NEON 16S/ITS qPCR Standard Operating Procedure v.6

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I. Version History

1. Section III, Recommended Materials, was updated to allow the genomic DNA standards to vary from batch to batch. Exact standards in use are reported in the batch-level data; DNA extraction kit added.
2. Section IV.A.1 was changed to allow for direct isolation of bacterial gDNA from a 22-strain consortium.

II. Objective and Overview

To assess microbial abundance in soil and aquatic samples, quantitative polymerase chain reaction (qPCR) is performed using primers adapted for hypervariable regions V3 and V4 from bacterial and archaeal 16S ribosomal DNA (rDNA) and fungal-specific primers for the ITS-1 region of fungal rDNA (Table 1).

III. Recommended Materials

Material	Manufacturer	Catalog #
Fungal gDNA Standard		varies
Archaeal gDNA Standard		varies
Bacterial standard		varies
Quantus ONE dsDNA Assay Kit	Promega	E4871
Wizard® Genomic Purification Kit	Promega	A1120
10 mg/mL Lysozyme	Sigma	L6876
10 mg/mL Lysostaphin	Sigma	L7386
Kapa SYBR Green Master Mix	Kapa Biosystems	KK4602
Genomic-tip 100/G Kit	Qiagen	10243

IV. Procedure

A. Standard Preparation

Bacterial, archaeal, and fungal genomic DNA standards are used for generating standard curves and calculating gene copy numbers. The exact standard in use may vary from batch to batch based on standard availability and is tracked at the batch level for each data set.

1. Prokaryotic Standards

Archaeal genomic DNA (gDNA) standards are rehydrated according to the manufacturer's instructions, as needed.

For preparation of the bacterial genomic DNA from a microbial consortium, the entire contents of the vials are extracted directly using a commercial genomic DNA extraction kit according to the manufacturer's instructions. This ensures that all bacteria present in the consortium are represented in the gDNA.

Bacterial and archaeal gDNA concentrations are determined using the Quantus Fluorometer with the Quantus ONE dsDNA assay kit. The bacterial gDNA stock and archaeal gDNA are combined in equal proportions to create a gDNA prokaryotic standard, normalized by calculated gene copy based on the mass of the genome and concentration of extracted DNA. A ten-fold dilution series is prepared for the prokaryotic gDNA standard curve ranging from approximately 1 x 10^6 to 1 Gene Copies (GC)/µL. Exact standard curve concentrations may vary, as long as there is a six point standard curve.

2. Fungal Standards

Commercially available fungal genomic DNA (gDNA) standards are rehydrated according to the manufacturer's instructions. Genomic DNA concentrations are determined using the Quantus Fluorometer with the Quantus ONE dsDNA assay kit. Fungal gDNA standards are combined, and a ten-fold dilution series is prepared for the fungal gDNA standard curve ranging from approximately 1 x 10^6 to 1 GC/µL. Exact standard curve concentrations may vary, as long as there is a six point standard curve.

B. qPCR Analysis

DNA extracts will be diluted prior to analysis (100-fold for 16S and 10-fold for ITS). Quantitative PCR (qPCR) is performed using the Applied Biosystems 7500 Fast PCR platform with Kapa SYBR Green Master Mix according to the manufacturer's instructions. Each DNA extract is analyzed for 16S (archaeal and bacterial) and ITS (fungal) abundances using the appropriate primers as described in Table 1, and the appropriate cycling conditions as described in Tables 2 and 3. The data are analyzed using the Applied Biosystems 7500 software, version 2.3, according to the manufacturer's instructions.

Table 1 - qPCR Primer Sequences

Target	Primer	Sequence	Reference
16S v3-4	Forward	5'-CCTACGGGNBGCASCAG-3'	Pro341F and Pro805R[1]
	Reverse	5'-GGACTACNVGGGTATCTAATCC-3'	
ITS-1	Forward	5'-CTTGGTCATTTAGAGGAAGTAA-3'	Walters et al. (from Gardes and Bruns et al. Mol Ecol. 1993)[2]
	Reverse	5'-GCTGCGTTCTTCATCGATGC-3'	

[1] Takahashi, S., J. Tomita, K. Nishioka, T. Hisada, and M. Nishijima. 2014. *Development of a Prokaryotic Universal Primer for Simultaneous Analysis of Bacteria and Archaea Using Next-Generation Sequencing.* PloS one 9.8 (2014): e105592.

[2] Walters, W., E. R. Hyde, D. B.-L., G. Ackermann, G. Humphrey, A. Parada, J. A. Gilbert, J. K. Jansson, J. G. Caporaso, J. A. Fuhrman, A. Apprill, and R. Knight. 2015. Improved Bacterial 16S rRNA gene (V4 and V4-5) and Fungal Internal Transcribed Spacer Marker Gene Primers for Microbial Community Surveys." *mSystems Methods and Protocols* 1.1 (2015): e00009-15.

Table 2 - 16S qPCR Cycling Conditions

Step	Ramp Rate	Temperature	Duration	Collect Data	Cycles
Polymerase Activation	100%	95 °C	3 minutes		Hold
Denature	100%	95 °C	30 seconds		**35**
Anneal	100%	50 °C	30 seconds		
Extend	100%	72 °C	30 seconds	On Hold	
Hold	100%	72 °C	5 min		Hold
Melt Curve Step 1	100%	95 °C	15 seconds		1
Melt Curve Step 2	100%	60 °C	1 minute	On Ramp	
Melt Curve Dissociation Step	1%	95 °C	15 seconds		
Melt Curve Step 3	100%	60 °C	15 seconds		

Table 3 - ITS qPCR Cycling Conditions

Step	Ramp Rate	Temperature	Duration	Collect Data	Cycles
Polymerase Activation	100%	95 °C	3 minutes		Hold
Denature	100%	95 °C	30 seconds		**35**
Anneal	100%	50 °C	1 minute		
Extend	100%	72 °C	1 minute	On Hold	
Hold	100%	72 °C	10 min		Hold
Melt Curve Step 1	100%	95 °C	15 seconds		1
Melt Curve Step 2	100%	60 °C	1 minute	On Ramp	
Melt Curve Dissociation Step	1%	95 °C	15 seconds		
Melt Curve Step 3	100%	60 °C	15 seconds		

C. Analysis Criteria

Data analyses will be performed using the Applied Biosystems 7500 software, version 2.3, according to the manufacturer's instructions with automatic baseline setting and automatic or manual threshold setting, with no more than two significant digits.

D. Acceptance Criteria

1. Assay Acceptance Criteria

For each qPCR assay, data is reported to the client if the following acceptance criteria are satisfied:

1. The standard curve contains at least three concentrations of standard for which there are three positive replicates.
2. The R^2 value for the standard curve is greater than or equal to 0.95.

If any of these criteria are not met in an assay, all samples in the assay are repeated.

2. Sample Acceptance Criteria

For individual samples tested by qPCR, data are reported to the client if the following acceptance criteria are satisfied:

1. The acceptance criteria in section C. 1. were satisfied for the assay in which the sample was tested.
2. The sample was detected as positive for at least two of three replicates.

NTC results are used to establish background amplification and primer dimer formations found in SYBR testing[3]. The NTC results are used to determine the limit of quantification (LOQ), which is defined as the lowest concentration of DNA standard that has all 3 replicates with higher CT values than all 5 NTC replicates. Any sample below the LOQ will be reported with a quality flag.

Samples not passing the above criteria, and samples passing the above criteria whose average quantity is calculated to be above the range of the standard curve, are re-tested at the discretion of the client.

[3] Thermo Fisher Scientific – US. Amplification of the No Template Control (NTC). (n.d.). Retrieved October 30, 2018, from https://www.thermofisher.com/us/en/home/life-science/pcr/real-time-pcr/real-time-pcr-learning-center/real-time-pcr-basics/real-time-pcr-troubleshooting-tool/gene-expression-quantitation-troubleshooting/amplification-no-template-control.html#3