Methods In this study, 129 patients with varying degrees of liver fibrosis and 223 controls without liver fibrosis were recruited. Further 41 patients with no liver, but kidney fibrosis were also included to evaluate interference with expressions of kidney fibrosis. Urinary low molecular weight proteome was then analysed by capillary electrophoresis coupled to mass spectrometry (CE-MS).

Results CE-MS identified 50 urinary peptides associated with liver fibrosis. When combined into a classifier, LivFib-50, it separated liver fibrosis from controls with an area under the curve (AUC) of 0.95 (95% CI: 0.90–0.98, p<0.0001) with 83.5% sensitivity and 95.1% specificity (figure 1). In the first validation cohort, LivFib-50 demonstrated an AUC of 0.94 (95% CI: 0.89–0.97, p<0.0001). In a second validation cohort, LivFib-50 was adjusted for age and demonstrated an AUC of 0.91 (95% CI: 0.76–0.98, p<0.0001). Age-adjusted LivFib-50 showed 84.2% sensitivity (95% CI: 60.4–96.6) and 82.4% specificity (95% CI: 56.6–96.2) for detection of liver fibrosis. The sequence-identified peptides were mainly fragments of collagen chains, uromodulin and Na/K-transporting ATPase subunit γ. We also identified ten putative proteolytic cleavage sites; eight were specific for matrix metallopeptidases and two for cathepsins.

Conclusions Profiling of urinary peptides in liver fibrosis offers potential diagnostic markers. The discovered proteolytic sites could enhance our knowledge about the pathophysiology of liver fibrosis.

EVALUATING THE PERSPECTIVES OF TRAINEES ON THE HEPATOLOGY TRAINING PATHWAY

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