TANBead Stool Cell Extraction kit

I. Introduction

The TANBead Stool DNA extraction kit is designed for fast purification of high-quality microbial and host DNA from stool samples. Combined with TANBead Automated Extractor, the nucleic acids can be easily extracted without any risks of cross-contamination. Additionally, this kit utilizes advanced technology for robust yields of pure DNA ready for down-stream PCR, next-generation sequencing (NGS), or other applications. The kit uses highly efficient lysis and washing technology for fast removal of inhibitors such as proteins, nucleases, and other impurities. Compare with traditional extraction protocol, we provide a simpler and more efficient solution for those who struggle with time-consuming and complex methods.

II. Advantages

- Isolate 1 to 96 samples in 50 minutes.
- Increases nucleic acids recovery from stool sample with high input and low elution volumes in 96 deep-well plate formats.
- Automation-ready, no organic extraction or ethanol precipitation is required.
- Complete removal of contaminants and inhibitors.

III. Application data

To verify which type of stool samples can be treated for DNA extraction, the extraction of host genomic DNA and bacterial DNA from various animal sample types was carried out by using the TANBead Stool DNA extraction kit. Tested samples were prepared by using different types of animal stool specimens from omnivorous animals to herbivorous animals **(Table 1)**. To analyze the extracted DNA from a human stool specimen, the total yields of extracted DNA were measured using the NanoDrop and the bacterial and eukaryotic gDNA was determined by qPCR of 16S rRNA and GAPDH, respectively **(Table 2)**. In addition, the extracted DNA were analyzed by 16S rRNA sequencing to define operational taxonomic units (OTU)[1-2], the abundance distribution of dominant 35 genera between two samples are displayed in the species abundance heatmap[3-4] **(Figure 1)**.

50 mg of various animal stool specimens		DNA yield (µg)
Omnivorous	Cat	27.37±0.62
	Dog	17.14±0.36
Herbivorous	Rabbit	28.07±0.21
	Chinchilla	28.65±0.18
	Goat	20.10±0.51
	Tortoise	28.16±0.60
	Guinea pig	27.62±1.16
	Cow	29.48±0.46

Table 1. The performance of the TANBead Stool Cell DNA extraction kit was conducted with various animal stool specimens (Triplicate for each sample).

DNA yield (μg)	qPCR detection (Ct)	
	16S rRNA	*GAPDH*
7.81±0.12	15.54±2.22	31.90±1.20

Table 2. The performance of the TANBead Stool Cell DNA extraction kit was conducted with a human stool specimen (50 mg sample per test, n = 3).
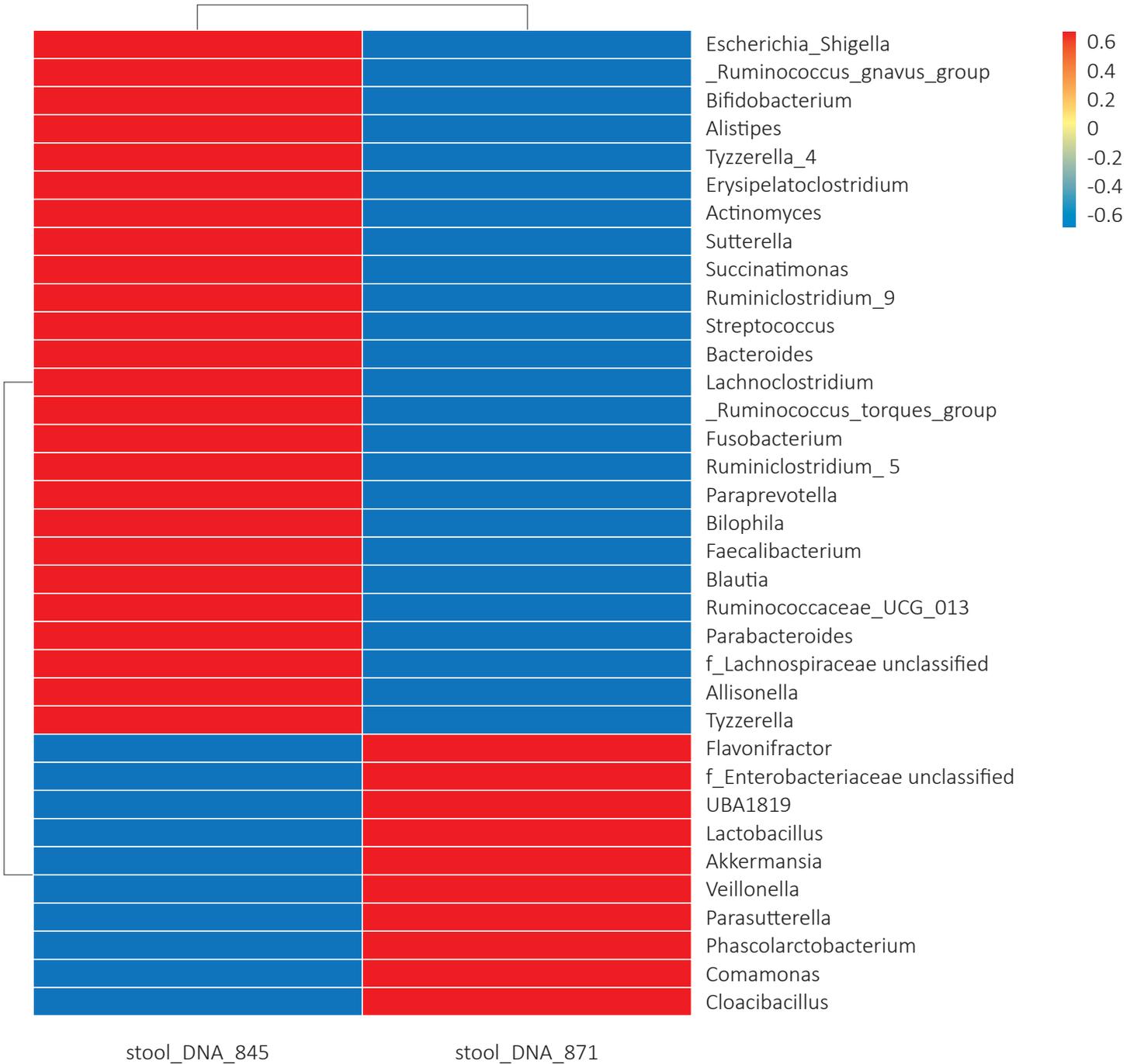

Figure 1. Species abundance heatmap of human stool samples extracted by TANBead Stool Cell DNA extraction kit. The relative abundances are colored based on the percentage of each OTU compared with total OTU count present in that sample (Blue: low percentage of OTUs to sample; Red: high percentage of OTUs). Plotted by sample name on the X-axis and OTU on the Y-axis represents the genus. The absolute value of 'z' represents the distance between the raw score and the mean population of the standard deviation. 'z' is negative when the raw score is below the mean, and vice versa.

IV. Specifications

Target	Instrument model	M8	M4800	M9600	SLA 32 SLA E13200
Host or Bacterial DNA	Input sample	At least 50 mg / test			
	Elution volume	80 µl			
	Incubation time	10 mins			
	Extraction time	41 mins	41 mins	50 mins	44 mins
	Throughput	8 samples	48 samples	96 samples	32 samples
	Application	Real-time PCR, NGS			

V. Conclusion

The significance of stool microbiome on health has been reported in many studies of medicine and research. We have demonstrated that TANBead Stool Cell DNA extraction kit is an ideal laboratory tool to automatically isolate DNA from stool samples, the purified DNA is ready for direct use in downstream applications, such as qPCR and NGS. Therefore, it is a powerful tool for sample preparation of noninvasive colon cancer screening, microbiota analysis, biology research, etc.

VI. Refernces

1. Blaxter M, Mann J, Chapman T, et al. Defining operational taxonomic units using DNA barcode data. *Philos Trans R Soc B Biol Sci.* 2005;360(1462):1935-1943.
2. Haas B.J., Gevers D, Earl A.M., et al. Chimeric 16S rRNA sequence formation and detection in Sanger and 454-pyrose quenced PCR amplicons. *Genome Res.* 2011;21(3):494-504.
3. Quast C, Pruesse E, Yilmaz P, Gerken J, Schweer T, Yarza P, Peplies J, Glöckner F.O. The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. *Nucl. Acids Res.* 41 (D1): D590-D596.
4. Ondov B.D., Bergman N.H., Phillippy A.M. Interactive metagenomic visualization in a Web browser. *BMC Bioinformatics.* 2011;12(1):385.