

Proteomic Profiling of iCCA: A Multicentric Study within the DKTK Network

Intrahepatic cholangiocarcinoma (iCCA) is a rare and highly aggressive primary liver cancer associated with limited therapeutic options, late-stage diagnosis, and poor prognosis. Despite recent advances in genomic profiling, the biological complexity and clinical heterogeneity of iCCA remain poorly understood.

To address this, we are currently assembling a multicentric cohort of iCCA tumor samples through the German Cancer Consortium (DKTK) partner sites and the Clinical Communication Platform (CCP). Tumor samples will be processed using standardized and semi-automated protocols, followed by deep proteomic profiling via high-resolution liquid chromatography–mass spectrometry (LC-MS/MS). A central goal of this project is to integrate clinical parameters—including patient demographics, treatment histories, and outcomes—with proteomic data to identify molecular patterns associated with prognosis and therapeutic response.

The study builds on prior work from an independent American iCCA cohort, where proteomic analysis identified two major tumor subtypes: one enriched in extracellular matrix components, and another characterized by altered RNA processing and a higher risk of recurrence. Using a machine learning-based classification model, we could already validate these results in a local Freiburg iCCA cohort.

With the expanded DKTK cohort, we now aim to further validate and refine these molecular subtypes, discover novel protein-level biomarkers, and support the development of proteome-informed clinical strategies.

Preferred type of presentation

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