Subsequently increased numbers of referrals are being made to secondary care, escalating the demand of colonoscopies and other current investigation methods.

**Methods** Data was collected from a prospectively maintained database between January 2011 and December 2017. 1950 patients who were assessed via our telephone triage service were included in the study. Patients were followed up until either diagnosis or discharge. The specific investigation(s) each patient underwent was recorded. And costed as per NHS tariff (2018). Using current sensitivity/specificity data related to FIT all true positive/negatives, false positives/negatives, positive predictive value and negative predictive value was calculated as if FIT was used as the diagnostic test used for each patient. This was then compared to the costing as per the current methods.

**Results** Median age was 65 (IQ 47–82) with 43.37% male and 56.3% female. 2898 investigations were carried out with a diagnostic yield of 26 cancers (18 colon, 8 rectal), 138 polyps and 29 high risk polyps (HGD ≥ 10 mm), £713,948 was spent in total for the investigations. The commonest investigation was colonoscopy and totalled £533,169. The total cost for each cancer was £28,500 per diagnosis. Sensitivity (92.1% CI 86.9–95.3) and specificity (85.8% CI 78.3–90.1) for FIT in colorectal cancer was taken from NICE and was costed via the manufacturer(s). The total cost for the overall microbiota profiles were consistent within individuals, eight genera were significantly different between fresh, OG day 10, and FIT day 10 conditions. *Blautia*, *Anaerostipes*, *Bifidobacterium*, and *Lachnospiraceae* were higher in FIT samples stored for 10 days at room temperature, with *Parabacteroides*, *Bacteroides*, and *Sutterella* lower (all P>0.05). Storage of FIT samples over 20 days resulted in no significant difference in alpha- or beta-diversity, but *Parabacteroides* reduced significantly between day 0 (mean 0.9% relative abundance) and 20 (mean 0.2% relative abundance; P=0.006). Storage at -80°C and concentrating samples by SV or FD had no effect on alpha-diversity, beta-diversity or taxonomic profiles.

**Conclusions** Faecal microbiome diversity and overall taxonomic profiles were relatively consistent across test conditions. FIT kits may provide an accurate, convenient, and cost-effective means of studying the faecal microbiome in large, representative, populations.

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**P304** USING Faecal IMMUNOCHEMICAL TESTS (FIT) FOR LARGE-SCALE GUT MICROBIOTA ANALYSIS

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**Introduction** Accumulating evidence suggests that the gut microbiome is important in GI disease. There is an urgent need for large-scale population-based studies to better understand intestinal microbiota as a disease risk factor. However stool sampling is complex, unacceptable to some and is influenced by confounders such as bowel preparation.

We aimed to test if accurate microbiome data can be obtained from Faecal Immunochemonal Test (FIT) kits (OC Sensor, Mast diagnostics) when compared to DNA Genotek tubes (OMNIgene® GUT; OG) (current accepted standard) and fresh faeces. We considered microbiome profile stability over time, mimicking real world scenarios and explored if speed of vacuum (SV) or freeze-dry (FD) concentration of samples is necessary.

**Methods** A faecal sample was provided by 10 healthy volunteers and immediately sampled for DNA extraction after varying periods of storage and conditions 1) Fresh 2) FIT Day 0 3) FIT Day 0 SV 4) FIT Day 0 FD 5) OG Day 10 6) FIT Day 10 7) FIT Day 10 -80°C 8) FIT Day 10 -80°C SV 9) FIT Day 10 -80°C FD 10) Fresh -80°C 11) FIT day 20. 125 samples including negative and positive controls underwent V4 16S rRNA gene sequencing. All samples were rarefied to 10,000 reads.

**Results** Alpha-diversity was consistent within individuals regardless of test condition with richness (P=0.9) and Shannon diversity (P=0.44) comparable across conditions. Beta-diversity based on Bray-Curtis dissimilarity showed samples grouped by patient (P<0.001) and not test condition (P=0.28), which was consistent with presence/absence Jaccard index (patient P<0.001; condition P=0.84). While overall microbiota profiles were consistent within individuals, eight genera were significantly different between fresh, OG day 10, and FIT day 10 conditions. *Blautia*, *Anaerostipes*, *Bifidobacterium*, and *Lachnospiraceae* were higher in FIT samples stored for 10 days at room temperature, with *Parabacteroides*, *Bacteroides*, and *Sutterella* lower (all P>0.05). Storage of FIT samples over 20 days resulted in no significant difference in alpha- or beta-diversity, but *Parabacteroides* reduced significantly between day 0 (mean 0.9% relative abundance) and 20 (mean 0.2% relative abundance; P=0.006). Storage at -80°C and concentrating samples by SV or FD had no effect on alpha-diversity, beta-diversity or taxonomic profiles.

**Conclusions** Faecal microbiome diversity and overall taxonomic profiles were relatively consistent across test conditions. FIT kits may provide an accurate, convenient, and cost-effective means of studying the faecal microbiome in large, representative, populations.