



Development and Evaluation of Whole Cell- and Genomic DNA-based Microbiome Reference Standards

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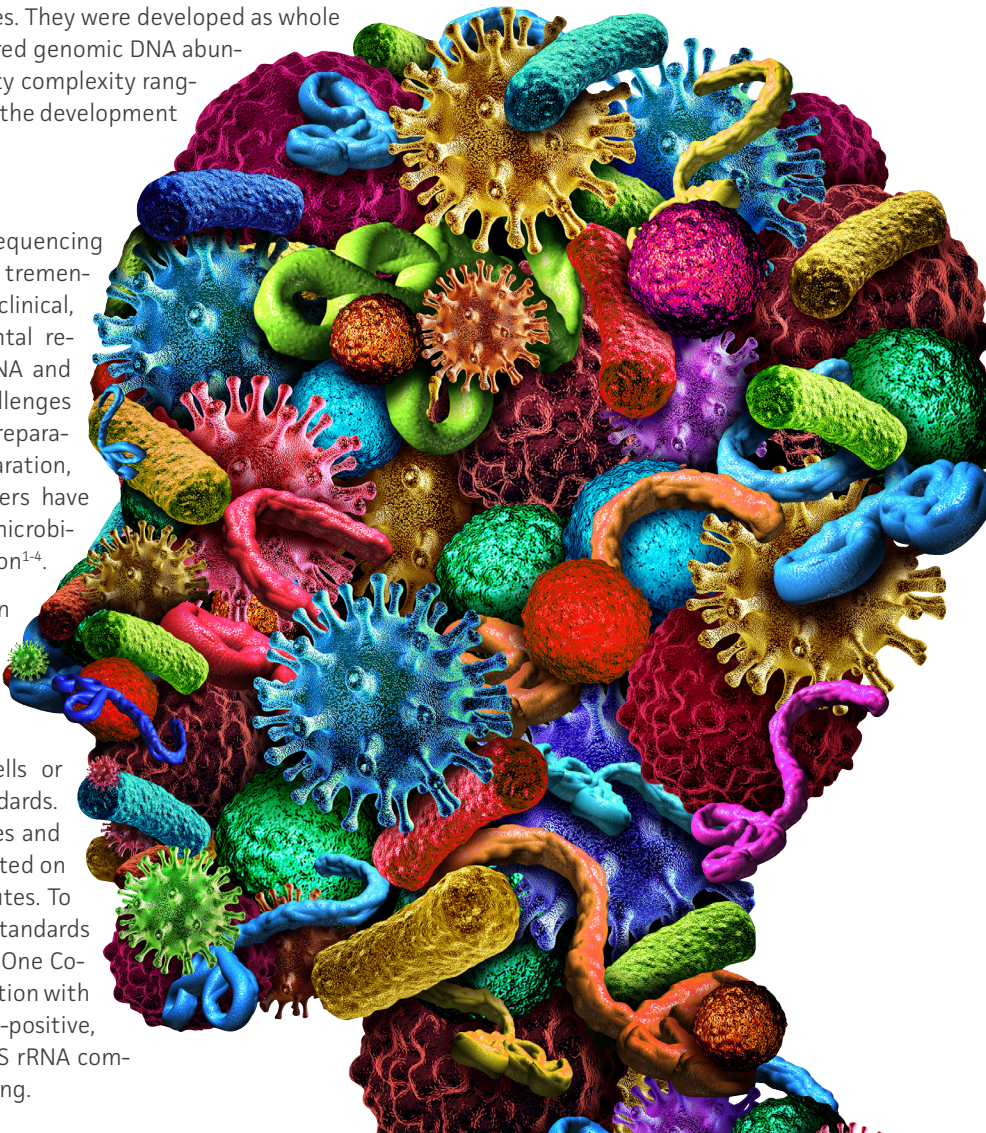
Abstract

ATCC has developed ATCC® Microbiome Standards for use in a broad array of applications ranging from method optimization to data interpretation. These standards are fully sequenced, characterized, and authenticated mock microbial communities that mimic mixed metagenomic samples. They were developed as whole cell or nucleic acid preparations with even or staggered genomic DNA abundance, and medium or high levels of mock community complexity ranging from 10 to 20 strains per sample. Here, we explore the development and use of the ATCC® Microbiome Standards.

Introduction

Advancement and accessibility of next-generation sequencing technologies have influenced microbiome analyses in tremendous ways, opening up applications in the areas of clinical, diagnostic, therapeutic, industrial, and environmental research. However, due to the complexity of 16S rRNA and metagenomic sequencing analysis, significant challenges can be posed by biases introduced during sample preparation, DNA extraction, PCR amplification, library preparation, sequencing, or data interpretation. Many researchers have published studies on these biases, and leaders in the microbiome field have highlighted the need for standardization¹⁻⁴.

One of the primary challenges in assay standardization is the limited availability of reference materials. To address these biases and provide a measure of standardization within microbiome research and applications, ATCC has developed a set of mock microbial communities, which includes lyophilized whole cells or genomic DNA, for use as microbiome reference standards. These standards mimic mixed metagenomics samples and comprise fully sequenced, characterized strains selected on the basis of select phenotypic and genotypic attributes. To further enhance the use of microbiome reference standards and eliminate the bias associated with data analysis, One Codex has developed a data analysis module in collaboration with ATCC that provides simple output in the form of true-positive, relative abundance, and false-negative scores for 16S rRNA community profiling and shotgun metagenomic sequencing.



Development of ATCC® Microbiome Standards

ATCC® Microbiome Standards comprise fully sequenced, characterized strains selected on the basis of phenotypic and genotypic attributes, such as cell wall type (Gram stain classification), GC content, genome size, unique cell wall characteristics, and spore formation (Table 1). These standards were prepared as lyophilized whole cells or genomic DNA and were developed with even or staggered relative abundance and medium or high levels of mock community complexity (10 or 20 strains per sample) (Figure 1).

TABLE 1. Table 1. Selection attributes for strains included in ATCC® Microbiome Reference Standards

| Genus species | ATCC® No. | Gram Status | Genome Size (Mb) | % GC | 16S Copies | GenBank ID | Special Features | Microbiome |
|-------------------------------------|-----------|-------------|------------------|------|------------|-------------------|-----------------------|---------------------|
| <i>Bacillus cereus</i> | 10987™ | Positive | 5.42 | 35.2 | 12 | NC_003909.8 | Endospores former | Soil |
| <i>Bifidobacterium adolescentis</i> | 15703™ | Positive | 2.09 | 59.2 | 5 | NC_008618.1 | Anaerobe | Gut |
| <i>Clostridium beijerinckii</i> | 35702™ | Positive | 6.49 | 30 | 14 | NC_009617.1 | Spores former | Gut/soil |
| <i>Deinococcus radiodurans</i> | BAA-816™ | Negative | 3.29 | 66.7 | 7 | NC_001263.1 | Thick cell wall | Gut/environment |
| <i>Enterococcus faecalis</i> | 47077™ | Positive | 3.36 | 37.5 | 4 | NC_017316.1 | Biofilm producer | Gut |
| <i>Escherichia coli</i> | 700926™ | Negative | 4.64 | 50.8 | 7 | NC_000913.3 | Facultative anaerobe | Gut |
| <i>Lactobacillus gasseri</i> | 33323™ | Positive | 1.89 | 35.3 | 6 | NC_008530.1 | Nuclease producer | Vaginal/gut |
| <i>Rhodobacter sphaeroides</i> | 17029™ | Negative | 4.60 | 68.8 | 3 | NZ_AKVW01000001.1 | Metabolically diverse | Aquatic |
| <i>Staphylococcus epidermidis</i> | 12228™ | Positive | 2.56 | 31.9 | 5 | NC_004461.1 | Thick cell wall | Skin/mucosa |
| <i>Streptococcus mutans</i> | 700610™ | Positive | 2.03 | 36.8 | 5 | NC_004350.2 | Facultative anaerobe | Oral |
| <i>Acinetobacter baumannii</i> | 17978™ | Negative | 4.34 | 39 | 6 | NZ_CP009257.1 | Filaments, capsule | Environment |
| <i>Actinomyces odontolyticus</i> | 17982™ | Positive | 2.39 | 65.5 | 2 | NZ_DS264586.1 | Type 1 fimbriae | Oral |
| <i>Bacteroides vulgatus</i> | 8482™ | Negative | 5.16 | 42.2 | 7 | NC_009614.1 | Anaerobe | Gut |
| <i>Helicobacter pylori</i> | 700392™ | Negative | 1.67 | 38.9 | 2 | NC_000915.1 | Helix shaped | Stomach/gut |
| <i>Neisseria meningitidis</i> | BAA-335™ | Negative | 2.27 | 51.5 | 4 | NC_003112.2 | Diplococcus | Respiratory tract |
| <i>Porphyromonas gingivalis</i> | 33277™ | Negative | 2.35 | 48.4 | 4 | NC_010729.1 | Anaerobe, collagenase | Oral |
| <i>Propionibacterium acnes</i> | 11828™ | Positive | 2.56 | 60 | 4 | NC_006085.1 | Aerotolerant anaerobe | Skin |
| <i>Pseudomonas aeruginosa</i> | 9027™ | Negative | 6.26 | 66.6 | 4 | NC_009656.1 | Facultative anaerobe | Skin |
| <i>Staphylococcus aureus</i> | BAA-1556™ | Positive | 2.82 | 32.8 | 6 | NC_007795.1 | Thick cell wall | Skin/respiratory |
| <i>Streptococcus agalactiae</i> | BAA-611™ | Positive | 2.16 | 35.6 | 7 | NC_004116.1 | Serogroup B | Vaginal/environment |

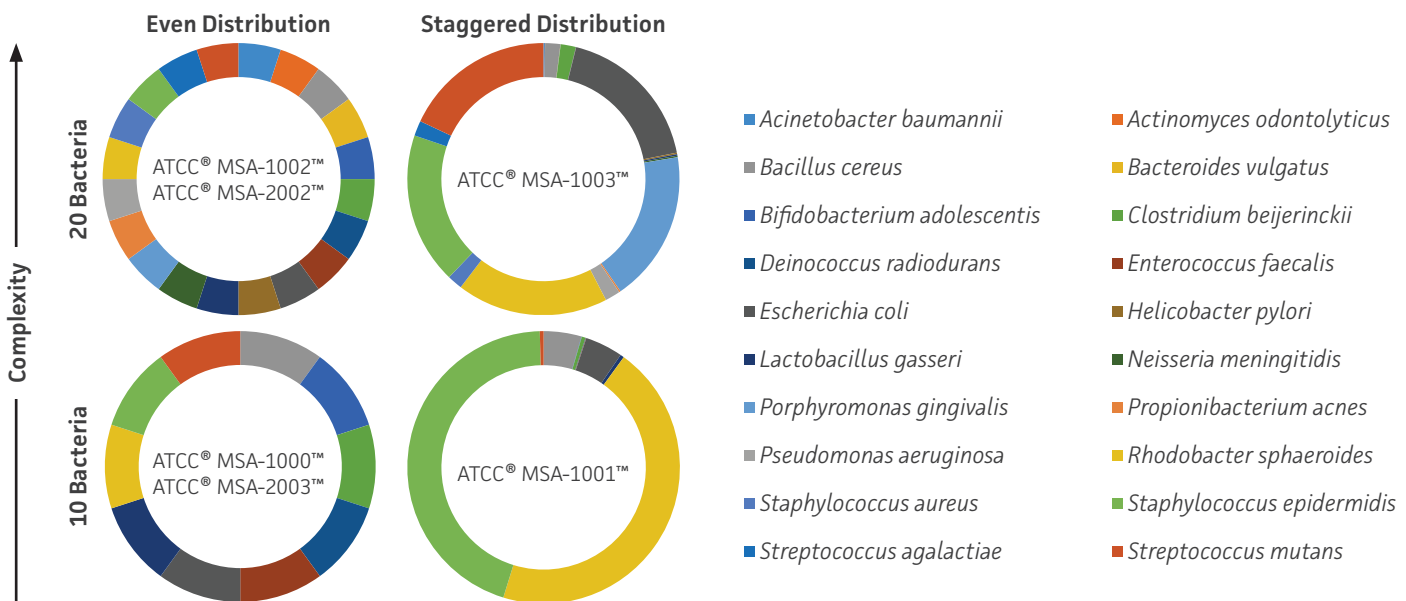


FIGURE 1. ATCC® Microbiome Standards. ATCC® MSA-1000™, MSA-1001™, MSA-1002™, and MSA-1003™ are genomic DNA standards, and ATCC® MSA-2002™ and MSA-2003™ are lyophilized whole cell standards.

Using ATCC® Microbiome Standards to Evaluate PCR Amplification, Library Preparation, and Sequencing

To evaluate factors that contribute to biases associated with PCR amplification, library preparation, and sequencing, we performed an inter-laboratory comparison following the earth microbiome protocol, which targets the V4 region for 16S community profiling. The data revealed significant inter-laboratory variability in the number of true positives (70–95%) and false positives (83–100%) as well as in the relative abundances (Figure 2A). We also compared three different regions of the 16S rRNA gene (V1V2, V3V4, and V4) using the genomic DNA microbiome standards. The results revealed that only the V1/V2 region of the 16S rRNA gene was able to profile the bacteria to the species level (true positives = V1V2: 90–100%, V3V4: 90–95%, V4: 90–95%, along with significant differences in the expected versus observed relative abundances) (Figure 2B). Overall, the data clearly reveals the need for reference standards to standardize critical methods used in microbiome analyses.

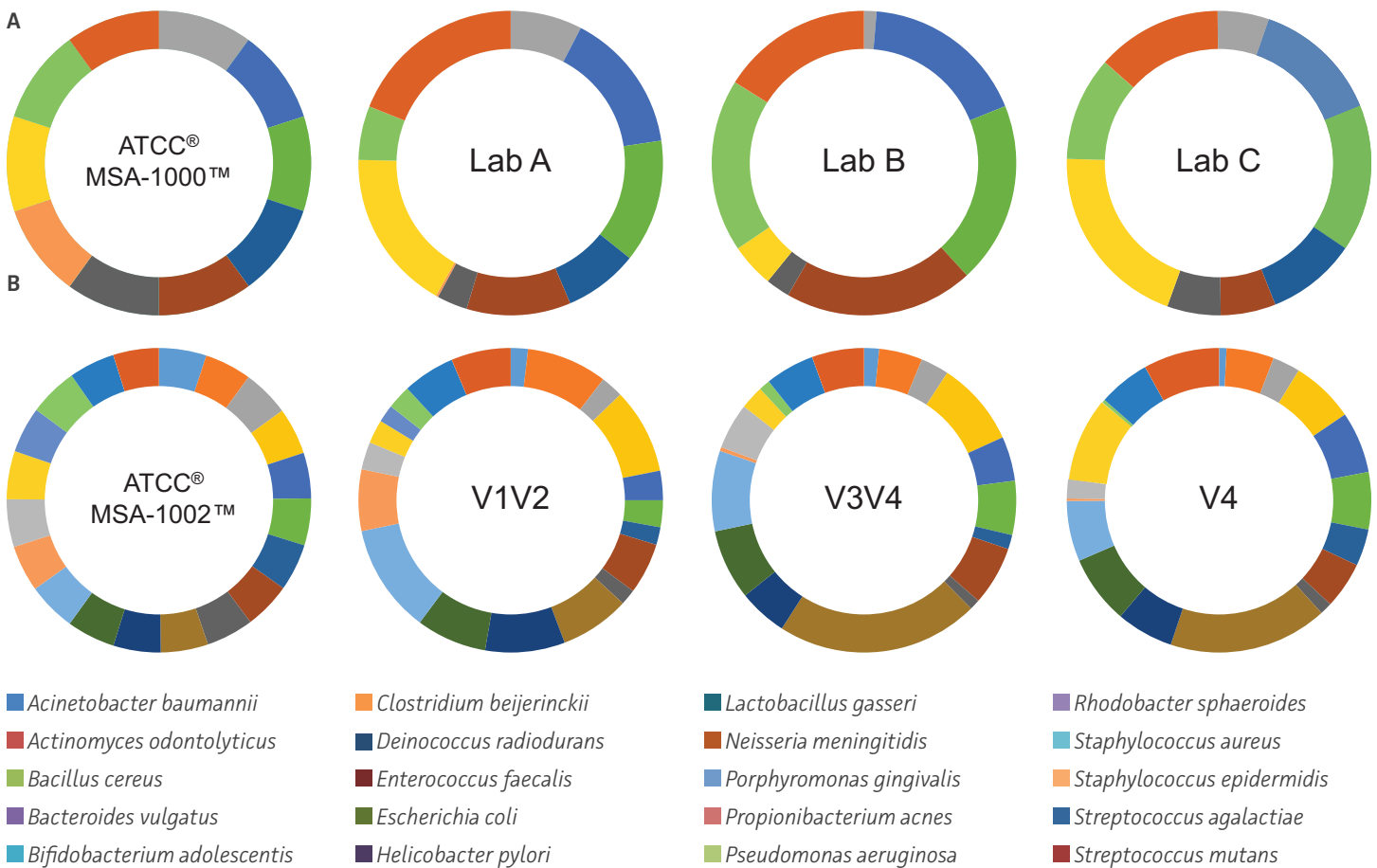


FIGURE 2. The use of standards during PCR amplification, library preparation, and sequencing. A) Inter-laboratory variations in identity and relative abundances. 16S rRNA V4 sequence data from different laboratories. Percent ratios of expected and observed organisms in the even genomic mock community comprising 10 organisms (ATCC® MSA-1000™). The blinded samples were sent to commercial vendors where they used their standard 16S protocol (Earth Microbiome Project) on the Illumina® platform. B) Choice of 16S rRNA primer regions affects identity and relative abundances. 16S rRNA community profiling results from the ATCC® MSA-1002™ standard using primer sets covering the V3V4, V1V2, and V4 regions on the Illumina® platform. The FASTQ files were analyzed using One Codex. For details on how to calculate the true-positive, false-positive, and relative abundance score, visit <http://app.onecodex.com/atcc>.

Using ATCC® Microbiome Standards to Evaluate Data Analysis

To evaluate biases associated with variations between data analysis platforms, we compared simulated data sets and two laboratory data sets that were produced using the ATCC® MSA-1000™ genomic DNA standard on the One Codex and NEPHELE⁵ data analysis platforms (Figure 3). The simulated data were generated by using a next-generation sequencing read simulator (ART)⁶ and the GenBank ID data and 16S rRNA copy number from each individual bacterial strain (Table 1). Here, all data were generated using primers against the V1/V2 region of the 16S rRNA gene. The results indicate that the One Codex platform identified all bacteria at the species level, while the NEPHELE platform identified bacteria at the genus level with wide variations in the relative abundances.

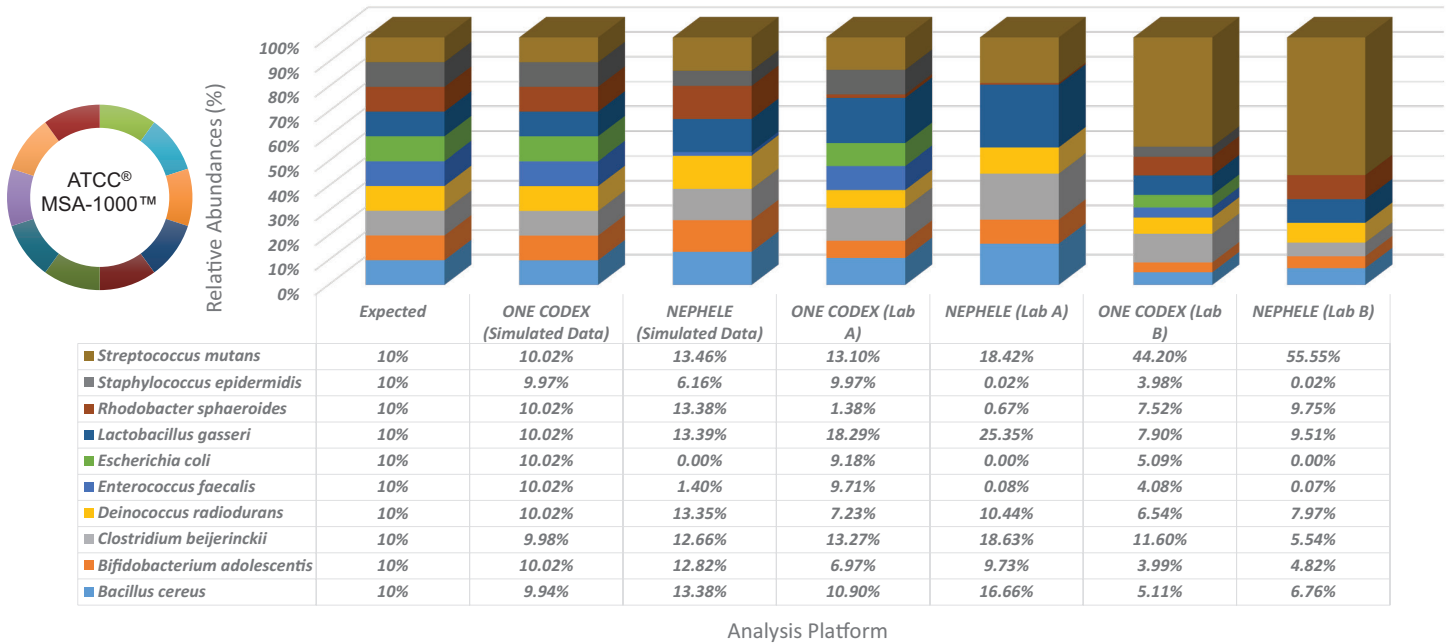


FIGURE 3. Data analysis platform affects identification and relative abundances. Simulated data sets and two laboratory data sets generated using the ATCC® MSA-1000™ genomic DNA standard using the 16S rRNA (V1/V2) primer set were evaluated on the One Codex and NEPHELE (<https://nephele.niaid.nih.gov>) platforms.

Combining the ATCC® Microbiome Standards with the Power of One Codex

To further enhance the use of ATCC microbiome reference standards and eliminate the bias associated with data analysis, we developed a data analysis module in collaboration with One Codex (<https://app.onecodex.com/atcc>) to provide simple output in the form of true-positive, relative abundance, and false-positive scores for 16S community profiling and shotgun metagenomic sequencing methods. Here, we compared the One Codex data analysis module side-by-side with three other commonly used analysis platforms. The results demonstrated significant variations among the number of true positives, the relative abundances, and the inability to identify all organisms at the species level (Figure 4). In contrast, the One Codex analysis tool, which was specifically customized for the ATCC microbiome reference standards, generated relative abundances close to the expected ratio.

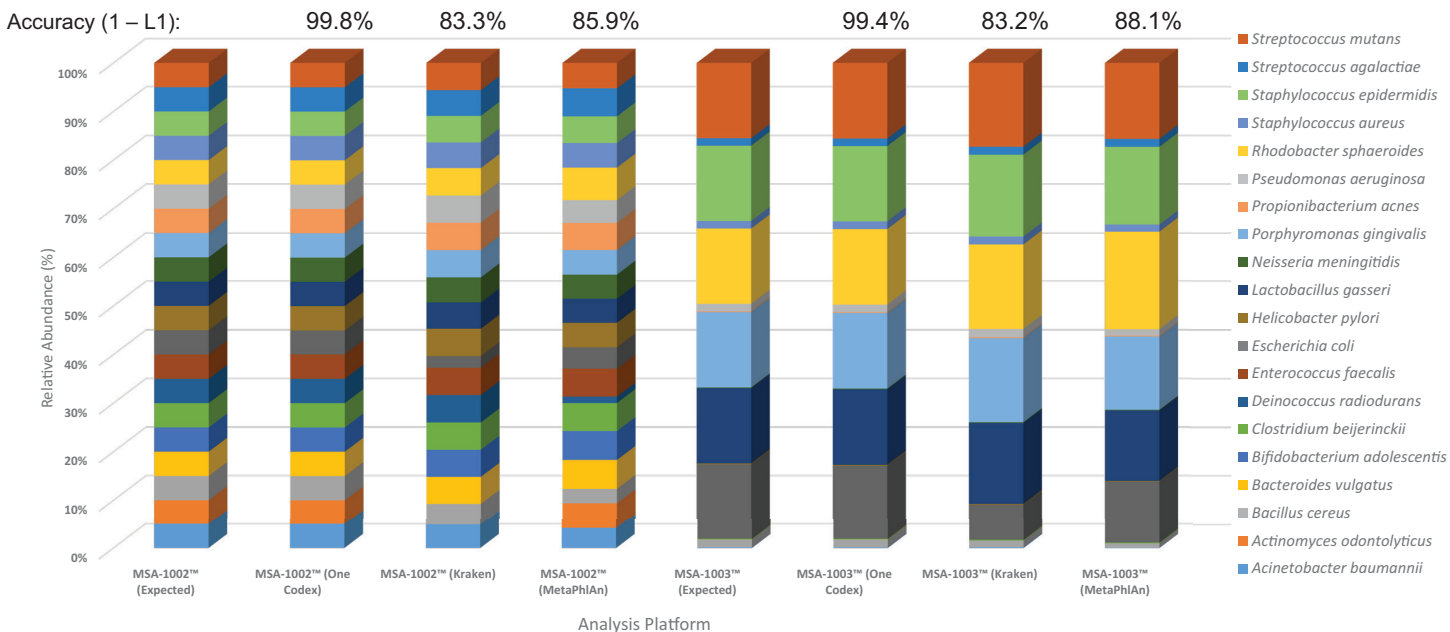


FIGURE 4. Data analysis platform affects identification and relative abundances. ATCC® MSA-1002™ and ATCC® MSA-1003™ were used to compare the performance of the One Codex, Kraken, and MetaPhlAn data analysis platforms. The percentages located above the bars represent the overall accuracy between platforms, as compared using L1-distance. Only One Codex demonstrated the accuracy necessary to robustly quantify microbiome sequencing errors.

Conclusions

Our data clearly reveals the need for standardization in microbiome analyses. Here, we demonstrate that bacterial identification and the evaluation of relative abundances in mixed samples can be affected by the 16S rRNA region chosen for amplification, general inter-laboratory differences, and variations between data analysis platforms. ATCC® Microbiome Standards combined with the One Codex data analysis module provide a comprehensive solution for standardizing data from a wide range of sources, and generating consensus among microbiome applications and analyses.

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About One Codex

One Codex is the leading bioinformatics platform for microbial genomics, supporting taxonomic and functional analysis of metagenomic (WGS), 16S, and other sequencing data. We specialize in creating robust, scalable, and secure bioinformatics solutions for metagenomics and microbial genomics, with a strong focus on ease of use. Founded in 2014, the One Codex platform counts thousands of users across leading academic institutions, biotechnology companies, and public sector organizations. One Codex is built on top of Amazon Web Services and is the only microbial genomics offering providing HIPAA-level security, as well as other strong compliance and audit guarantees. To learn more, visit <http://www.onecodex.com>.

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