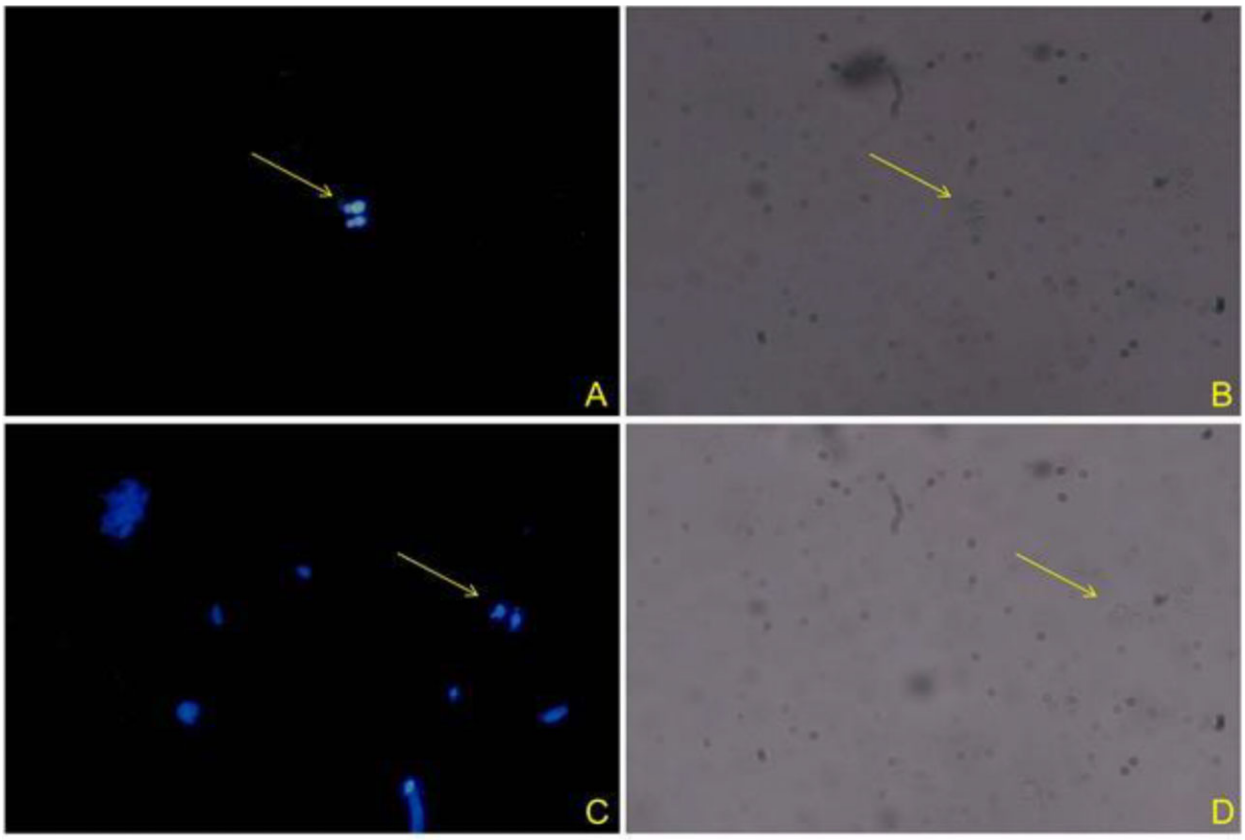


**P416**

**Efficient and accurate diagnosis of otomycosis using an ensemble deep learning model**

Mao Chenggang[1], Li Aimin[1], Wang Juehui[2], Sun Yi[1], Peng Dan[1]
[1]Jingzhou Hospital Affiliated To Yangtze University, Jingzhou, China
[2]Jingzhou University, Jingzhou, China

Poster session 3, September 23, 2022, 12:30 PM - 1:30 PM

Objectives: Otomycosis accounts for >15% of the cases with external otitis worldwide. And otomycosis is more frequently observed in humid regions and people enjoying the culture of ear cleaning in China. *Aspergillus* and *Candida* are the major pathogens that could cause long-term infection. Early endoscopic and microbiological examinations are important for appropriate medical treatment to otomycosis. However, accurate diagnosis always needs experts such as otologist and microbiologist. Deep learning model is a novel efficient method to provide quick diagnosis which is an automatically diagnostic program using a large database of images acquired in the cliniC. This paper puts forward a mechanic learning model to address the diagnosis of otomycosis caused by *Aspergillus* and *Candida* accurately and quickly.

Methods: We proposed a computer-aided decision system that is based on a deep learning model consisting of two subsystems, a java-based web application, and picture classification. The web application subsystem mainly provides a user-friendly page for collecting consulted pictures as well as displaying the calculation results. The picture classification subsystem mainly uses trained neural network models for end-to-end data inference. The end user only needs to upload a few pictures of the ear endoscope, and the system will return the classification results to the user in the form of category probability value.

In order to accurately diagnose otomycosis, we generally kept endoscopic images and took the secretion for fungal culture for further identification. Positive fluorescence fungal staining, culture, and further DNA sequencing were taken to confirm the pathogens, *Aspergillus* or *Candida* sp. In addition, impacted cerumen, external otitis, and normal external auditory canal endoscopic images are retained for reference. We merged these four types of images into an endoscopic images gallery.

Results: In order to achieve better accuracy and generalization ability after model training, we selected 2750 samples from nearly 4000 ear endoscopic images as training samples and 454 as validation samples. On the selection of deep neural network models, we tested the resnet, senet, and efficientnet neural network models with different numbers of layers. Considering the accuracy and operation speed, we finally chose the efficientnet-b6 model and output the probability values of the four categories of otomycosis, external otitis, impacted cerumen, and normal cases. After multiple iterative sample training, the overall validation sample accuracy reached 94.71%, and the average cross-validation accuracy of the 4 classifications reached 94.3%.

Conclusion: The results suggest that the system can be used as a reference for general practitioners to make better decisions in the diagnosis of otomycosis.

**P417**

**Evaluation of matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS)-Bruker Biotyper Sirius for identification of invasive molds**

Mousami Dalvi, Sampada Patwardhan, Parikshit Prayag, Bharat Purandhare, Rajeev Soman
Deenanath Mangeshkar Hospital, Pune, India

Poster session 3, September 23, 2022, 12:30 PM - 1:30 PM

Objectives: Susceptibility to various antifungal drugs varies between different species and subspecies within the same genus. Phenotypic identification of fungi has limitations for species-level identification. Correct identification of species and subspecies in invasive mold infections is important to initiate the appropriate antifungal therapy. Matrix Assisted Laser Desorption Ionization Time-of-Flight mass spectrometry (MALDI-TOF MS) with its proteomic analysis overcomes this limitation and helps in administering the correct anti-fungal therapy. A total of seven mold isolates from invasive fungal infections were evaluated for identification by MALDI-TOF MS and conventional morphological methods.

Methods: Total of seven isolates from invasive mold infections were identified by the conventional method of culturing specimens on Sabouraud's dextrose agar and Potato Dextrose agar with incubation at room temperature and 37°C in Biological oxygen demand (BOD) incubator. Micro-morphological identification of the fungus was done by Lacto Phenol Cotton Blue (LPCB) mount. Same isolates were processed on MALDI-TOF MS Bruker Biotyper Sirius (Bruker Daltonics, Bremen Germany) following recommended extraction protocol using ethanol absolute, acetonitrile, and 70% formic acid.

Results: As per the below Figure.

Conclusion: In four out of seven isolates phenotypic identification upto species level based on LPCB micromorphology was confirmed on MALDI-TOF MS. In the remaining three isolates we could only give a genus level identification based on LPCB mount. These three isolates were further identified upto the level of species after processing on MALDI as *Aspergillus tamarii*, *Phaeoacremonium cinerum*, and *Fusarium equiseti*. All mold isolates were identified with good quality mass spectra. In our experience, mold identification by MALDI-TOF MS using the Bruker Biotyper Sirius platform definitely has an edge over conventional phenotypic methods in species-level differentiation of various molds, impacting targeted antifungal management.