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Summary

Gut microbiota to predict clinical features of pancreatitis: Basic science and clinical perspective

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This presentation reviewed emerging evidence that gut microbiome alterations are associated with acute pancreatitis severity and downstream complications, though clinical implementation remains premature pending validation and mechanistic clarity.

KEY POINTS

- The speaker presented data from the PMAP study, a prospective European multicenter trial of approximately 400 patients, which achieved an AUC of 0.85 and negative predictive value over 90% for predicting acute pancreatitis severity using rectal and buccal microbiome signatures collected within 72 hours of admission.
- A German cohort of over 200 acute pancreatitis patients followed for a median of 2.8 years showed that ten identified microbial species correlated with development of recurrent acute pancreatitis (24% of patients), chronic pancreatitis (6%), and type 3 diabetes (7%).
- The speaker stated that healthy controls have different microbiome composition compared to patients in early acute pancreatitis, with dysbiosis potentially contributing to severity via leaky gut and altered microbial metabolites, though direct evidence linking these mechanisms to organ failure is still lacking.
- A 2008 Lancet probiotics trial in severe/moderate acute pancreatitis showed higher mortality in the probiotics group; the speaker stated that current International Association of Pancreatology guidelines recommend against probiotics based on this evidence.
- The speaker emphasized that clinical implementation of microbiome-based prediction is premature, citing needs for external validation, standardized collection methods, accounting for confounders (diet, medications, alcohol, obesity), and distinguishing whether dysbiosis is cause or consequence of disease.

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