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Comparison of collection methods for fecal samples for discovery metabolomics in epidemiological studies

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Abstract

Background—The gut metabolome may be associated with the incidence and progression of numerous diseases. The composition of the gut metabolome can be captured by measuring metabolite levels in the feces. However, there is little data describing the effect of fecal sample collection methods on metabolomic measures.

Methods—We collected fecal samples from eighteen volunteers using four methods: no solution, 95% ethanol, fecal occult blood test (FOBT) cards, and fecal immunochemical test (FIT). One set of samples was frozen after collection (day 0), and for 95% ethanol, FOBT, and FIT, a second set was frozen after 96 hours at room temperature. We evaluated 1) technical reproducibility within sample replicates, 2) stability after 96 hours at room temperature for 95% ethanol, FOBT, and FIT, and 3) concordance of metabolite measures with the putative “gold standard,” day 0 samples without solution.

Results—Intraclass correlation coefficients (ICC) estimating technical reproducibility were high for replicate samples for each collection method. ICCs estimating stability at room temperature were high for 95% ethanol and FOBT (median ICC>0.87) but not FIT (median ICC=0.52). Similarly, Spearman correlation coefficients (r_s) estimating metabolite concordance with the “gold

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standard” were higher for 95% ethanol (median $r_s=0.82$) and FOBT (median $r_s=0.70$) than for FIT (median $r_s=0.40$).

Conclusions—Metabolomic measurements appear reproducible and stable in fecal samples collected with 95% ethanol or FOBT. Concordance with the “gold standard” is highest with 95% ethanol and acceptable with FOBT.

Impact—Future epidemiologic studies should collect feces using 95% ethanol or FOBT if interested in studying fecal metabolomics.

Keywords

metabolomics; feces; collection methods; reproducibility; stability

Introduction

Metabolomics is the systematic measurement of the low molecular weight compounds, often loosely termed “metabolites”, in biospecimens (1, 2). These metabolites typically come from the host, microbial symbionts, environmental exposures, or combinations of these sources (e.g. an environmental molecule modified by a bacterial enzyme) and can be measured using either a targeted or an untargeted approach. Targeted metabolomics platforms measure a limited number of specific metabolites of known identity making them well-suited for hypothesis-driven studies. In contrast, untargeted platforms measure as many metabolites as possible, of known and unknown identity, in a biospecimen allowing for the discovery of novel metabolic associations and disease pathways (3). Metabolomic phenotypes have been associated with diet (4–8), behaviors such as smoking (9, 10) and physical activity (11), and diseases such as diabetes (12), Crohn’s disease (13), prostate cancer (14, 15), and colorectal cancer (16–19). The majority of epidemiologic studies have measured metabolomic phenotypes (i.e. the full complement of measured metabolites) within blood (e.g. serum) (4–6, 9–12, 14–17); fewer have analyzed urine samples (7, 8, 14), and although only a few relatively small studies have analyzed fecal samples using untargeted platforms, they have found potential diagnostic markers of disease (13, 18). These studies highlight the need for future epidemiologic studies with large-scale fecal sample collection. However, methodological research to inform the collection protocols of these future studies is essential.

As epidemiologic studies increase collections of fecal samples for microbiome analysis (20, 21), we expect a considerable increase in the number of investigations on the relationship between fecal metabolites, which reflect complex interactions between dietary inputs, intestinal bacteria and host metabolism (22), and risk, or progression, of diseases such as colorectal cancer.

It is widely recognized that the microbiome alters the metabolome in ways that are associated with, and in mouse models, cause disease (23, 24). It is therefore advantageous to assess these phenotypes concurrently and, in epidemiological studies, use sample collection methods that are amenable to multiple molecular analyses (25). When selecting a suitable collection method for fecal samples in population-based research, key quality considerations

include technical reproducibility (i.e. consistency of metabolites measurement for replicate samples collected and stored in the same manner), stability at ambient temperature for a period of time that mimics field conditions, and concordance of metabolite measurements with samples frozen soon after collection, which is currently considered the “gold standard” for microbiome and other “omic” analyses (26).

Therefore, we conducted a fecal metabolomics study to evaluate the technical reproducibility, stability, and concordance of three collection methods (95% ethanol, fecal occult blood test (FOBT) cards, and fecal immunochemical test (FIT) tubes) as compared with the “gold standard”. By design, this study was nested in a larger study of collection methods for fecal samples in microbiome analyses thereby permitting the identification of suitable collection methods for both fecal metabolome and microbiome studies. For microbiome analyses, we found that the fecal sample collection methods, considered herein, were relatively reproducible, stable and concordant with the “gold standard” sample that was frozen following collection (day 0) with no solution (Vogtmann et al, under re-review). In addition, a prior study of seven fecal sampling methods for microbiome analyses found that FOBT cards and samples stored in *RNAlater* had the highest stability, while FOBT cards and samples stored in 70% ethanol had the highest concordance with the “gold standard” sample that was frozen shortly after collection with no solution (27). This earlier study did not, however, consider the potential of each collection method for metabolomic analyses nor did it include FIT tubes, which are commonly used in colorectal cancer screening programs and thus a potential untapped resource in future diagnostic and etiologic studies of cancer if they were to be stored in -80°C freezers rather than discarded. Moreover, samples collected with *RNAlater* have a high sodium sulfate content making this collection incompatible with mass spectrometry-based metabolomics platforms (25) and highlighting the need for methods research to ascertain which fecal collection methods are most suitable for a variety of molecular analyses in future epidemiologic studies.

Materials and Methods

Study participants

A sample of 18 individuals (9 males and 9 females) was randomly selected from a larger microbiome methods study of 52 volunteers who were recruited from Mayo Clinic employees. Eligibility requirements for the main microbiome methods study included the following: minimum age of 18 years, no use of antibiotics or probiotics within the two weeks prior to enrollment, no history of pelvic radiation, and no current chemotherapy treatment. At study enrollment, participants self-reported demographic and health characteristics, tobacco use, alcohol consumption, oral health habits, and recent antibiotic exposure using a standardized questionnaire that was created for this study. All participants provided informed consent. The study was approved by the Mayo Clinic Institutional Review Board and by the National Cancer Institute Office of Human Subjects Research.

Fecal specimen collection

Following enrollment, participants were invited to return to the clinic at a later date to provide a fecal specimen. On the collection day, each participant was provided with an

Exakt Pak canister (Inmark Packaging, Austell, GA, USA) for on-site fecal specimen collection. Immediately following collection, the study coordinator delivered each specimen to the laboratory for processing. Average time from collection to laboratory processing was 14 minutes.

In the laboratory, each fecal specimen was mixed manually using a spatula, and aliquots for the different collection methods were generated in random order. For each participant, approximately 1–2 grams of feces, representing a full scoop of feces, was placed in a Sarstedt feces tube (Numbrecht, Germany) containing no solution or 2.5 mL of 95% ethanol (Sigma-Aldrich, St. Louis, Missouri). Triple-slide Hemocult II Elite Dispensapak Plus for FOBT (Beckman Coulter, Brea, California) were smeared thinly with feces and the flap was closed. FIT tubes (Polymedco, Inc., Cortlandt Manor, New York) were created by dipping the fecal specimen with the FIT probe and the tube was shaken. Aliquots from each FIT tube were created and stored in cryovials. One set of replicates of the no solution, 95% ethanol, and FIT cryovials were frozen following processing at -80°C (day 0). One set of replicate FOBT cards was developed using two drops of Hemocult Sensa Developer applied to the guaiac paper on the back of the card (i.e., the testing strategy for occult blood in colorectal cancer screening) and then frozen at -80°C (day 0). Average time from the beginning of processing to freezer for day 0 samples was 15 minutes. The remaining samples were left at ambient temperature for 96 hours. After 96 hours, the ambient temperature FOBT cards were developed and all remaining samples were frozen at -80°C (day 4). In total, 160 frozen samples from 18 participants, including blinded duplicate samples from 5, randomly selected, participants yielding 23 samples per collection method except for FIT tube/day 4, which had one sample missing (Figure 1), were shipped on dry ice to Metabolon (Durham, NC) for biochemical profiling. Following receipt, samples were stored at -80°C until processed.

Metabolomics analysis

Samples were prepared using an automated system. In brief, fecal samples collected with no solution and 95% ethanol were dried, weighed and then re-suspended at a 50:1 (50ul H₂O for every 1mg of feces weight) ratio for homogenization and processing; thus, these samples were processed with equivalent amounts of material. For FOBT cards, all material was collected from the cards and re-suspended at a 30:1 ratio; thus, these samples were also processed at equivalent amounts. Finally, for the FIT tubes, a weight for the fecal component of these samples was not available; thus, 100ul of the suspension on a per sample basis was processed. To remove protein, dissociate small molecules bound to protein or trapped in the precipitated protein matrix, and to recover chemically diverse metabolites, proteins were precipitated with methanol under vigorous shaking followed by centrifugation. Following removal of the organic solvent, sample extracts were stored overnight under nitrogen before preparation for analysis.

All fecal samples were analyzed using ultra-performance liquid chromatography (UPLC) and high resolution/tandem mass spectrometry (MS/MS). The sample extract was dried then reconstituted in solvents compatible to each of the four collection methods. Each reconstitution solvent contained a series of standards at fixed concentrations to ensure

injection and chromatographic consistency. One aliquot was analyzed using acidic positive ion conditions, chromatographically optimized for more hydrophilic compounds. In this method, the extract was gradient eluted from a C18 column using water and methanol with 0.05% perfluoropentanoic acid and 0.1% formic acid. Another aliquot was also analyzed using acidic positive ion conditions; however, it was chromatographically optimized for more hydrophobic compounds. In this method, the extract was gradient eluted from the same C18 column using water, methanol and acetonitrile with 0.05% perfluoropentanoic acid and 0.01% formic acid. A third aliquot was analyzed using basic negative ion optimized conditions following gradient elution with a separate C18 column using methanol, water, and 6.5 mM ammonium bicarbonate at pH 8. A fourth aliquot was analyzed using negative ionization following elution from an HILIC column using water, acetonitrile, and 10 mM Ammonium Formate, pH 10.8.

Raw data was extracted, peak-identified and processed by Metabolon using proprietary software as described elsewhere (28–30). In brief, compounds of exogenous, human, and microbial origin, were identified by comparison to library entries of purified standards or recurrent unknown entities. Metabolon maintains a dynamic and proprietary biochemical reference library of more than 4,500 known metabolites (based on authenticated standards) and more than 9,000 novel metabolites (without an identified chemical structure); each library entry contains the retention time/index (RI), mass to charge ratio (m/z), and chromatographic data (including MS/MS spectral data). Biochemical identifications are based on three criteria: retention index within a narrow RI window of the proposed identification, accurate mass match to the library \pm 10 ppm, and the MS/MS forward and reverse scores between the experimental data and authentic standards. The MS/MS scores are based on a comparison of the ions present in the experimental spectrum to the ions present in the library spectrum. Integrated ion peaks were quantified using area-under-the-curve. Each collection method was run separately; however, all samples for a given collection method were run on the same plate on the same day. For each collection method, metabolite peak values were rescaled to set the median equal to 1, and the missing values were imputed with the minimum value for a given metabolite.

In addition to our blinded duplicate samples, Metabolon included three types of controls that were analyzed in concert with the experimental samples. First, a pooled matrix sample, which was generated by taking a small volume of each experimental sample, served as a technical replicate throughout the data set. Second, extracted water samples served as process blanks. Finally, a cocktail of quality control standards that were carefully chosen not to interfere with the measurement of endogenous compounds were spiked into every analyzed sample to monitor instrument performance and aid chromatographic alignment. Experimental samples were randomized across the platform run with quality control samples spaced evenly among the injections. Metabolon determined instrument variability by calculating the median relative standard deviation (RSD) for the standards that were added to each sample prior to injection into the mass spectrometers; median instrument variability was 2%, 2%, 3%, and 4% for fecal samples collected with no solution, 95% ethanol, FOBT cards, and FIT tubes, respectively. In addition, Metabolon determined overall process variability by calculating the median RSD for all endogenous metabolites (i.e., non-instrument standards) present in 100% of the pooled matrix samples; median process

variability was 6%, 8%, 8%, and 11% for fecal samples collected with no solution, 95% ethanol, FOBT cards, and FIT tubes, respectively. These values for instrument and process variability met Metabolon's acceptance criteria (28).

Statistical analysis

For the analyses of technical reproducibility, stability, and concordance, we first limited the set of metabolites to those with $\geq 80\%$ detectability (i.e. above the detection limit in a given batch) in day 0 samples collected with no solution, which was considered the “gold standard”. For analyses including samples collected with 95% ethanol, FOBT, or FIT, we further restricted the set of metabolites to those with $\geq 80\%$ detectability in the collection method of interest. Limiting these analyses to only those metabolites with high detectability ensured an adequate number of samples for calculating ICCs in this small sample. For analyses, metabolite values were natural log-transformed to make them more normally distributed.

We defined “technical reproducibility” as a standard intraclass correlation coefficient, where σ_B^2 is the between-individual variability and σ_W^2 is the within-individual variability owing to sample handling or laboratory variability:

$$\frac{\sigma_B^2}{\sigma_B^2 + \sigma_W^2}$$

For each metabolite and each collection method, we calculated the values σ_B^2 and σ_W^2 using a linear mixed effects regression model with a random effect for subject. We calculated ICCs separately for day 0 and day 4 samples. Non-replicate samples were included in the ICC calculation since they contribute to the estimation of between-individual variability.

We similarly defined “stability” as an intraclass correlation coefficient, where σ_B^2 is the between-individual variability and σ_T^2 is the within-sample variability over time:

$$\frac{\sigma_B^2}{\sigma_B^2 + \sigma_T^2}$$

Our estimation of stability used data from replicate samples that were frozen at different time points (day 0 or day 4). For each metabolite, we calculated the values σ_B^2 and σ_T^2 using a linear mixed effects regression model with hierarchical random effects for subject and time of freezing to incorporate all available measurements for a given collection method. Note that measurement error (i.e. σ_W^2 when evaluating technical reproducibility) does not factor into our definition of stability

We defined “concordance” as the Spearman correlation coefficient (r_s) between metabolite values from samples frozen on day 0 for a given collection method and metabolite values from samples frozen on day 0 with no solution (i.e., “gold standard”). The Spearman

correlation evaluates whether the rank order of metabolite values for a given collection method was preserved as compared with the “gold standard”. For the five individuals with duplicate day 0 samples we randomly selected a single sample for each of the collection methods so that there were two observations per participant, one for a given collection method (95% ethanol, FOBT, or FIT) and one for no solution.

RESULTS

Fecal samples from nine men and nine women, aged 22 to 56 years, were analyzed in this study. Two thirds of participants (66.7%) had at least a Bachelor’s degree, and a large majority (88.9%) was non-Hispanic white (Supplemental Table 1).

In total 859, 874, 704, and 496 metabolites were detected in fecal samples collected with no solution, 95% ethanol, FOBT cards, and FIT tubes, respectively (Supplemental Table 2). For the three collections methods with day 0 and day 4 samples, restricting to the subset of metabolites detected in day 0 samples only, there were 871, 703, and 466 metabolites in 95% ethanol, FOBT cards, and FIT tubes, respectively (Figure 2 and Supplemental Table 2). Further restricting to the subset of metabolites with 80% detectability, there were 625, 552, 461, and 243 metabolites in no solution, 95% ethanol, FOBT cards, and FIT tubes, respectively (Figure 2 and Supplemental Table 2).

In day 0 fecal samples with no solution, approximately half of all detected metabolites were classified as lipid (27%) or amino acid (20%) metabolites; a smaller percentage of detected metabolites were xenobiotic (12%), nucleotide (5%), peptide (4%), cofactor and vitamin (4%), carbohydrate (3%), or energy (1%) metabolites, and approximately 26% were unnamed metabolites. Although the number of detected metabolites varied considerably by collection method (Figure 2) the proportions of compounds classified as lipid (22% to 27%), amino acid (19% to 23%), xenobiotic (12%), nucleotide (5% to 7%), peptide (4%), cofactors and vitamins (4% to 5%), carbohydrate (3% to 4%), energy (1% to 2%), and unnamed (23% to 27%) metabolites were similar (Supplemental Figure and Supplemental Tables 3–6).

There were 508, 435, and 220 metabolites, with 80% detectability, in fecal samples collected with 95% ethanol, FOBT cards, and FIT tubes, respectively, that overlapped with the subset of 625 metabolites, with 80% detectability, in fecal samples collected with no solution (Table 1). Overall, 19%, 30%, and 65% of the metabolites with 80% detectability in no solution did not have 80% detectability in 95%, FOBT cards, and FIT tubes, respectively. The subset of overlapping metabolites was used to calculate technical reliability, stability, and concordance. The median ICC (interquartile range; IQR) for technical reproducibility for day 0 samples was 0.94 (0.86–0.98) for no solution, 0.86 (0.68–0.96) for 95% ethanol, 0.87 (0.75–0.95) for FOBT cards, and 0.83 (0.65–0.94) for FIT tubes (Figure 3 and Supplemental Table 7). The median ICCs for technical reproducibility for day 4 samples collected with 95% ethanol, FOBT, and FIT were similar to the day 0 ICCs (Supplemental Table 7). The median ICC (IQR) for stability was 0.87 (0.65–0.98) for 95% ethanol, 0.86 (0.69–0.99) for FOBT cards, and 0.52 (0.00–0.97) for FIT tubes (Figure 4 and Supplemental Table 7). For concordance, the median Spearman Correlation coefficient

(IQR) with no solution was 0.82 (0.72–0.90) for 95% ethanol, 0.70 (0.51–0.85) for FOBT cards, and 0.40 (0.15–0.72) for FIT tubes (Figure 5 and Supplemental Table 7).

Known microbial metabolites were detected in fecal samples collected under varying conditions. For example, enterolactone, which is formed by the action of intestinal bacteria on lignan precursors, was detectable in all samples regardless of collection method (Supplemental Table 3–6) and freezing time (data not shown). Other microbial metabolites related to the degradation of polyphenols were detected under some but not all conditions. For example, in day 0 samples, caffeate was detected in 100% of samples that were collected with no solution, 95% ethanol, or FOBT cards but was not detected in fecal samples collected with FIT tubes; benzoate, on the other hand, was detected in 100% of samples collected with no solution or FOBT cards but in only 87% of samples that were collected with either 95% ethanol or FIT tubes, and 3-(3-Hydroxyphenyl)propionate was detected in 100% of samples collected with no solution or 95% ethanol but only in 91% of FOBT samples and 57% of FIT samples. Metabolon classified known metabolites by “super-pathway”, representing chemical classes, and “sub-pathway”, corresponding to the specific role of a compound in metabolism, on the basis of the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways (31). A complete list of metabolites, sorted by super- and sub-pathways, for each collection method frozen on day 0, can be found in Supplemental Tables 3 through 6.

DISCUSSION

This study found that metabolite measures obtained from an untargeted UPLC/MS-MS platform had high technical reproducibility for fecal samples collected with no solution, 95% ethanol, FOBT cards, or FIT tubes. In contrast, when comparing samples that were frozen after 4 days at room temperature to those that were frozen on day 0 for a given collection method, metabolite stability was high (median ICC>0.87) for fecal samples collected with 95% ethanol or FOBT cards, but low (median ICC=0.52) for the majority of metabolites measured in FIT tubes. Similarly, concordance with the putative “gold standard” was higher for fecal samples collected with 95% ethanol (median r_s =0.82) or FOBT (median r_s =0.70) and frozen on day 0 than for fecal samples collected with FIT tubes (median r_s =0.40) and frozen on day 0.

To our knowledge, the impact of fecal collection method on metabolomic measurements, particularly fecal samples collected with no additive, 95% ethanol, FOBT cards, or FIT tubes, has not previously been assessed using an untargeted metabolomics platform. Moreover, the impact of incubating fecal samples collected with each of these methods for 96 hours at room temperature, a time period reflective of potential field conditions in a large population-based study, has not previously been studied. Our study shows that fecal samples collected with no additive are suitable for untargeted metabolomics analysis when frozen shortly after collection. Fecal samples that were collected with 95% ethanol or FOBT cards also appear suitable for untargeted metabolomics analysis and, more importantly, yield similar results when frozen after four days at ambient temperature or shortly after collection. FIT tubes that were frozen on day 0 are of intermediate quality, but given the existence of better methods, we recommend against this collection method. In contrast, FIT tubes that are

left at room temperature for an extended period of time should not be used for untargeted metabolomics analysis. Although freezing samples right after collection with no solution yielded the greatest number of metabolites with high detectability and the highest estimates of technical reproducibility, this method of collection may not be practical for large epidemiological studies. Alternatively, fecal samples collected with 95% ethanol or FOBT cards appear well adapted to field conditions in which samples may be left at room temperature for an extended period of time.

In addition to the raw number of metabolites and these three measures of quality, researchers should consider which classes of compounds are of potential importance. For example, future studies with integrated measures of the metabolome and microbiome have the tremendous potential to increase our understanding of the mediating role of gut microbial metabolism in disease etiology. Accordingly, specific microbial metabolites may be of particular interest to researchers who are using fecal metabolomics to study interactions between dietary components and the microbiota. To aid in this effort, we have highlighted a small number of known microbial metabolites (enterolactone, caffeate, benzoate, and 3-(3-Hydroxyphenyl)propionate) with varying degrees of detectability by collection method and have included comprehensive lists of all detected metabolites by collection method in the supplemental material. Based on our results, fecal samples collected with no solution and frozen on day 0 as well as samples collected with 95% ethanol provide the largest number of metabolites with high detectability (80%) and the greatest coverage of metabolic super-pathways. In comparison, samples collected with FOBT cards as compared with no solution had a similar number (<20% difference) of metabolites with high detectability for metabolites related to the amino acid, carbohydrate, and energy super-pathways but substantially fewer metabolites related to (20% difference) cofactors and vitamins, lipid, nucleotide, peptide, and xenobiotic super-pathways. FIT tubes had many fewer detected metabolites for all metabolite classes as compared with other collection methods.

Metabolomics is a burgeoning technology and its potential to produce biomarkers of exposure and disease is considerable. Nevertheless, its integration into population-based research remains in its early stages (2). Rigorous methods studies identifying sources of variability in metabolite measurements for various types of biological specimens is critical (18, 32, 33). Presently, relatively few human studies have used untargeted metabolomics platforms to analyze fecal samples. In a small colorectal cancer case-control study approximately 1000 metabolites in lyophilized fecal samples by HPLC-GC/MS-MS were measured (18). Assay reproducibility in replicate samples exceeded 0.7 for 91% the 579 metabolites that were detected in at least 10% of the fecal specimens, and statistically significant differences between cancer cases and controls were found for 41 metabolites including some that appeared to reflect differences in gut microbial diversity. This study found potential markers to aid diagnosis and improve understanding of disease etiology thereby underscoring the need for future epidemiologic studies, including prospective cohort studies, with large-scale fecal sample collection and thus the need for research on how fecal collection methods and freezing conditions impact metabolite measurements.

A number of other small case-control (34, 35), cross-sectional (36, 37), and intervention (38–40) studies have used NMR spectroscopy to generate metabolic phenotypes of various

types of fecal samples, including crude fecal samples (37), fecal water extracts (34–37, 40) and lyophilized feces (38, 39). Although these studies have shown reasonable reproducibility, they have been more targeted, capturing a smaller less diverse set of metabolites than untargeted approaches, and collectively have not used standardized sample collection, storage, or preparation methods. Interestingly, a number of NMR-based metabolomics studies have demonstrated associations between the fecal metabolome and microbiome (40, 41), further strengthening the case for the inclusion of fecal sample collection in population-based studies in combination with the development of standardized fecal sample collection methods suitable for multiple molecular analyses.

Limitations of this study include its small sample size and potentially limited generalizability as participants were relatively young, well-educated and primarily non-Hispanic white. It is possible that the quality metrics for fecal metabolomics considered herein may vary by collection methods among individuals with clinical or underlying disease or among individuals in different age or racial/ethnic groups. In addition, the samples in this study were collected at one-time point; consequently, we were unable to estimate within individual variability over time, which is an important consideration in population-based metabolomics studies. Using an untargeted metabolomics approach, one study found that, on average, approximately 40% of the biologic variability in serum metabolite measurements could be attributed to variation occurring within an individual over time; this estimate translates to a need for large sample sizes, upwards of 1000 individuals, to detect metabolite-disease associations in case-control studies (32). While sources of variability in urine, serum, and plasma metabolite measurements have been studied (32, 42, 43), data on sources of variability in fecal metabolite measurements is lacking.

Future methods work should be extended to the general population and should collect multiple fecal samples over a period of time to assess within individual variability over time. In addition, the feasibility of each collection method, including freezing time, should be carefully weighed when designing large population-based studies. For example, FOBT cards can be shipped in the mail, making them particularly suitable for large, geographically diverse cohorts. Finally, additional research is needed to ascertain whether these collection methods are suitable for other multiomic technologies, such as whole genome shotgun metagenomics and proteomics. In conclusion, metabolite measures, obtained from an untargeted UPLC/MS-MS platform, from fecal samples collected with 95% ethanol or FOBT cards are reflective of those from fecal samples with no solution that were frozen shortly after collection (i.e. “gold standard”) and appear reproducible and stable following incubation at room temperature.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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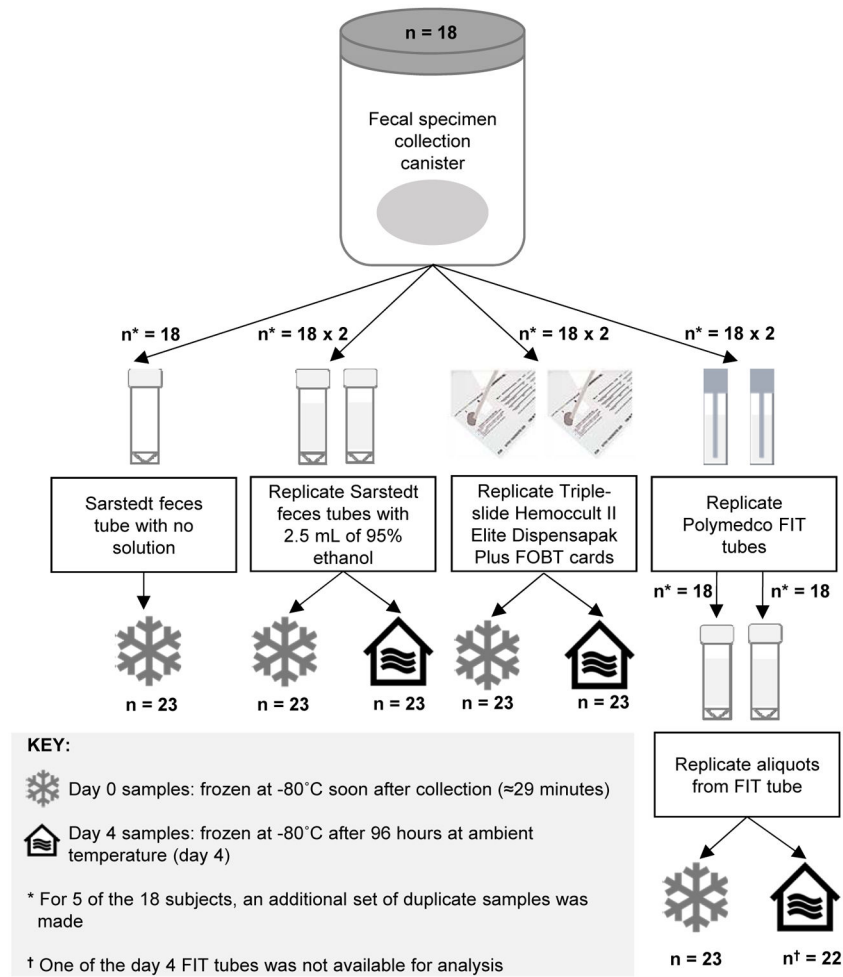


FIGURE 1.
Flowchart of study design

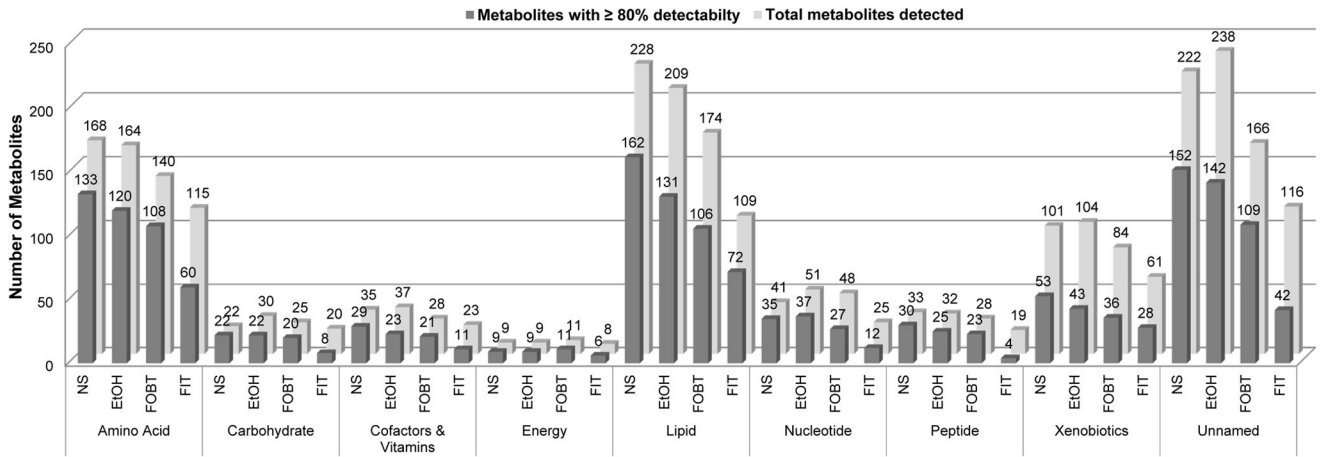


FIGURE 2.

Number of metabolites in fecal samples, frozen on day 0, by collection method and metabolic super pathway

Abbreviations: NS, no solution; EtOH, 95% ethanol; FOBT, fecal occult blood test; FIT, fecal immunochemical test

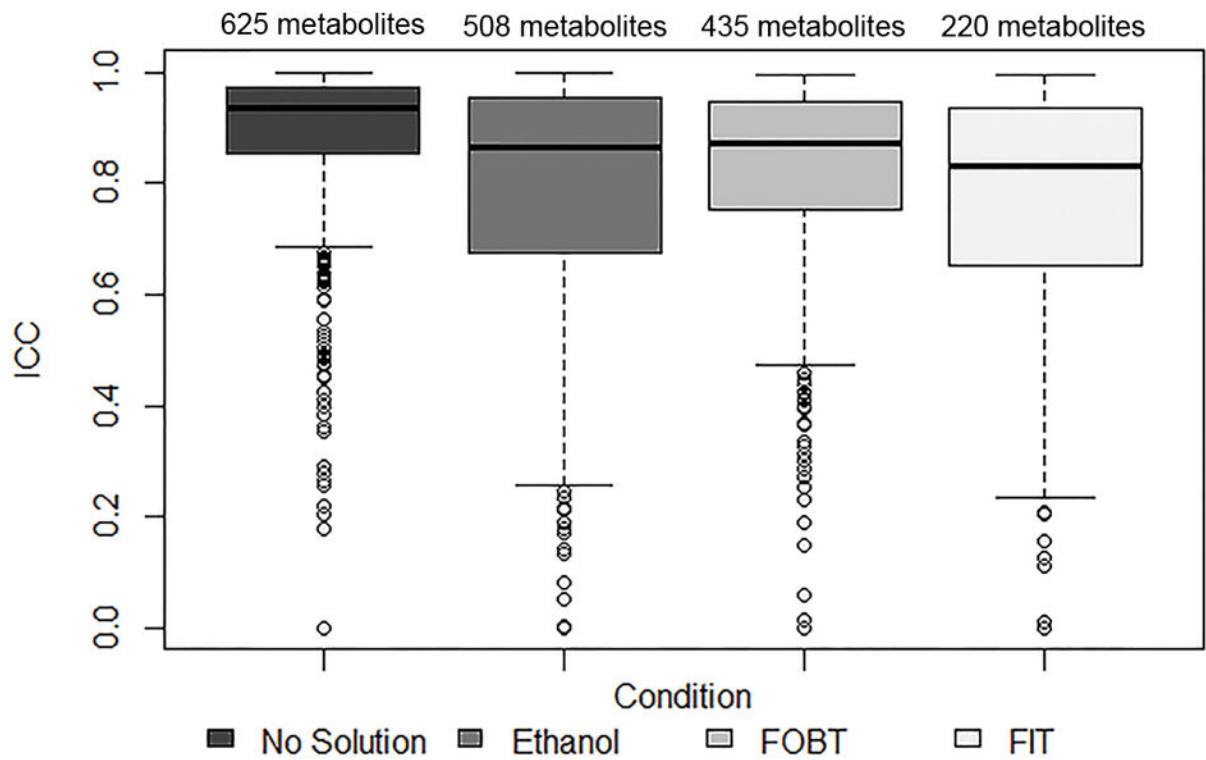


FIGURE 3.

Technical reproducibility, estimated using intraclass correlation coefficients, of replicate fecal samples, frozen on day 0, for metabolites with 80% detectability in samples with no solution and in samples collected with 95% ethanol, FOBT, or FIT

Abbreviations: ICC, intraclass correlation coefficient; NS, no solution; FOBT, fecal occult blood test; FIT, fecal immunochemical test

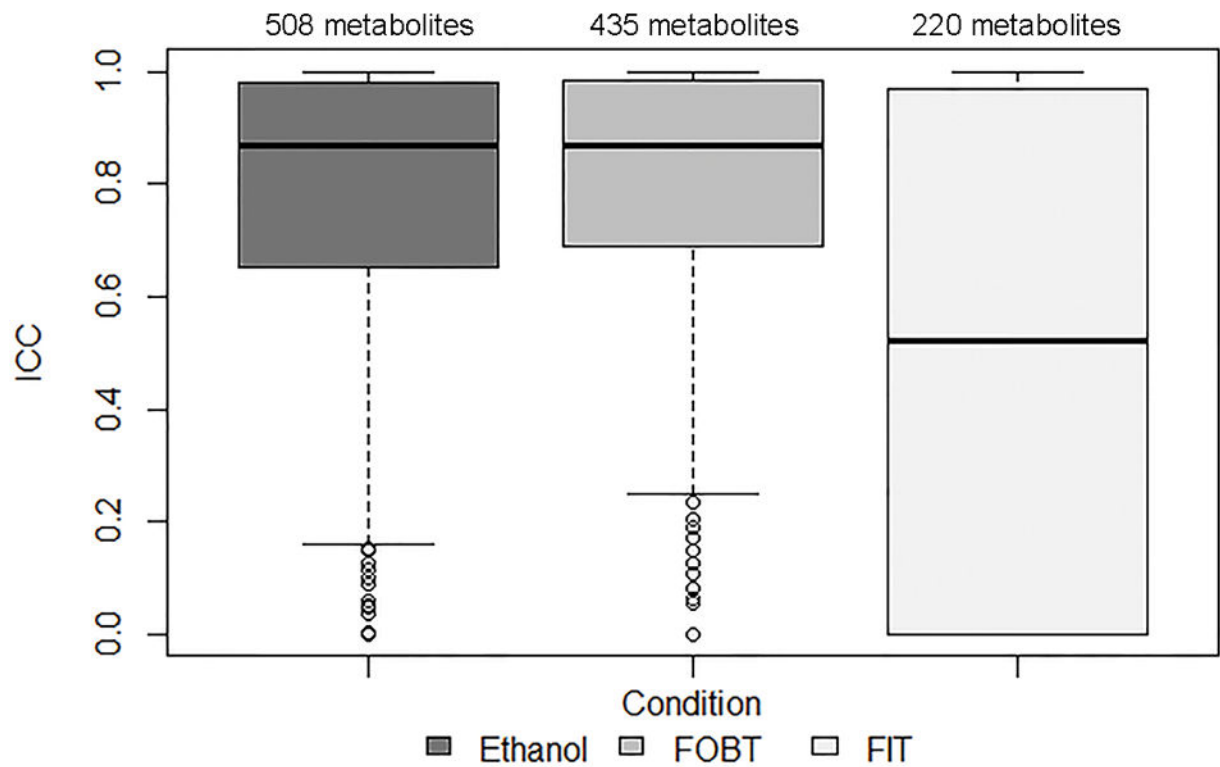


FIGURE 4.

Stability, estimated using intraclass correlation coefficients estimated from fecal samples that were frozen on day 4 after 96 hours at ambient temperature and replicate fecal samples that were frozen on day 0, for metabolites with 80% detectability in samples with no solution and in samples collected with ethanol, FOBT, or FIT

Abbreviations: ICC, intraclass correlation coefficient; NS, no solution; FOBT, fecal occult blood test; FIT, fecal immunochemical test

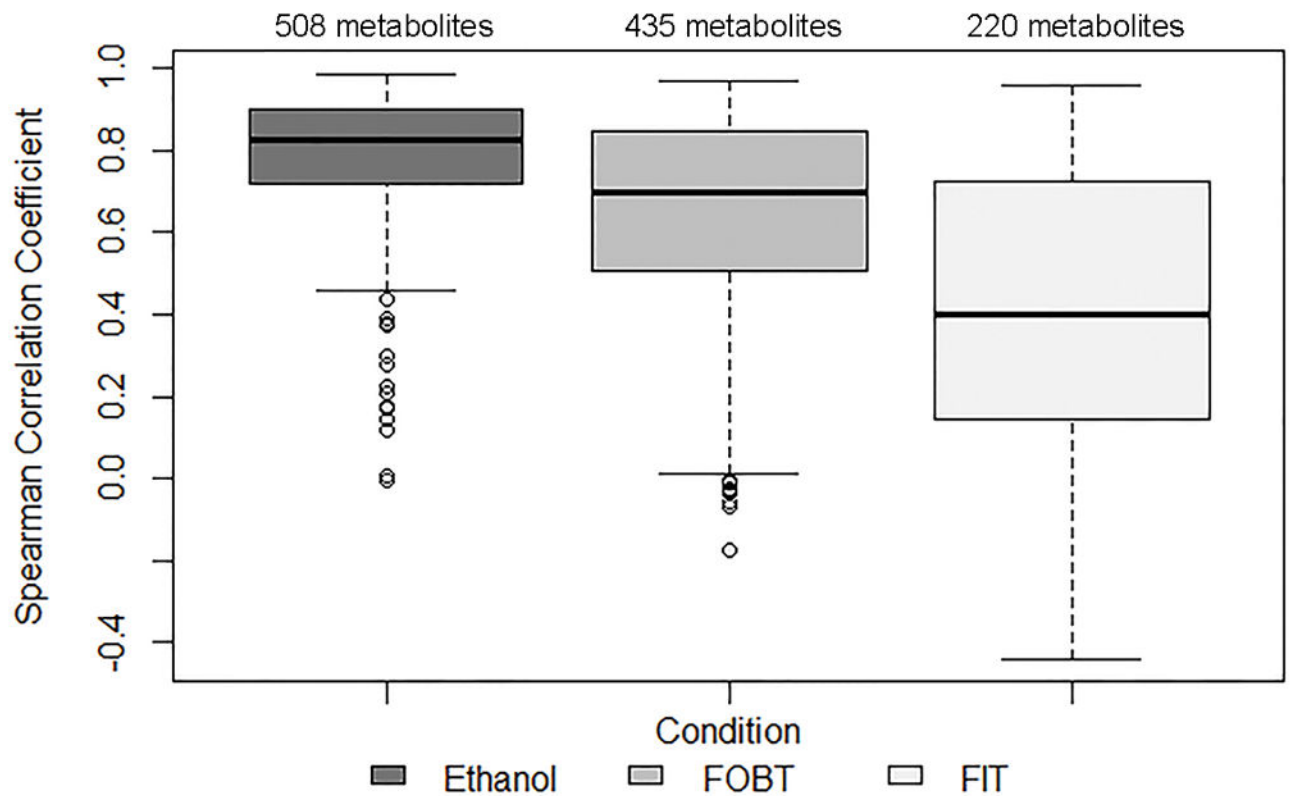


FIGURE 5.

Concordance, estimated using Spearman correlation coefficients, of fecal samples that were collected with ethanol, FOBT, or FIT and frozen on day 0 with fecal samples that were frozen on day 0 with no solution for metabolites with 80% detectability in samples with no solution and in samples collected with ethanol, FOBT, or FIT

Abbreviations: NS, no solution; FOBT, fecal occult blood test; FIT, fecal immunochemical test

Comparison of the number of metabolites, with 80% detectability, in no solution (NS) to the number of metabolites, with 80% detectability, in fecal samples collected with 95% ethanol, FOBT cards, or FIT tubes

TABLE 1

Condition	Total no. Metabolites	No. of metabolites in condition and NS ¹	No. metabolites in NS only	No. metabolites in condition only
No solution (gold standard)	625	---	---	---
95% Ethanol	561	508	117	53
FOBT	473	435	190	38
FIT	258	220	405	38

¹ Subset of metabolites used in technical reliability, stability, and concordance calculations

Abbreviations: NS, no solution; FOBT, fecal occult blood test; FIT, fecal immunochemical test