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## 18S Metagenomics in a Field Setting



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**Protocol status:** Working

**We use this protocol and it's working**

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## Abstract

This protocol is was used to conduct DNA 18S metagenomics on FPI's Genomics in the Jungle - 2018 field course at the Green Lab, located and Inkaterra Guides Field Station, Madre de Dios, Peru.

## Guidelines

This protocol starts from already extracted DNA

## Materials

### STEP MATERIALS

⊗ Agencourt Ampure XP **Beckman Coulter Catalog #A63880**

## Protocol materials

⊗ Agencourt Ampure XP **Beckman Coulter Catalog #A63880**

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## Troubleshooting










## Amplification


### 1 **Remove samples and the following reagents and let thaw, once thawed keep on ice block**

- 10mM DNTPs
- 25 mMgCl
- 5x Go Taq Buffer
- Forward primer 5'-CAGCAGCCGCGGTAATTCC-3' (10uM)
- Reverse primer 5'-CCCGTGTGAGTCAAATTAAGC-3' (10uM)
- GoTaq Hotstart Polymerase 5u/ul

**Make PCR cocktail for # of samples \* 1.1** (10% extra). Don't forget to include 1 PCR negative control for each separate PCR

#### **Run PCR according to the following cycle conditions:**

- Initial denaturation  95 °C for 120s
- 25 cycles of  98 °C for  00:00:30 ,  51 °C for  00:00:30 ,  72 °C for  00:00:45
- Final extension  72 °C for  00:05:00

Upon completion remove, label, and store at  4 °C , or take directly to electrophoresis

### 2 **Equipment**


- BlueGel system
- MiniOne system



#### **Create .8 - 1.0% agarose 1 gel with 13 combs**

- Measure 1 g of agarose
- Mix agraose with 100 mL of 1xTBE
- Microwave the mixture until agarose is completely dissolved (1-3 min)
- Pour the agarose gel into the tray with the comb in place.
- Allow the agarose gel to harden (20-30 min)



**Insert the agarose gel into electrophoresis equipment and add 1xTBE buffer until the agarose gel is submerged**

**Spot check with**  2  $\mu\text{L}$  **of each sample**



**Mix**  1  $\mu\text{L}$  **of loading dye to**  2  $\mu\text{L}$  **of each sample and load the gel.** (If Green Taq buffer with built in loading dye was used, skip this step).

**Load**  5  $\mu\text{L}$  **of 100bp ladder into the agarose gel.**











**Turn on the electrode and let the DNA run until the band is identifiable**

## Barcoding PCR

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- A barcoding PCR was run to attach barcodes from the 96-barcode kit for the MinION to each sample
- We did not use special PCR mastermix at this stage, using instead a mix similar to that of the PCRs above
- We used  1  $\mu\text{L}$  of each barcode primer and  2  $\mu\text{L}$  of every positive PCR amplicon in a total volume of 25  $\mu\text{L}$

We ran the PCR at the following conditions:

- Initial denaturation of hotstart taq at  95  $^{\circ}\text{C}$  for  00:02:00
- Denaturation at  95  $^{\circ}\text{C}$  for  00:00:30
- Annealing at  62  $^{\circ}\text{C}$  for  00:00:30
- Extension at  72  $^{\circ}\text{C}$  for  00:00:45
- Total number of cycles - 18
- Final Extension at  72  $^{\circ}\text{C}$  for  00:05:00

## Quantification

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## Equipment

### Equipment

Quantus Fluorometer

NAME

DNA and RNA Quantifier

TYPE

Promega

BRAND

E6150

SKU

<https://www.promega.com/products/fluorometers-luminometers-multimode-readers/fluorometers/quantus-fluorometer/?catNum=E6150>

LINK



- dsDNA dye
- Qubit Assay Tubes
- Your DNA sample


**Pulse vortex your sample and spin down.**

**Add**  200  $\mu\text{L}$  **of dsDNA dye into the qubit assay tube.**

- Make sure to cover up the tube from light

**Transfer**  1  $\mu\text{L}$  **of DNA sample into qubit assay tube**


**Pulse vortex and spin down**

**Let it sit for**  00:05:00 **in room temperature**

- Covered from the light

**Gently vortex and spindown the sample**

**Calibrate the Quantus Fluormeter by standard and reference testing.**

- Follow the same process but use  1  $\mu\text{L}$  ddH<sub>2</sub>O and Lambda DNA.

**Insert the qubit assay tube into the Quantus Flurometer**



## Normalisation and Pooling

### 5 **Dilute each sample to 50 nM**

- Mix 5 uL of the sample with calculated amount of ddH<sub>2</sub>O (based on DNA concentration above) to make each sample the same concentration of 50 nM
- Then pool 5 uL of each dilution into a single tube.
- This is now your library.

## SPRI Cleanup

- 6 Run a SPRI cleanup of the library using your choice of bead purification systems/kits in a 1:1 ratio. Resuspend in the same volume.



Agencourt Ampure XP **Beckman Coulter Catalog #A63880**