gutflix
GI learning, personalised

Summary

A LIMOSILACTOBACILLUS REUTERI-CENTERED LACTIC ACID BACTERIA CONSORTIUM DEFINES RESPONSE TO PD-1 BLOCKADE PLUS CHEMOTHERAPY IN GASTRIC CANCER VIA METABOLIC REMODELING

Weiqi Xu

UEG Week Barcelona 2026 | Presentation

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

October 19, 2026

In 143 gastric cancer patients receiving PD-1 inhibitor plus chemotherapy, response was not driven by overall microbiome diversity but by a specific consortium centered on Limosilactobacillus reuteri, which was significantly more abundant in responders (P=0.0088).

KEY POINTS

- Responders (n=74) and non-responders (n=69) showed no difference in global gut microbial diversity (Shannon index P>0.05, no PCoA separation).
- L. reuteri formed a central hub co-occurring with five other lactic acid bacteria (L. gasseri, L. crispatus, L. johnsonii, L. fermentum, L. paragasseri), and this six-species consortium significantly segregated responders from non-responders (dbRDA P=0.005).
- L. crispatus (P=0.0055), L. fermentum (P=0.037), and L. gasseri (P=0.036) were each significantly more abundant in responders, with higher community-wide detection frequencies.
- KEGG genes for GABA and lactate core metabolism were enriched in responders and positively correlated with the L. reuteri consortium (P<0.05), while virulence and proteolysis genes were enriched in non-responders.
- Phocaeicola and Parabacteroides distasonis dominated in non-responders, identified by LEfSe and confirmed by MaAsLin2 after adjusting for BMI, sex, and age.

VIEW THIS CONTENT ON GUTFLIX

https://gutflix.eu/search/d/938593d0-d12c-11f1-8831-daaa6dbee0a2

AI-generated summary

This summary was generated by an AI large language model based on the content transcript. It is for informational purposes only and should not be considered a substitute for clinical judgment. Always rely on your professional expertise and the full clinical context when making clinical decisions.