Primary sclerosing cholangitis (PSC) is a rare, progressive disease with no effective treatment and reliable prognostic biomarkers. CCL24, a chemokine with a fibro-inflammatory activity is overexpressed in damaged bile ducts. CCL24 blockade with the neutralizing antibody CM-101 was shown to be safe and active in early clinical trials and is currently being evaluated in a PSC phase 2 clinical study.

**Aim**

We present a machine learning analysis of serum proteins and clinical stages of PSC, aimed to highlight proteins associated with the disease, including exploration of serum CCL24 levels as a potential predictor of PSC-related complications, such as cirrhosis.

**Method**

Sera from 30 healthy controls (HC) and 45 patients with PSC were profiled with Olink PEA, quantifying the expression of 2870 proteins and used to train an elastic net model.

**Results**

Machine learning successfully predicted the presence of PSC, focusing on a 16-protein signature for disease severity. Further, CCL24 was linked to cirrhosis in patients with PSC.

**Conclusions**

Robust proteomic profiling of patients with PSC led to a useful model highlighting a protein signature in disease presence and progression, and CCL24 as linked to cirrhosis. These findings underscore the significance of targeting CCL24 in PSC treatment while the proteomic pattern associated with ELF score may offer promise as a biomarker in the ongoing clinical trial utilizing CM-101—a neutralizing monoclonal antibody targeting CCL24.

**References**


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