CT RC&D Compost Tea Project 2025
Compost Tea Application in Organic Vegetable Production: A Five-Farm Field Trial

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Abstract

Actively aerated compost tea (AACT) is widely applied in organic vegetable production as a biological soil amendment, yet the conditions under which it reliably produces agronomic returns remain poorly characterized. This study reports results from a single-season five-farm field trial examining the effect of AACT application on crop yield across tomato, kale, and cucumber plots under organic management. Crop yield was the primary outcome variable. Five applications of biologically active tea were delivered as combined foliar and drench treatments alongside equivalent food-amendment-only controls using a randomized paired block design with four spatial blocks per site. Soil biological status, soil chemistry, plant tissue nutrition, and qualitative field microscopy were collected as contextual measurements to support interpretation of yield outcomes.

A statistically significant yield increase was observed at one of five farms. At Lathorp Farm (LATH) — a new field with no prior compost application history — tea-treated Big Beef tomato plots yielded 35.4% more than controls (19.9 vs 14.7 lbs/sqft; $t(3) = -8.37$, $p = .004$, Cohen's $d = 4.18$), supported by a coherent evidence chain spanning biological, chemical, and nutritional measurement layers consistent with accelerated decomposition, mineralization, and solubilization by the tea-associated microbial community. No statistically significant yield response was observed at the remaining four sites despite measurable soil chemistry and biological responses at several of them.

The ratio of microbial biomass carbon (MBC) to total organic carbon — termed the Microbial Quotient (MQ; Sparling, 1992) showed a near-monotonic relationship with yield response across the five sites. The only site with an MQ classified as biologically adequate (1.21%) produced the only significant yield response; sites with suppressed or

low MQ values (0.27–0.50%) showed soil chemistry responses without agronomic translation. These findings suggest that the biological receptivity of the receiving soil — rather than delivered microbial load — is the primary determinant of single-season AACT efficacy, and that the pre-season MQ may serve as a useful screening criterion for identifying soils most likely to respond to biological inoculant application within a single growing season.

1. Introduction

This study reports results from a single-season five-farm field trial testing the effect of AACT application on crop yield across five organic vegetable farms representing a range of management histories and baseline biological states. Contextual measurements of soil biological status, soil chemistry, and plant tissue nutrition were collected alongside yield to support interpretation of the yield outcomes. The pre-season Microbial Quotient (Sparling, 1992) is examined as a candidate for identifying soils most likely to respond to biological inoculant application within a single growing season.

The trial was conducted as part of the CT RC&D Compost Tea Equipment Mobile Unit 2025 Educational Pilot Project, undertaken in cooperation with CT NOFA and funded by the Climate Smart Farming: Agriculture and Forestry Grant, awarded and administered by the Connecticut Department of Agriculture. The project was designed to introduce Connecticut farmers to the use of compost tea as an organic soil health tool through on-farm experimental trials, contributing both to practitioner knowledge and to the evidence base for biological amendment adoption under regional conditions. Five farms were selected through an application process open to all operating farms statewide: Reservoir Community Farm (RESV) in Bridgeport, Common Ground High School (CGHS) in New Haven, Lathrop Farm (LATH) and Sweet Acre (ACRE) in Lebanon, and Artza Mendi Farm (ARTZA) in Baltic. Trial methods followed the framework described in Pérez Orozco et al. (2023), adapted for the compost tea application context. The multi-layer measurement design was intended to generate findings applicable both to the participating farms and to the broader evidence base for biological amendment adoption under regional conditions.

Compost tea as an organic agriculture method

Soil biological health is increasingly recognized as a foundation of sustainable and organic vegetable production, mediating the mineralization of organic nutrients, the solubilization of mineral-bound elements, and the physical architecture of the soil environment through fungal hyphal networks and aggregate formation (Ingham, 1999; Coleman et al., 2004). In conventionally managed soils, decades of tillage, synthetic fertilizer inputs, and reduced organic matter additions frequently suppress microbial biomass and community complexity relative to the organic carbon pool available to support them, creating a condition in which nutrient cycling is dominated by chemical rather than biological processes (Wardle, 1992; Wardle et al., 1995).

Compost teas and extracts are organic methods used to inoculate soils and plants with beneficial microbes found in high-quality compost and vermicompost (Ingham, 2005; Scheuerell & Mahaffee, 2002). The microbial communities introduced through these preparations are known to facilitate nutrient cycling, suppress plant diseases, decompose organic matter, promote plant growth, and support broader soil health and bioremediation functions (Coleman et al., 2004; Ingham, 1999; Mahala et al., 2021). Actively aerated compost tea (AACT) has gained increasing adoption among organic growers as a field-applicable biological amendment intended to stimulate these functions in situ, with increasing interest from farms seeking to reduce their dependency on synthetic fertilizer applications and to transition toward biologically driven nutrient management systems (Ingham, 2005). AACT is produced by aerating a dilute compost suspension with supplemental food amendments over a 24–48 hour period, generating a liquid inoculant rich in bacterial and fungal biomass applied to soil and plant surfaces as a combined drench and foliar treatment. The biological rationale rests on the premise that introducing a diverse and active microbial community to the rhizosphere and soil surface can accelerate the conversion of soil organic matter and mineral substrates into plant-available nutrients, supplementing the nutrient delivery capacity of a biologically depleted resident community (Ingham, 2005). Whether and under what soil conditions this mechanism operates at agronomically meaningful rates is a central question to address.

Despite widespread practitioner adoption and the mechanistic plausibility of AACT as a biological soil amendment, the peer-reviewed evidence base for its agronomic efficacy is inconsistent, and systematic testing remains essential for informed farmer adoption. Positive yield and nutritional responses have been reported in some trials, particularly in soils with low baseline biological activity, while other trials have found no significant effect or mixed results across crop types and management contexts (Scheuerell & Mahaffee, 2002; Hargreaves et al., 2009). Several factors have been proposed to explain this inconsistency: variability in tea biological quality between batches, differences in application timing and rate, crop-specific responses, and the confounding influence of site-level soil conditions on the responsiveness of the receiving soil to inoculant application. While some published AACT trials have measured soil chemistry and tissue nutrition alongside yield (Hargreaves et al., 2009), the broader literature has not systematically characterized pre-application soil biological conditions as predictors of agronomic response, leaving practitioners without a diagnostic framework for identifying soils most likely to benefit from inoculant application within a single growing season (Scheuerell & Mahaffee, 2002).

A key gap in the AACT literature is the absence of a systematic framework for predicting which soils are most likely to benefit from biological inoculant application in a given season. Sparling (1992) demonstrated that the ratio of microbial biomass carbon to total organic carbon (Cmic:Corg, or Microbial Quotient, MQ) is a sensitive indicator of soil biological status and management history, with values typically ranging from 1–4% in healthy soils and declining under arable cropping and disturbance. This ratio expresses how active the microbial community is relative to the available carbon substrate — distinguishing between carbon-rich but biologically suppressed soils and soils where the microbial community is actively processing available substrate. Without a pre-application diagnostic criterion of this kind, AACT is applied uniformly across soils with widely varying biological status, conflating soil contexts that represent fundamentally different intervention conditions. This may partly explain the apparent inconsistency of AACT outcomes across the literature, where variable and often unreported baseline soil biological conditions could contribute to divergent responses to otherwise similar treatment protocols (Scheuerell & Mahaffee, 2002; Hargreaves et al., 2009).

2. Materials and Methods

2.1 Trial Site Characteristics

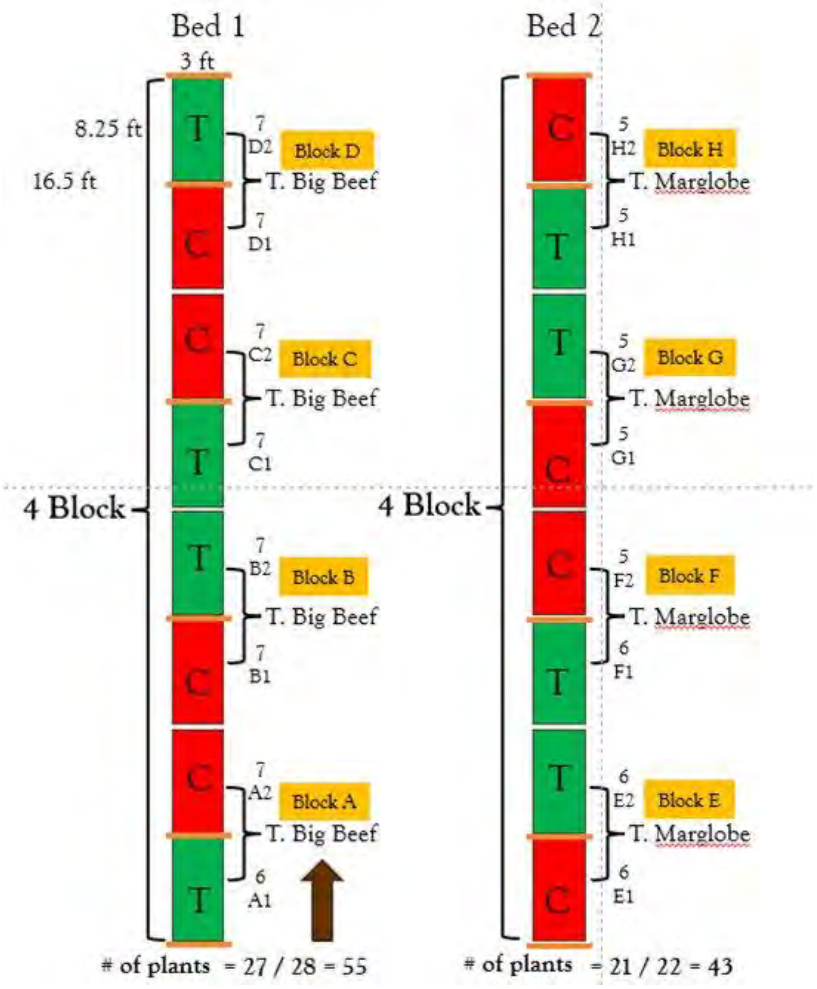
Five farms participated representing similar soil types but a range of management histories, and production contexts. LATH was a new fine sandy loam field with no prior compost application history, managed with black plastic cover and straw mulch. ARTZA was a newly established fine sandy loam plot with a woodchip base mulch. RESV comprised raised beds under organic management with limited irrigation. ACRE was a fine sandy loam greenhouse site with a history of compost application. CGHS was a gravelly sandy loam with a history of compost application. Site-level characteristics and structure are summarized in Tables 1 and 2. Plots for the trial and crop selections were determined by farmers in agreement with the field researchers, following the participatory on-farm research framework described in Pérez Orozco et al. (2023). Site-specific events affecting trial integrity are detailed in Section 3.9.

2.2 Plot Design

The trial used a randomized paired block design (Pérez Orozco et al., 2023). Each plot was physically divided into four spatial blocks running the length of the plot, providing four replications per farm. Within each block, one sub-unit was assigned to the control treatment and one to the tea treatment, with sub-unit plant counts determined by plot density. An example of the randomized paired block layout is illustrated in Figure 1.

The trial set out to test statistically whether five AACT applications per season would result in higher yields in the selected crops, and secondarily whether such applications would help prevent or minimize disease and pest pressure. The present paper reports yield and soil biology outcomes; systematic disease and pest assessment is noted as a direction for future work.

Figure 1. Schematic of the randomized paired block design at Sweet Acre Farm (ACRE), illustrating the arrangement of treatment (T, green) and control (C, red) sub-units across four blocks in two beds. Numbers indicate plant counts per sub-unit.



Example from ACRE: Bed 1 = Big Beef tomato (27/28 plants); Bed 2 = Marglobe tomato (21/22 plants). Each block contains one T and one C sub-unit. Block order was randomized independently within each bed.

2.3 Compost Tea Production and Distribution

The project provided a Compost Tea Mobile Unit which included a trailer, a 50-gallon conic brewer, a 55-gallon 3-point PTO spray rig, a 4-gallon backpack sprayer, a compost tea filter and amendments. Given the distance between farms and for logistics purposes, tea brew production and distribution followed a two-hub design. Compost tea for LATH, ACRE, and ARTZA was brewed at the LATH farm using a 50-gallon conic brewer charged with well water. The source of the vermicompost used for brewing tea was supplied by Wiggle Room LLC, Baltic, CT. Tea for CGHS and RESV was brewed at CGHS using a 7-gallon conic brewer charged with municipal water. All brews used a consistent compost-to-water ratio of 0.2 lbs/gallon and a 24-hour brew cycle with

identical food amendments (kelp, fish hydrolysate, humic acid) scaled proportionally to volume. Within each hub, farms received tea from the same brew batch per application event.

2.4 Compost Input, Tea Quality Characterization and Treatment Application

Compost input quality was assessed using the Microbiometer dry soil protocol (Prolific Earth Sciences Inc.), yielding MBC (µg C/g) and Fungal to Bacteria Ratio (F:B) as co-outputs of a single colorimetric extraction. These outputs are not independent. Finished tea MBC (µg C/ml) was measured using the Microbiometer liquid protocol. A minimum threshold of approximately 15–25 µg C/ml was applied as the operational floor for biologically active tea, consistent with the Low range for compost tea by Microbiometer measurement (Prolific Earth Sciences Inc., n.d.). Throughout the season, attention was given to operational factors known to influence brew biological quality: water temperature, dissolved oxygen levels, brewer efficiency, pH, diversity and ratio of microbial food amendments, and consistency of vermicompost input quality (Ingham, 2005). These parameters were recorded at brew completion where instrumentation was available. Tea quality data are reported in Table 3.

Each plot received a standardized application volume of 4 gallons per event, applied as a combined foliar spray and soil drench distributed across all plants within the plot. Control plots received an equivalent volume of water with identical food amendments at the same per-plant volume, ensuring that any treatment effect is attributable to the microbial fraction of the tea rather than the food amendments alone. Five applications were made across the 2025 growing season (June–September) at approximately three-week intervals (see schedule, Table 4). Site-level per-plant application volumes and estimated delivered loads are reported in Table 2 and illustrated in Figure 3. Foliar applications were made to cover both upper and lower leaf surfaces to maximize epiphytic microbial contact. Soil drench volumes were applied at the base of each plant with the intent of reaching the active root zone; however, drench penetration depth was not verified independently. Applications were not made consistently at times during the day that would help reduce microbial desiccation from heat and evaporation.

2.5 Biological Measurements

Crop yield was the primary outcome variable of this trial. Soil biological, chemical, plant tissue, and field microscopy measurements were collected as contextual indicators to support interpretation of yield outcomes and are reported in that capacity.

Soil MBC and F:B were measured using the Microbiometer soil test kit at 6-inch depth from the designated crop plot at each site pre-season (May) and post-season (September): Big Beef tomato at LATH, ACRE, and ARTZA; Hungarian tomato at RESV; Curly kale at CGHS. Twelve subsamples per plot were composited separately for control and tea sub-plots. The pre-season Microbial Quotient was calculated as MBC / (OM% / 1.724 × 10,000) × 100, following Sparling (1992).

2.6 Field Microscopy: Qualitative Microbial Analysis

Qualitative field microscopy observations were conducted in parallel with Microbiometer MBC and F:B ratio measurements throughout the trial. Observations were made using a compound microscope with a standard wet-mount preparation from a 1:5 soil or tea dilution in de-chlorinated water, examined at 100x and 400x total magnification following the preparation protocol described by Ingham (1999).

For compost tea quality assessment, microscopy was performed on each batch of brewed tea prior to application. Observations characterized the presence and approximate relative abundance of microorganisms across trophic layers — bacteria, fungi (hyphae and spores), protozoa (flagellates, amoebae, and ciliates where present), nematodes, and microarthropods — alongside organic matter humification state and aggregate formation in the compost substrate (Table 5). These observations allowed each brew to be assessed not only for total microbial biomass (via Microbiometer) but for the trophic diversity and community character of the biological inoculant being delivered. Vermicompost input quality was not assessed separately in each batch but was considered consistent, supported by prior qualitative microscopy characterizing the material as biologically mature, with well-developed aggregate structure, a balanced bacterial and fungal community, and a multi-trophic assemblage including flagellates, testate amoebae, and bacterivore nematodes as the dominant higher trophic groups, with microarthropods present at low abundance.

For soil assessment, microscopy was performed on composite samples collected from both the control and tea treatment plots at each site at pre-season and post-season time points, matched to the Microbiometer sampling schedule. Observations followed the same trophic layer framework applied to the tea assessments, allowing qualitative comparison of the soil biological community before and after the five application events. Soil microscopy characterized the presence of bacterial-dominated vs. fungal-dominated communities, protozoan community composition (succession state), organic matter humification stage, and evidence of aggregate structure and particle binding.

Field microscopy observations are reported descriptively and were used to contextualize and corroborate the quantitative MBC and F:B ratio findings from the Microbiometer. Quantitative scoring of microscopy observations using a structured assessment instrument was not applied in this trial; this is identified as a methodological refinement for future cycles (see Section 5.1).

2.7 Soil Chemistry

Soil chemical analysis was conducted at Logan Labs on samples collected pre- and post-season from the same designated crop plot at each site at 6-inch depth, matched to the biological sampling structure. Mehlich III extraction was used for a full nutrient panel; selected parameters are reported in Table 7. Soil paste extract was additionally analyzed for plant-available nutrient fractions; selected parameters are reported in Table 8. Complete analytical datasets for both methods are available from the corresponding author on request.

2.8 Plant Tissue Analysis

Foliar tissue samples were collected approximately one week after the third application. For both tomato and kale, 15 plants were sampled per treatment per plot and submitted to Penn State Agricultural Analytical Services Laboratory for macro- and micronutrient analysis (Table 9). Normal reference ranges are those of Penn State for general tomato and kale production.

2.9 Yield

Yield was recorded by participating farmers as cumulative seasonal harvest weight of marketable produce across all harvest events within each sub-unit per block (Table 10). Sub-unit area was used to normalize yield to lbs/sqft, enabling comparison across plots of varying size (sub-unit dimensions reported in Table 2). Percentage yield change = [(tea − control) / control] × 100.

2.10 Statistical Analysis

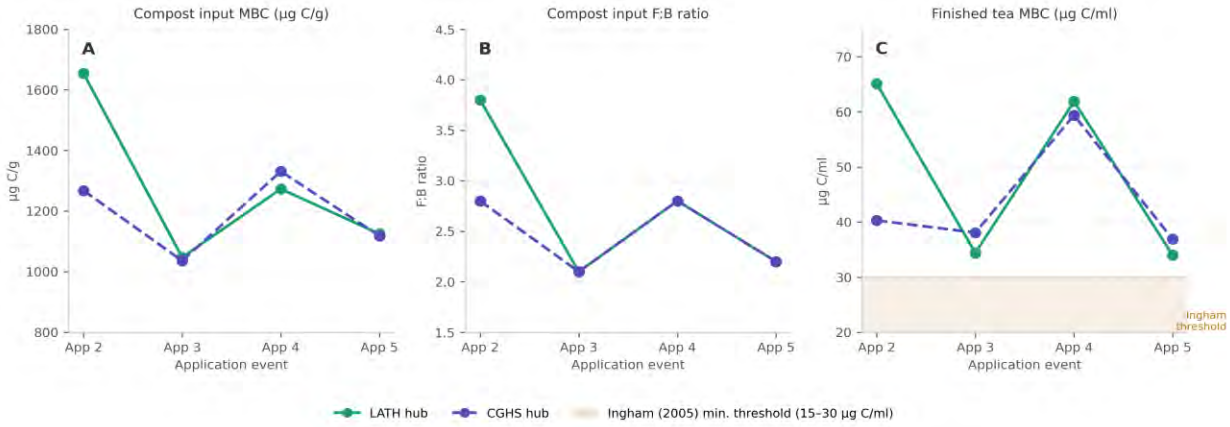
Yield data were analyzed using two-tailed paired samples t-tests exploiting the blocked plot design (df = 3 for four paired observations). Effect size was estimated using Cohen's d. All analyses were conducted in NUMIQO statistical software. Statistical testing was conducted only for comparisons with a minimum of four blocks per treatment; others are reported as descriptive means only.

3. Results

3.1 Compost Input Quality and Brew Consistency

Tea MBC ranged from 34.0 to 65.1 µg C/ml at LATH hub and 36.9 to 59.4 µg C/ml at CGHS hub. Using the Microbiometer compost tea ranges as a reference (Prolific Earth Sciences Inc., n.d.), which define a Low range of approximately 15–25 µg C/ml and an Excellent range of approximately 55–65 µg C/ml, brew quality varied across the season. Applications 2 and 4 at LATH hub and Application 4 at CGHS hub reached the Excellent range (59.4–65.1 µg C/ml), while Applications 3 and 5 at both hubs fell in the upper portion of the Low range or at the Low-to-Excellent transition (34.0–40.3 µg C/ml). All brews exceeded the 15 µg C/ml minimum floor. Input MBC and F:B were closely aligned between hubs across applications 3–5, indicating the same compost batch was likely used. Application 2 diverged, with LATH showing higher compost input quality coinciding with the strongest tea output recorded (65.1 µg C/ml). Brew consistency across the season is illustrated in Figure 2.

Figure 2. Compost input quality and finished tea consistency across application events (apps 1–5).

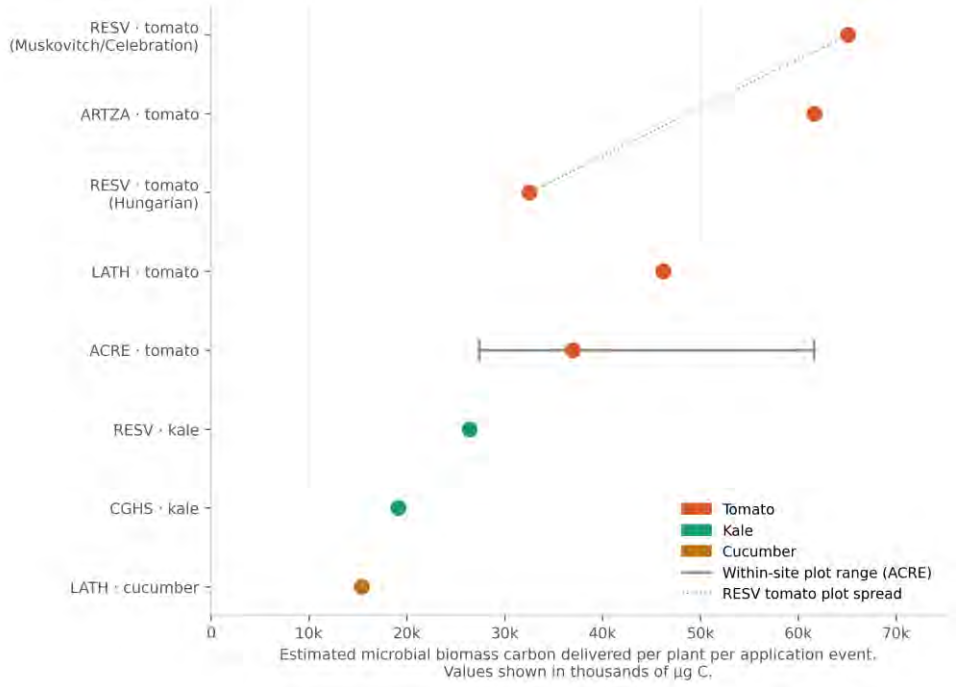


Panel A: compost input MBC (µg C/g). Panel B: compost input F:B. Panel C: finished tea MBC (µg C/ml). LATH hub solid; CGHS dashed. Application 1 excluded (ND).

3.2 Delivered Microbial Load and Treatment Delivery

Delivered load ranged from 15,388 to 65,061 µg C per plant. All tomato sites received well above the 15 µg C/ml minimum floor (Table 2, Figure 3). Delivery rank did not explain yield response direction or magnitude.

Figure 3. Estimated microbial biomass carbon delivered per plant per application event.



Values in thousands of µg C.

3.3 Yield

LATH Big Beef showed the only statistically significant treatment effect: tea 19.9 vs control 14.7 lbs/sqft (+35.4%; $t(3) = -8.37$, $p = .004$, $d = 4.18$). All other tested comparisons were non-significant. Harvest frequency varied in two sites and is recorded in Table 11.

3.4 Soil Microbial Biomass Carbon, Fungal:Bacterial Ratio, and Microbial Quotient

Sections 3.4 through 3.9 report the contextual biological, chemical, tissue, and qualitative observations collected to support interpretation of the yield findings in Section 3.3.

Pre-season MQ ranged from 0.27% (RESV) to 1.21% (LATH). Following Sparling (1992), LATH was the only site in the adequate range; CGHS (0.50%) and ARTZA (0.45%) were classified as Low; ACRE (0.30%) and RESV (0.27%) as Suppressed. All plots showed substantial MBC gains across the season. Post-season MBC was higher in tea plots at CGHS (+119 µg C/g) and ARTZA (+59 µg C/g). At LATH and ACRE, where pre-season treatments were biologically imbalanced, tea sub-plots showed larger ΔMBC despite starting lower. F:B increased at all sites in both treatments; post-season F:B was higher in tea at RESV, CGHS, and ARTZA.

Post-season MQ was calculated from post-season MBC and OM% values (Table 12). Three findings are notable. First, LATH control MQ remained stable (1.21%→1.24%) despite a near-doubling of absolute MBC, because organic matter also nearly doubled (+6.0% OM), keeping the ratio constant. LATH tea post-season MQ (1.07%) was lower than the pre-season control threshold (1.21%) for the same reason: tea plots accumulated OM (+6.4%) at a rate that outpaced proportional MBC growth, indicating that within a single season AACT may build organic carbon faster than the proportional microbial community to process it. Second, CGHS tea post-season MQ reached 1.17% crossing the apparent response threshold for the first time. CGHS control also approached it at 0.99%. Neither treatment crossed the threshold pre-season. CGHS ended the season biologically positioned where LATH began, suggesting it may be a candidate for yield response in a second season if K deficiency and Cu deficiency are corrected first. Third, all sites except RESV tea showed meaningful MQ improvement

across the season: ARTZA tea (0.53%→0.87%), ACRE tea (0.26%→0.86%), RESV ctrl (0.27%→0.63%). The non-responding sites were not biologically static — they were developing. Full post-season MQ values are reported in Table 12.

3.5 Soil Chemistry — Mehlich III

Potassium was deficient at all sites. LATH tea (+37 ppm) and ACRE tea (+82 ppm) were the only plots showing post-season K gains. Organic matter increased substantially at LATH (~6%) and ACRE (3–5%). Silicon increased from pre-season to post-season at all sites in both treatments (gains of 1.6–9.9 ppm). The RESV tea treatment showed pH acidification (7.1→6.2). The ARTZA ctrl pre-season NO_3 outlier (290.3 ppm) is attributed to chicken manure deposition. Selected parameters are reported in Table 7.

Full Mehlich III exchangeable cation data revealed a consistent pre-season Ca:Mg imbalance across all five sites, with ratios ranging from 4.2:1 at LATH to 13.6:1 at CGHS against an optimal target of 3–7:1, with Ca and Mg together comprising approximately 80% of base saturation (Marschner, 2012). LATH was the only site within the optimal range. Post-season, four of five sites moved toward better Ca:Mg balance in both treatments through Mg gains and Ca losses or stability. LATH was the exception: both treatments showed Ca:Mg widening substantially across the season (ctrl 4.21→6.50; tea 4.28→6.30), probably driven by large Ca releases from decomposing straw mulch (+832 ppm ctrl, +945 ppm tea) that outpaced proportional Mg gains (+80 and +97 ppm respectively). Tea did not consistently widen or narrow Ca:Mg ratios relative to control at any site; post-season treatment differences ranged from −0.27 to +0.33 with no directional pattern. Full exchangeable cation data are available from the corresponding author on request.

Using Logan Labs' site-specific desired values as the reference standard, potassium was the only nutrient showing universal deficits: all five sites were below Logan's desired K values in both treatments pre-season, and all five worsened post-season as crop uptake depleted an already-insufficient pool. Magnesium deficits were flagged only at CGHS, where both treatments fell below desired values pre-season (ctrl −36 ppm, tea −35 ppm) and marginally post-season, consistent with Ca base saturation

persistently above the 70% ceiling (76–79%) dominating the exchange complex and limiting Mg occupancy. All other sites met Logan's desired Mg values within their soil-specific calibration. Calcium deficits were flagged at two sites: LATH pre-season in both treatments (ctrl −100 ppm, tea −88 ppm), where Ca base saturation also fell below the 60% floor (57.8% ctrl pre-season) — confirming genuine Ca undersupply at the exchange complex level, not merely low absolute concentration — and a minor Ca deficit in the RESV tea treatment post-season associated with the pH acidification event. At ARTZA, K base saturation exceeded the 5% ceiling pre-season (ctrl 5.1%, tea 7.3%) before collapsing below the 2% floor post-season — K moving from excess to deficiency within a single growing season. No phosphorus or sulfur deficits were reported by Logan Labs at any site.

3.6 Soil Chemistry — Paste Extract

All soluble salt levels remained below the 960-ppm toxicity threshold. Soluble P was below the 1–3 ppm desired range at LATH pre-season. ACRE tea post-season reached 16.9 ppm soluble K, the only site approaching the desired 15–20 ppm range. Bicarbonate exceeded the <50 ppm threshold at LATH tea post (60 ppm). Soluble Fe rose to 9.76 ppm in the RESV tea treatment, consistent with pH-driven Fe mobilization. Selected parameters are reported in Table 7.

3.7 Plant Tissue Analysis

Nitrogen was below normal at all sites except ARTZA in both treatments. Iron was elevated at all tomato sites in both treatments. Three apparent treatment differences are boundary artifacts within 0.02 units of a reference boundary (RESV Mg, ARTZA P, LATH Mg). ACRE Zn moved from Low (22.6) to Normal (28.6 ppm) in the tea treatment. CGHS tea N was notably lower than control (2.54 vs 2.95%). Full results in Table 9.

3.8 Field Microscopy: Qualitative Observations

Qualitative microscopy observations were made on each brew batch prior to application and on paired soil composite samples from the control and tea plots at each site before and after the five application events. Observations characterized trophic community composition, aggregate structure, organic matter character, and biological fullness of the preparation or soil sample.

Table 5 below summarizes brew observations across the ten application events. CGHS hub brews showed progressive trophic development across the season, advancing from a bacterial-dominant community with aggregates at Application 1 through to a community including flagellates, testate amoebae, a ciliate, and a nematode by Applications 3 and 4. LATH hub brews remained more bacterial-dominant throughout, with fungal elements appearing from Application 2 onward but no higher trophic predators observed across the season. This difference in brew trophic character is consistent with the higher F:B ratios recorded in LATH brews (Table 3) and suggests differences in compost input maturity, aeration dynamics between hubs and seasonal ambient temperature.

Pre-trial soil microscopy confirmed no observable biological difference between the designated control and tea plots at any site, consistent with the randomized paired block assignment. All five sites presented bacterial-dominant communities with varying degrees of aggregate development, reflecting the range of management histories described in Section 2.3. LATH and ACRE presented the densest pre-season biological communities; CGHS, ARTZA, and RESV appeared more sparsely colonized with minimal aggregate structure.

Post-trial observations showed greater microbial composition and micro-aggregate development in tea plots relative to controls at four of five sites (LATH, ACRE, CGHS, ARTZA). RESV showed the least treatment differentiation post-trial, with both control and tea described as full and bacterial-dominant. Table 6 summarizes pre- and post-trial soil observations by site and treatment. The qualitative direction of change in tea plots is consistent with the MBC and F:B ratio gains recorded by the Microbiometer, and the greater micro-aggregate development in tea plots at most sites is consistent with the organic matter gains observed in Mehlich III data. Both control and tea plots showed increased biological activity post-season relative to pre-season, consistent with seasonal microbial development expected across all plots.

3.9 Pest and Disease Incidence: Qualitative Observations

Systematic comparative pest and disease incidence data were not collected during the trial, as the volume of farm tasks carried out by participating farmers precluded the additional structured monitoring required. This gap relative to the secondary research aim is discussed in Section 4.10. Farmer observations across the five sites indicated that overall pest and disease pressure was low during the 2025 growing season and did not materially affect the primary yield comparisons at most sites.

Three site-specific exceptions were documented. At ARTZA, flea beetle damage caused complete loss of the eggplant trial plants shortly after transplanting; that secondary crop trial was discontinued and is excluded from all analyses. The ARTZA tomato trial was unaffected and continued to completion. At LATH, Big Beef tomato seedlings showed early blight symptoms before transplanting; two plants in the control plot were subsequently lost and replaced, maintaining block structure. At LATH, Marketmore cucumber seedlings exhibited Anthracnose fungal disease symptoms before transplanting, and the grower applied chemical fungicides during the growing season to manage the disease. The cucumber trial was productive but had a shortened season, and the chemical applications represent a management confound for the LATH cucumber comparison specifically. No systematic chemical inputs were applied to the tomato plots.

4. Discussion

4.1 Biological Transfer Capacity as a Mediating Variable

The central finding of this trial is that a statistically significant yield response to AACT was observed at only one of five sites, and that the site where it occurred was the only one with a pre-season Microbial Quotient in the adequate range. To interpret this pattern, the contextual biological and chemical measurements were integrated into a post-hoc explanatory framework centered on the concept of biological transfer capacity — the ability of the soil microbial community to convert nutrients stored in organic matter and mineral soil fractions into plant-available forms at rates that match crop demand across the growing season. Biological transfer capacity is not a property of the soil chemistry or the organic matter; it is a functional property of the biological

community — specifically its size relative to substrate, its metabolic efficiency, its community composition, and the functional guild diversity that determines which nutrient transformation pathways are operating.

Before examining those biological pathways, the soil chemistry data were reviewed against Logan Labs' site-specific desired values to assess each site's pre-season chemical capacity — whether sufficient nutrients were present in accessible forms to potentially sustain crop production. This prior question matters because biological transfer capacity operates on what is already in the soil: a highly active microbial community can accelerate conversion of stored nutrients into plant-available forms, but it cannot manufacture nutrients that are absent, and it cannot fully compensate when crop withdrawal rates exceed replenishment capacity.

By Logan Labs' calibration, K was the only nutrient deficient at all five sites before the season began — a universal starting constraint. Beyond K, sites differed substantially. ACRE entered the season with Ca, Mg, and P all at or above desired values — only K was flagged, and the exchange complex was well-stocked. CGHS had adequate Ca and P but Mg deficits in both treatments, with Ca base saturation persistently above the 70% ceiling, crowding Mg and K from their functional exchange positions. RESV had adequate Ca and Mg but severe pre-season K deficits. ARTZA had adequate Ca and Mg with K initially above desired, but K base saturation crashed from above the 5% ceiling (7.3% tea pre-season) to below the 2% floor (1.8%) by season's end — K exhausted by crop demand during the season. LATH was the most chemically undersupplied at planting: Ca was below desired values in both treatments and Ca base saturation was below the 60% floor (57.8% ctrl pre-season), confirming genuine Ca undersupply at the exchange complex level alongside K deficits. Yet LATH ended the season with Ca, Mg, and K all meeting or exceeding desired values, driven potentially by the decomposer community acting on Ca- and Mg-rich straw mulch and K-solubilizing bacterial activity. At LATH, biological activity did not supplement an already-adequate supply — it built one. This distinction between biology accelerating access to an existing reserve versus biology actively constructing a depleted one is central to understanding why the yield response occurred where it did.

This concept integrates five rate-limiting processes along the nutrient pathway from storage to plant uptake. First, mineralization of organic nitrogen, phosphorus, and sulfur is rate-limited by the size and activity of the decomposer community — reflected in this trial by the Microbial Quotient (MQ = MBC / total organic carbon × 100; Sparling, 1992). Second, solubilization of mineral-bound phosphorus and potassium is rate-limited by the density of phosphate-solubilizing and potassium-solubilizing bacterial guilds — not captured by total MBC but implied by community composition and evidenced in this trial by paste extract K and P gains (Mahala et al., 2021). Third, spatial delivery of immobile nutrients from soil particles to root surfaces is rate-limited by fungal hyphal network density and extent — reflected here by the F:B ratio (Wardle et al., 1995). Fourth, aggregate-mediated nutrient release from protected macro- and microaggregate pools is rate-limited by the fungal community's capacity to produce glomalin and maintain aggregate structure — not directly measured in this trial but implicated by the organic matter gains and F:B trajectory observed at LATH and ACRE. Bacteria drive microaggregate formation while fungi, particularly arbuscular mycorrhizal fungi, are the primary architects of macroaggregate stability through hyphal enmeshment and extracellular binding agents (Philippot et al., 2024). Fifth, nutritional receptivity — the degree to which the ionic balance of the soil solution and root uptake environment allows delivered nutrients to actually enter the plant — is rate-limited by cation competition and antagonism at root uptake sites (Marschner, 2012). This fifth constraint operates at the plant physiology layer, downstream of all four biological processes: even a complete biological chain cannot correct an ionic imbalance that blocks uptake at the root surface. It is the only BTC constraint that microbial inoculation cannot directly resolve.

The paste extract and plant tissue data allow the biological transfer capacity framework to be interrogated directly: at which sites did microbial activity measurably improve nutrient availability in the soil solution, and did those improvements reach the plant?

At LATH, the tea community produced detectable improvements in soluble K (+2.0 ppm paste) and Mg (+1.3 ppm paste) post-season, alongside larger exchangeable Ca gains in the Mehlich III data (+945 vs +832 ppm). The Ca signal translated clearly into plant

tissue — tea Ca was 15.3% higher than control (3.02 vs 2.62%), the largest single-nutrient tissue improvement in the trial — consistent with the decomposer community accelerating Ca and Mg release from decomposing straw mulch alongside K-solubilizing bacterial activity. K improved in the paste but not in tissue, likely reflecting rapid crop uptake of a pool being generated and consumed simultaneously. P and Zn showed no tea advantage in tissue despite adequate soil P, consistent with elevated tissue Fe (137–134 ppm; normal 40–100 ppm) blocking uptake at the root through competitive antagonism regardless of any solubilization activity.

At ACRE, the paste record shows the largest microbial solubilization signal in the trial: soluble K reached 16.9 ppm in tea plots versus 8.9 ppm in controls post-season, and soluble Mg reached 18.3 versus 12.9 ppm. Multiple tissue nutrients were directionally higher in tea — Ca (+7.4%), Mg (+9.8%), K (+2.7%), P (+6.9%) — and the most analytically striking improvement was Zn: control tissue Zn was Low (22.6 ppm) while tea tissue Zn was Normal (28.6 ppm, +26.5%), despite Fe remaining elevated in both treatments. This correction is consistent with siderophore-mediated Zn mobilization by the tea community partially overcoming Fe–Zn competitive antagonism at the root. The paste and tissue data confirm that the tea community was biologically effective at ACRE across multiple nutrient pathways — the flat yield reflects demand already met by the resident community, not a failure of the inoculant.

At ARTZA, paste values post-season were lower in tea than control for K (6.5 vs 8.3 ppm), Mg (4.8 vs 6.4 ppm), and P (1.25 vs 1.35 ppm) the control recovered more soluble nutrients than the tea. Tissue Mg was identical in both treatments (0.45%, both below normal), and tissue K was lower in the tea treatment (4.01 vs 4.43%). There is no evidence in either the paste or tissue data that the tea community improved nutrient availability at ARTZA. K exhaustion across the season and the double antagonism of Ca and K suppressing Mg uptake at root exchange sites operated independently of any biological contribution from the inoculant.

At CGHS, the tea community reduced soluble K availability relative to the control: paste K was lower in tea post-season (3.1 vs 5.4 ppm) despite stronger MBC gains in the tea treatment (+293 vs +248 µg C/g). Tissue N was 13.9% lower in tea (2.54 vs 2.95%),

consistent with net N immobilization by the activated microbial community consuming mineral N to build biomass under high C:N substrate conditions rather than releasing it to the plant. The CGHS community was biologically active and successionally advanced — CGHS hub brews showed the most advanced trophic development of either hub — yet that biological activity consumed nutrients rather than delivering them. At CGHS, the BTC chain was intercepted not by a deficiency of biological activity but by a chemistry-layer configuration — severe K deficit, Mg below desired values, Ca base saturation above the 70% ceiling crowding other cations, and high C:N substrate driving immobilization — that redirected microbial metabolism away from net mineralization.

At RESV, tea showed directional paste improvements in K (+1.3 ppm), Mg (+1.7 ppm), and P (+0.40 ppm) post-season, but none translated meaningfully into tissue. The dominant paste signal in the tea treatment was Fe: 9.76 ppm versus 5.41 ppm in the control — a near-doubling driven by pH acidification (7.1→6.2) rather than biological solubilization. Elevated soluble Fe at this level is a constraint rather than a benefit, potentially suppressing Zn and P uptake through competitive antagonism at the root and partially explaining why the paste improvements did not reach tissue.

Across the five sites, the paste-to-tissue evidence follows the same gradient as the MQ ranking. At sites where the biological community was adequately sized relative to substrate — LATH and ACRE — microbial activity produced measurable improvements in both the soil solution and plant tissue. At sites where MQ was suppressed or chemistry-layer constraints intercepted the nutrient pathway — CGHS, RESV, and ARTZA — paste improvements were absent, reversed, or failed to reach the plant. This gradient is the strongest cross-layer evidence in the trial that MQ explains not only single-season yield response but whether microbial activity will translate into nutrient delivery at all.

The central role of biological community composition in mediating soil functions — including nutrient cycling — has been emphasized in the soil modelling literature, where biological actors are argued to be the primary drivers of plant productivity, C storage, and nutrient cycling yet are rarely represented explicitly in agronomic models or field assessments (Vogel et al., 2024). The BTC framework operationalizes this insight at the

farm-trial scale by identifying the specific biological rate-limiting steps that determine whether stored nutrients reach the plant. A soil can have abundant nutrients in storage and still have low biological transfer capacity if the microbial community is suppressed relative to available substrate, metabolically inefficient, compositionally imbalanced, or lacking specific functional guilds — precisely the conditions observed across the four non-responding sites in this trial.

Ranking farms by their pre-season MQ (Sparling, 1992) produces a near-monotonic relationship with yield response magnitude that persists across substantial variation in soil type, crop, and management context. LATH (MQ 1.21%, adequate) was the only site to show a significant yield response. Sites with MQ 0.27–0.50% showed soil chemistry and biological responses without agronomic translation. The MQ threshold separating response from non-response appears to fall between 0.50% and 1.21%, though the five-site design does not provide sufficient resolution to locate it precisely.

The post-season MQ trajectory supports a multi-season interpretation of the non-responses. Rather than representing biological failure, four of five non-responding sites showed MQ development across the season. CGHS tea crossed the apparent response threshold post-season (1.17%), ARTZA tea reached 0.87%, and ACRE tea reached 0.86%. This suggests AACT application may be building the biological foundation for future yield response even where single-season agronomic returns were not observed. The practical implication is that MQ should be applied not only as a pre-application screening criterion but as a seasonal monitoring tool, tracking biological development across successive seasons to identify when a site has crossed into the responsive range.

4.2 The Complete Evidence Chain at LATH

LATH produced a coherent multi-layer evidence chain. Soil biology: tea showed larger ΔMBC (+495 vs +441 µg C/g ctrl) and higher post-season F:B (1.7 vs 1.6). Soil chemistry: both Mehlich III and paste extract showed higher soluble Mg and K in tea plots, alongside dramatic Ca gains (+945 vs +832 ppm exchangeable Ca). Plant tissue: Ca directionally higher in tea (3.02% vs 2.62%). Yield: +35.4%, statistically significant with a very large effect size. The functional mechanism consistent with this pattern is

accelerated decomposition and mineralization of the decomposing straw mulch substrate, alongside solubilization of K and Mg by potassium-solubilizing bacteria known to be enriched in biologically active AACT (Ingham, 2005; Mahala et al., 2021). The higher post-season TEC in the tea treatment (11.3 vs 9.7 M.E.) is consistent with greater humic incorporation driven by accelerated decomposer activity. The shift toward greater fungal dominance (F:B 1.7 vs 1.6) additionally supports hyphal delivery of micronutrients directly to plant roots. In biological transfer capacity terms, LATH is the only site where all five BTC components appear to have been sufficiently active: a decomposer community of adequate size (MQ 1.21%), a growing fungal component capable of nutrient delivery (F:B 0.6→1.7), paste extract gains consistent with solubilizing guild activity, and organic matter decomposition driving humic incorporation into the exchange complex. One forward-looking observation warrants attention: the straw mulch decomposition that drove the yield response also widened the exchangeable Ca:Mg ratio substantially across the season (ctrl 4.21→6.50; tea 4.28→6.30), driven by Ca releases (+832 ppm ctrl, +945 ppm tea) that substantially outpaced Mg gains (+80 and +97 ppm). LATH entered the season as the only site within the optimal Ca:Mg range (3–7:1); it ended the season in the ratio range that characterized the non-responding sites pre-season. If straw mulch decomposition continues at a similar rate in subsequent seasons without targeted Mg correction, this emerging Ca:Mg imbalance may progressively constrain the nutritional receptivity that allowed the year-one yield response to occur. Field microscopy corroborates this interpretation: post-trial tea plots at LATH were described as very full with diverse aggregate sizes and visible fungi — a qualitative advance over the pre-trial state and a clear contrast with the control treatment, with the formation of microaggregates providing additional visual confirmation of the biological response pattern (Table 6; Philippot et al., 2024).

4.3 The CGHS Paradox: Biology Without Yield

CGHS showed the strongest absolute MBC response of any site (+119 µg C/g post-season advantage) yet produced a non-significant negative yield trend (−22.6%). Potassium was severely deficient across both treatments, with paste extract soluble K lower in the tea treatment post-season (3.1 vs 5.4 ppm) detailed in Section 4.1. The

lower tissue N in the tea treatment (2.54% vs 2.95%) is consistent with net N immobilization by the activated community, which can occur when the C:N ratio of decomposing organic substrates exceeds approximately 25:1, drawing down plant-available N rather than releasing it — a threshold well established in soil biochemistry. The specific high-C:N substrate driving this at CGHS was not identified. In biological transfer capacity terms, two distinct mechanisms operated at different points in the BTC chain: K deficiency constraining the solubilizing guild pathway, and probable N immobilization at the mineralization pathway. K correction is the priority intervention at CGHS. Notably, the CGHS hub brews showed the most advanced trophic succession of either hub across the season — reaching ciliate and testate amoeba presence by Application 3 (Table 5) confirming that the inoculant being delivered was biologically active and successionally advanced. The interception of the agronomic response occurred at the chemistry layer, not at the point of inoculant quality.

4.4 The ACRE Dissociation: Chemistry Without Yield

ACRE produced the largest soil chemistry response in the trial — K tea +82 ppm Mehlich III, paste K reaching 16.9 ppm, soluble Mg gains (18.3 vs 12.9 ppm), Zn tissue Low to Normal — with no agronomic return. The soil chemistry response is consistent with active solubilization and mineralization by the tea-inoculated community — the K gains in particular are characteristic of potassium-solubilizing bacterial activity described by Mahala et al. (2021). However, ACRE had already developed sufficient biological transfer capacity to meet crop demand, leaving no yield gap for additional activity to fill. This is consistent with patterns reported in the broader AACT literature: biological amendments produce their strongest responses in soils with genuine biological deficits (Scheuerell & Mahaffee, 2002). In biological transfer capacity terms, ACRE's resident community had already developed the functional guild diversity and decomposer mass needed to supply crop demand; AACT augmented all five BTC pathways but found no nutrient gap that was not already being bridged. Field microscopy at ACRE produced the most qualitatively striking post-trial contrast of any site: tea plots advanced from a sparsely colonized pre-season state to an established community with diverse fungi, testate amoebae, and flagellates, while control plots showed only minor development. This biological response is the strongest qualitative confirmation of the chemistry layer

findings at ACRE and underscores that the tea was biologically effective — the flat yield reflects demand already met, not a failure of biological activity (Table 6).

4.5 Delivered Microbial Load as a Non-Predictor

RESV and ARTZA — the two highest-delivery tomato sites — showed no significant yield response. LATH, with a mid-range delivered load (46,212 µg C per plant), produced the only significant result. The functional processes of decomposition, mineralization, and solubilization depend not on how many organisms are delivered but on whether the receiving soil has the biological architecture — the biological transfer capacity — to support and sustain those processes once the inoculant integrates with the resident community. Delivered MBC adds to the community pool; whether that addition moves the needle on any of the five BTC rate-limiting steps depends entirely on what is already present and what constraints are operating.

4.6 Brew Quality Variability as a Structural Property

All brews exceeded the 15 µg C/ml minimum floor (Prolific Earth Sciences Inc., n.d.) despite substantial variability across the season. Applications 2 and 4 reached the Excellent range (≥59 µg C/ml) while Applications 3 and 5 fell at the Low-to-Excellent transition (34–40 µg C/ml). The close alignment of compost input quality across applications 3–5 strengthens cross-site comparability for those events. Compost source quality appears to be the primary lever for improving tea consistency.

4.7 The Silicon Signal

Silicon increased from pre-season to post-season at all sites in both treatments (gains of 1.6–9.9 ppm Mehlich III), confirming that soil biological activity sufficient to drive silicate weathering — requiring active heterotrophic respiration and organic acid production — is occurring at all sites. Microorganisms weather silicate minerals through proton release, organic acid secretion, and metal-complexing agents, releasing K, Mg, P, Ca, Fe, and Si from mineral lattices (Philippot et al., 2024). Silicate-solubilizing bacteria produce the same organic acids implicated in phosphate and potassium solubilization, confirming that the broader solubilizing functional community is active across all participating sites. Both tea and control plots showed substantial Si gains from pre- to post-season at all five sites, with post-season differences between

treatments small and inconsistent in direction (tea marginally higher at four sites, control marginally higher at ARTZA). This pattern indicates that the solubilizing biological activity responsible for silicate weathering was operating in both treatments and was not uniquely driven by the AACT inoculant, confirming that a baseline solubilizing community was already active across all participating sites.

4.8 RESV pH Acidification: Treatment Effect or Management Confound?

The RESV tea treatment showed pH decline from 7.1 to 6.2 post-season while the control remained stable (6.7→6.8). The associated soluble Fe rise (9.76 vs 5.41 ppm) is consistent with pH-driven Fe mobilization and represents a potential micronutrient toxicity risk if the acidification persists. Whether this reflects a genuine treatment effect or an irrigation confound cannot be resolved from the available data. Microbial activities — including nitrification, organic acid production by bacteria and fungi, and organic sulfur mineralization — are established drivers of soil pH shifts of 1–2.5 units under active community conditions (Philippot et al., 2024), making a microbially driven acidification mechanism plausible alongside the irrigation confound. Field microscopy at RESV showed the least treatment differentiation of any site post-trial — both control and tea plots described as full and bacterial-dominant with good aggregate structure — suggesting that the acidic soil environment suppressed any differential biological response that the inoculant might otherwise have produced (Table 6).

4.9 Nutrient Antagonisms as Contextual Constraints on Crop Uptake

The nutrient antagonism data reveals a failure mode that is conceptually distinct from the biological transfer capacity constraints discussed in Section 4.1. BTC failure operates at the soil biology layer: nutrients do not reach the soil solution in adequate quantity because the microbial community is too small, compositionally wrong, or missing specific functional guilds. Microbial inoculation via AACT can potentially address this. Uptake failure operates at the plant physiology layer: nutrients are present in the soil solution but are blocked at the root surface by competitive antagonism between ions. No level of microbial activity can reconfigure the ionic environment at a root uptake site. A well-structured microbial community with adequate MQ and functional guild diversity remains unable to correct a severe Ca:Mg or K:Mg imbalance,

because the constraint is not biological in origin. The one partial exception is mass-action compensation. A highly active solubilizing community can flood the soil solution with enough of a suppressed nutrient to partially overcome competitive exclusion, as the ACRE Zn correction may illustrate — but this is compensation at the margins of an ionic imbalance, not correction of it. At the ratio extremes observed in this trial (Ca:Mg 7:1 at CGHS; K HIGH alongside Mg LOW at ARTZA), the gap may be too large for biological activity to bridge.

Plant tissue analysis confirmed several antagonism patterns operating independently of the AACT treatment. Antagonistic interactions between nutrients — in which excess of one element suppresses uptake of another through competition at root uptake sites, rhizosphere precipitation, or cation exchange interference — are well-established in plant nutrition science (Marschner, 2012). Their presence in both treatment and control tissues at multiple sites confirms these as pre-existing soil and plant nutrition conditions, not treatment effects.

The most pervasive cross-site pattern is Fe excess. Tissue iron was elevated above the Penn State normal range (40–100 ppm) at all five tomato sites in both treatments, ranging from 110 to 167 ppm. This is a site-level condition unrelated to AACT application. Elevated Fe is a known antagonist of Zn and P uptake through competition at shared root transporter sites and rhizosphere precipitation of iron-phosphate complexes (Marschner, 2012). Consistent with this mechanism, tissue Zn was Low at LATH (19.4 and 18.1 ppm in control and tea treatments respectively; normal 25–71 ppm) in both treatments, and tissue P was Low at LATH (0.26–0.27%; normal 0.30–0.52%) and at the low boundary at ACRE (0.29–0.31%) in both treatments. At LATH — the only site producing a significant yield response — the Fe–Zn and Fe–P antagonisms may have partially capped the magnitude of the response despite favorable biological conditions. The most analytically striking tissue observation in the dataset is the ACRE control-to-tea Zn correction: control tissue Zn was Low (22.6 ppm) while tea treatment tissue Zn was within normal range (28.6 ppm), despite Fe remaining elevated in both treatments (121.5 vs 167.5 ppm). This suggests that the elevated solubilizing activity associated with the tea community — including microbial production of Zn-complexing

siderophores and organic acids that mobilize Zn from mineral forms — was sufficient to partially overcome Fe-Zn competitive suppression, an effect not detectable from yield data alone (Philippot et al., 2024).

Cation competition between Ca, K, and Mg produced site-specific antagonism patterns that compound the soil-chemistry constraints already identified. At ARTZA, tissue K was above normal in the control (4.43%; normal 2.30–4.10%) alongside Low tissue Mg (0.45%; normal 0.55–1.00%), and the Ca:Mg ratio was 4.6–4.9. Both K and Ca compete with Mg for uptake at root cation exchange sites (Marschner, 2012); the simultaneous elevation of K and Ca relative to Mg at ARTZA represents a double antagonism likely explaining the Mg deficiency independently of soil Mg supply. Mg is the central atom of chlorophyll and a required cofactor for ATP synthesis; deficiency at this level constrains photosynthetic efficiency. At CGHS, the Ca:Mg ratio reached 7.0–7.2 in both treatments — the most extreme imbalance in the dataset — adding a cation competition constraint to the K and N limitations already identified at that site. At RESV and ACRE, Ca:Mg ratios of 4.6–6.2 alongside borderline Mg levels indicate moderate cation competition pressure. Post-season exchangeable Ca:Mg data (full Mehlich III cation panel) showed that tea did not consistently widen Ca:Mg ratios relative to controls at any site; post-season differences ranged from −0.27 to +0.33 with no directional pattern. At ACRE specifically, both treatments narrowed the Ca:Mg ratio slightly across the season (ctrl 8.97→8.24; tea 8.49→7.97), with tea Mg increasing (+18 ppm) and Ca essentially stable (+11 ppm). The hypothesis that activated PSB communities disproportionately release Ca from Ca-dominant mineral substrates — worsening existing Ca:Mg imbalances — is mechanistically plausible given the established PSB literature (Marschner, 2012; Philippot et al., 2024) but is not supported by the exchangeable cation data from this trial. A more notable observation is that the pre-season Ca:Mg ratios across all five sites align with the yield response pattern in the same direction as MQ: LATH (4.2:1, within the optimal 3–7:1 range) was the only responding site; RESV (7.3:1) was at the upper boundary; ARTZA (8.4:1), ACRE (8.7:1), and CGHS (13.6:1) were above it. The Ca:Mg imbalance at the non-responding sites represents a persistent soil chemistry constraint that operates independently of biological amendment activity and requires targeted mineral correction — particularly at CGHS

(13.6:1) and ACRE (8.7:1) before biological amendment can be expected to translate consistently into yield. The post-season trajectory across four of five sites (all narrowing toward better balance in both treatments) suggests that the season's biological activity was moving these soils in the right direction, but the starting imbalances are large enough that multi-season correction will be required. LATH is the exception requiring attention: the straw mulch decomposition that drove the yield response also widened the Ca:Mg ratio from 4.2:1 to 6.3–6.5:1, creating an emerging constraint for future seasons if not corrected with Mg amendment.

Two additional site-specific observations are noted. At CGHS, tissue Cu was severely deficient in both treatments (1.9 and 1.6 ppm; normal 5–25 ppm for kale). This is the most extreme micronutrient deficiency in the dataset and was present in both treatments, confirming it as a pre-existing site condition. Kale Fe was within normal range at CGHS (67–71 ppm; kale normal 60–301 ppm), so Fe antagonism is not the explanation; this likely reflects soil Cu availability or binding into unavailable organic complexes. Cu deficiency constrains lignin synthesis, enzyme function, and disease resistance in ways that are difficult to detect from yield data alone. At RESV and ACRE, tissue B was elevated above normal (59–71 ppm; normal 25–45 ppm for tomato) in both treatments. Elevated B can antagonize K uptake and at sustained high levels affects sugar transport physiology; while acute toxicity is unlikely at these concentrations, the B excess represents a nutritional imbalance that warrants monitoring. Collectively, the antagonism burden — particularly Fe excess, Ca:Mg imbalance, and Cu deficiency — represents a second class of pre-application screening criterion alongside the MQ. Sites where severe ionic imbalances are present require mineral correction before biological amendment can be expected to translate into yield, regardless of the quality of the inoculant or the adequacy of the resident biological community. Future trial design should incorporate pre-season cation balance assessment — Ca:Mg ratio, K:Mg ratio, and tissue Fe from the prior season where available — as a parallel screening step to MQ, identifying sites that need chemistry correction before biological intervention.

4.10 Limitations

The primary limitation is the single-plot design: one paired plot per farm, providing one observation per treatment per site. Statistical significance at LATH does not constitute evidence that AACT reliably produces a 35% yield increase in new-field tomato production. The MQ-yield relationship is strongly suggestive but not statistically testable with five data points. Pre-season biological imbalance at LATH and ACRE means yield differences may partly reflect pre-existing heterogeneity. Harvest frequency varied at CGHS and RESV. Tissue analysis represents a mid-season snapshot. Multi-season follow-up would be needed to separate treatment effects from year-specific variation. Additionally, while the trial was designed to assess whether AACT applications would help prevent or minimize disease and pest pressure as a secondary aim, no systematic disease or pest assessment was conducted within the scope of this paper. This represents a meaningful gap relative to the original project aims and is identified as a priority for future trial cycles. Volumetric application rate expressed as a land-area equivalent (gallons per acre) was not standardized across sites: plot sizes ranged from approximately 198 to 450 square feet while the liquid volume applied per event remained the same, resulting in variable effective rates across farms. This represents a confound that future trials should resolve by standardizing application rate on a per-area or per-plant basis consistently across all sites. The proximity of control and tea plots within the same bed row creates a potential drift or migration effect — airborne droplets during foliar application and lateral movement of soil microbes between adjacent plots could reduce the biological contrast between treatments. Corrugated plastic barriers were used during spray applications in this trial to minimize cross-contamination, but complete spatial separation of treatments would be preferable in future designs. Pre-trial seedling health was not formally verified at all sites before plot establishment — as documented in Section 3.9, pre-trial seedling disease at LATH affected two crop comparisons and introduced an uncontrolled chemical input for the cucumber comparison specifically. Future trials should include a seedling health assessment at transplanting as an eligibility criterion for plot inclusion, and any unplanned chemical applications within a trial plot should be recorded and reported as a covariate. Time of day of application was not systematically recorded across all sites and seasons, which

precludes analysis of whether application timing relative to temperature and evaporation conditions influenced delivered biological viability.

5. Conclusions

This trial examined the effect of AACT applications on crop yield across five farms. A statistically significant yield increase was observed at one of five farms: LATH Big Beef tomato produced a 35.4% yield advantage ($t(3) = -8.37$, $p = .004$, $d = 4.18$), supported by a coherent multi-layer evidence chain consistent with accelerated decomposition, mineralization, and solubilization by the tea-associated microbial community.

The most consistent finding was the relationship between pre-season MQ (Sparling, 1992) and yield response. LATH (MQ 1.21%, adequate) was the only site to show a significant yield response. Sites with MQ 0.27–0.50% showed soil chemistry and biological responses without agronomic translation. Three practical conclusions follow: AACT is most likely to produce single-season yield returns in soils with genuine biological deficits; delivered microbial load is not a reliable predictor of agronomic response; and single-season yield is an insensitive and incomplete measure of the treatment's effect on soil biological development.

Two site-specific findings warrant direct management attention. At CGHS, severe potassium deficiency and probable N immobilization intercepted the chain of evidence before it could reach the plant; K correction is a prerequisite for AACT efficacy at that site. At RESV, pH acidification in the tea treatment (7.1→6.2 post-season) warrants monitoring, as it was associated with elevated soluble iron. Multi-season, multi-plot follow-up trials are needed to validate the MQ as a predictive tool for AACT response and to characterize the threshold above which single-season yield responses become reliably detectable.

5.1 Recommendations for Future Trials

The following recommendations are drawn directly from the trial findings.

1. Pre-screen sites with the Microbial Quotient before application. The MQ threshold between responding and non-responding sites appears to fall between 0.50% and 1.21%. Future trials should stratify sites by MQ class to test the threshold directly.

2. Replicate within sites. A minimum of three replicate plots per site, spatially separated, is needed to enable within-site statistical power and distinguish treatment effects from pre-existing heterogeneity.

3. Correct acute nutrient deficiencies before measuring AACT response. Pre-season soil chemistry screening and correction of acute macronutrient deficiencies should precede AACT application at any trial site.

4. Include multi-season follow-up at non-responding sites. Sites in the Suppressed MQ range should be followed for a minimum of three consecutive seasons to determine whether a yield response emerges as biological transfer capacity rebuilds.

5. Add functional guild measurements alongside total MBC. At minimum, phosphate-solubilizing and potassium-solubilizing bacteria counts, and ideally nitrogen mineralization rate assays, should be added to test whether soil chemistry changes can be attributed to specific functional guilds.

6. Standardize brew quality with a minimum input threshold. A minimum compost input quality threshold (MBC and F:B) should be established before each brew and batches falling below it replaced.

7. Control and record irrigation equally between treatments. Equal measured irrigation delivery to control and tea sub-plots and recording of irrigation events as a covariate would resolve the RESV confound.

8. Add a mid-season soil biology time point. A mid-season time point after the third application would detect whether MBC and F:B respond to treatment and whether those changes precede changes in paste extract chemistry.

9. Measure nitrogen mineralization rate directly. An incubation-based net N mineralization assay would determine whether the activated microbial community is mineralizing or immobilizing N under site-specific substrate conditions.

10. Consider the MQ as a pre-treatment screening criterion for extension programs. If the MQ-yield relationship holds across a larger trial, MQ could serve as a

binary screening criterion recommending AACT application only to sites above a validated threshold.

11. Include farmer data collection stipends in future trial proposals. Systematic yield recording is a burden on farm operators during an active growing season. Inconsistent harvest event recording — observed at CGHS and RESV in this trial — reduced the precision of yield comparisons and is identified as a limiting factor in the current dataset. Future grant proposals and trial agreements should include explicit financial stipends to incentivize consistent and complete data collection by participating farmers, following the participatory research framework described by Pérez Orozco et al. (2023).

12. Align application timing to crop growth stages in future trials. Fixed-interval application schedules, as used in this trial, do not account for variation in crop nutrient demand and biological receptivity across the growing season. Future protocols should consider growth-stage-based application events: (i) root zone inoculation at transplanting to establish beneficial microbes before planting; (ii) one to two applications during early vegetative growth to support seedling establishment and root system development; (iii) applications at flowering and early fruiting to enhance nutrient uptake and support fruit quality during peak demand. This approach is likely to produce more differentiated biological and yield responses than calendar-interval applications and should be tested alongside or in place of fixed-interval scheduling.

13. Operationalize biological transfer capacity measurement in future trials. The five BTC components identified in this paper can each be measured with established methods. (i) Decomposer community size relative to substrate (MQ, Microbial Quotient): Microbiometer MBC and OM%, already applied here. (ii) Metabolic efficiency (qCO_2 = basal respiration / MBC): Solvita CO_2 burst combined with MBC; lower qCO_2 indicates a more efficient, less stressed community. (iii) Functional guild density: phosphate-solubilizing and potassium-solubilizing bacterial plate counts, and AMF colonization rate via root staining. (iv) Aggregate stability: slake test or wet-sieving (Herrick et al., 2001) combined with glomalin-related soil protein assay. (v) Nutritional receptivity: pre-season cation balance panel including Ca:Mg ratio, K:Mg ratio, and soil or prior-season tissue

Fe. Combining these five measurement layers with the paired block design already used in this trial would allow direct attribution of yield responses to specific BTC constraints, moving from correlational observation toward mechanistic explanation — the kind of explicit biological process representation that Vogel et al. (2024) identify as a priority for soil science modelling.

Appendix A. Cross-Layer Evidence Linkage Summary

The cross-layer evidence linkage table is provided as a separate file: evidence_linkage_table.png. It presents one row per farm with a complete four-layer dataset (soil biology, soil chemistry, plant tissue, yield), with directional indicators (↑ tea outperforms ctrl; ↓ ctrl outperforms tea; → no meaningful difference) and a Chain Evidence classification for each site. The MQ (Sparling, 1992) is shown for each farm alongside the chain classification: Complete (LATH), Disrupted (RESV), Partial (ACRE), Incomplete (ARTZA), or Broken (CGHS). A planned secondary eggplant trial at ARTZA was terminated by flea beetle damage causing complete plant loss after transplanting and is excluded from all analyses; the ARTZA tomato trial reported here was unaffected.

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Tables

Tables are numbered in the order they are first cited in the text. Landscape tables are presented on landscape pages for readability.

Table 1. Participating Farm Characteristics.

Code	Full Name	Location	Primary Crop (sampled)	Soil Type	Management Notes	Hub	Pre-season MQ (%)	MQ Class	Pre-season Ca:Mg	Chain of Evidence
LATH	Lathrop Farm	Lebanon, CT	Tomato / Big Beef	Fine sandy loam	New field; no prior compost application; black plastic + straw mulch	LATH	1.21	Adequate	4.2:1	Complete
ACRE	Sweet Acre Farm	Lebanon, CT	Tomato / Big Beef	Fine sandy loam (greenhouse)	Greenhouse production; history of compost application	LATH	0.30	Suppressed	8.7:1	Partial
ARTZA	Artza Mendi Farm	Baltic, CT	Tomato / Big Beef	Fine sandy loam	Newly established plot; woodchip base mulch	LATH	0.45	Low	8.4:1	Incomplete
CGHS	Common Ground High School	New Haven, CT	Kale / Curly	Gravelly sandy loam	History of compost application	CGHS	0.50	Low	13.6:1	Broken
RESV	Reservoir Community Farm	Bridgeport, CT	Tomato / Hungarian	Raised beds	Organic management; limited irrigation	CGHS	0.27	Suppressed	7.3:1	Disrupted

Table 2. Plot Structure and Treatment Delivery by Site

Site	Crop	Variety	Hub	Tea plants	Ctrl plants	Tea ml/plant	Ctrl ml/plant	Gal/acre†	µg C/plant (avg)‡	Notes
LATH	**Tomato**	Big Beef	LATH	16	16	946	946	1,162	46,212	New field; black plastic + straw mulch
LATH	**Cucumber**	Marketmore	LATH	48	48	315	315	1,162	15,388	Balanced
RESV	**Tomato**	Hungarian	CGHS	20	20	757	757	2,723	32,521	Raised beds; limited irrigation
RESV	**Tomato**	Muskovitch; Celebration	CGHS	10	10	1,514	1,514	5,445	65,061	5 plants/variety/treatment
RESV	**Kale**	Curly; Lozanato; Russian	CGHS	74	78	606–632	561–606	5,445	~26,400	Control 4 plants higher across 3 varieties
ACRE	**Tomato**	Big Beef	LATH	27	28	561	541	1,760	27,405	Greenhouse; history of compost application
ACRE	**Tomato**	Marglobe	LATH	21	22	720	688	1,760	35,172	Greenhouse; history of compost application
ARTZA	**Tomato**	Big Beef	LATH	12	12	1,262	1,262	1,613	61,649	New woodchip mulch plot
CGHS	**Kale**	Lozanato	CGHS	35	35	433	433	3,319	18,602	History of compost application
CGHS	**Kale**	Russian	CGHS	33	34	459	446	3,319	19,719	Control 1 plant higher

† Gal/acre from plot area and 4-gallon application. ‡ µg C/plant applies to treatment only.

Table 3. Brew Quality Record by Hub and Application Event

Identification				Compost input (Microbiometer dry soil)					Finished tea (Microbiometer liquid)				
Hub	Sites served	App	Date	MBC (µg C/g)	Eval	F:B	%F	%B	MBC (µg C/ml)	Eval	DO (mg/L)	Brew Temp °F	pH
LATH	**LATH/ACRE/ARTZA**	1	09-Jun-25	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
LATH	**LATH/ACRE/ARTZA**	2	30-Jun-25	1653.9	Excellent	3.8	79.2	20.8	65.1	Excellent	7	78.2	7.5
LATH	**LATH/ACRE/ARTZA**	3	21-Jul-25	1047.3	Below Avg.	2.1	68	32	34.4	Below Avg.	7.3	73.9	7.4
LATH	**LATH/ACRE/ARTZA**	4	11-Aug-25	1272.9	Above Avg.	2.8	73.6	26.4	61.9	Excellent	6.4	79.5	7.4
LATH	**LATH/ACRE/ARTZA**	5	01-Sep-25	1125	Below Avg.	2.2	69	31	34	Below Avg.	7.3	66.5	7.5
CGHS	**CGHS/RESV**	1	02-Jun-25	ND	ND	ND	ND	ND	40.1	Avg.	ND	ND	ND
CGHS	**CGHS/RESV**	2	23-Jun-25	1267.5	Above Avg.	2.8	73.7	26.3	40.3	Avg.	6.3	67.6	7
CGHS	**CGHS/RESV**	3	14-Jul-25	1036	Below Avg.	2.1	67.7	32.3	38.1	Avg.	6.8	84	6.9
CGHS	**CGHS/RESV**	4	04-Aug-25	1331	Above Avg.	2.8	73.5	26.5	59.4	Excellent	6.4	81.8	7.5
CGHS	**CGHS/RESV**	5	25-Aug-25	1118	Below Avg.	2.2	69.2	30.8	36.9	Avg.	7.2	68.7	7.6
LATH hub avg (apps 2–5)			**1274.8**		**2.73**	**72.5**	**27.6**	**48.85**					
CGHS hub avg (apps 1–5)			**1188.1**		**2.48**	**70.5**	**29.5**	**42.96**					

MBC = microbial biomass carbon. F:B = fungal:bacterial ratio. ND = not determined. All measured brews exceeded the 15 µg C/ml minimum floor (Prolific Earth Sciences Inc., n.d.).

Table 4. Trial Application Schedule by Hub.

Application	LATH Hub Date	CGHS Hub Date	Sites (LATH hub)	Sites (CGHS hub)	Approx. interval (days)
1	09-Jun-25	02-Jun-25	LATH, ACRE, ARTZA	CGHS, RESV	—
2	30-Jun-25	23-Jun-25	LATH, ACRE, ARTZA	CGHS, RESV	21 (LATH); 21 (CGHS)
3	21-Jul-25	14-Jul-25	LATH, ACRE, ARTZA	CGHS, RESV	21 (LATH); 21 (CGHS)
4	11-Aug-25	04-Aug-25	LATH, ACRE, ARTZA	CGHS, RESV	21 (LATH); 21 (CGHS)
5	01-Sep-25	25-Aug-25	LATH, ACRE, ARTZA	CGHS, RESV	21 (LATH); 21 (CGHS)

Table 5. Compost tea brew quality: qualitative microscopy observations by hub and application event.

Hub	Application	Qualitative Observations
LATH	1	Sparse; some aggregates; bacterial dominant
LATH	2	Full; good aggregate structure; some fungi; diverse bacteria
LATH	3	Aggregates; bacteria; minor fungi; some flagellates
LATH	4	Stable aggregates; no large predators; bacterial dominant
LATH	5	Abundant aggregates; one nematode; full
CGHS	1	Abundant organic matter; good aggregate structure; no large predators; bacterial dominant
CGHS	2	Fuller than Application 1; well-established aggregates; flagellates; bacterial dominant
CGHS	3	Good aggregate structure; nematode; abundant flagellates; one ciliate; testate amoeba; fungi present
CGHS	4	Full; diverse microbes; flagellates; testate amoeba; some fungi
CGHS	5	Abundant organic matter; aggregates; bacterial dominant; flagellate activity

Table 6. Soil microscopy: qualitative observations by site and treatment, pre- and post-trial.

Site	Treatment	Pre-Trial	Post-Trial
LATH	Control	Dense; small aggregates; abundant bacteria; healthy	Small aggregates; bacterial dominant; full; few flagellates
LATH	Tea	(No difference from control pre-trial)	Very full; diverse aggregate sizes; some fungi; abundant movement
ACRE	Control	Bacterial dominant; some aggregates; healthy but somewhat barren	Small aggregates; bacterial dominant; one flagellate; space between bacteria
ACRE	Tea	(No difference from control pre-trial)	Established aggregates; diverse fungi; testate amoebae; flagellates; full
CGHS	Control	Bacterial dominant; tiny aggregates; somewhat barren	Sparse; some aggregate structure; no predators; sandy
CGHS	Tea	(No difference from control pre-trial)	Abundant aggregates; full; some fungi; flagellates; one nematode
ARTZA	Control	Minimal aggregates; bacterial dominant; no predators; healthy	Good aggregate structure; bacterial dominant; space between bacteria; no predators
ARTZA	Tea	(No difference from control pre-trial)	Full; good aggregate structure; bacterial dominant; nematode; flagellate
RESV	Control	Minimal structure; bacterial dominant; some sand	Some aggregates; bacterial dominant; full; similar to tea treatment
RESV	Tea	(No difference from control pre-trial)	Good aggregate structure; bacterial dominant; full; sandy

Table 7. Selected Mehlich III Soil Chemistry Parameters — Key Agronomic Indicators by Site, Treatment, and Season

Site	Crop / Variety	pH				OM (%)				TEC (M.E.)				K (ppm)				NO_3 (ppm)				Si (ppm)			
		Pre Ctrl	Pre Tea	Post Ctrl	Post Tea	Pre Ctrl	Pre Tea	Post Ctrl	Post Tea	Pre Ctrl	Pre Tea	Post Ctrl	Post Tea	Pre Ctrl	Pre Tea	Post Ctrl	Post Tea	Pre Ctrl	Pre Tea	Post Ctrl	Post Tea	Pre Ctrl	Pre Tea	Post Ctrl	Post Tea
RESV	Tomato / Hungarian	6.7	7.1	**6.8**	**6.2**	14.5	15.8	**14.1**	**16.1**	10.9	8.3	**9.2**	**10.7**	71	56	**41**	**37**	23.1	3.3	**6.6**	**4.2**	6.7	7	**9.2**	**9.9**
CGHS	Kale / Curly	6.7	6.7	**6.7**	**6.6**	8.2	8.6	**8.5**	**8.9**	12.4	12	**11**	**11.3**	146	85	**58**	**39**	23.8	18.3	**5.4**	**8.3**	5.2	5.3	**9.7**	**10.6**
LATH	Tomato / Big Beef	6.4	6.6	**6.9**	**7**	6.4	6.6	**12.4**	**13**	4.9	5.8	**9.7**	**11.3**	59	72	**82**	**109**	5.1	21.9	**16.5**	**24.9**	7.9	8.5	**17.5**	**18.4**
ACRE	Tomato / Big Beef	6.9	7.1	**6.4**	**6.8**	13.9	12.4	**17**	**17.3**	15.8	13.6	**15.3**	**14.6**	143	67	**111**	**149**	9.7	14.9	**27.6**	**37.9**	17.4	19.3	**22.4**	**23.5**
ARTZA†	Tomato / Big Beef	6.4	6.7	**6.6**	**6.5**	11.7	9.8	**13.5**	**13**	7.9	7	**7.4**	**7.5**	157	200	**74**	**54**	290.3	8.4	**4.1**	**2.6**	5.1	5.7	**8.4**	**7.3**

Pre = May (pre-season); Post = September (post-season). K cells shaded red = below 100 ppm (deficient threshold). Post-season values bold. Yellow row = ARTZA. † ARTZA ctrl pre NO_3 = 290.3 ppm (chicken manure artifact). LATH and ACRE rows have pre-season treatment imbalance — see Table 5 notes. Mehlich III extraction throughout; pH by water extract.

Table 8. Soil Paste Extract — Key Soluble Nutrient Parameters by Site, Treatment, and Season

Site	Crop / Variety	pH (opt 6–7)				HCO_3 (ppm, <50)				Sol. P (ppm, 1–3)				Sol. K (ppm, 15–20)				Sol. Mg (ppm, 8–12)				Sol. Fe (ppm, 0.5–3)			
		Pre Ctrl	Pre Tea	Post Ctrl	Post Tea	Pre Ctrl	Pre Tea	Post Ctrl	Post Tea	Pre Ctrl	Pre Tea	Post Ctrl	Post Tea	Pre Ctrl	Pre Tea	Post Ctrl	Post Tea	Pre Ctrl	Pre Tea	Post Ctrl	Post Tea	Pre Ctrl	Pre Tea	Post Ctrl	Post Tea
RESV	Tomato / Hungarian	6.7	7.1	**6.8**	**6.2**	38	26	**35**	**49**	0.18	0.18	**0.42**	**0.82**	2.3	1.9	**2.3**	**3.6**	4.3	2.8	**4.7**	**6.4**	5.28	5.67	**5.41**	**9.76**
CGHS	Kale / Curly	6.7	6.7	**6.7**	**6.6**	35	31	**52**	**51**	0.72	0.76	**1.07**	**0.94**	7.9	10.7	**5.4**	**3.1**	2.8	3.1	**5.2**	**5.4**	1.43	1.57	**3.71**	**3.28**
LATH	Tomato / Big Beef	6.4	6.6	**6.9**	**7**	27	23	**46**	**60**	0.07	0.1	**0.5**	**0.56**	1.6	3	**6.7**	**8.7**	2.2	4.9	**6.8**	**8.1**	1.14	1.87	**3.85**	**3.89**
ACRE	Tomato / Big Beef	6.9	7.1	**6.4**	**6.8**	38	41	**62**	**52**	0.22	0.26	**0.54**	**0.57**	8.1	7.1	**8.9**	**16.9**	6	7	**12.9**	**18.3**	1.23	2.26	**1.84**	**1.65**
ARTZA	Tomato / Big Beef	6.4	6.7	**6.6**	**6.5**	27	32	**50**	**51**	0.48	0.69	**1.35**	**1.25**	6	6.1	**8.3**	**6.5**	1.6	1.6	**6.4**	**4.8**	3	6.41	**7.19**	**5.1**

Pre = May; Post = September. Red cells = outside desired range shown in column header. Post-season values bold. Desired ranges from Logan Labs reference values. Saturated paste extract method throughout. Samples from designated crop plot per site.

Table 9. Plant Tissue Nutrient Analysis by Site and Treatment — Penn State Agricultural Analytical Services Laboratory

Site	Crop / Variety	Treatment	N (%)	P (%)	K (%)	Ca (%)	Mg (%)	S (%)	Mn (ppm)	Fe (ppm)	Cu (ppm)	B (ppm)	Zn (ppm)
Penn State Ref. Range	Tomato		3.75–4.25	0.3–0.52	2.3–4.1	1–4.75	0.55–1	0.3–1.21	30–100	40–100	10–20	25–45	25–71
	Kale		3.1–5.51	0.3–0.7	2–4.01	1.3–2.51	0.25–0.7	0.3–0.76	30–250	60–301	5–25	30–101	30–250
RESV	Tomato / Hungarian	Control	2.98	0.36	3.52	2.52	0.55	0.9	30.5	152.2	21.1	59.8	34.9
RESV	Tomato / Hungarian	Tea	2.92	0.4	3.51	2.63	0.54	0.92	30.2	150.7	20.1	55.2	35.1
CGHS	Kale / Curly	Control	2.95	0.48	3.43	2.1	0.3	0.5	40.1	67.3	1.9	34.9	29.7
CGHS	Kale / Curly	Tea	2.54	0.45	3.41	2.23	0.31	0.38	40.6	70.6	1.6	34.6	29.3
LATH	Tomato / Big Beef	Control	3.51	0.27	2.69	2.62	1	0.46	83.4	137.3	10.5	33.7	19.4
LATH	Tomato / Big Beef	Tea	3.39	0.26	2.43	3.02	1.02	0.51	73.4	134.7	10.5	32.8	18.1
ACRE	Tomato / Big Beef	Control	3.39	0.29	2.55	3.8	0.61	1.26	77.3	121.5	12.3	70.9	22.6
ACRE	Tomato / Big Beef	Tea	3.42	0.31	2.62	4.08	0.67	1.26	80.8	167.5	12.6	66.9	28.6
ARTZA	Tomato / Big Beef	Control	3.86	0.52	4.43	2.09	0.45	0.41	52.6	110.1	13.5	46.3	28.2
ARTZA	Tomato / Big Beef	Tea	4.16	0.53	4.01	2.19	0.45	0.48	66.5	124.5	15.8	48.1	29.6

Blue = below normal range (Low). Amber = above normal range (High). Yellow = boundary artifact: value within ≤0.02 units of reference range boundary; interpret as measurement uncertainty. Green rows = tea treatment; white = control treatment. Penn State Agricultural Analytical Services Laboratory normal ranges (Penn State, 2024). Tissue sampled ~1 week after 3rd application; 15-plant composites per treatment. % values = g/100g; ppm = mg/kg dry weight.

Table 10. Yield Comparison (lbs/sqft) Between Control and Tea Treatments — Paired Samples t-test

Farm	Hub	Crop	Variety	Ctrl mean (lbs/sqft)	Tea mean (lbs/sqft)	Diff	% change	t	df	p	Cohen's d	Sig.	Harvest events
LATH	LATH	Tomato	Big Beef	14.7	19.9	5.2	+35.4%	-8.37	3	0.004	4.18	*	8 (consistent)
LATH	LATH	Cucumber	Marketmore	29.4	31.7	2.3	+7.8%	-0.47	3	0.669	0.24	ns	4 (consistent)
RESV	CGHS	Tomato	Hungarian	17.7	19.8	2.1	+11.9%	-0.39	3	0.72	0.2	ns	5–7 (variable)
RESV	CGHS	Tomato	Celebration	16.6	11.6	-5	-30.1%	—	—	—	—	desc	—
RESV	CGHS	Tomato	Muskovitch	8.8	9.3	0.5	+5.7%	—	—	—	—	desc	—
RESV	CGHS	Kale	Curly	5.7	7.7	2	+35.1%	—	—	—	—	desc	—
RESV	CGHS	Kale	Lozanato	5.9	3.4	-2.5	-42.4%	—	—	—	—	desc	—
RESV	CGHS	Kale	Russian	6.7	5.6	-1.1	-16.4%	—	—	—	—	desc	—
ACRE	LATH	Tomato	Big Beef	88.9	86.6	-2.3	-2.6%	0.38	3	0.73	0.19	ns	20–21 (consistent)
ACRE	LATH	Tomato	Marglobe	47.5	48.8	1.3	+2.7%	-0.29	3	0.79	0.14	ns	21–22 (consistent)
ARTZA	LATH	Tomato	Big Beef	29.5	26.9	-2.6	-8.8%	0.38	3	0.73	0.19	ns	15 (consistent)
CGHS	CGHS	Kale	Curly	42.3	32.7	-9.6	-22.7%	1.51	3	0.229	0.75	ns	4–9 (variable)
CGHS	CGHS	Kale	Lozanato	28.7	43.6	14.9	+51.9%	—	—	—	—	desc	—
CGHS	CGHS	Kale	Russian	26.6	44.1	17.5	+65.8%	—	—	—	—	desc	—

** p < 0.05. ns = not significant. desc = insufficient blocks for statistical test. Paired t-test, df = 3. % change: green > +5%, red < −5%.*

Table 11. Harvest Events per Block by Site, Crop, Variety, and Treatment

Farm	Hub	Crop	Variety	Treatment	Block 1	Block 2	Block 3	Block 4	Range	Notes
LATH	**LATH**	Tomato	Big Beef	Control	8	8	8	8	8	
LATH	**LATH**	Tomato	Big Beef	Tea	8	8	8	8	8	
LATH	**LATH**	Cucumber	Marketmore	Control	4	4	4	4	4	
LATH	**LATH**	Cucumber	Marketmore	Tea	4	4	4	4	4	
RESV	**CGHS**	Tomato	Hungarian	Control	5	5	6	5	5–6	Variable harvest frequency within treatment†
RESV	**CGHS**	Tomato	Hungarian	Tea	6	7	7	6	6–7	Variable harvest frequency within treatment†
RESV	**CGHS**	Tomato	Celebration	Control	6	—	—	—	6	1 block only; descriptive
RESV	**CGHS**	Tomato	Celebration	Tea	6	—	—	—	6	
RESV	**CGHS**	Tomato	Muskovitch	Control	6	—	—	—	6	1 block only; descriptive
RESV	**CGHS**	Tomato	Muskovitch	Tea	7	—	—	—	7	
RESV	**CGHS**	Kale	Curly	Control	2	1	—	—	1–2	Variable†
RESV	**CGHS**	Kale	Curly	Tea	4	1	—	—	1–4	Variable†
RESV	**CGHS**	Kale	Lozanato	Control	4	3	—	—	3–4	Variable†
RESV	**CGHS**	Kale	Lozanato	Tea	4	1	—	—	1–4	Variable†
RESV	**CGHS**	Kale	Russian	Control	1	3	—	—	1–3	Variable†
RESV	**CGHS**	Kale	Russian	Tea	2	2	—	—	2	
ACRE	**LATH**	Tomato	Big Beef	Control	20	20	21	21	20–21	Variable†
ACRE	**LATH**	Tomato	Big Beef	Tea	20	21	21	20	20–21	
ACRE	**LATH**	Tomato	Marglobe	Control	21	22	22	22	21–22	Variable†
ACRE	**LATH**	Tomato	Marglobe	Tea	21	22	22	22	21–22	
ARTZA	**LATH**	Tomato	Big Beef	Control	15	15	15	15	15	
ARTZA	**LATH**	Tomato	Big Beef	Tea	15	15	15	15	15	
CGHS	**CGHS**	Kale	Curly	Control	9	7	6	8	6–9	Variable†
CGHS	**CGHS**	Kale	Curly	Tea	9	7	5	4	4–9	Variable†
CGHS	**CGHS**	Kale	Lozanato	Control	4	4	—	—	4	2 blocks; descriptive
CGHS	**CGHS**	Kale	Lozanato	Tea	2	6	—	—	2–6	Variable†
CGHS	**CGHS**	Kale	Russian	Control	4	4	—	—	4	2 blocks; descriptive
CGHS	**CGHS**	Kale	Russian	Tea	8	5	—	—	5–8	Variable†

† Variable harvest frequency within plot. Harvest events reflect crop readiness and field logistics, not experimental design. Yield is cumulative seasonal total across all harvest events per block. Blank/— = blocks not established or not harvested. Comparisons with fewer than 4 blocks per treatment are reported as descriptive means only in Table 10.

Table 12. Pre- and Post-Season Soil MBC, F:B Ratio, and Microbial Quotient (MQ) by Site, Crop, and Treatment

Site	Crop / Variety (sampled plot)	Pre-season ctrl		Pre-season tea		Post-season ctrl		Post-season tea		ΔMBC (post−pre)		Post diff (tea−ctrl)		Pre-season MQ (%)		Post-season MQ (%)		Notes
		MBC (µg C/g)	F:B	MBC (µg C/g)	F:B	MBC (µg C/g)	F:B	MBC (µg C/g)	F:B	Ctrl	Tea	MBC	F:B	Ctrl	Tea	Ctrl	Tea	
RESV	Tomato / Hungarian	229	0.4	299	0.6	**511**	**0.7**	**493**	**0.9**	+282	+194	**-18**	**+0.2**	0.27%	0.33%	**0.63%**	**0.53%**	
CGHS	Kale / Curly	238	0.4	312	0.6	**486**	**0.9**	**605**	**1.1**	+248	+293	**+119**	**+0.2**	0.50%	0.63%	**0.99%**	**1.17%**	
ARTZA	Tomato / Big Beef	305	0.6	300	0.6	**595**	**1.2**	**654**	**1.3**	+290	+354	**+59**	**+0.1**	0.45%	0.53%	**0.76%**	**0.87%**	
ACRE	Tomato / Big Beef	242	0.5	185	0.2	**786**	**1.6**	**865**	**1.5**	+544	+680	**+79**	**-0.1**	0.30%	0.26%	**0.80%**	**0.86%**	† Pre-season imbalance; ΔMBC primary metric
LATH	Tomato / Big Beef	450	0.9	312	0.6	**891**	**1.6**	**807**	**1.7**	+441	+495	**-84**	**+0.1**	1.21%	0.81%	**1.24%**	**1.07%**	† Pre-season imbalance; ΔMBC primary metric

MBC in µg C/g. MBC and F:B are co-outputs of a single Microbiometer extraction and are not independent. MQ = MBC / (OM% / 1.724 × 10,000) × 100 (Sparling, 1992). MQ colour: green ≥1.0% (Adequate); yellow 0.5–0.99% (Low); red-orange <0.5% (Suppressed). † Pre-season treatment imbalance at LATH and ACRE; ΔMBC is the primary comparative metric.

Appendix A. Cross-Layer Evidence Linkage by Site. Arrows indicate direction of tea vs. control difference (↑ tea > ctrl; ↓ ctrl > tea; → no meaningful difference). Chain classifications: Complete = all four layers consistent; Partial = biology + chemistry without yield; Incomplete = biology without chemistry or yield; Disrupted = chemistry layer interrupted; Broken = biology active but all downstream layers intercepted.

Site	MQ (%)	MQ Class	Biology (ΔMBC tea vs ctrl)	F:B (post-season)	Chemistry: Key Signal	Tissue: Key Signal	Yield	Chain
LATH	1.21	Adequate	↑ +495 vs +441 µg C/g	↑ 1.7 vs 1.6 (tea)	↑ K +37 ppm tea; OM +6% both; Ca +945 tea vs +832 ctrl ppm	↑ Ca 3.02% tea vs 2.62% ctrl	+35.4%* (p=.004, d=4.18)	Complete
ACRE	0.30	Suppressed	↑ +680 vs +544 µg C/g	→ 1.5 vs 1.6 (ctrl slightly higher)	↑ K +82 ppm tea; Sol K 16.9 ppm tea; Ca/Mg gains	↑ Zn Low→Normal in tea (22.6→28.6 ppm)	-2.6% ns	Partial
ARTZA	0.45	Low	↑ +354 vs +290 µg C/g	↑ 1.3 vs 1.2 (tea)	K deficient both; no post-season K gain in tea	No significant treatment differences	-8.8% ns	Incomplete
CGHS	0.50	Low	↑ +293 vs +248 µg C/g	↑ 1.1 vs 0.9 (tea)	K deficient; Sol K lower in tea post (3.1 vs 5.4 ppm); N immobilisation	↓ N 2.54% tea vs 2.95% ctrl	-22.6% ns	Broken
RESV	0.27	Suppressed	→ +194 vs +282 µg C/g (ctrl higher)	↑ 0.9 vs 0.7 (tea)	↓ pH 7.1→6.2 tea; ↑ Fe 9.76 ppm tea	No significant treatment differences	+11.9% ns	Disrupted