Core Receiving and Splitting

In 2 collections

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ABSTRACT

The method covers how soil cores were received and depth stratified.

MATERIALS

- Site Cores (Cores A, B, C1-4)
- Core Extruder (Long stick with flask disk on end by broom in 1446)
- Aluminum Foil
- 70% ethanol
- Kimwipes
- Gloves
- Bench Scraper
- Ruler/Measuring tape in cm
- Sharpies/writing utensils
- 4mm sieves and base
- Processing kit (Box with tubes, bags, tins, and labels)
    - 50 mL conical tubes (for both top and bottom)
        - 1 pH
        - 1 P - extraction
        - 6 N (3 for extraction and 3 for extractant)
        - 9 for microbial biomass (3 MicB, 3 MicB_Back, 3 MicB_Fum; only MicB gets filled with soil)
        - 6 unlabeled 50 ml tubes for P extract (will get labeled following pH measurements)
    - Whirlpak bags
        - DNA (Top and Bottom)
        - Removed rock and roots (Top, Middle, and Bottom)
        - Large aluminum pans (4 total for Top (2), Middle, Bottom; Extras are stored in 1106 if needed)
    - Small aluminum weigh boats
        - GWC – 3 each for top and bottom

1 When cores are received first check that there are cores labeled Core A, Core B, and Cores C1-4 included in the sample cooler.

2 Place Core A and C4 back into the site bag and store vertically in the 4 °C refrigerator in 1446.

3 Spray down the table with a 70% EtOH solution and wipe down using kimwipes.

3.1 Keep each core, if processing multiple simultaneously, in its own dedicated area/table.

4 Wearing gloves, tear two large sections of foil (~2.5 ft in length) and place them overlapping by half onto the cleaned tabletop.

5 Using a permanent marker write the site code at one end of the foil.

6 Lay the Core B core on the foil horizontally and remove the caps (top and bottom) noting which section of the core is top on the foil.

7 Clean the core extruding tool with 70% EtOH, align the flat end of the extruder with the bottom exposed soil.

8 While maintaining a horizonal position on the bench slide the tube up the core extruders handle to release the core onto the foil.

9 Take photographs of the soil core with and without a measuring tape making sure to include the site label in the photos.

10 Record the cores total length and how well it maintained the shape of the tube in the core processing files.

10.1 Processing_Template *actual template

10.2 Make sure to save the Processing_Template document with the site codes for example: “Processing_PRS1_PRS2.xlsx”

11 In the Processing file record the core receiving and splitting information.

12 Using a bench scraper and a measuring tape slice the core at 10 cm from the top and 10 cm from the bottom. Record the depth range for each section on the processing forms.

13 Using 70% EtOH wipe out clean (rinsed with water) 4 mm sieve. Stacking the sieve on top of the lower pan scrape each section (top, middle, and bottom) into its own clean and labeled sieve.

13.1 In only the top 10 cm section add cores C1-3 during sieving to homogenize.

13.2 Do not combine the top middle and bottom sections at any point.

14 Gently shake and stir (with a clean sterilized gloved hand) the soil in the sieve being careful not to force soil through sieve.

14.1 If the soils have a high clay content you may need to use a sterilized paint brush to break up the particles using a stippling motion (vertical tapping).

14.2 Break up large aggregates between fingers and continue sieving.

15 Once sieving is completed collect all items remaining on the sieve into a whirlpak bag labeled with the site code, removed, and depth fraction for example (1000S_PRS1_Removed_ TOP). Record the mass of the bag and the total mass (bag + removed rocks/roots) on the corresponding section of the Processing file.

15.1 Do not tare out the whirlpak prior to adding soil.

16 To measure gravimetric water content (GWC) on the top and bottom core sections record the mass of the empty tin and the mass of the tin + 10 g of soil. Place the tins in the 60 °C degree oven for 48:00:00 to 72:00:00 or a 100 °C degree oven for 24:00:00. GWC is collected in triplicate and make sure the tins are labelled with the 1000S_SITE_GWC_DEPTH_1-3. 6d

16.1 Make sure to record the wet mass and dry mass (after 24:00:00 or 48:00:00) in the processing file. 3d

17 Collect a minimum of 10 g of soil for DNA into a whirlpak bag for the top and bottom sections. These samples will be labelled with the site code, DNA, and depth fraction (Top and Bottom). For example: 1000S_PRS1_DNA_Top

18 Collect 20 g (within 0.1 g) of soil for pH into a 50 mL falcon tube for the top and bottom sections. The samples should be labelled with the site code, pH, and depth fraction. For example: 1000S_PRS1_pH_Top.

19 Collect ~ 12 g of soil for phosphorus extraction into a 50 mL falcon tube for the top and bottom sections. The samples should be labelled with the site code, P, and depth fraction. For example: PROS_P_Top.

19.1 Following pH samples with a pH less than 7 will be extracted using the Bray Method, while samples with pH greater than 7 will be extracted using the Olsen Method.

20 To measure microbial biomass and N extractions place exactly 8 g (within 0.02 g) of soil into six 50 mL falcon tubes for the top and bottom sections. Record the mass onto the MicrobialBiomass_N tab. The 6 tubes will be labelled with three for microbial biomass and three for N extraction. For example: PRS1_N_Top_1-3 & PRS1_MicB_TOP_1-3

21 The remaining sieved soil will be placed in a labelled clean aluminum pie pan and covered with foil and stored at 4 °C.

21.1 Soils are air dried in the BSC hood in 1521. Depending on the mineral composition soils can take longer to air dry.

21.2 Book time for the BSC hood using this calendar: 1521 BSC Hood Calendar

22 Repeat the sieving and subsampling steps for the bottom section and sieve and store the middle

section.

22.1 Reminder Core A and Core C4 are not processed at this time.

23 Store samples in the appropriate location:

23.1 Store the DNA samples in a zip-top bag labelled 1000 soils and in the -80 °C .

These samples are typically on the middle shelf of the furthest east -80 °C in the corridor behind 1521.

23.2 Refrigerate the pH and P extraction samples until done processing cores.

23.3 Place GWC tins in the drying oven in 1446 at 60C for 48:00:00 to 72:00:00 . 5d

23.4 Dry the remaining soils in the BSC hood for 48:00:00 to 72:00:00 or until dry. After soils are dry collect a 50 mL Olympus centrifuge tube of OM analysis and seal the remainder in labeled Polypropylene jars for archive. 5d