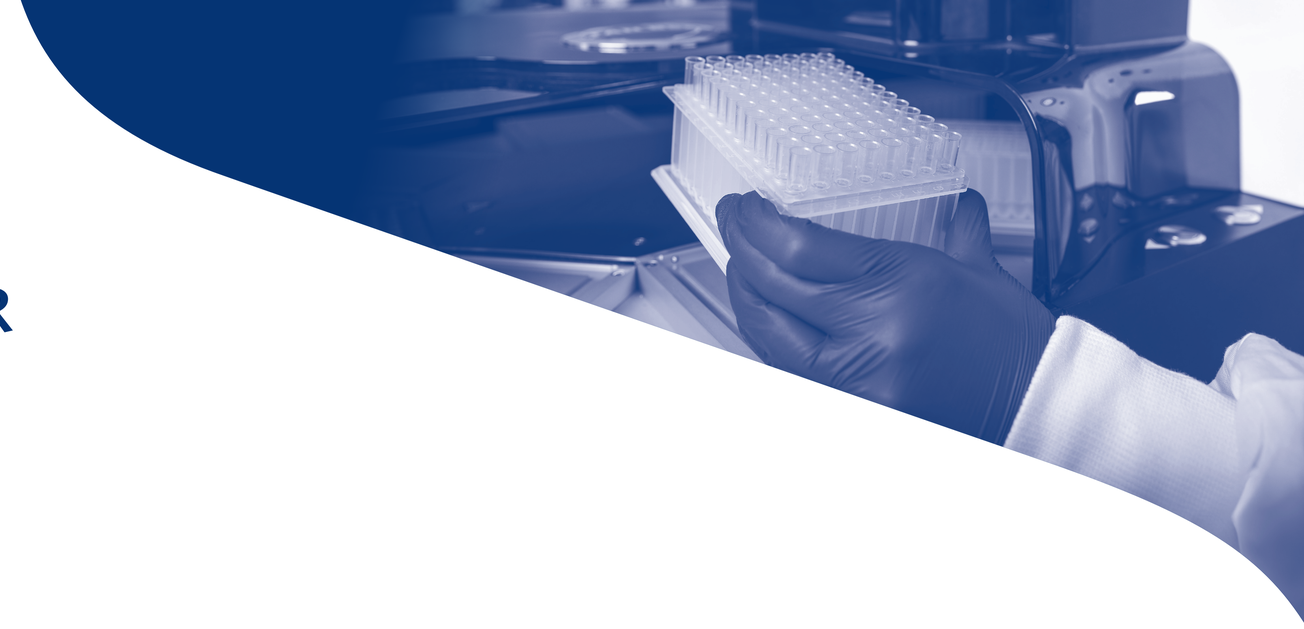

DOUGLASS HANLY MOIR PATHOLOGY

A Sonic Healthcare Practice

Review of MetaPanel™

MetaPanel™: A diagnostic metagenomic gastrointestinal pathogen assay detecting pathogens and antimicrobial resistance genes in patients with chronic gastrointestinal symptoms

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Gastrointestinal (GI) infection is routinely diagnosed by culture, PCR or a combination of both. However, the diagnosis is limited to pathogens that are targets in the multiplex PCR assay or detected on routine culture media. Up to 47% of patients presenting to general practitioners (GPs) with GI complaints remained unresolved.[1] In March 2024, MetaPanel™, a comprehensive, shotgun metagenomic next-generation sequencing assay, was introduced through Sonic Healthcare Australia Pathology laboratories. This assay has evolved from an initial proof of concept,[2] and now reports 115 DNA pathogens, including bacteria and selected bacterial virulence factors, protozoa, helminths, viruses, fungi and microsporidia, in addition to 60 antimicrobial resistance (AMR) gene families and a research-use-only dysbiosis measure, incorporating diversity and richness scores.

Table 1. A sample from the MetaPanel target list

Bacteria

Aeromonas spp. (4 species)	*Clostridium perfringens*, toxigenic	*Klebsiella pneumoniae*, hypervirulent	*Staphylococcus aureus*, toxigenic
Arcobacter spp. (2 species)	*Edwardsiella tarda*	*Listeria monocytogenes*	*Treponema pallidum*
Campylobacter spp. (6 species)	*Escherichia* spp. (2 species)	*Neisseria gonorrhoeae*	*Tropheryma whipplei*
Chlamydia trachomatis	*Grimontia hollisae*	*Plesiomonas shigelloides*	*Vibrio* spp. (6 species)
Clostridioides difficile, toxigenic	*Helicobacter* spp. (5 species)	*Salmonella* spp. (2 species)	*Yersinia* spp. (2 species)

Virulence factors

Cholera toxin	*Clostridium perfringens* enterotoxin	EPEC virulence factor (*E. coli*)	Listeriolysin O
Clostridium difficile binary toxin positive	EAEC virulence factor (*E. coli*)	ETEC heat-labile toxin (*E. coli*)	*Staphylococcus* enterotoxin A–H
Clostridium difficile toxin A &/or B	EHEC O157:H7 virulence factor	ETEC heat-stable toxin (*E. coli*)	*Staphylococcus* leukocidin ED
	EIEC invasion plasmid antigen	STEC shiga toxin (*E. coli*)	*Yersinia* stable toxin
		Klebsiella mucoid regulator	

Viruses

Adenovirus spp. (7 species)	*Cytomegalovirus* (CMV)	*Herpes simplex virus* (2 species)	

Parasites/Protozoa

Cryptosporidium spp. (6 species)	*Cyclospora cayetanensis*	*Entamoeba* spp. (2 species)	*Giardia intestinalis*

Parasites/Helminths

Ancylostoma duodenale	*Dipylidium caninum*	*Hymenolepis* spp. (2 species)	*Strongyloides stercoralis*
Ascaris lumbricoides	*Enterobius vermicularis*	*Necator americanus*	*Taenia* spp. (2 species)
Clonorchis sinensis	*Fasciola hepatica*	*Opisthorchis* spp. (2 species)	*Trichuris trichiura*
Dibothriocephalus latus	*Fasciolopsis buski*	*Schistosoma* spp. (2 species)	

Fungi/Microsporidia

Anncaliia algerae	*Encephalitozoon* spp. (3 species)	*Enterocytozoon bieneusi*	*Histoplasma capsula*
Candida auris			

Methods

A review of the first 725 MetaPanel samples was undertaken, focusing on type of referrer, patient demographics, detected pathogens, detected AMR genes, and proportion with low diversity and richness (defined as falling in the lowest decile of a healthy cohort). Putative pathogens were considered those with some evidence of an organism being present and included indeterminate results (with genomic reads just below the confident), with the exception of indeterminate *Campylobacter concisus, Aeromonas* and *Salmonella* species based on validation studies.

Results

- **Demographics:** 56% female; average age 48 years (range 1–97; 7.7% <18 years)
- **Referrer type:** of the 438 individual referrers:
  - 72% GPs, 12.9% integrated health practitioners who together referred 60.7% of patients
  - 16% gastroenterologists who referred 27% of patients
  - 12% other specialists, including infectious diseases (ID) physicians (n=7)
  - >1 sample referred by 125 clinicians (28.5%) with median of 3 samples (2–20)
  - 71.3% had clinical history available and all confirmed symptomatic

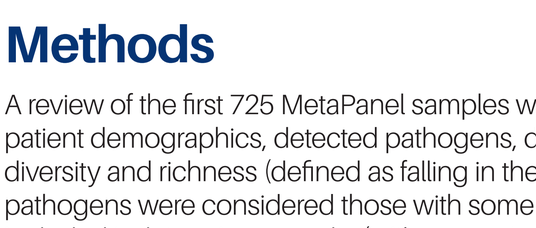

Figure 1. Number of pathogens per test (detected and indeterminate)

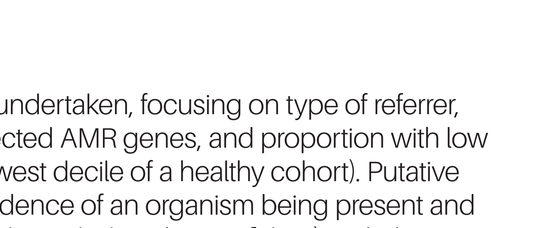

Figure 2. Number of confidently detected pathogens by referrer type

- **Detected pathogens:**
  - 34 unique pathogens identified in 201 patients (27.7%; 144 (19.9%) confident, 57 (7.9%) indeterminate), with 18 patients having 2 pathogens (Figure 1)
  - ID physician referrals had a higher percent positivity of confidently detected pathogens than GPs and gastroenterologists (Figure 2)
  - Most common pathogens were *Campylobacter concisus* (n=56), enteropathogenic *E. coli* (EPEC) (17), toxigenic *Clostridium perfringens* (14) and *Tropheryma whipplei* (14)
  - Worms were detected in 5 patients: *Enterobius vermicularis* (4), *Schistosoma mansoni* (1) (Figure 3)
  - 23/34 (67.6%) of the detected pathogens would not likely be detected using standard testing algorithms

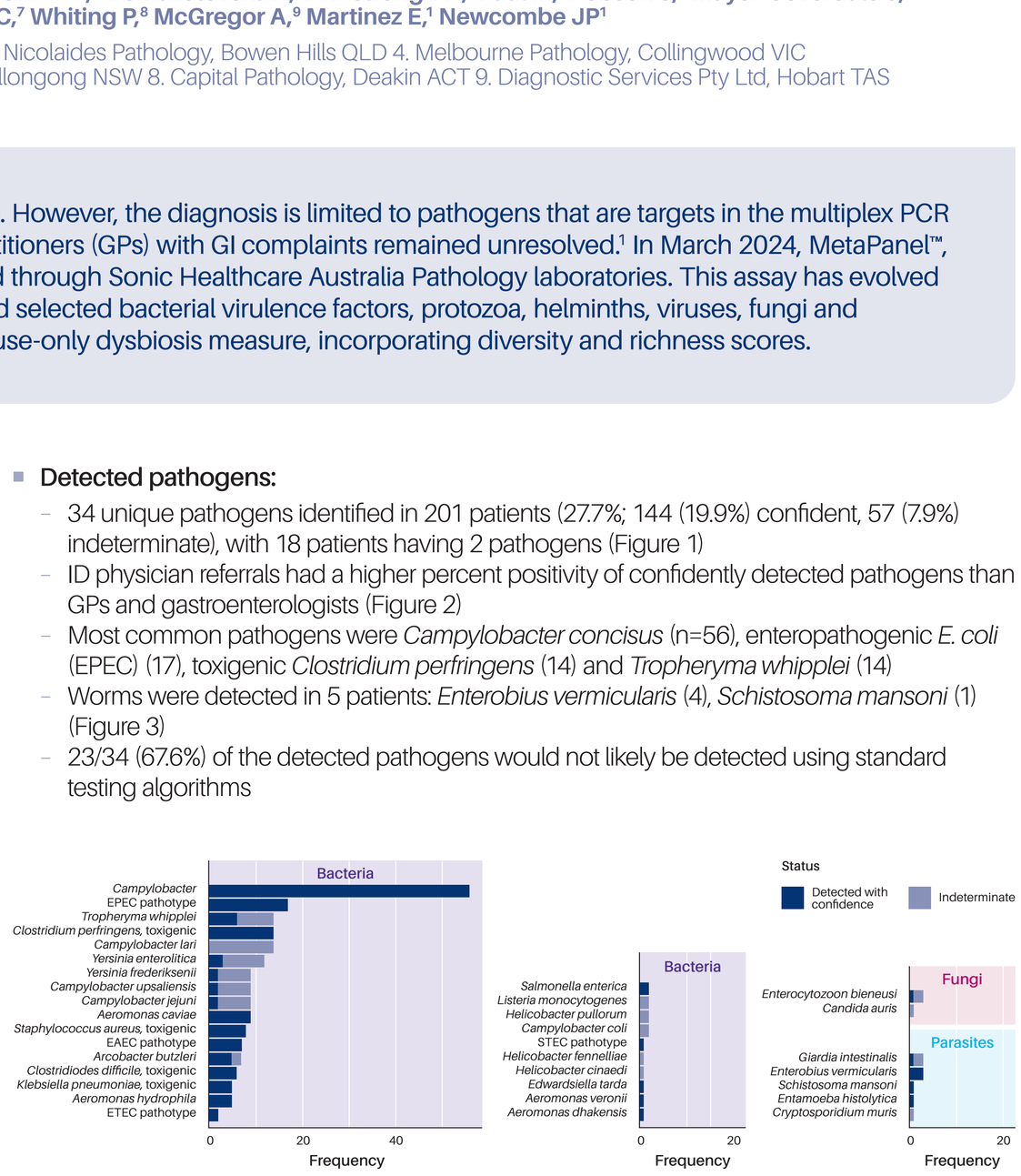

Figure 3. Pathogen frequency (detected and indeterminate)

- **AMR gene detection:**
  - 26 unique AMR genes were detected in 185 patients (25.5%) (Figure 4)
  - 61/149 (40.9%) of ESBL, AmpC and qnr genes were not detected with their known hosts suggesting they were plasmid mediated
- **Microbial diversity and richness:**
  - 73.6% of samples were classified as being of low diversity and/or richness supportive of underlying dysbiosis (Figure 5)

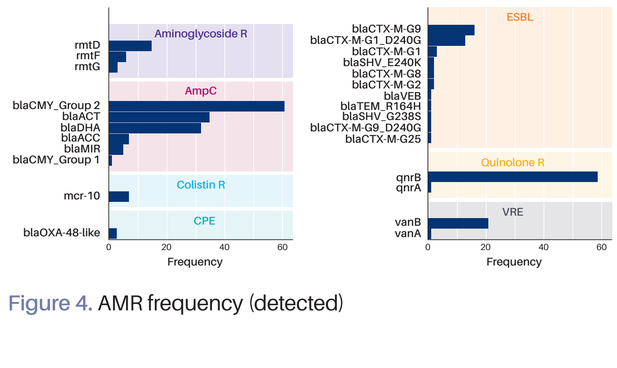

Figure 4. AMR frequency (detected)

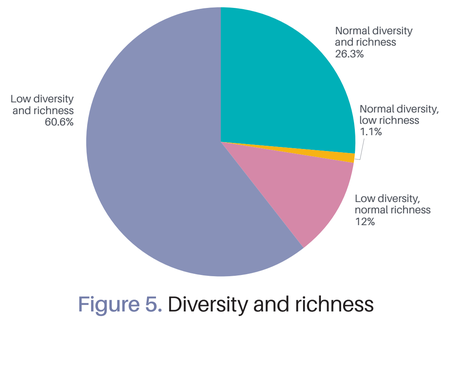

Figure 5. Diversity and richness

Conclusion

Early results support the utility of a faecal metagenomics assay (MetaPanel™) in diagnosing difficult-to-detect GI pathogens and carriage of relevant AMR genes. Further studies are underway to investigate the impact of MetaPanel on patient management and clinical outcomes.

Scan the QR code for further information or visit sonicmicrobiomics.com.au

References

1. Gordon J, Miller G & Valenti L. The management of unresolved gastrointestinal symptoms in Australian general practice. *Aust Fam Physician*. 2015;44(9):621–623.
2. Angel NZ, et al. Metagenomics: a new frontier for routine pathology testing of gastrointestinal pathogens. *Gut Pathog*. 2025 Jan 18;17(1):4. PMID: 39827146

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