Ruprecht-Karls-Universität Heidelberg
Medizinische Fakultät Mannheim
Dissertations-Kurzfassung

Deep view of hepatocellular carcinoma gene expression signatures and their comparison with other cancers

Autor: Yuquan Qian
Institut / Klinik: II. Medizinische Klinik
Doktorvater: Prof. Dr. med. Dr. rer. nat. A. Teufel

Gene expression signatures correlate genetic alterations with specific clinical features, providing the potential for clinical usage. Over the last two decades, numerous HCC-dependent gene expression signatures have been developed. However, unlike breast and colorectal cancers, none of HCC gene expression signatures have been utilized in clinical practice. This study is the first to widely investigate the specificity of HCC gene expression signatures, which is an essential aspect for their clinical applications.

In this thesis, I investigated the specificity of public HCC gene expression signatures by conducting a comparative transcriptomic analysis and comparing them with the clinically or commercially available gene expression signatures for breast and colorectal cancer. My results reveal that (1) the evaluated HCC gene expression signatures display significant potential specificity to other cancers, notably breast and colorectal cancer. However, none of these gene expression signatures exhibit strict specificity to HCC exclusively. (2) Additionally, my work demonstrates that all these HCC gene expression signatures have no or very little overlap in terms of common core genes and enriched pathways. (3) My study also highlights the absence of a standardized and consistent approach in generating these HCC gene expression signatures, specifically in regards to gene expression platform, algorithm to screen signature genes, and source of the samples. Thus, in order to develop HCC gene expression signatures with greater specificity to HCC, rigorous and feasible standards in data formatting, sample storage, and gene expression signature generation methods were proposed in this study, which we believe can aid in the development of more targeted therapies for this challenging cancer.

In conclusion, my thesis has revealed that (1) the present HCC gene expression signatures lack specificity, (2) variations in core genes, enrichment pathways, and generation methods could be the underlying reasons. (3) My data also help to develop more specific HCC gene expression signatures by proposing corresponding criteria during the establishment of gene expression signatures.