MGIEasy
Stool Microbiome DNA Extraction Kit

MGIEasy Stool Microbiome DNA Extraction Kit is designed for extracting and purifying high quality microbial genomic DNA from fresh and frozen human stool samples. With grinding beads, it can achieve unbiased extraction of microbial species from samples, including G-/G+ bacteria, fungi, protozoa, etc. The extracted product can be used for metagenomic analysis, intestinal flora research, probiotics research, etc.

Focuses on the extraction of microbial gDNA

The extracted product is a higher-quality microbial gDNA without species bias, which can be directly used in metagenomic analysis, human intestinal flora study, rare microbial mining, etc.

Good extraction performance

High extraction yield, good extraction purity, and can effectively remove PCR inhibition

Automation friendly

Compatible with the high-throughput automated sample preparation system MGISP-960 and the high-throughput automated nucleic acid extraction system MGISP-NE384

High safety

Free of hazardous components such as phenol, make experiment safe

Product info

Product Name	MGIEasy Stool Microbiome DNA Extraction Kit
Cat. No.	940-000122-00 & 940-000123-00
Specification	96 preps, 384 preps
Period of Validity	12 months
Storage Condition	2 °C-30 °C
Compatible Samples	Fresh or frozen human stools
Input volume	200-500 µL
Elution volume	100-150 µL
Compatible Automation	High-throughput automated sample preparation system MGISP-960, 96 samples/run High throughput nucleic acid extraction system MGISP-NE384, 384 sample/run
TAT	Manual： ~ 90 min， MGISP-960： ~ 90 min， MGISP-NE384： ~ 60 min

Order info

Name	Cat. No.	Model	Specification	Unit	Certification
MGIEasy Stool Microbiome DNA Extraction Kit	940-000122-00	SD02T-96	96 preps	Kit	RUO
MGIEasy Stool Microbiome DNA Extraction Kit	940-000123-00	SD02T-384	384 preps	Kit	RUO

Performance

Case1

Sample type: fresh human stools

Input volume: 500 µL

Output volume: 100 µL

Extraction method: manual extraction

Result: extraction yield > 10 µg, A260 / A280 > 1.8, C_T value < 20, that is, the kit has good extraction performance and can effectively remove PCR inhibition

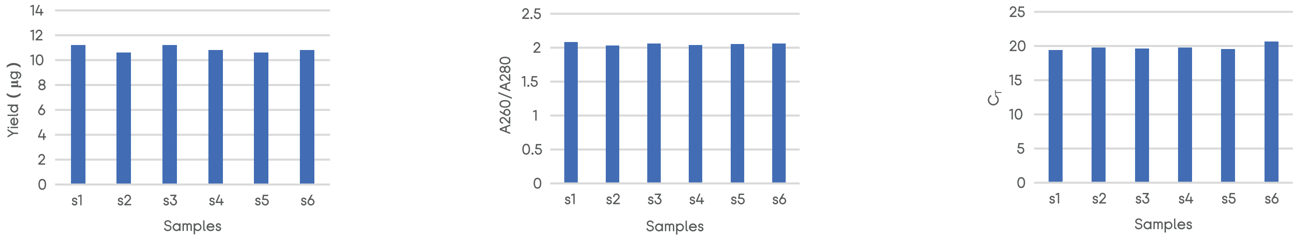

Figure 1 Extraction performance of MGI's kit

Case2

Sample type: fresh human stools

Input volume: 500 µL

Output volume: 100 µL

Extraction method1:

manual vs automation platform (MGISP-960)

Extraction method2:

manual vs automation platform (MGISP-NE384)

Result:

The A260/A280 and C_T values of manual and automatic extraction were basically consistent, which means MGI's kit can compatible with multiple automation platforms.

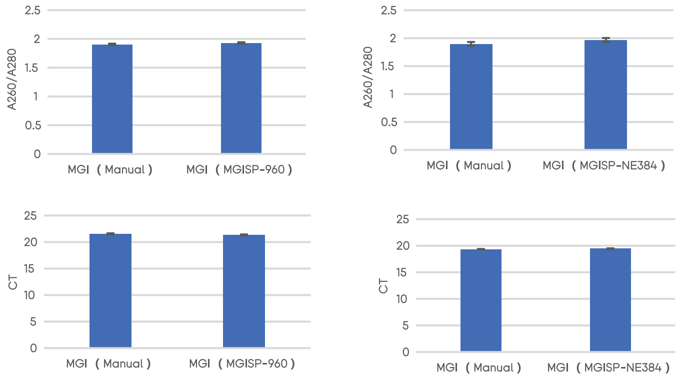

Figure 2 Comparison of manual and automated extraction methods of MGI's kit

Case3

Sample: fresh stool samples from nine people

Input volume: 1 mL and 200 µL for the MGI's kit;

Downstream operations: metagenomic analysis

Result:

A) PCoA was calculated based on species level, showing the species differentiation among samples. The better the overlap of the results for one subject, the smaller the differentiation. As shown in the figure A, the samples of 7 out of 9 subjects were well overlapped, indicating that different inputs do not affect the species abundance in the samples. (B) Bray dissimilarity is a measure used in ecology to measure the differentiation in species composition. The smaller the value is, the smaller the differentiation is. As shown in the figure B, all samples of one people were analyzed by MGI extraction kit, and it was found that the results were all clustered in a region with a very low value, indicating that different inputs almost make no difference on the species abundance. In conclusion, the MGI extraction kit can extract gDNA from sample with no microbial species bias.

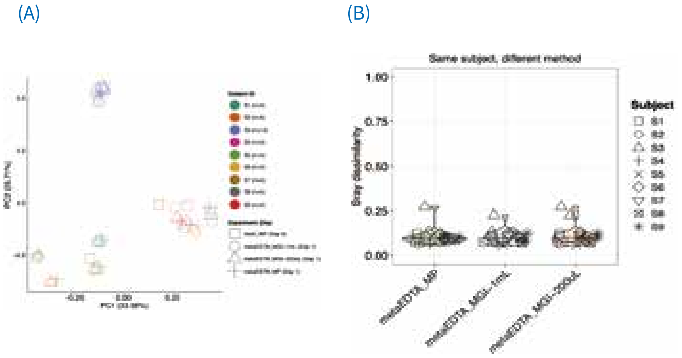

Figure 3 Metagenomic analysis

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