF MS

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Background: General bacteria can be routinely identified using an on-plate-mass spectrometric method. However, identification of filamentous fungi requires cumbersome pretreatment. Therefore, we devised simple pretreatment methods and verified the identification accuracy using *Aspergillus* spp., the most frequently isolated filamentous fungi in the past five years in Japan.

Materials/methods: Forty-nine clinical isolates of *Aspergillus* spp. (12 *A. fumigatus*, 13 *A. flavus*, one *A. versicolor*, two *A. sydowii*, eight *A. niger*, one *A. nidulans*, 12 *A. terreus*) were pretreated using the manufacturer's protocol (conventional method: Biomerieux Japan and Bruker Daltonics). Two variant pretreatment methods were evaluated in this study. In the yeast-like pretreatment method (MF method), a single colony is suspended in sterilized water, followed by addition of ethanol. Formic acid (70%) and matrix were added on the target plate. In the improved method, the cell suspension is mixed with 70% formic acid and added on the matrix on a target plate to shorten the operation time. Fungi were identified using VITEK mass spectrometry (MS) and MALDI Biotyper, and the identification accuracy was verified.

Results: The improved method showed higher working efficiency. Verification of the accuracy of species identification showed that the identity of all strains obtained using the conventional and variant methods (both MF and improved), followed by MS, were identical. In contrast, the identification result obtained using Biotyper were in agreement between the conventional and MF methods for 13 strains (26.5%) and the improved method for 29 strains (59.2%), with a score value of ≥ 1.7 . Comparison based on the type of fungi showed that the agreement rate with the conventional method was higher for *A. niger* with the MF method and for *A. fumigatus* and *A. terreus* with the improved method.

Conclusions: We compared the agreement rates of the conventional method and the two variant pretreatment methods. All strains examined yielded identical results with the conventional pretreatment method and either of the variant treatments in MS. Thus, we suggest that the working efficiency can be improved while maintaining high identification probability using the improved pretreatment method for MS-based filamentous fungi identification.