

# Protocol: Quantifying species abundance using 16S Sanger Sequencing and CASEU

Jack Reddan

May 23, 2022

## Contents

<b>1</b>	<b>Culture Collection</b>	<b>2</b>
1.1	Overview	2
1.2	Materials	2
1.3	Method	2
<b>2</b>	<b>gDNA Isolation</b>	<b>2</b>
2.1	Overview	2
2.2	Materials	2
2.3	Method	2
<b>3</b>	<b>16S rDNA Amplification</b>	<b>3</b>
3.1	Overview	3
3.2	Materials	3
3.3	Method	3
<b>4</b>	<b>16S rDNA Purification</b>	<b>4</b>
4.1	Overview	4
4.2	Materials	4
4.3	Methods	4
<b>5</b>	<b>Sanger Sequencing</b>	<b>4</b>
5.1	Overview	4
5.2	Materials	4
5.3	Method	4
<b>6</b>	<b>Appendix</b>	<b>4</b>
<b>A</b>	<b>PCR Master Mix</b>	<b>4</b>
<b>B</b>	<b>PCR Program</b>	<b>4</b>

# 1 Culture Collection

## 1.1 Overview

This section describes collecting cultures for which you wish to quantify species abundances. In addition to any experimental mixtures, pure cultures of community members are needed for the analysis.

## 1.2 Materials

- Pure and mixed liquid cultures
- 2-mL microcentrifuge tubes

## 1.3 Method

1. In a 2-mL microcentrifuge tube, Collect 1 ODmL of liquid culture for all mixtures and pure cultures. Spin-down and remove supernatant.
2. Either store pellets at  $-20^{\circ}\text{C}$ , or continue to [gDNA Isolation](#).

# 2 gDNA Isolation

## 2.1 Overview

This section describes how to isolate gDNA to be used for 16S rDNA amplification. These steps are for the QIAGEN DNeasy Blood & Tissue Kit. If you happen use a different kit, please follow its instructions, and then proceed to [16S rDNA Amplification](#).

## 2.2 Materials

- QIAGEN DNeasy Blood & Tissue kit
- 100% ethanol
- Cell pellets from cultures collected in [Culture Collection](#)

## 2.3 Method

Follow the subsequent instruction in parallel for all samples to be processed.

1. Resuspend pellet in 180  $\mu\text{L}$  of buffer ATL, and add 20  $\mu\text{L}$  of Proteinase K. Mix thoroughly by vortexing. Incubate at  $56^{\circ}\text{C}$  for 1 hour, and vortex every 15 minutes.
2. Vortex for 15s, then add 200  $\mu\text{L}$  of buffer AL and mix thoroughly by vortexing. Immediately add 200  $\mu\text{L}$  of 100% ethanol and, again, mix thoroughly by vortexing.

3. Pipet the mixture from step 2 into a DNeasy Mini spin column placed in a 2-mL collection tube. Centrifuge at  $\geq 6000 \times g$  for 1 min. Afterwards, discard flow-through and collection tube.
4. Place DNeasy Mini spin column into a new 2-mL collection tube and add 500  $\mu\text{L}$  of buffer AW1. Centrifuge at  $\geq 6000 \times g$  for 1 min. Afterwards, discard flow-through and collection tube.
5. Place DNeasy Mini spin column into a new 2-mL collection tube and add 500  $\mu\text{L}$  of buffer AW2. Centrifuge at  $20000 \times g$  for 3 min. Afterwards, discard flow-through and collection tube.
6. Place DNeasy Mini spin column into a clean 1.5-mL microcentrifuge tube. Add 200  $\mu\text{L}$  of buffer AE and incubate at room temperature for 1 min. Centrifuge at  $\geq 6000 \times g$  for 1 min to elute.
7. Check gDNA concentration on the nano spectrophotometer. Then store at  $-20^{\circ}\text{C}$  or continue to **16S rDNA Amplification**.

## 3 16S rDNA Amplification

### 3.1 Overview

This section describes how to amplify the 16S rDNA using Phusion polymerase for Sanger sequencing. If you are using a different polymerase, please follow its specific instructions and proceed to **Sanger Sequencing**.

### 3.2 Materials

- ddH<sub>2</sub>O
- Phusion polymerase
- 5X High Fidelity (HF) reaction buffer
- dNTPs
- 27F forward primer
- 1492R reverse primer
- gDNA template from **gDNA Isolation**

### 3.3 Method

Follow the subsequent instruction in parallel for all gDNA samples collected in **gDNA Isolation**.

1. Mix the ddH<sub>2</sub>O, dNTPs, forward/reverse primers, 5X HF buffer, and polymerase according to [Appendix A](#) for  $N + 1$  reactions, where  $N$  is the number of gDNA samples to be processed.
2. Pipet 38  $\mu$ L of the PCR master mix into 200- $\mu$ L PCR tubes. Then add 2  $\mu$ L of template gDNA, at a concentration of 100 ng/ $\mu$ L, to the mix for each sample.
3. Place reactions into the thermocycler and run the PCR program specified in [Appendix B](#).
4. Once the run is complete, check for synthesis of the desired product using gel electrophoresis.
5. If the proper product was amplified, either store the reaction at  $-20^{\circ}$  C or proceed to [16S rDNA Purification](#)

## 4 16S rDNA Purification

### 4.1 Overview

### 4.2 Materials

### 4.3 Methods

## 5 Sanger Sequencing

### 5.1 Overview

### 5.2 Materials

### 5.3 Method

## 6 Appendix

### A PCR Master Mix

### B PCR Program

## References