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Letters to the editor

Comment on "Development of machine learning-based personalized predictive models for risk evaluation of hepatocellular carcinoma in hepatitis B virus-related cirrhosis patients with low levels of serum alpha-fetoprotein"

Dear Editor,

Xu et al. [1]. have recently published a study focusing on developing personalized risk prediction models for hepatocellular carcinoma (HCC) in patients with hepatitis B virus-related cirrhosis, particularly in those with low levels of serum alpha-fetoprotein (AFP). This research emphasizes the use of machine learning techniques to improve risk assessment and facilitate early HCC detection in this high-risk population, where conventional biomarkers may fall short. By employing these tailored predictive models, the study seeks to enhance the precision of risk evaluations and potentially support more targeted monitoring and intervention approaches for individuals at elevated risk of HCC. However, some potential concerns need to be addressed and clarified further.

Firstly, as outlined in the abstract [1], "*This study aimed to develop personalized predictive models by combining machine learning (ML) technology with a demographic, medical history, and noninvasive biomarker data.*" Nevertheless, the models developed in this study did not account for medical history. It is well established that antiviral treatment plays a crucial role in managing the risk of HCC in patients with hepatitis B virus [2,3]. Different antiviral therapies can significantly affect patient outcomes. For instance, a multicenter cohort study [4] of 372 individuals receiving entecavir demonstrated that virological response to this drug was associated with a reduced likelihood of disease progression in patients with cirrhosis. This finding suggests that entecavir positively influences virological response in cirrhotic patients, potentially slowing HCC progression. Therefore, integrating antiviral treatment strategies into the predictive frameworks could enhance the models' predictive accuracy and clinical relevance.

Secondly, the level of hepatitis B virus DNA represents a pivotal biomarker for evaluating the likelihood of HCC and possesses considerable clinical and prognostic relevance. A research investigation conducted by Lin et al. delineates the robust association between heightened HBV DNA concentrations and the onset of HCC. This observation highlights the profound and multifaceted impact of HBV on the process of hepatocarcinogenesis, offering critical insights into the fundamental mechanisms that govern tumorigenesis in individuals with chronic infection. Consequently, the integration of HBV DNA quantification within this established predictive risk models is not merely justified but is imperative for enhancing the precision of HCC risk stratification.

Thirdly, it is important to mention that several critical details are missing in this study [1]. It is unclear whether the patients had newly diagnosed HCC or liver cirrhosis, which could significantly impact disease progression and prognosis. Additionally, there is no information regarding whether the patients were undergoing radiation therapy or chemotherapy, both of which could influence laboratory results, such as alkaline phosphatase, serum alpha-fetoprotein, direct bilirubin, and hemoglobin levels. Furthermore, the stage of HCC, a key determinant of prognosis and treatment strategy, is not provided. In addition, the lack of information about liver resection or other interventions also complicates the interpretation of the prediction model. These omissions limit the model's applicability and present challenges for clinical decision-making and personalized treatment planning.

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Declaration of interests

None.

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[1] Xu Y, Zhang B, Zhou F, Yi YP, Yang XL, Ouyang X, et al. Development of machine learning-based personalized predictive models for risk evaluation of hepatocellular carcinoma in hepatitis B virus-related cirrhosis patients with low levels of serum alpha-fetoprotein. Ann Hepatol 2024;29(6):101540.
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