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Efficient and accurate diagnosis of otomycosis using an ensemble deep learning model
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Objectives: Ototmycosis accounts for >15% of the cases with external ear infections. 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 machine learning model to address the diagnosis of otomycosis caused by Aspergillus and Candida accuracy and quickly.

Methods: We proposed a computer-aided diagnosis system that is based on a deep learning model consisting of two sub-systems, a meta-based web application, and picture classification. The web application sub-system 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 sectum for fungal culture for further identification. Positive fluorescent fungal staining, culture, and further DNA sequencing were taken to confirm the pathogens, Aspergillus or Candida sp. In addition, impregnated cerumen, external otitis, and normal external auditory canal endoscopic images are retained for reference. We merged these five types of images into an endoscopic image 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 vgg16, vgg19, 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 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.

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Evaluation of matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS)-Bruker Biotyper Sirius for identification of invasive molds
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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 antifungal 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 55°C in Biological oxygen demand (BOD) incubator. Micro-morphological identification of the fungi was done by Laser Phased 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 figures.

Conclusions: 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 fumigatus, Phacoderomum curvatum, and Bactaris sp. 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.
Objectives: Candida auris is an emerging fungal pathogen responsible for hospital outbreaks. It represents a serious threat due to its drug resistance profile and its potential spread within healthcare facilities. Since the global alert by the CDC in 2016, specific control measures are now available to prevent the further spread of the pathogen. These measures should be implemented immediately as soon as a case is identified to prevent patient-to-patient transmission. Until recently, culture was the main technique used for the detection of C. auris from patient and environmental samples. Nevertheless, PCR protocols have been reported and commercial kits are now available. Our objective was to compare culture and PCR in routine for the management of a case of C. auris infection in a hospital setting.

Methods: We report here the case of a patient infected by C. auris following injuries in a public road traffic accident in Delhi. Following the medical evacuation and transfer of the patient to our hospital in Paris, C. auris was isolated from several surgical swabs from the elbow. Identification of the species level was initially performed by MALDI-TOF Mass spectrometry and confirmed by ITS sequencing. Antifungal susceptibility testing was performed by Etest and EUCAST. Surveillance of the index case included bronchoalveolar surveillance for 2 weeks and then once a week. Contact was also screened for C. auris colonization once a week by oral swabbing and groin. Samples were analyzed by standard mycological cultures and a specific C. auris qPCR kit (kit Fungaplex Candida auris®).

Results: In total 133 samples were analyzed for the patient and 52 controls. For the index case, 142 samples were positive in culture for C. auris including, elbow lesions, skin and axilla, groin, and rectal swabs. Other Candida species (C. albicans, C. glabrata) were also recovered from the same samples for the patient. For the controls, all 111 samples were negatives for C. auris by culture, but not more several other yeast species (C. albicans, C. glabrata, C. krusei, C. parapsilosis, C. tropicalis, K. krusei, and Rhodotorula glutinis). By using qPCR, all culture-positive samples were positives (C ranged from 29.7 to 38.0, with a median at 31.6). Two culture-squares samples (one biopsy and one auditory swab) were also qPCR positive. All samples from controls were negatives by qPCR. The strain was resistant to fluconazole (≥2 μg/ml) and susceptible to all other antifungals (amphotericin B, caspofungin, voriconazole, and anidulafungin). Whole genome sequencing of the C. auris strain is in progress to determine the clade.

Discussion: The Fungaplex C. auris qPCR kit described good sensitivity and specificity, even for the frequent structure of samples growing with two or three Candida species. These results highlight the usefulness of the PCR for surveillance of infected patients as well as for controls.