Microbial Changes Upon Chemotherapy Induced GI Toxicity in Colon Cancer Patients–a Population Study

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BACKGROUND

- Microbial drug metabolism can modulate chemotherapy efficacy and toxicity, linking microbiome composition to treatment outcomes. [1,2]
- Irinotecan, a broad-spectrum anticancer agent, disrupts the gut microbiome, where bacterial β-glucuronidase reactivates its metabolites (SN38G → SN38), driving diarrhea and mucositis. [3]
- Severe GI toxicity occurs in 50–80% of patients treated with irinotecan, often leading to dose delays, reductions, or hospitalization. [4]

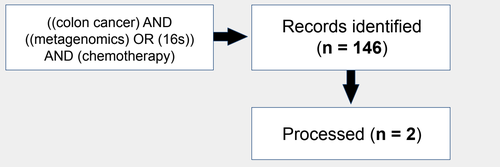
STUDY OVERVIEW

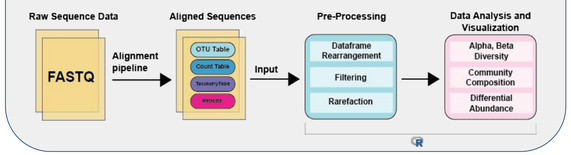
We harmonize existing clinical and pre-clinical microbiome datasets to compare microbiome changes upon irinotecan-induced GI toxicity.

- **Rationale:** Identify bacteria linked to chemotherapy-induced GI toxicity.
- **Clinical data:** colon cancer patients grouped by diarrhea response, pre/post-treatment microbiomes analyzed (e.g., Bacteroides intestinalis). [5]
- **Pre-clinical data:** mouse models assessed before and after irinotecan. [6]

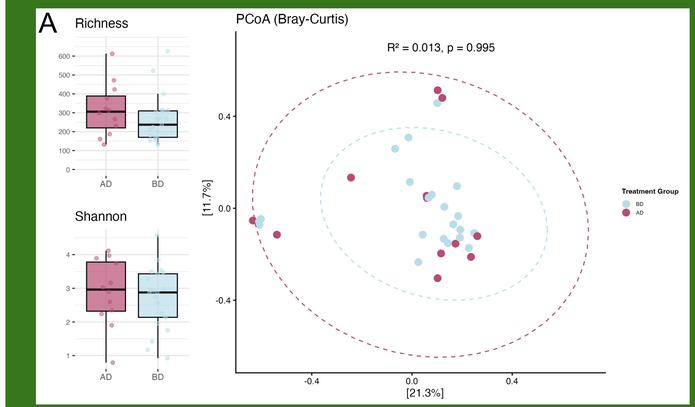
METHODS

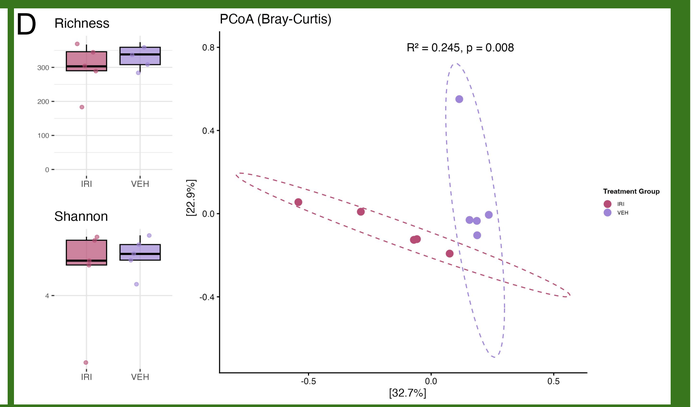
Identification of studies via PubMed:

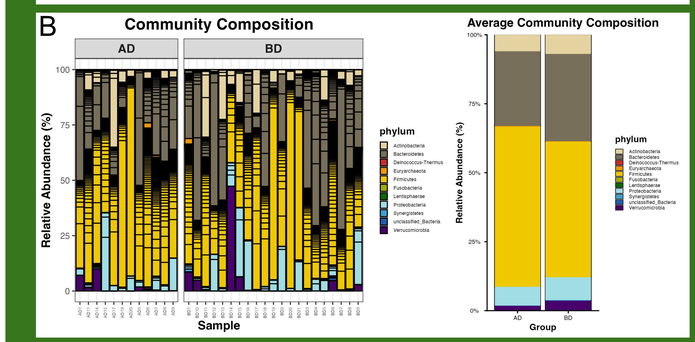


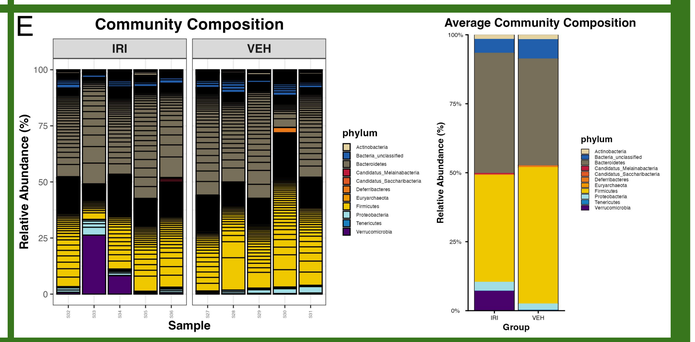


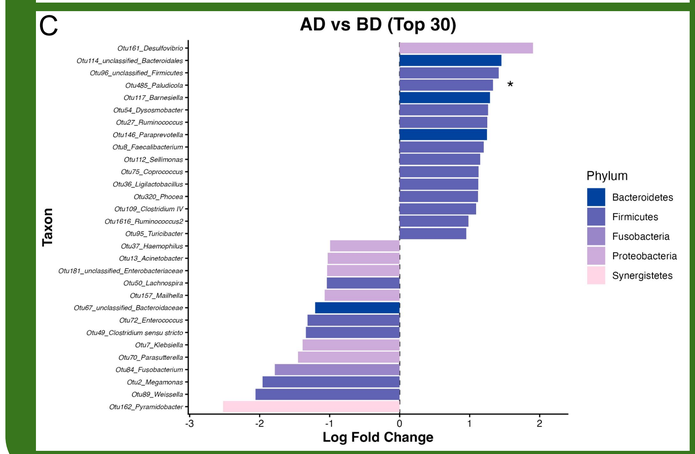
Linking Clinical (A-C) and Pre-Clinical (D-F) Microbiome Changes with Irinotecan Toxicity

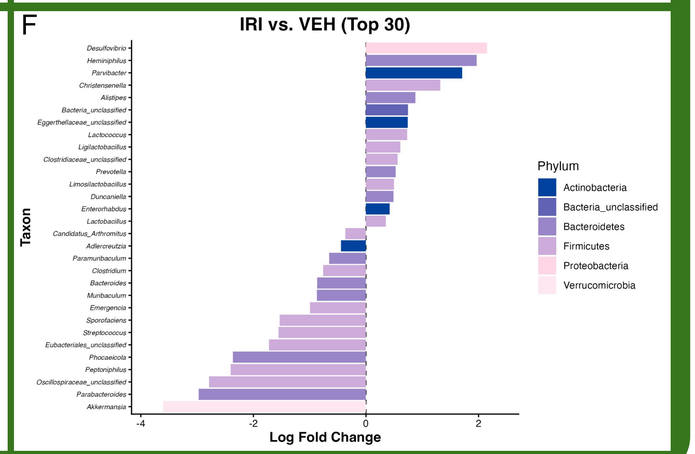












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GOAL

- Identify microbial signatures consistently associated with irinotecan-induced GI toxicity across clinical and pre-clinical models to guide mechanistic and translational studies.

RESULTS

- Established a microbiome analysis pipeline: alpha/beta diversity, PCoA, and differential abundance.
- Observed microbial shifts associated with chemotherapy-induced GI toxicity in colon cancer patients and mouse models.
- Desulfovibrio (DSV), a sulfate-reducing, β-glucuronidase–producing bacterium, emerged as the top concordant taxon across both human and mice.
- These findings suggest that hydrogen sulfide produced by DSV may be a significant proinflammatory molecule for chemotherapy induced GI toxicity.

NEXT STEPS

- Apply harmonized pipeline to all identified studies to build a comprehensive toxicity–microbiome map.
- Identify potential microbiome-targeted interventions to mitigate chemotherapy toxicity.

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