ASSESSING MORTALITY RISK IN CHRONIC PANCREATITIS: A PREDICTION MODEL INCORPORATING CLINICAL VARIABLES AND PROMOTER HYPERMETHYLATION IN CELL-FREE DNA

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A prediction model combining clinical factors and promoter hypermethylation of five genes achieved an AUC of 0.84 in stratifying mortality risk among 97 chronic pancreatitis patients.

KEY POINTS

- The final model included age, sex, exocrine insufficiency, endocrine insufficiency, and methylation status of five genes: SFRP2, HIC1, MLH1, RASSF1A, and CDKN2B.
- High-risk patients (n=30) had 53% five-year survival versus 94% in low-risk patients (n=67), with a hazard ratio for death of 10.2 (95% CI 4.9-21.1).
- The methylation-based model (AUC 0.84) outperformed a clinical-variables-only model (AUC 0.76), demonstrating added value of the methylation markers.
- The study analyzed 16 genes using bisulfite-based PCR in patients with chronic pancreatitis, a disease lacking globally accepted severity scoring systems.
- Authors hold a patent on a diagnostic panel including promoter hypermethylation status of eight genes related to pancreatic cancer methylation markers.

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