

MICROBIOME PROFILING: FAECAL METAPROTEOMICS VERSUS 16S rRNA SEQUENCING IN COLORECTAL NEOPLASIA

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Poster

Colorectal

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A comparison of metaproteomics and 16S rRNA sequencing for profiling faecal microbiota in colorectal neoplasia patients reveals complementary strengths, with metaproteomics offering superior species-level resolution and 16S providing broader genus-level detection.

KEY POINTS

- Faecal samples from 12 colorectal cancer patients, 10 advanced adenoma patients, 11 non-advanced adenoma patients, and 20 controls were analyzed using both metaproteomics and 16S rRNA sequencing
- Metaproteomics identified 261 species and 250 subspecies compared to only 14 species for 16S rRNA, but detected fewer genera (81 versus 180)
- Both methods identified CRC-associated genera *Bacteroides*, *Parvimonas*, and *Prevotella*, while *Fusobacterium* was detected exclusively by metaproteomics and *Peptostreptococcus* exclusively by 16S
- Considerable overlap existed at family level for the top 12 most abundant bacteria (9 of 12 families), but less overlap at genus level (5 of 12 genera)
- Researchers studying colorectal neoplasia-associated microbiota may benefit from combining both analytical methods to achieve more complete bacterial diversity profiling

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