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Rapid and reliable species identification of wild mushrooms by MALDI-TOF MS

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The morphological inspection has been traditionally used for the identification of mushrooms, whereas recent DNA sequencing applied successfully. This study focuses on a simpler and more rapid methodology for the identification of wild mushrooms via protein profiling based on MALDI-TOF MS. A preliminary study using 6 commercial mushrooms suggested that a more reproducible spectrum was obtained from a portion of the cap than from the stem of a fruiting body. We used 157 wild mushroom-fruiting bodies collected in 2014. Sequencing analysis of rDNA provided 134 identifications of mushrooms by genus or species. MALDI-TOF MS analysis (Bruker) yielded a reproducible spectrum for 114 of 157 samples. Profiling scores that matched each other within the database gave correct species identification (with scores of ≥2.0) for 110 samples (96%). An in-house prepared database was constructed from 106 independent species. We used 48 wild mushrooms that were collected in 2015 to validate the in-house database. As a result, 21 mushrooms were identified at the species level with scores ≥2.0 and 5 mushrooms at the genus level with scores ≥1.7, although the signals of 2 mushrooms were insufficient for analysis. The remaining 20 samples were recognized as "unreliable identification" with scores <1.7. Subsequent DNA analysis confirmed that the correct identifications were achieved by MALDI-TOF MS for the 26 former samples, whereas the 18 mushrooms with poorly matched scores were species that were not included in the database. Thus, the proposed MALDI-TOF MS could be a powerful tool for the rapid and reliable identification of mushrooms.

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