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Summary

BASELINE GASTRIC BACTERIA-FUNGI CROSSTALK DYSBIOSIS DRIVES REFRACTORY HELICOBACTER PYLORI ERADICATION: AN INTEGRATED MULTI-OMICS COHORT STUDY

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Gut Microbiota | Stomach & H. Pylori | Mechanisms & Personalised Medicine | Digestive Oncology | Oesophagus

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Baseline gastric bacterial diversity and inter-kingdom microbial signatures predict H. pylori eradication failure in gastric MALT lymphoma, with post-treatment Aspergillus proliferation marking refractory disease.

KEY POINTS

- In 19 prospectively followed gastric MALT lymphoma patients receiving standard quadruple H. pylori eradication therapy, baseline bacterial Shannon diversity was significantly higher in the remission group versus the refractory group (2.6±0.2 vs. 1.9±0.1, $p<0.01$).
- Refractory patients exhibited baseline enrichment of opportunistic pathogens such as Acinetobacter and Candida, while responsive patients showed enrichment of 16 KEGG pathways including quorum sensing and ABC transporters.
- Post-treatment, refractory patients underwent profound fungal community restructuring with proliferation of Aspergillus, Penicillium, and Cladosporium, while responsive cases maintained stable fungal profiles.
- Aspergillus abundance positively correlated with the Ki-67 proliferation index ($r=0.62$, $p=0.01$) and persisted despite H. pylori eradication, with regions enriched in neutrophils both before and after treatment.
- LASSO regression identified Sphingopyxis as the paramount independent prognostic factor (coefficient=2.25), and an integrated multi-omics sPLS-DA model achieved an AUC of 0.81, outperforming clinical-only models (AUC=0.774).

– The speaker emphasizes that profiling baseline Sphingopyxis levels and fungal burden may provide a precision medicine framework to stratify high-risk patients, though external validation is required before clinical use.

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