Topic : Basic Research

GENOMIC BIOMARKERS TO PREDICT RESPONSE TO COMBINATION IMMUNOTHERAPY IN HEPATOCELLULAR CARCINOMA

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Background : Combination immunotherapy, such as atezolizumab plus bevacizumab, is now the standard of care for inoperable hepatocellular carcinoma (HCC). However, the lack of predictive biomarkers and understanding of response mechanisms remains a challenge.

Methods : Using data from the IMbrave150plus cohort, we applied the immune signature score (ISS) predictor to stratify HCC patients treated with atezolizumab plus bevacizumab or sorafenib into potential high and low response groups. By applying multiple statistical approaches including Bayesian covariate prediction algorithm, we refined the signature to 10 key genes (ISS10) for clinical use while maintaining similar predictive power to the full model.

Results : The study identified a significant association between the ISS and treatment response. Among patients classified as high responders, those treated with the combination exhibited improved overall and progression-free survival compared to those treated with sorafenib. Analysis of immune cell subpopulations revealed distinct characteristics between ISS subtypes. The ISS10 high subtype displayed a more favorable immune environment with higher proportions of anti-tumor macrophages and activated T-cells, potentially explaining its better response. Additionally, the study found a link between the ISS10 and hepatic stem cell features, suggesting potential avenues for further investigation.

Conclusions : Our study suggests that ISS and ISS10 are promising predictive biomarkers for enhanced therapeutic outcomes in HCC patients undergoing combination immunotherapy. These markers are crucial for refining patient stratification and personalized treatment approaches to advance the effectiveness of standard-of-care regimens.

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