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BioTechniques

A comparison of DNA/RNA extraction protocols for high-throughput sequencing of microbial communities

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ABSTRACT

One goal of microbial ecology researchers is to capture the maximum amount of information from all organisms in a sample. The recent COVID-19 pandemic, caused by the RNA virus SARS-CoV-2, has highlighted a gap in traditional DNA-based protocols, including the high-throughput methods the authors previously established as field standards. To enable simultaneous SARS-CoV-2 and microbial community profiling, the authors compared the relative performance of two total nucleic acid extraction protocols with the authors' previously benchmarked protocol. The authors included a diverse panel of environmental and host-associated sample types, including body sites commonly swabbed for COVID-19 testing. Here the authors present results comparing the cost, processing time, DNA and RNA yield, microbial community composition, limit of detection and well-to-well contamination between these protocols.

ACCESSION NUMBERS

Raw sequence data were deposited at the European Nucleotide Archive (accession number ERP124610), and raw and processed data are available at Qiita (study identifier 12201). Processing and analysis code is available on GitHub (https://github.com/justinshaffer/Extraction_test_MagMAX).

METHOD SUMMARY

To allow for downstream applications involving RNA-based organisms such as SARS-CoV-2, the authors compared the two extraction protocols designed to extract DNA and RNA with the authors' previously established protocol for extracting only DNA for microbial community analyses. Across ten diverse sample types, one of the two protocols was equivalent or better than the authors' established DNA-based protocol. The authors' conclusion is based on per-sample comparisons of DNA and RNA yield, number of quality sequences generated, microbial community alpha- and beta-diversity and taxonomic composition, limit of detection and extent of well-to-well contamination.

KEYWORDS:

16S rRNA • DNA extraction • high-throughput sequencing • limit of detection • microbial community • microbiome • RNA extraction • shotgun metagenomics • well-to-well contamination

Our growing understanding of microbial communities continues to reveal knowledge important for fostering human and environmental sustainability [1–4]. Nearly every day, new links are made between the human microbiome and human health [5–7], and the development of methods related to studying microbial communities is ever-expanding [8–10]. One major roadblock to studying microbial communities is that single methods rarely capture information from all organisms in a sample or from across diverse sample types [11–13].

The ongoing COVID-19 pandemic driven by SARS-CoV-2 has infected over 40 million human individuals and killed 1.1 million (as of 18 October 2020) [14]. Such an event represents an invaluable opportunity to study the effects of a novel pathogen on microbial interactions relevant to human hosts and other ecosystems [15–17]. Currently, the authors' protocol benchmarked for high-throughput microbiome sequencing focuses on extracting high-quality DNA from samples [18] and therefore will not capture RNA-based genomes such as that of SARS-CoV-2, which is a positive-sense, single-stranded RNA virus [19].

Here the authors aim was to identify an extraction protocol that extracts high-quality RNA while also producing DNA output and community composition comparable to the authors' previously benchmarked protocol [18]. The authors also considered technical differences

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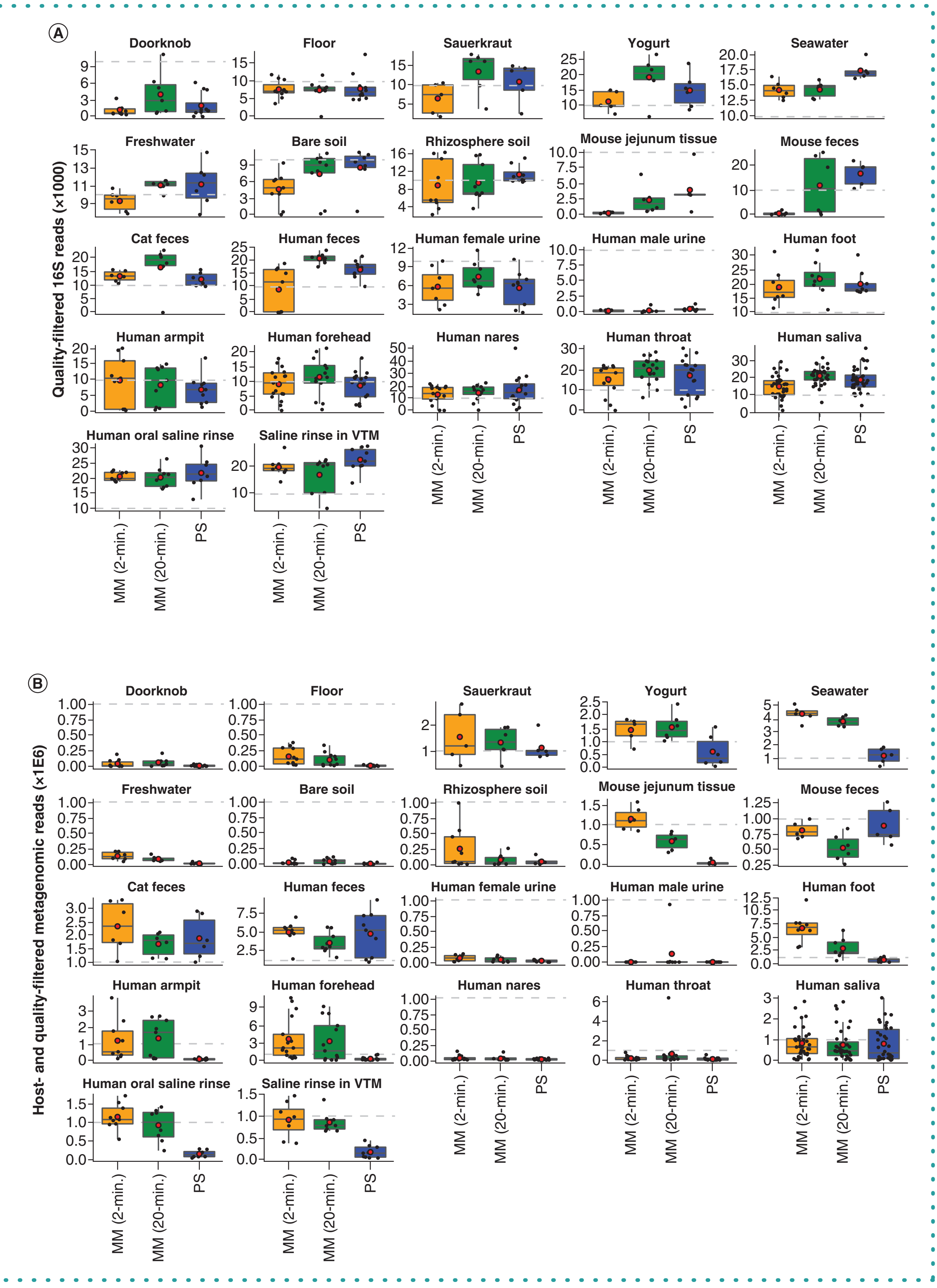

Figure 1. Sequences per sample across extraction protocols and sample types. Average number of quality sequences for **(A)** 16S and **(B)** metagenomics data (n = 660 samples included). Red circles indicate means. Dashed lines indicate our expectation of **(A)** 10,000 from 16S and **(B)** 1 million reads from metagenomics, respectively, for human fecal samples. Note that additional samples included here absent from our statistical test (n = 45) include those for which technical replication across protocols was not feasible due to recommended sampling protocols (e.g., human nares, human throat), so we included biological replicates instead. Sample types missing here lacked representation by both MagMAX protocols.
MM: MagMAX; PS: PowerSoil.

Table 1. Limit of detection across extraction protocols.								
Extraction protocol	**Sample set**	**Threshold (%)**	**LOD Gram-negative**	**LOD Gram-positive**	**LOD mixed culture**	**Read depth**	**Samples retained**	**Samples retained (%)**
MagMAX 2-min	High biomass	50	–	–	5.73E+02	362	76	80
		80	–	–	5.73E+04	1392	69	73
		90	–	–	5.73E+04	3512	64	67
		95	–	–	5.73E+06	9144	46	48
	Low biomass	50	1.60E+03	3.10E+03	–	637	69	73
		80	1.60E+04	3.10E+03	–	1631	63	66
		90	1.60E+04	3.10E+03	–	3007	59	62
		95	1.60E+05	3.10E+04	–	5526	52	55
MagMAX 20-min	High biomass	50	–	–	5.73E+05	8499	68	71
		80	–	–	5.73E+07	14,522	55	57
		90	–	–	5.73E+07	20,158	30	31
		95	–	–	5.73E+07	27,541	3	3
	Low biomass	50	1.60E+01	3.10E+01	–	491	79	83
		80	1.60E+03	3.10E+03	–	776	71	75
		90	1.60E+03	3.10E+03	–	1031	68	72
		95	1.60E+04	3.10E+03	–	1354	64	67
PowerSoil	High biomass	50	–	–	5.70E+01	1050	87	92
		80	–	–	5.73E+07	14,632	36	38
		90	–	–	NA	106,110	0	0
		95	–	–	NA	944,308	0	0
	Low biomass	50	1.60E+03	3.10E+00	–	1836	69	72
		80	1.60E+04	3.10E+02	–	3797	62	65
		90	1.60E+05	3.10E+03	–	5997	57	59
		95	1.60E+05	3.10E+03	–	9345	40	42

Titrations of cultured cells were used to identify the number of reads needed per sample to meet various thresholds of detection (i.e., percentage of reads mapped to expected taxa vs background contaminants). Read depths corresponding to a threshold of 50% were used for filtering samples prior to community analyses of microbial 16S data, as recommended [20]. Retention of samples following filtering based on read depth for each threshold is shown.
Gram+: *Bacillus subtilis*; Gram–: *Paracoccus denitrificans*; Mixed culture: *B. subtilis* and *P. denitrificans*; NA: Not applicable.

regarding the detection ability [20] and extent of contamination [21–23] among protocols. The authors compared DNA and RNA yield, number of quality sequences, microbial community alpha- and beta-diversity and taxonomic composition, limit of detection (LOD) and extent of well-to-well contamination across common sample types and among three extraction protocols.

Methods

Sample collection

To compare extraction protocols, the authors collected biological materials from a broad range of human and environmental samples, focusing on types widely used in studies of microbial communities and SARS-CoV-2 detection [18,24,25]. Each unique sample was aliquoted across extraction plates for comparison of extraction efficiency among protocols. The authors included a total of 33 human skin samples, 30 human oral samples, eight built environment samples, six fecal samples, six human urine samples, six soil samples, four water samples, four fermented food samples and two tissue samples. The authors collected most sample types using wooden handle cotton swabs (Puritan, CA, USA) following the standard Earth Microbiome Project protocol [26]. To make comparisons relevant to SARS-CoV-2 detection, the authors collected additional samples, mimicking those collected from patients, using BBL CultureSwab plastic handle polyester swabs (category number 220135; BD Biosciences, NJ, USA) following the CDC's specimen collection guidelines [24,25].

The authors collected samples to allow for technical replication across three extraction protocols. Human skin samples included those from the foot, armpit, forehead and nostril interior. Foot and armpit samples were collected from three individuals by rubbing five cotton swabs simultaneously on the sole of each foot or armpit for 30 s. Forehead and nostril samples were collected from 12 individuals by rubbing two polyester swabs over the forehead for 30 s or in each nostril for 15 s each. Human oral samples included throat, saliva and oral saline rinses and the same rinses diluted in viral transport medium [27]. Throat samples were collected from 12 individuals by rubbing two polyester swabs across the pharynx for 30 s. Saliva was collected from 12 individuals using active spitting into a 50-ml centrifuge tube. Saline rinses were collected from three individuals by swishing 10 ml 0.9% saline for 30 s and spitting into a 50-ml centrifuge tube. To mimic storage in viral transport medium, 5 ml of saline rinse was mixed with 100 μl 50× viral transport medium in a 15-ml centrifuge tube. Built environment samples included floors and door handles. Floor and door handle samples were collected from two rooms using

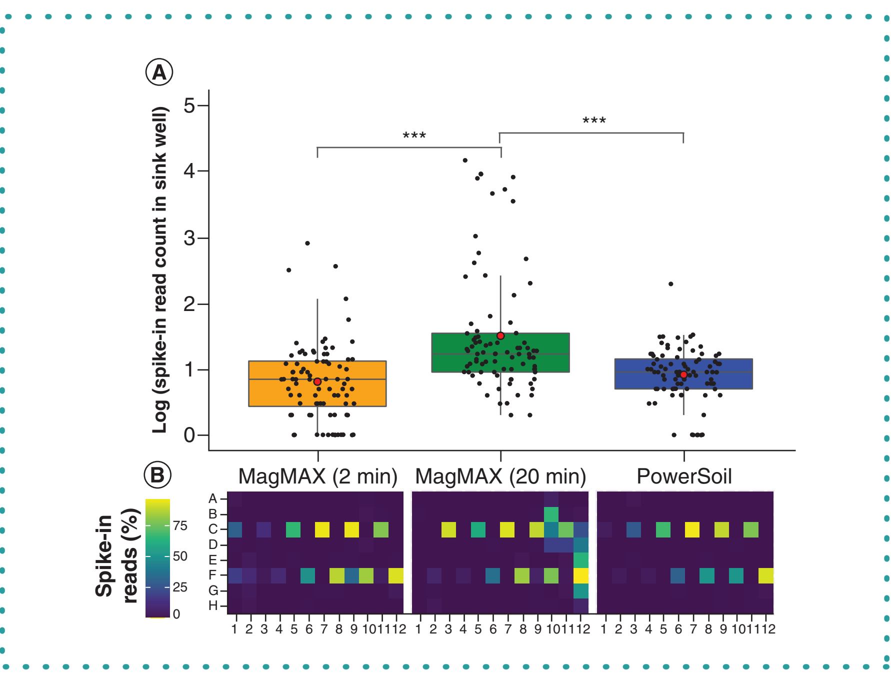

Figure 2. Well-to-well contamination across extraction protocols. Plasmids harboring synthetic 16S sequences were spiked into a single well per plate column (i.e., alternating from row C to F across columns: C1, F2, C3, F4, etc.) of each high-biomass sample plate prior to extraction. **(A)** The number of reads matching synthetic 16S sequences was quantified for all wells that did not receive a spike-in. Asterisks indicate significant differences between pairs of extraction protocols as determined by a Kruskal-Wallis post-hoc Dunn's test with a Benjimini-Hochberg correction for multiple comparisons. **(B)** The percentage of spike-in reads among all reads per well shown as a heatmap.
*** $p < 0.001$.

cotton swabs and two rooms using polyester swabs by rubbing nine swabs simultaneously across the surface of a 1 sq ft tile for 30 s or one entire door handle, respectively. Fecal samples included human, mouse and cat samples. Human feces were collected from two individuals using commode collectors (commode specimen collection system, Thermo Fisher Scientific, MA, USA). Mouse feces were collected from two individuals and stored in 1.5-ml microcentrifuge tubes. Cat feces were collected from two individuals and stored in plastic zip-top bags. Human urine samples included samples from female and male individuals. Urine was collected from three female and three male individuals and stored in commode collectors or 50-ml centrifuge tubes. Soil samples included tree rhizosphere and bare soil. For each type, soil was collected from two adjacent sites down to a depth of 20 cm using a sterile trowel and stored in plastic zip-top bags. Water samples included fresh- and seawater collected from two sites at the San Diego River and two sites at the Scripps Institution of Oceanography, respectively. Water was collected and stored in 50-ml centrifuge tubes. Fermented food samples included yogurt and sauerkraut samples. Two varieties of one brand of each food were purchased commercially and stored in 50-ml centrifuge tubes. Tissue samples included jejunum tissue from eight mice. Approximately 3.8 cm of the middle small intestine was removed, and any fecal matter inside was squeezed out lengthwise. Each tissue section was added to a 2-ml microcentrifuge tube containing 1 ml sterile 1× phosphate-buffered saline and approximately 40 mg sterile 1-mm silicone beads and homogenized at 6000 rpm for 1 min with a MagNA Lyser (Roche Diagnostics, CA, USA). The liquid homogenate from three intestinal sections from cohoused mice was pooled to create a single sample (one sample per cage). All samples were stored at -80°C within 3 h of collection and frozen for a maximum of 24 h before extraction. To compare LOD – defined as the number of cells required to detect a microbe in the sequence data – the authors included serial dilutions of cultures of *Bacillus subtilis* (Firmicutes) and *Paracoccus denitrificans* (Alphaproteobacteria) [20]. Input cell densities ranged from 2.0 to 9.6E7 cells for *B. subtilis* and 0.0 to 3.1E7 cells for *P. denitrificans*. To compare well-to-well contamination [23], the authors included plasmid-borne, synthetic 16S rRNA gene spike-ins (i.e., 4 ng of unique spike-in to one well of each column in the plate) [28] and at least five extraction blanks per plate.

DNA and RNA extraction

The authors compared two extraction protocols that use a 96-sample magnetic bead cleanup format: the MagAttract PowerSoil DNA isolation kit (category number 27000-4-KF; Qiagen, CA, USA) and the MagMAX microbiome ultra nucleic acid isolation kit (category number A42357; Applied Biosystems, CA, USA). The authors considered that the PowerSoil kit protocol includes heating the lysis solution to 60°C when mixing with samples as well as a subsequent 20-min bead-beating step, whereas the MagMAX kit uses no heating and only a 2-min bead-beating step. Additional heating and extended bead-beating may alter the extent of cellular lysis and degradation of extracellular nucleic acids and, subsequently, microbial community composition. The authors therefore included a third protocol, a

Table 2. Results from a forward, stepwise model selection of factors influencing microbial community beta-diversity.							
Data type	**Distance metric**	**Factor**	**Adjusted R^2**	**df**	**AIC**	**F**	**p-value**
16S	Unweighted UniFrac	Sample type	0.87	24	-556.59	172.97	0.0002
		Host identity	0.01	30	-583.89	2.85	0.0002
		Extraction protocol	0.001	2	-588.47	3.92	0.004
	Weighted UniFrac	Sample type	0.76	24	-165.42	79.55	0.0002
		Host identity	0.06	30	-320.67	7.83	0.0002
		Extraction protocol	0.001	2	-323.72	3.21	0.02
	Jaccard	Sample type	0.89	24	-651.49	206.18	0.0002
		Host identity	0.02	30	-756.85	5.76	0.0002
		Extraction protocol	0.001	2	-762.48	4.40	0.0008
	RPCA	Sample type	0.86	24	-495.50	154.16	0.0002
		Host identity	0.03	30	-619.04	6.49	0.0002
		Extraction protocol	0.001	2	-625.14	4.61	0.0002
Metagenomics	Unweighted UniFrac	Sample type	0.93	26	-958.24	317.60	0.0002
		Host identity	0.01	31	-1062.60	5.57	0.0002
		Extraction protocol	0.001	2	-1067.53	4.08	0.0006
	Weighted UniFrac	Sample type	0.87	26	-602.92	173.32	0.0002
		Host identity	0.02	31	-676.11	4.42	0.0002
		Extraction protocol	0.003	2	-693.97	10.09	0.0002
	Jaccard	Sample type	0.94	26	-1084.87	391.42	0.0002
		Host identity	0.01	31	-1217.42	6.67	0.0002
	RPCA	Sample type	0.85	26	-496.04	143.29	0.0002
		Host identity	0.03	31	-620.86	6.36	0.0002
		Extraction protocol	0.005	2	-645.41	13.24	0.0002

Values are based on permutation tests of variation explained by redundancy analysis, done separately for four unique metrics for both 16S and metagenomics data. The full model included bead-beating time (i.e., 2 vs 20 min), sample biomass (i.e., high vs low biomass), sample type, host subject identity and extraction protocol (i.e., MagMAX 2-min, MagMAX 20-min, PowerSoil) as model variables. The 16S data were rarefied, as noted for Figure 3. Metagenomics data were rarefied to 17,000 host- and quality-filtered reads per sample or had samples with fewer than 17,000 reads excluded when using RPCA distances (n = 647 samples). Rarefaction depths were selected to maintain at least 75% samples from both high- and low-biomass datasets.
AIC: Akaike information criterion; df: degrees of freedom; RPCA: Robust principal component analysis.

variant of the MagMAX protocol, including 60°C incubation and 20-min bead-beating steps, and refer to the three protocols as PowerSoil, MagMAX 20-min and MagMAX 2-min.

For extraction, aliquots of each sample were transferred to unique wells of a 96-well extraction plate. For samples collected with swabs, the entire swab head was broken off into the lysis plate. For liquid samples, the authors transferred 200 μl. For bulk samples, the authors used cotton swabs to collect approximately 100 mg of homogenized material and broke the entire swab head off into the lysis plate. Extractions were performed following the manufacturer's protocol, except for the modifications made to the previously described MagMAX 20-min protocol. Lysis was performed with a TissueLyser II (Qiagen). Bead clean-ups were performed with the KingFisher flex purification system (Thermo Fisher Scientific). Extracted nucleic acids were stored at -80°C prior to quantification of RNA yield, fragment length distribution and integrity as well as quantification of DNA yield and downstream sequencing.

16S rRNA gene and shotgun metagenomics sequencing

The authors prepared DNA for 16S rRNA gene and shallow shotgun metagenomics sequencing as described previously [10,29–31]. For 16S data, raw sequence files were demultiplexed using Qiita [32], and suboperational taxonomic units were generated using Deblur [33]. For shallow shotgun metagenomics data, raw sequence files were demultiplexed using BaseSpace (Illumina, CA, USA), quality-filtered using Atropos [34] and human read-depleted by alignment to human reference genome GRCh38 using bowtie2 [35]. Filtered reads were aligned to the Web of Life database [36] using Shogun [31] with default parameters and using bowtie2 as the aligner, followed by read classification with the Web of Life Toolkit App [36,37]. Raw sequence data were deposited at the European Nucleotide Archive (accession number ERP124610), and raw and processed data are available at Qiita (study identifier 12201). Processing and analysis code is available on GitHub (https://github.com/justinshaffer/Extraction_test_MagMAX).

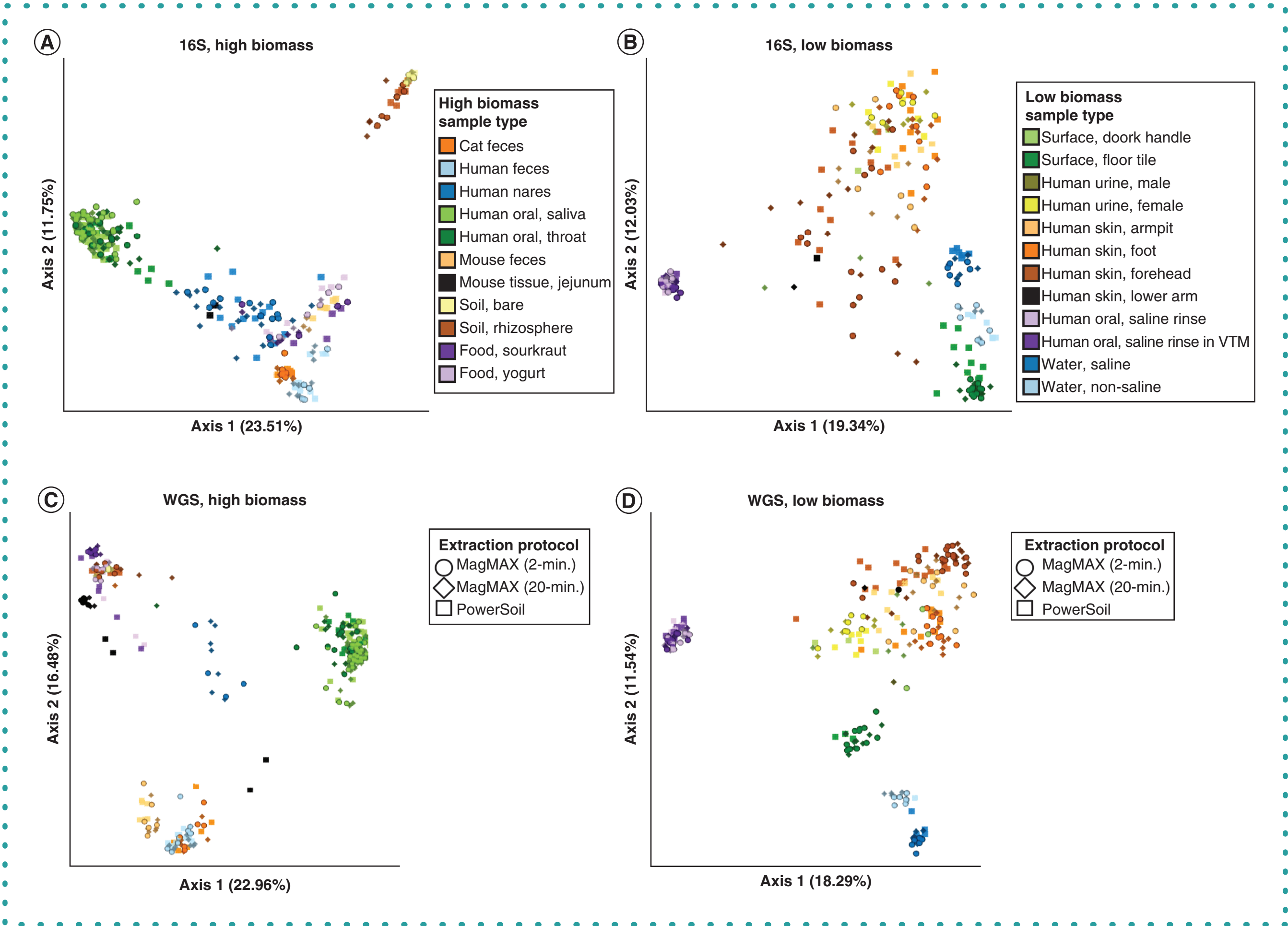

Figure 3. Beta-diversity among extraction protocols and sample types. Principal coordinates analysis (PCoA) plots showing unweighted UniFrac distances based on 16S data for **(A)** high biomass samples and **(B)** low biomass samples, and shotgun metagenomics data for **(C)** high biomass samples and **(D)** low biomass samples. Colors indicate sample types and shapes indicate extraction protocols. Mock community and control blanks were excluded for clarity. 16S data were rarefied to 5,000 quality-filtered reads per sample for both high- and low-biomass samples (n = 611 samples). Metagenomics data were rarefied to 35,000 host- and quality-filtered reads per high-biomass sample (n = 287 samples), and to 20,000 reads per low-biomass sample (n = 242 samples). When using RPCA distances rather than using rarefied data, we excluded samples with fewer reads than the rarefaction depth for that dataset. Rarefaction depths were selected to maintain at least 75% samples from both high- and low-biomass datasets.

Results & discussion

The authors found DNA yield to be similar across the three extraction protocols and note that when considering all sample types (n = 615 samples), the extraction efficiency of the PowerSoil protocol was more similar to that of the MagMAX 20-min protocol compared with MagMAX 2-min protocol (paired-sample Wilcoxon signed-rank test: PowerSoil vs MagMAX 20-min W = 10,540; p = 0.6 and PowerSoil vs MagMAX 2-min W = 81,170; p = 0.01) (Supplementary Figure 1). The authors observed a similar pattern for the number of quality-filtered 16S reads (PowerSoil vs MagMAX 20-min W = 11,482; p = 0.1 and PowerSoil vs MagMAX 2-min W = 4651; p = 2.74E-11). However, for quality- and human-filtered shotgun metagenomics reads, both MagMAX protocols varied from the PowerSoil protocol (PowerSoil vs MagMAX 20-min W = 15,873; p = 1.41E-11 and PowerSoil vs MagMAX 2-min W = 17,148; p = 2.24E-15) (Figure 1 & Supplementary Figure 2).

From a technical perspective, the authors' comparison of the LOD of each protocol indicates that the MagMAX 2-min protocol requires ten times the number of cells required by PowerSoil for accurate detection in mixed bacterial cultures (Table 1). This is compared with the 10,000 times required by the MagMAX 20-min protocol (Table 1). This pattern is mirrored when considering sample retention following filtering based on LOD thresholds, for which the MagMAX 2-min is better with high-biomass samples and the MagMAX 20-min with low-biomass samples. However, the authors observed an increase in well-to-well contamination in the MagMAX 20-min protocol compared with the MagMAX 2-min protocol (Figure 2). As all other parameters were consistent between the two MagMAX protocols, this indicates that mimicking lysis parameters from the PowerSoil protocol in the MagMAX protocol can have undesirable consequences.

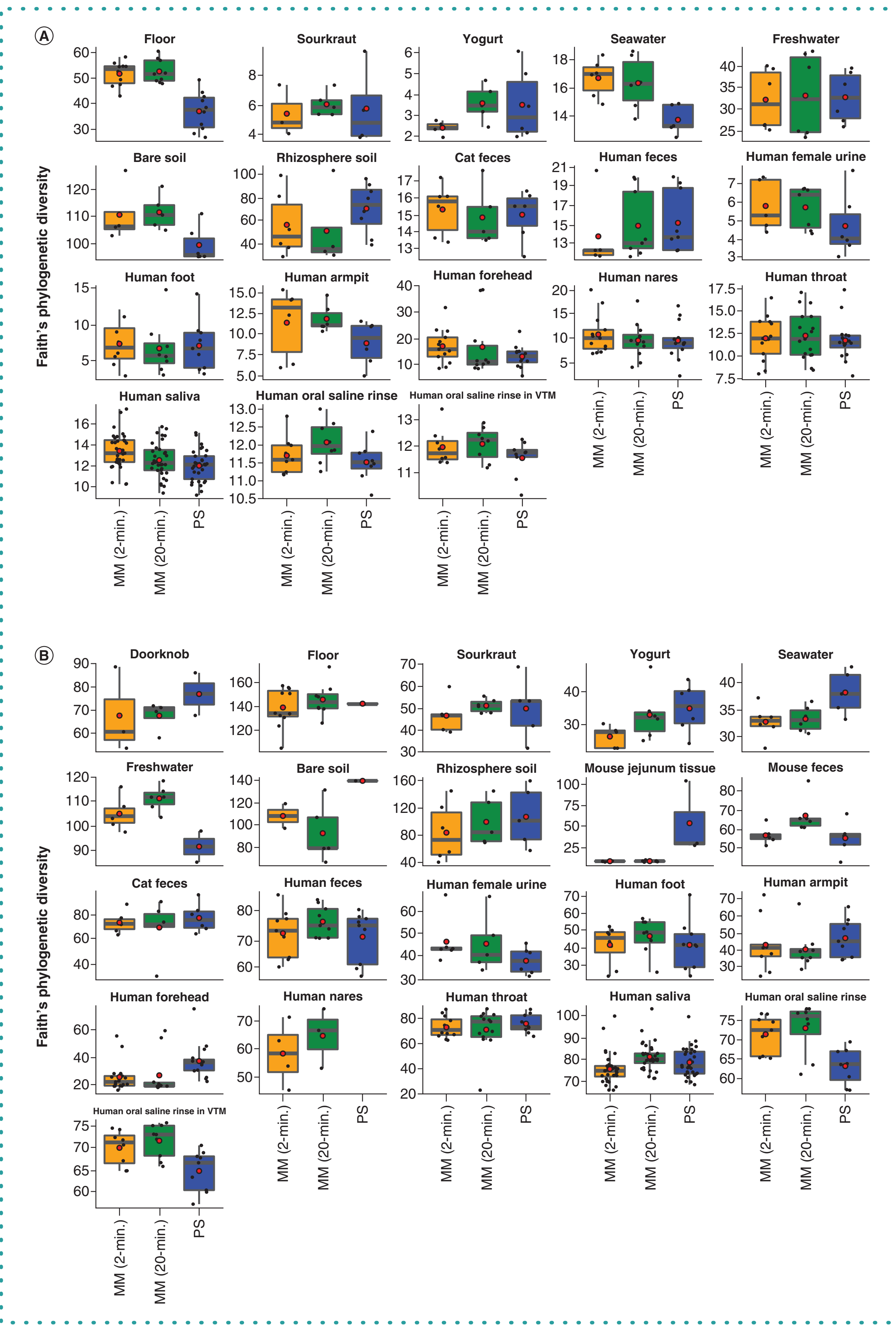

Figure 4. Alpha-diversity across extraction protocols and sample types. Faith's Phylogenetic Diversity among the three extraction protocols based on **(A)** 16S and **(B)** metagenomics data. Red circles indicate means. Data were rarefied as noted for Figure 3.
MM: MagMAX; PS: PowerSoil.

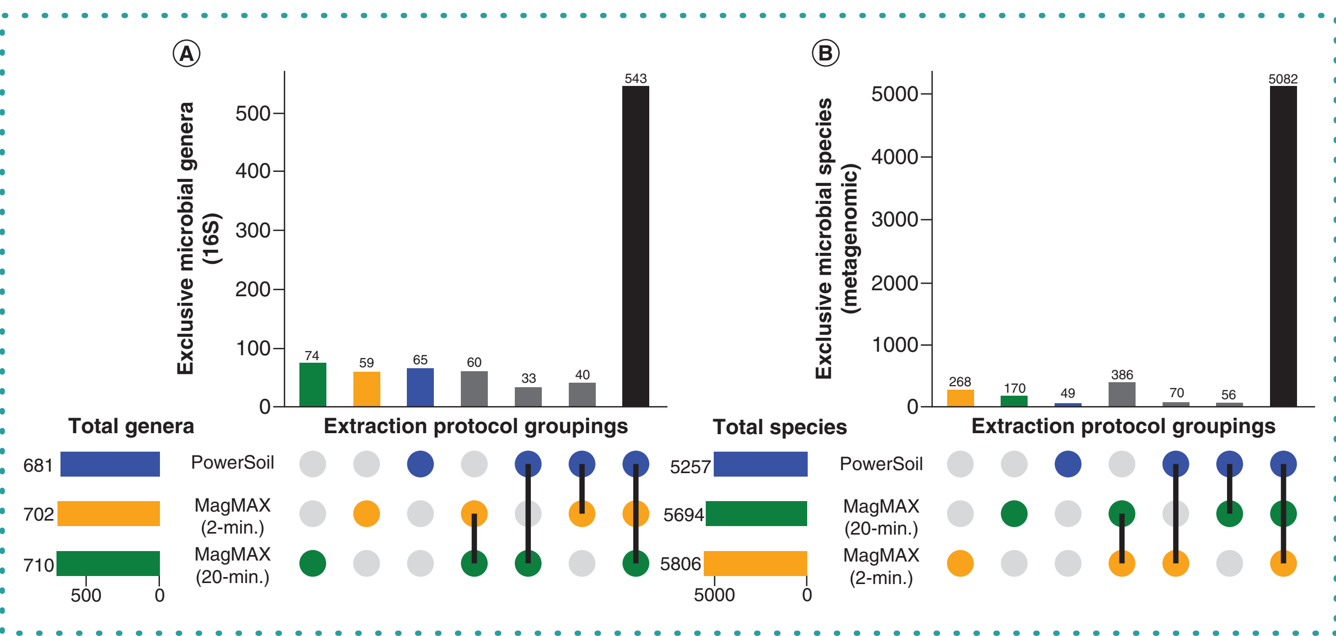

Figure 5. Taxonomic bias among extraction protocols. Upset plots showing (A) genera for 16S data and (B) species for metagenomics data, highlighting taxa shared among extraction protocols. Data were rarefied as noted for Figure 3.

The extended bead-beating time may lead to lysate leaking into the thin ridges of the 96-well plate, which is covered by a plastic film. From this perspective, the authors favor the MagMAX 2-min protocol.

With respect to microbial community composition, the authors found bias introduced by extraction protocol to be small compared with variation among sample types or replicates of the same sample (i.e., one to two orders of magnitude weaker in explaining beta-diversity) (Tables 1 & 2 & Supplementary Figures 3 & 4). The authors also found strong correlations in microbial community beta-diversity among samples between any two extraction protocols; however, relationships with the PowerSoil protocol were slightly stronger for MagMAX 2-min compared with MagMAX 20-min (Supplementary Table 1). The authors used principal coordinates analysis of unweighted UniFrac distances to visualize these trends and confirmed that samples clustered strongly by type and host subject and not by extraction protocol for both 16S and metagenomics data (Figure 3 & Supplementary Figures 5 & 6). Estimates of alpha-diversity were more comparable to those from PowerSoil for the MagMAX 2-min protocol (paired-sample Wilcoxon signed-rank test: PowerSoil vs MagMAX 2-min $W = 5916$; $p = 0.0001$ and PowerSoil vs MagMAX 20-min $W = 7058$; $p = 1.53E-06$) (Figure 4 & Supplementary Figure 7). Finally, the majority of genera (16S) and species (metagenomics) were shared across all three extraction protocols; however, for both datasets, the MagMAX 2-min protocol shared a greater number of exclusive taxa with the PowerSoil protocol than the MagMAX 20-min protocol did (Figure 5).

Together, these results highlight that, despite variation in DNA yield, sequence read counts and LOD of microbial cells among extraction protocols, differences in microbial taxonomic and community composition resulting from the different methods were minor for both 16S and metagenomics microbial sequence data. However, between the two MagMAX protocols, the authors note that for beta-diversity, alpha-diversity and taxonomic composition, the MagMAX 2-min protocol generated results more comparable to the PowerSoil protocol.

Importantly, whereas RNA yield was comparable between the two MagMAX protocols (Figure 6A), the authors observed a higher quality of extracted RNA using the MagMAX 2-min versus MagMAX 20-min protocol (Figure 6B & C). In addition to reduced well-to-well contamination from a shorter bead-beating time during lysis for the MagMAX 2-min versus MagMAX 20-min protocol, the lack of incubation of the lysis buffer resulted in relatively high-quality RNA produced with the former compared with the latter (Figure 6).

Conclusion

We conclude that the MagMAX 2-min extraction protocol is comparable to our established PowerSoil protocol with respect to characterizing microbial community composition and therefore should allow for comparisons such as meta-analysis across 16S and metagenomics data produced using both protocols and downstream methods similar to those used here. In addition to extracting both DNA and RNA, the more rapid processing time (i.e., approximately 2 h faster than PowerSoil per 96 samples), use of fewer consumables (i.e., approximately 70% of plastics) and lower cost (i.e., \$5.56 vs \$5.65 per sample) highlight the MagMAX 2-min protocol as a comparable and efficient alternative to the PowerSoil protocol that also allows for downstream applications using RNA.

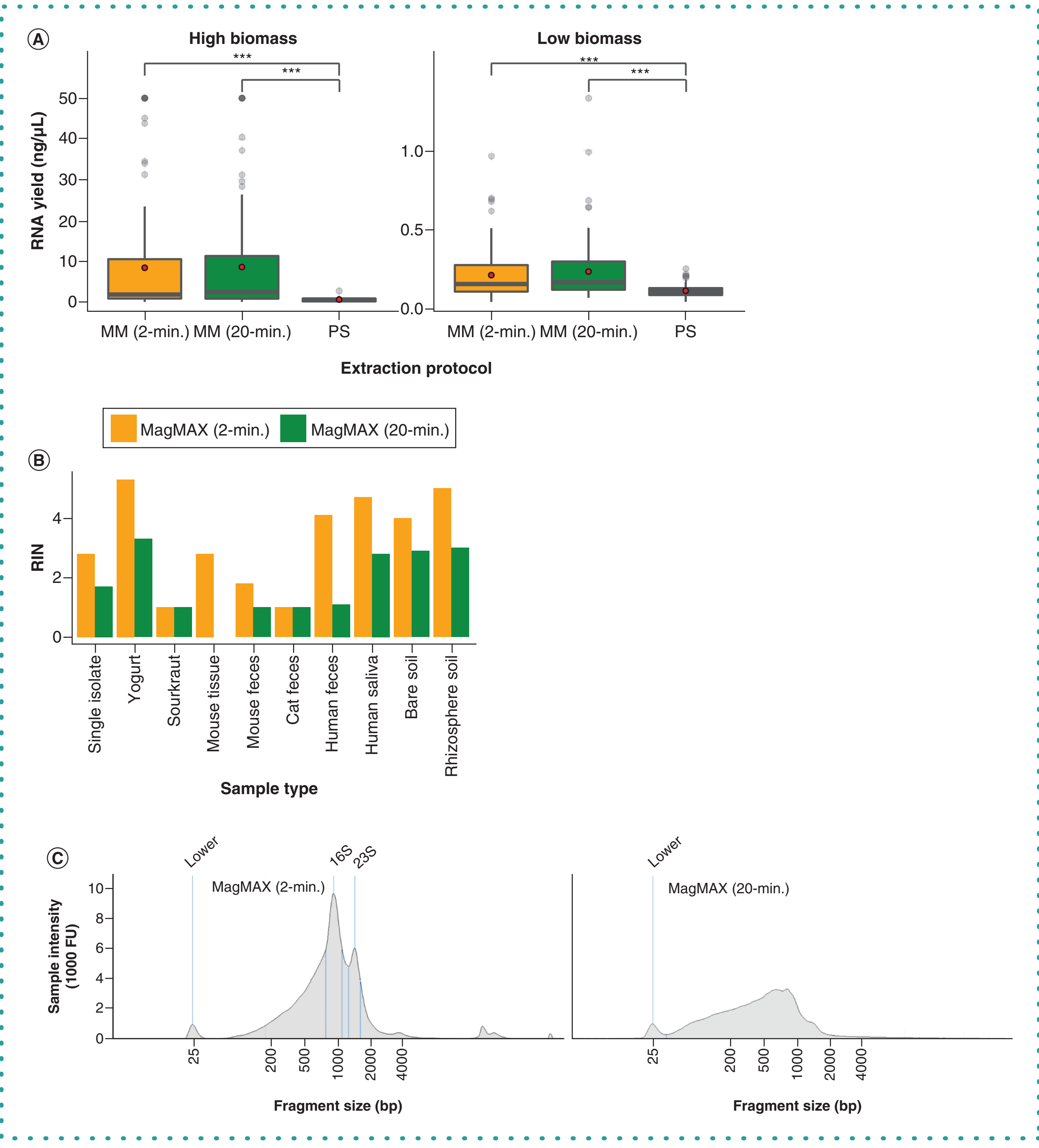

Figure 6. RNA output across extraction protocols. (A) RNA yield quantified using the Qubit RNA assay. Red circles indicate means. Asterisks indicate significant differences between pairs of extraction protocols as determined by paired-sample Wilcoxon signed-rank tests; ***$p < 2.2E\text{-}16$. Values at 50 ng/μl are at the upper limit of detection for the Qubit assay, and may underestimate actual yields for those samples. **(B)** RNA Integrity Number (RIN) across a subset of samples for the MagMAX extraction protocols, estimated using the TapeStation high-sensitivity (HS) RNA assay. PowerSoil extracts were excluded from the assay due to poor RNA yield, however we note that this may be to our exclusion of the RNAse step available in that protocol. **(C)** RNA fragment length distribution estimated using the TapeStation HS RNA assay for one human fecal sample. The distribution for the MagMAX (2-min) is on the left and that for the MagMAX (20-min) on the right. The positive control marker at 25-bp is annotated. Peaks corresponding to expected lengths for 16S and 23S rRNA are annotated for the 2-min. protocol and are missing from output from the 2-min. one.
MM: MagMAX; PS: PowerSoil.

Future perspective

Future optimization of molecular methods for microbial community analyses should focus on increasing representation of all microbes in a sample as well as diverse sample types, including those used here. Achieving these goals will allow for more widely adopted use of the same methods. As no single study can be completely comprehensive, making advances that allow us to better compare across studies, particularly past studies, is an important step [38]. Alongside the development of computational methods that bioinformatically reduce experimental variation, continuing to explore new molecular methods for capturing important ecological interactions will support our growing understanding of microbial communities.

Executive summary

- Established protocols were compared for DNA extraction with two alternative protocols that also extract RNA.
- The authors included a diverse panel of sample types, ranging from host-associated to environmental.
- Controls were included for detecting well-to-well contamination and LOD of microbial cells.
- The authors observed sample type-specific differences in DNA extraction efficiency among three extraction protocols.
- Both new protocols were similar with respect to RNA extraction efficiency but varied in RNA quality.
- Sample type and host identity were stronger drivers of microbial community beta-diversity compared with the extraction protocol used.
- A protocol was identified that generates both DNA and RNA and produces data that are highly similar to their established protocol with respect to microbial community alpha-diversity, beta-diversity and taxonomic composition.
- The similarity between the optimal protocol and the authors' existing protocol will allow for meta-analyses across both with negligible technical bias.

Supplementary data

To view the supplementary data that accompany this paper please visit the journal website at: www.future-science.com/doi/suppl/10.2144/btn-2020-0153

Author contributions

JP Shaffer, C Marotz, P Belda-Ferre, RA Salido, CS Carpenter, LS Zaramela, JJ Minich, G Humphrey, AD Swafford, S Miller-Montgomery and R Knight designed the study; JP Shaffer, C Marotz, P Belda-Ferre, RA Salido, CS Carpenter, L Zaramela, M Bryant and G Humphrey provided samples; JP Shaffer, C Marotz, CS Carpenter and S Fraraccio performed extractions; RA Salido, M Bryant, K Sanders and G Humphrey performed quality control and sequencing; JP Shaffer, C Marotz, P Belda-Ferre, C Martino, S Wandro, M Estaki and RA Salido performed data analyses; and JP Shaffer wrote the manuscript, with contributions from all authors.

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Ethical conduct of research

The authors state that they have obtained appropriate institutional review board approval; the human subject work conducted here has been approved through University of California, San Diego IRB#150275. In addition, informed consent has been obtained from the participants involved.

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