

Bayer HWSC Soil Health Protocol

Funding sources: Areawide, Bayer (led by Mirsky)

Collaborators MD, IL, LA, TX, VA

Data and Protocol is located in this Google Folder:

https://drive.google.com/drive/folders/1peQWtT2M7OTAq_9cVtF9F0KJtf-YOmrX?usp=sharing

Contacts for questions:

Protocol questions: Eugene Law (eplaw@udel.edu or 315-256-7466)

Cornell Soil Health Lab: soilhealth@cornell.edu or 607-227-6055

Part 1: Soil Health Indicators

Objective: Determine the effects of cover crop, HWSC, and those combined on indicators of soil health, with an emphasis on soil carbon storage.

Hypotheses:

- a) Cover cropping will improve physical and chemical indicators of soil health in surface soils by increasing inputs of organic matter as cover crop residues and reducing soil erosion and crusting.
- b) HWSC will not affect soil health indicators.

Treatments: Full 2x2 factorial of (+/- HWSC and +/- cover crop)

Replication: At each collaborating site the full treatment factorial will be replicated at least three times with rotation entry points of both corn and soybean starting with cover crop planting Fall 2021/cash crop planting Spring 2022.

See the full HWSC protocol for more information about experimental design and field layout:

-  HWSC Protocol 1: corn and soybean.docx

Data Collection:

Applies to both soybean and corn phases of rotation. Soil samples will be collected in spring 2022 and the end of the project (ideally in the spring of 2026) to evaluate indicators of soil health (every 4 years).

SOIL SAMPLES WILL BE TAKEN FROM THE CENTER SOYBEAN HEADER WIDTH OF EACH PLOT, OUTSIDE OF THE CENTRAL 100 ft SUBPLOT.

Enter all data in the appropriate folder (your state > Farmer/crop rotation) here:

https://drive.google.com/drive/folders/1C5Y3GYix-C_knm3_8iTy1OsyscAawcz8g?usp=sharing

A. Soil Health Indicators Analyzed at Cornell Soil Health Laboratory:

1. Soil health indicator sampling (sampling protocol adapted from CASH manual: <http://www.css.cornell.edu/extension/soil-health/manual.pdf>):
 - a. Sample every plot in both fields (minimum of 24 samples: 4 trmts * 3 reps * 2 crop rotations).
 - i. Use a standard soil probe (2.2 cm dia.) to a depth of 6 inches.
 1. [Example probe](#)
 - ii. Bulk ~20 cores taken from random locations within the center soybean header width but **outside** of the 100 ft central sampling area to prevent soil disturbance where we are quantifying impact mill effects on soil seedbanks.
 - iii. When collecting each core:
 1. Remove surface debris.
 2. Insert soil probe perpendicular to soil surface to a depth of six inches
 3. Twist probe slightly to break suction and gently remove from soil.
 4. Gently extract soil core from probe and place into a clean 5 gal bucket
 - iv. After collecting ~20 cores from a plot, gently break up and mix individual cores by hand to create a homogenized bulk sample.
 - v. Transfer ~4 cups of the bulk sample to a labeled one gallon freezer bag
 - vi. Keep samples out of direct light and in a cool place until they are shipped.
2. Ship bulk soil samples to Cornell Soil Health Testing Laboratory as soon as possible:
 - a. Send samples and submission forms to:

Cornell Nutrient Analysis Lab
c/o Soil Health Lab
G01 Bradfield Hall
306 Tower Rd.
Ithaca, NY 14853
soilhealth@cornell.edu
607-227-6055
 - b. Packaging and shipping requirements (see CASH manual)
 - i. Bag each individual sample in a 1-gallon plastic (Ziploc) bag. Freezer bags are preferred. Make sure the bag is properly labeled with the field and plot number.

1. Example: VA102, plot 101
 - ii. **Double bag your soil sample in a Ziploc bag.** You can either place the single sample within another 1-gallon plastic bag or place multiple sample bags in a secondary, larger plastic bag.
 - iii. Place the double-bagged samples in a cardboard box. The size of the box depends on the number of samples. In general we recommend a small USPS Flat Rate Box for a single sample or a Priority Mail Medium Flat Rate box for up to 6 samples.
 - iv. Complete the Submission Forms for your site in the Google shared drive: [Bayer Soil Health Project](#). Please complete the forms before printing for shipping purposes so that we have a record stored in the drive. **It is important to enter the county from where the soil sample was taken.** You will need to enter the following information into the Submission Forms:
 1. County of origin - box 1
 2. Plot ID - will be filled out if plot maps have been uploaded, otherwise enter in box 7 (field ID/sample name). This should match the Plot IDs on the sample bags and used in your plot map for the experiment.
 - a. Example: VA102, plot 101
 3. Date sampled - box 8
 4. GPS Coordinates - box 11
 5. Soil Name (if known) - box 12
 6. Tillage Type (box 13) and Crop Information (box 14) if necessary. These will already be filled out if you have completed your Production Practices data sheet, but please check for correctness.
 - v. Place a copy of the completed submission form in the box, on top of the packaging material. Protect the form within its own plastic bag.
 - vi. Add packing material (such as crumpled paper or bubble wrap) to minimize sample movement within the box. Add ice packs (also within their own plastic bags) only if shipping during the hottest days of summer. Ice packs and coolers are not returned.
3. Soil health indicators to be assessed by Cornell Soil Health Lab:
 - a. pH and nutrient testing (including P, K, micronutrients, OM)
 - b. Wet aggregate stability
 - c. Active carbon
 - d. Total C and N
 - e. Soil respiration

B. Bulk Density Protocol - carried out at each site independently

1. Bulk Density sampling - **NOTE: Bulk density measurements are dependent on the accuracy of soil core volumes, total sample weight, rocky fragment percentage, and soil moisture content at sampling.** If you have not measured bulk density before please read this entire protocol in detail and contact Eugene with any questions before you start sampling. The sampling procedure is similar to the procedure for the samples being sent to Cornell, but there are several important differences that require us to collect separate samples for bulk density.
 - a. Sample every plot in both fields (minimum of 24 samples: 4 trmts * 3 reps * 2 crop rotations).
 - i. Use a standard soil probe (2.2 cm dia.) to a target depth of 6 inches (15 cm). If you use a soil probe with a different interior diameter (ID), note that in your final datasheet. **Note: Accurately sampling to 6 inches is critical. Mark your probe and measure the first few cores in each plot to ensure that you are consistently within ¼ in of the target depth.**
 1. [Example probe](#)
 - ii. Bulk **exactly 10 cores** taken from random locations within the center soybean header width but **outside** of the 100 ft central sampling area to prevent soil disturbance where we are quantifying impact mill effects on soil seedbanks.
 1. Avoid sampling in any recent tire tracks or obvious high-traffic areas.
 - b. When collecting each core:
 1. Remove surface debris.
 2. Insert soil probe perpendicular to soil surface to a depth of six inches.
 3. Twist probe slightly to break suction and gently remove from soil.
 4. Gently extract soil core from probe and place into a clean 5 gal bucket.
 - c. After collecting 10 cores from a plot, seal the bucket or transfer cores to a sealed plastic bag to prevent soil from drying while other samples are collected.
2. Lab processing steps:
 - a. Record wet weights of bulk samples.
 - b. Gently break up and mix individual cores by hand to create a homogenized bulk sample.
 - c. Sieve samples to 2 mm, retaining and recording weight of rocky fragments that do not pass the sieve
 - i. If samples are very rocky, pass them through a 4 mm sieve first.
 - d. Label and record tare weights of drying tins.
 - e. Weigh out 20-50 g of each sieved sample into a labeled drying tin.
 - i. Record subsample wet weight before drying.



- f. Dry samples at 60C until they reach constant weight.
 - i. After ~24 hours, record weights for a few samples, put them back in the oven, and re-weigh after an hour. If dry weights are within 0.1 g of each other, proceed with weighing remaining samples.
3. Enter soil probe ID, number of cores per bulk sample, bulk sample wet weight, rocky fragment weight, subsample wet weight, and subsample dry weight in your sites BD datasheet: [ADD LINK TO DATA FOLDER HERE](#)
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