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1255P Evaluating GPT-4 as an academic support tool for clinicians: A comparative analysis of case records from the literature

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Background: Artificial Intelligence (AI) and Natural Language Processing (NLP) advancements have led to sophisticated tools like GPT-4.0, allowing clinicians to explore its utility as a healthcare management support tool. Our study aimed to assess GPT-4's ability to suggest the definitive diagnosis and the most appropriate work-up to minimize unnecessary procedures.

Methods: We conducted a retrospective comparative analysis, extracting relevant clinical data from 10 cases published at NEJM after 2022 and inputting it into GPT-4 to generate diagnostic and workup recommendations. Primary endpoint: the ability to correctly identify the final diagnosis. Secondary endpoints: its ability to list the definitive diagnosis in the five most likely differential diagnoses and determine an adequate workup.

Results: The AI could not identify the definitive diagnosis in 2 out of the 10 cases (20% inaccuracy). Among the 8 cases correctly identified by the AI, 5 (63%) had the definitive diagnosis as the top differential diagnosis list. Regarding the suggested diagnostic tests and exams, requests for exams that would not aid in the patient's final diagnosis were made in 2 cases, representing 40% of the patients whose final diagnosis was not correctly identified by the AI. Moreover, the AI could not suggest adequate treatment for 7 cases (70%). Among them, the AI suggested inappropriate management for 2 cases, and the remaining 5 received incomplete or non-specific advice, such as chemotherapy, without specifying the best regimen.

Conclusions: Our study demonstrated GPT-4's potential as an academic support tool, although it cannot correctly identify the final diagnosis in 20% of the cases. There is also a limitation regarding the management suggested by AI. In cases where the main diagnostic hypothesis was incorrectly identified or not listed as the top differential diagnosis, the AI requested unnecessary additional diagnostic tests for 40% of the patients. Future research should focus on evaluating the performance of GPT-4 using a more extensive and diverse sample, incorporating prospective assessments, and investigating its ability to optimize diagnostic and therapeutic procedures to optimize healthcare utilization.

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1256P Value of detection of peripheral blood circRNA based on digital PCR in the diagnosis of lung adenocarcinoma

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Background: Lung cancer is a cancer type with high morbidity and mortality in the word, the clinical prognosis of lung cancer patients is still poor, the main reason is the lack of effective early screening and diagnosis methods. Plasma circRNAs detected by droplet digital PCR may be ideal markers for liquid biopsy. However, droplet digital PCR detection of circRNAs in plasma for (early) diagnosis of lung adenocarcinoma has been rarely reported.

Methods: RNA sequencing analysis was performed in plasma from patients with early lung adenocarcinoma and healthy individuals. Droplet digital PCR was used to verify the differentially expressed genes. We evaluated their diagnostic efficacy and predict their biological functions of target genes.

Results: The copy numbers of circLZIC and circCEP350 in the plasma of lung adenocarcinoma patients were significantly higher than in plasma of healthy people ($P < 0.01$), they are closely related to tumor size ($P < 0.05$) and TNM stage ($P < 0.05$),and the copy numbers in postoperative plasma of the same patient were significantly lower than those in preoperative plasma ($P < 0.05$).ROC curve analysis showed that circLZIC (AUC=0.782) and circCEP350 (AUC=0.764) alone and in combination (AUC=0.863) had diagnostic value in lung adenocarcinoma, circLZIC (AUC=0.786) and circCEP350 (AUC=0.546) alone and in combination (AUC=0.803) had diagnostic value in early lung adenocarcinoma.Bioinformatics analysis revealed that circLZIC and circCEP350 had more binding sites with multiple microRNAs. Their target genes were enriched in several signaling pathways.

Conclusions: The copy numbers of circLZIC and circCEP350 were higher in plasma of lung adenocarcinoma patients than in plasma of healthy controls, significantly correlated with tumor size and TNM stage, and closely related to the occurrence and development of tumors. These circRNAs may serve as molecular markers for the diagnosis of lung adenocarcinoma.

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1257P Double heterozygous prevalence in hereditary cancer syndromes in Northern Mexico population

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Background: Double heterozygous (DH) is a rare event, in DH patients, two pathogenic variants (PV) in two genes are present in the genomic DNA. Next-generation sequencing technologies with expanded gene, and affordable and more complete tools for diagnosis in hereditary cancer field, resulted in the identification of unexpected variants, including more than one variant in a single patient. The aim of this study was to identify the prevalence of double heterozygous and determine the effect of two pathogenic variants in hereditary cancer syndromes patients from Northeast Mexico.

Methods: This multicentric study included patients from the CECIL (The CUCC Early Cancer Detection Clinic) Hereditary Cancer Registry, and from the Hereditary Cancer Program from Tec Salud. Both centers accomplish patients of the Nuevo León state and adjacent states of Northern Mexico. Patients were recruited in a period of 7 years (from March of 2016 to March of 2023), a total of 872 patients were evaluated by Medical Geneticists and tested with NGS multigene cancer panel tests.

Results: A total of 294 (33.7%) patients had at least one PV, and 9 (3%) DH (two PV). Of all the DH patients, 8 (88.8%) had the clinical diagnosis of HBOC (Hereditary Breast Hereditary Cancer Syndrome), and one (11.1%) had Lynch Syndrome diagnosis. The mean age of cancer diagnosis was 42.8 years, compared with 40.3 mean for all the analyzed patients. None of the DH patients (0%) had synchronic or metachronic neoplasias diagnosed, compared to 19 (6.46%) with one PV patients. Among the identified variants BRCA1/2 and other homologous repair genes were found in 8 (88.8%) patients. The most frequent gene identified was MUTYH in 5 (55.5%) patients, surprisingly the variant c.1187G>A, known as a founder mutation in Northern Europe, was found in 4/5 (80%). These four Mexican patients had not known European ancestry.

Conclusions: This study suggest that the concurrence of two pathogenic variants did not impact the age of diagnosis or the risk of developing multiple neoplasia. variant c.1187G>A *MUTYH* founder mutation is frequent in our mestizo population and the most frequently found in the double heterozygous state.

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1258P Does FDG PET-based radiomics have an added value for prediction of overall survival in non-small cell lung cancer?

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Background: Machine-learning and radiomics are promising approaches to improve the clinical management of NSCLC. However the additive value of FDG-PET based radiomic compared to clinical and standard imaging variables is less investigated. We