immunotherapy could be adapted. Further investigations required to map the immune evasion machinery for each type of cancer and design the best targets for personalised immunotherapy of human malignancies.

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P02 Tumor microenvironment and microbiome in immunotherapy

A BIOINFORMATIC ANALYSIS: THE OVEREXPRESSION AND CLINICAL SIGNIFICANCE OF HVEM IN LIVER HEPATOCellular CARCINOMA

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Background The occurrence and development of liver cancer is related to the immune evasion caused by abnormal expression of immune costimulatory molecules in liver cancer cells. High expression of herpesvirus entry mediator (HVEM) was associated with tumor progression and reduced patient overall survival in multiple cancers. Overexpression of HVEM may lead to binding with inhibitory co-receptor B- and T-Lymphocyte Attenuator, downregulating T cell activation and proliferation, and mediating immune evasion in tumor immune microenvironment. However, clinical significance of HVEM overexpression in liver hepatocellular carcinoma (LIHC) and its relation to immunity remains unknown.

Materials and Methods We obtained expression profiles of HVEM in pan-cancer and LIHC through The Cancer Genome Atlas (TCGA) and Genotype-Tissue Expression. Expression of HVEM in LIHC was then validated by immunohistochemical staining in Human Protein Atlas (HPA). Additionally, we evaluated the prognostic value and association of clinicopathological factors to HVEM in LIHC with clinical survival data from TCGA. A risk prognostic nomogram model using Cox regression analysis was constructed to identify important LIHC prognostic indicators. Finally, we evaluated the correlation of HVEM with 24 immune cell infiltrates based on single sample gene set enrichment analysis.

Results Paired data from TCGA LIHC dataset indicated HVEM overexpression in LIHC compared to normal liver tissues (p < 0.001, normal = 50, tumor = 50). Unpaired data showed similar results (p = 0.001, normal = 160, tumor = 371). Additionally, immunohistochemical staining of HVEM in normal liver tissues was weak in HPA database but strong in LIHC tissues. High HVEM expression was strongly associated with worse overall survival [Hazard Ratio (HR) = 1.60 (1.13–2.26), p = 0.008], disease-specific survival [HR = 1.63 (1.03–2.26), p = 0.035], and progress free interval [HR = 1.35 (1.00–1.82), p = 0.048] in LIHC patients. Alpha-fetoprotein levels, Child-Pugh score, fibrosis ishak score, histological grade, T stage, M stage, and N stage are benchmarks associated with cancer progression. Logistic regression analysis revealed significantly higher HVEM expression in LIHC patients with greater cancer progression according to those benchmarks. Additionally, Cox risk regression analysis indicated that HVEM might be an independent prognostic factor for LIHC patients (p = 0.016). Nomogram calibration was performed on the constructed nomogram, revealing a C-index of 0.67, indicating good predictive ability. Functional enrichment and Gene Ontology analyses and Kyoto Encyclopedia of Genes and Genomes pathway analysis showed HVEM association with immune-related genes and pathways respectively. HVEM was positively correlated with the abundance of tumor-infiltrating immune cells like DC, B cells, CD8 T cells, macrophages, NK cells, Th1 cells, and Th2 cells, and negatively correlated with the abundance of TCM and TEM, suggesting association between HVEM and infiltration by immune cells.

Conclusions In conclusion, our findings demonstrated high expression of HVEM in LIHC patients and is a potentially dangerous prognostic predictor of LIHC. We also found a correlation between HVEM immune-related signaling pathways and immune cell abundance, which may affect progression and prognosis of LIHC patients.

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EASY AND SCALABLE TRANSFER OF AN IMMUNO-Oncology PANEL ACROSS A WIDE RANGE OF CANCER TISSUE TYPES

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Background Therapies based on checkpoint inhibitors have emerged as promising strategies in the treatment of cancer patients. The selection of the most efficient combination of immunotherapies along with the accurate prediction of cancer prognosis are unmet endeavors. Thus, scientists and clinicians need deeper knowledge of the immune profile of each patient as well as a detailed characterization of the tumor microenvironment (TME) to develop targeted therapies. Multiplex immunofluorescence (mIF) has become an important tool in the immune profiling of the TME. Ideally, multiplex IF assays should allow for the study of multiple markers in the same tissue sample while preserving the spatial information of tissue morphology. Despite a fast-growing need of multiplex methods, the broad implementation of mIF still remains challenging due to several technical barriers. Assays require robust validation but also a large degree of flexibility to be used across multiple tissue types.

Materials and Methods Here we present COMET™, an innovative solution to easily develop mIF assays that work as a fully automated staining and imaging platform allowing for hyperplex staining with up to 40-markers in just a few hours, without human intervention. COMET™ performs sequential immunofluorescence assays, which consist of sequential cycles of staining, imaging, and elution of two markers per cycle. With the aim of phenotyping different immune and cancer cells and their functional states in epithelial tumors, we...