# Evaluation of Treatment Response to Organisan Impact SIX Applied to Commercial Corn Across Early Vegetative Growth Stages

**January 2026**

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# 1. STUDY OVERVIEW

This trial evaluated the effects of Organisan-Impact SIX, a biostimulant treatment, on corn rhizosphere microbiome composition, soil nutrient cycling, and plant nutrient uptake at the Reese Farm in Finley, OH during the 2025 growing season. Organisan-Impact SIX was applied in-furrow at the time of plantingat a rate of 6 ounces per acre, via foliar application using a ground rig at V3 at a rate of 8 ounces/acre, and again at VT at 8 ounces/acre. Rhizosphere samples were collected from across the field at three vegetative growth stages: V2 (early vegetative), V5 (mid-vegetative), and V8 (late vegetative). Each growth stage included triplicate samples from the treated (Organisan-Impact SIX) strip and control (Check 13) strip, for a total of 18 sample sets.  Tissue sample was not replicated at the V2 growth stage, as the size of the plants limited the amount of plant material that could be harvested for testing.

Sampling involved collecting root samples, root-adjacent soil samples, and plant tissue samples (full plants at V2 stage or top collar leaves for V5 and V8 stages). Root samples were analyzed using shotgun metagenomic sequencing to characterize the rhizosphere microbial community and evaluate functional potential. Haney soil chemistry was performed on root-adjacent soil samples for nutrient availability assessment, and plant tissue was collected for nutrient analysis to quantify uptake. The integration of this data characterizes the complete Soil to Microbiome to Plant nutrient pathway and assesses the product's ability to enhance both soil nutrient availability and microbial functionality.

Statistical analyses employed Welch's t-tests for treatment comparisons at each growth stage, with significance thresholds of $p < 0.05$ for statistically significant effects and $p < 0.10$ for marginally significant trends. The sample size of $n = 3$ replicates per treatment per stage provides adequate statistical power to detect strong effects, though V2 tissue data was limited to $n = 1$ per treatment and is presented descriptively. Correlation analyses across paired treatment effects identified cross-domain relationships linking soil chemistry, functional pathways, community structure, and plant tissue composition.

## 2. SOIL FERTILITY EFFECTS

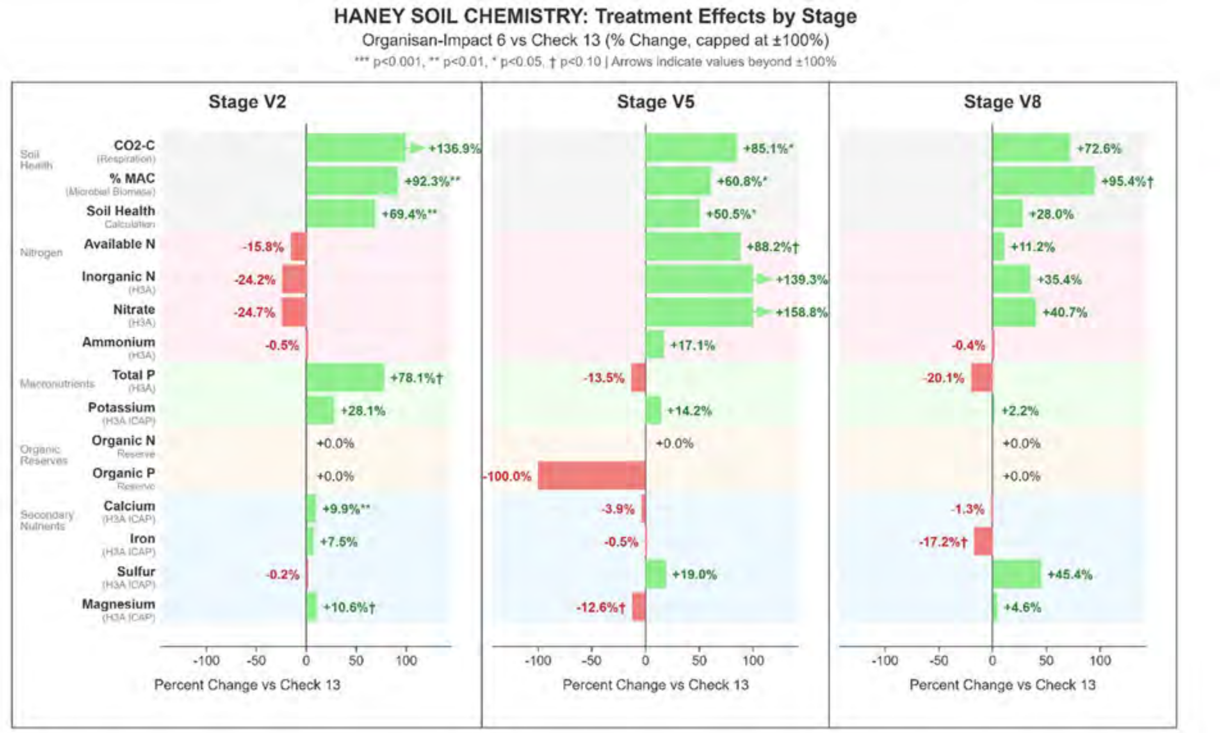

Figure 1. Soil Fertility Chemistry - Treatment Effects by Stage

Soil fertility analysis revealed consistent soil carbon enhancements as well as stage-dependent nutrient responses following biostimulant application. Across all stages, treated plots exhibited elevated CO2-C respiration, indicating sustained stimulation of microbial metabolic activity in the root-adjacent soil.

At V2, treated plots showed a statistically significant increase in soil calcium availability (H3A ICAP Calcium +9.9%, p = 0.043), indicating enhanced secondary nutrient availabily during early crop establishment. Treated samples showed enhanced available phosphorus (+78.1%) and available potassium (+28.1%), though neither reached statistical significance. Soil iron increased modestly (+7.5%) while sulfur remained essentially unchanged (-0.2%).

By V5, soil nutrients showed variable responses. Available nitrogen increased substantially (+88.2%), though this change did not reach statistical significance (p = 0.173). Available phosphorus declined modestly (-11.0%) while potassium maintained a positive trend (+14.2%). Sulfur availability increased (+19.0%) and organic matter showed notable accumulation (+34.4%). The elevated CO2-C respiration (+85.1%) at V5 indicates sustained microbial metabolic activity and carbon processing.

At V8, available nitrogen remained elevated (+11.2%) relative to controls, while phosphorus showed a decline (-20.0%). Sulfur availability increased substantially (+45.4%) and organic matter remained elevated (+27.0%). CO2-C respiration continued to exceed control levels (+72.6%), though the magnitude of increase moderated from earlier stages. Soil iron declined at V8 (-17.2%), potentially reflecting active mobilization to plant tissue.

**Table 2.1: Soil Available Nutrient Changes by Growth Stage**

| Soil Variable | **V2 Change** | **V5 Change** | **V8 Change** | **Pattern** |
|---|---|---|---|---|
| Available N | -15.8% | +88.2% | +11.2% | Variable |
| Available P | +78.1% | -11.0% | -20.0% | Early gain |
| Available K | +28.1% | +14.2% | +2.2% | Stable positive |
| H3A Calcium | +9.9%* | -3.9% | -1.3% | Early enhancement |
| CO2-C | +136.9% | +85.1% | +72.6% | Sustained activity |
| Organic Matter | +17.6% | +34.4% | +27.0% | Accumulation |

Note: * $p < 0.05$. Values represent percent change (Treated - Control) / Control.

# 3. MICROBIAL FUNCTIONS

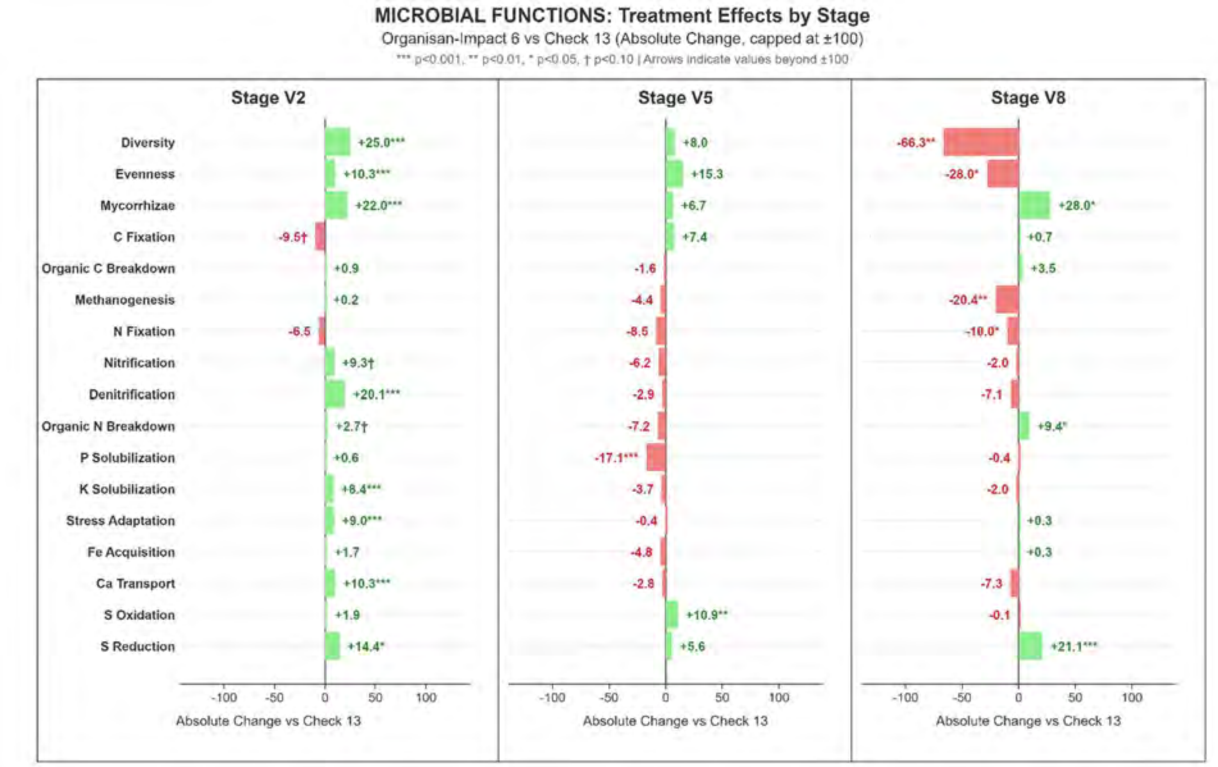

*Figure 2. Microbial Functional Pathways - Treatment Effects by Stage*

Metagenomic functional profiling revealed substantial early-season pathway activation with treatment. At V2, calcium transport potential increased significantly (+10.3 percentile points, p = 0.003), representing enhanced capacity for calcium mobilization in the rhizosphere. Potassium solubilization potential also increased significantly (+8.4 percentile points, p = 0.028), indicating improved capacity for converting mineral-bound potassium to plant-available forms.

A significant increase in denitrification pathway potential was observed at V2 (+20.1 percentile points, p = 0.005), reflecting enhanced microbial functional capacity that is conditionally relevant and dependent on soil moisture, aeration, and nitrate availability rather than indicative of realized nitrogen loss. Plant stress adaptation pathway potential was also significantly elevated (+9.0 percentile points, p = 0.007), suggesting enhanced microbial capacity to support plant resilience during early establishment. Sulfur reduction potential showed marginal elevation (+14.4 percentile points, p = 0.077).

Community structure metrics improved substantially at V2. Diversity increased significantly (+25.0 percentile points, p = 0.021) and evenness showed highly significant enhancement (+10.3 percentile points, p = 0.004). Mycorrhizae abundance increased significantly (+22.0 percentile points, p = 0.007), and the fungal to bacterial ratio shifted significantly toward fungal dominance (+16.0%, p = 0.001). These changes indicate treatment-induced restructuring toward a more diverse, balanced microbial community.

By V5, most pathway potentials moderated to near-control levels, indicating establishment of homeostatic nutrient cycling potential. Phosphorus solubilization potential declined significantly (-17.1 percentile points, p = 0.032), suggesting adequate phosphorus availability reducing microbial investment in mobilization pathways. Sulfur oxidation potential showed marginal elevation (+10.9 percentile points, p = 0.054). Community metrics remained positive but non-significant.

At V8, sulfur reduction potential remained significantly elevated (+21.1 percentile points, p = 0.002), indicating sustained treatment effects on sulfur cycling through late vegetative development. Organic nitrogen breakdown potential showed marginal elevation (+09.4 percentile points, p = 0.100). Community diversity showed a large decline (-66.3 percentile points, p = 0.083) compared to controls, contrasting with V2 increases and suggesting continued community restructuring throughout the growing season.

**Table 3.1: Microbial Functional Pathway Changes by Growth Stage**

| Pathway/Metric | V2 Change | V2 p | V5 Change | V8 Change | V8 p |
|---|---|---|---|---|---|
| Calcium Transport | +0.103 | 0.003** | -0.028 | -0.073 | ns |
| K Solubilization | +0.084 | 0.028* | -0.037 | -0.020 | ns |
| Denitrification | +0.201 | 0.005** | -0.029 | -0.071 | ns |
| Plant Stress Adapt. | +0.090 | 0.007** | -0.004 | +0.003 | ns |
| Sulfur Reduction | +0.144 | 0.077 | +0.056 | +0.211 | 0.002** |
| Diversity | +0.250 | 0.021* | +0.080 | -0.663 | 0.083 |
| Evenness | +0.103 | 0.004** | +0.153 | -0.280 | ns |
| Mycorrhizae Abund. | +0.220 | 0.007** | +0.067 | +0.280 | ns |

Note: ** $p < 0.01$, * $p < 0.05$. Values represent absolute difference in pathway scores.

# 4. PLANT TISSUE EFFECTS

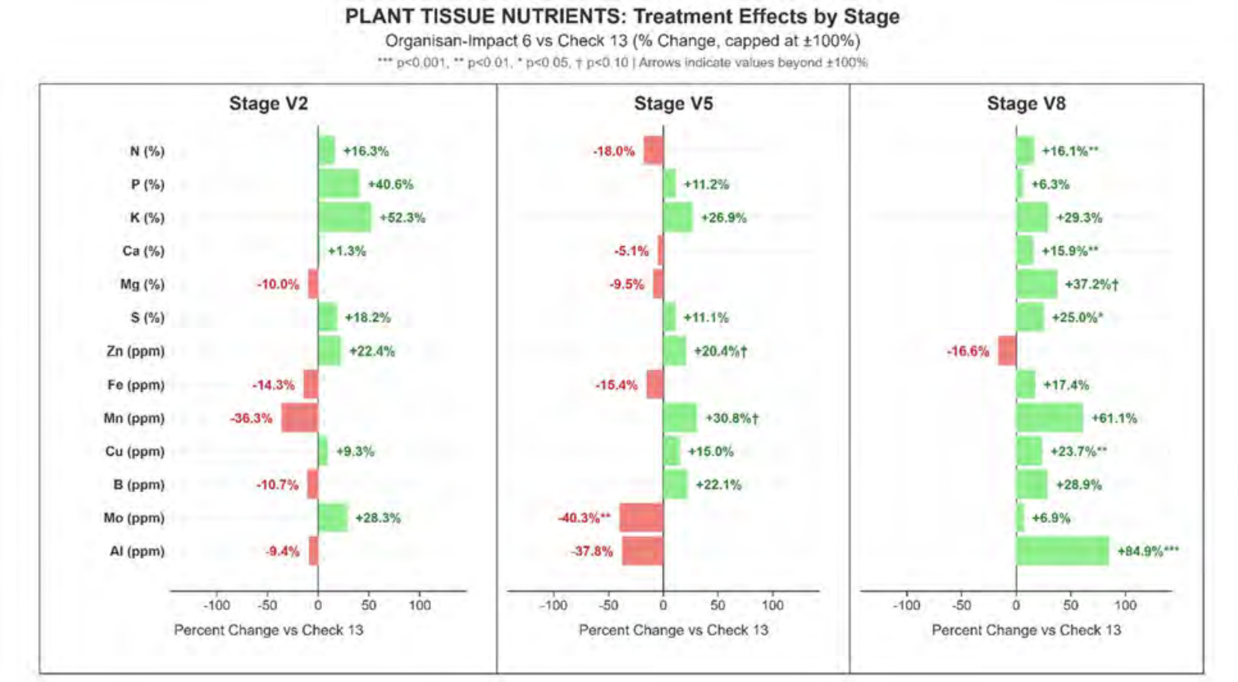

*Figure 3. Plant Tissue Nutrient Effects - Treatment Response*

Plant tissue nutrient analysis revealed stage-dependent responses with the clearest treatment benefit observed at V8. Tissue data at V2 was limited to a single replicate per treatment, precluding statistical analysis, so these values are reported descriptively. At V2, tissue phosphorus showed substantial elevation above control (+40.6%) and potassium was notably higher (+52.3%) in treated plants. Treatment resulted in positive effects on tissue nitrogen (+16.3%), as well as Sulfur, Zinc, Copper, and Molybdenum.

At V5, tissue nutrient responses were modest and non-significant . Potassium was elevated in treated plants (+26.9%) as well as phosphorus (+11.2%), while nitrogen declined slightly (-18.0%). Sulfur and calcium responses were variable, with sulfur slightly elevated (+11.1%) and calcium slightly reduced (-5.1%). Iron showed modest decline (-15.4%).

The most notable tissue findings occurred at V8, where treated plants showed elevated tissue nutrients across all nutrients measured, other than zinc. Calcium in treated tissues was elevated significantly (+15.9%, p = 0.044). This corresponds with early-stage enhancements in both soil calcium availability (+9.9% at V2) and calcium transport pathway activity (+0.103 at V2). Tissue nitrogen showed marginally significant elevation at V8 (+16.1%, p = 0.068), and sulfur was marginally higher (+25.0%, $p = 0.076$) in treated plants. Phosphorus (+6.3%) and Potassium (+29.3%) maintained elevated levels at V8, though not statistically significant.

The V8 calcium benefit represents a coherent Soil to Microbiome to Plant pathway response: early enhancement of soil calcium availability and microbial calcium transport potential translated to improved calcium delivery to plant tissue by late vegetative stage. This pattern suggests treatment effects accumulated progressively, with early microbial priming supporting later nutritional benefits.

Early season (V2) enhancement of soil Phosphorus and Potassium in response to treatment also led to sustained elevation of plant tissue P and K through V8, although the magnitude of the improvement generally decreased over time.  These effects, however, do not correspond with increases in microbial cycling potential for P and K, indicating that the treatment is yielding these responses through primarily chemical rather than biological means.

**Table 4.1: Plant Tissue Nutrient Changes by Growth Stage**

| Tissue Nutrient | **V2 Change** | **V5 Change** | **V8 Change** |
|---|---|---|---|
| Nitrogen, % N | +16.3% | -18.0% | +16.1% |
| Phosphorus, % P | +40.6% | +11.2% | +6.3% |
| Potassium, % K | +52.3% | +26.9% | +29.3% |
| Calcium, % Ca | +1.3% | -5.1% | +15.9%* |
| Sulfur, % S | +18.2% | +11.1% | +25.0% |
| Iron, ppm Fe | -14.3% | -15.4% | +17.4% |

Note: * $p < 0.05$. V2 tissue data limited ($n = 1$ per treatment).

# 5. CARBON CYCLING AND SOIL HEALTH

Carbon cycling analysis revealed pronounced treatment effects and soil health indicators across all growth stages, but with minimal changes to microbial carbon cycling potential:

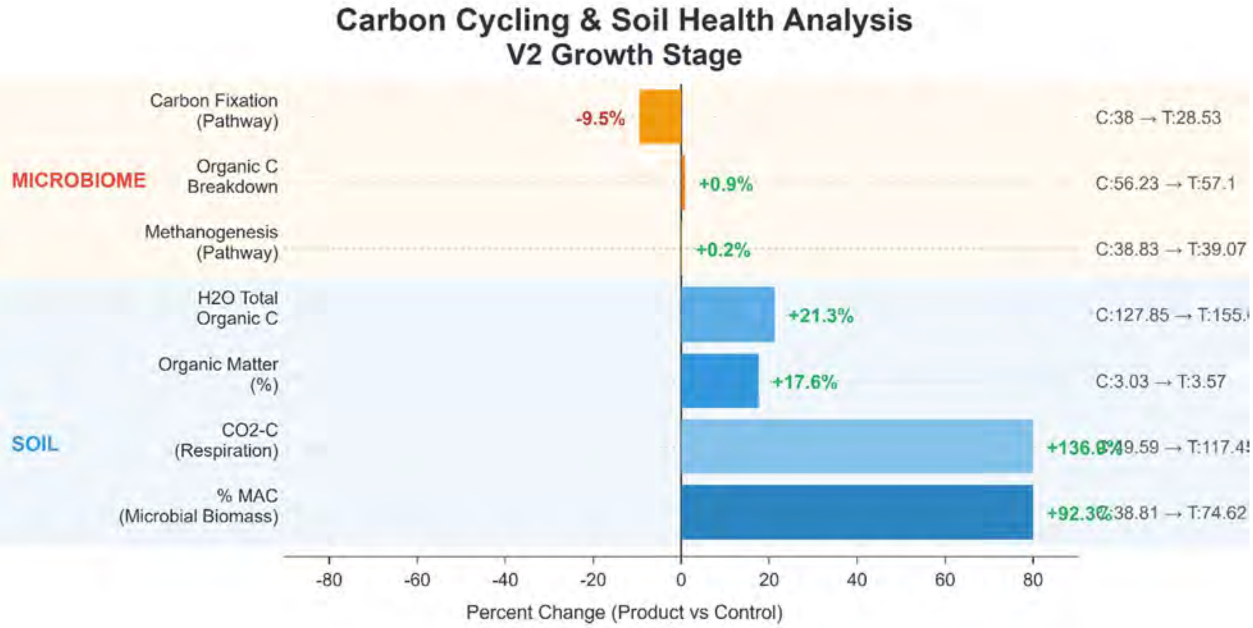

*Figure 4. Carbon Cycling and Soil Health Metrics at V2 Growth Stage*

At V2, CO2-C respiration increased substantially (+136.9%), indicating elevated microbial metabolic activity during early rhizosphere colonization. Organic matter increased (+17.6%) alongside improvements in the Soil Health Calculation and Water Extractable Organic Carbon, suggesting the treatment contributes directly to enhanced soil carbon pools and carbon sequestration, with only minimal effect on microbial carbon cycling potential at V2.

The relationship between microbial activity and carbon processing was further evidenced by integrated analysis correlations (Section 15, below). Percent Microbially Active Carbon (% MAC) correlated positively with mycorrhizae abundance (r = +0.775, p = 0.0142), indicating that improved carbon quality supported enhancement of beneficial fungal populations in treated areas.

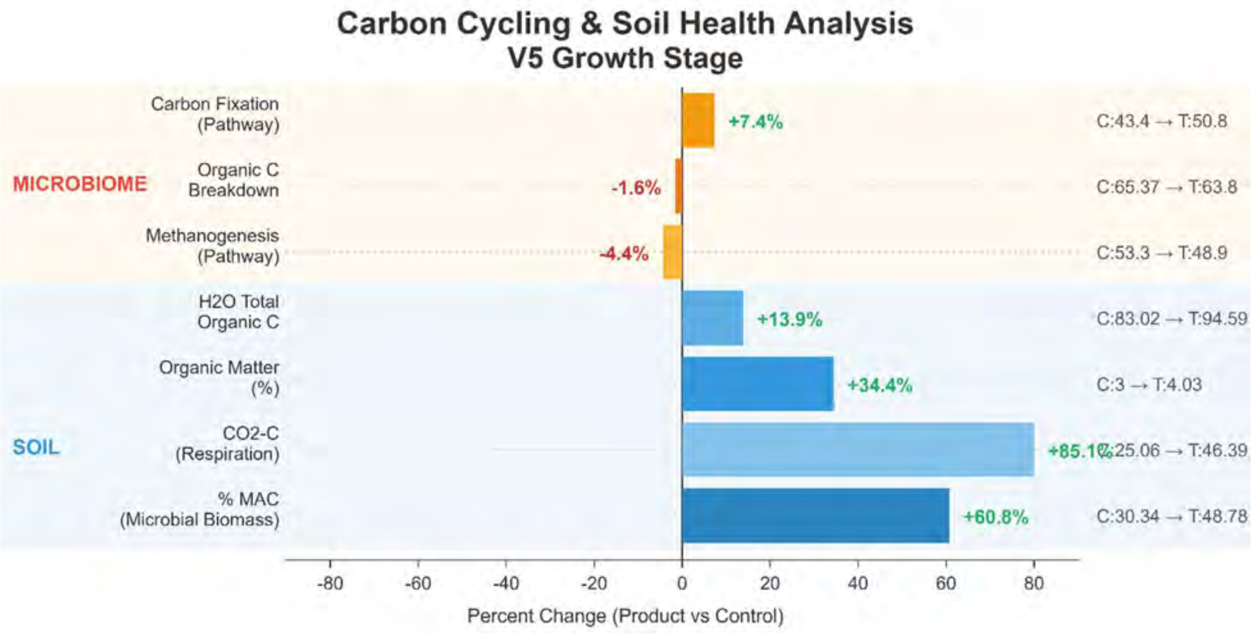

*Figure 5. Carbon Cycling and Soil Health Metrics at V5 Growth Stage*

At V5, soil carbon remained elevated in treated soils, including higher CO2-C respiration (+85.1%) and continued accumulation of organic matter (+34.4%), as well as H20 Total Organic C (+13.9%) and %MAC (+60.8%). The sustained respiration activity suggests ongoing microbial processing of organic inputs rather than rapid mineralization. Labile carbon pools (H2O Total Organic C) correlated positively with taxonomic richness ($r = +0.807$, $p = 0.0085$ (refer to Integrated Analysis Section 15), indicating that treatment-enhanced organic carbon availability supported greater microbial diversity.

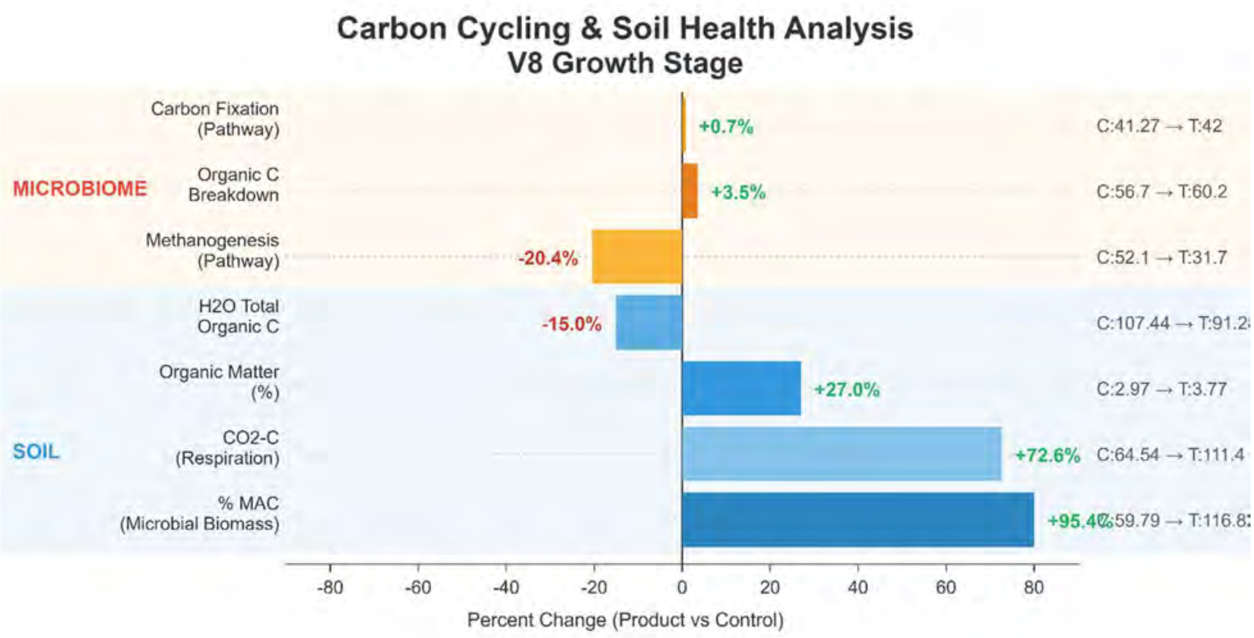

*Figure 6. Carbon Cycling and Soil Health Metrics at V8 Growth Stage*

At V8, CO2-C respiration remained above control levels (+72.6%) and organic matter accumulation persisted (+27.0%). The progressive decline in respiration enhancement magnitude from V2 to V8 (136.9% to 72.6%) suggests initial microbial activation followed by establishment of more stable cycling patterns later in the growing season. The Soil Health Calculation showed strong correlation with potassium availability ($r = +0.905$, $p = 0.0008$), indicating integration between carbon cycling and nutrient availability.

# 6. NITROGEN CYCLING

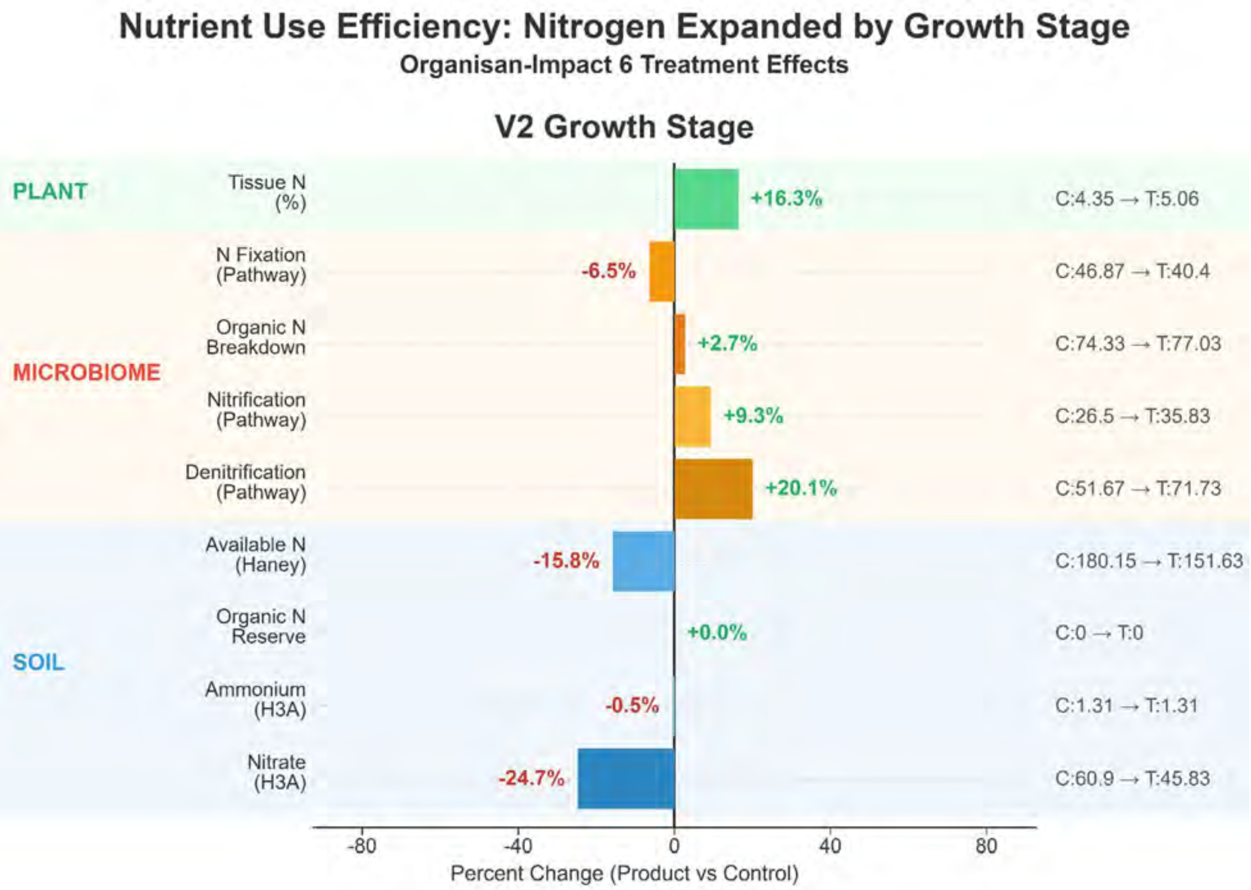

*Figure 7. Nitrogen Cycling Dynamics at V2 Stage*

Nitrogen cycling at V2 showed complex pathway activation. Available soil nitrogen was reduced (-15.8%) while tissue nitrogen increased (+16.3%, based on single-replicate data). Nitrification pathway potential showed non-significant elevation (+0.093), and  denitrification pathway potential showed a statistically significant increase (+0.201, $p = 0.005$). Correlation analysis revealed a strong inverse relationship between soil ammonium and nitrification activity ($r = -0.913$, $p = 0.0006$), reflecting the direct mechanistic link between nitrifying microbial activity and ammonium consumption.   These changes represent a trend of effective mobilization of Nitrogen, as depletion of soil inorganic nitrogen pools translates into improved plant tissue nitrogen in treated areas, facilitated by enhancing nitrogen cycling potential in the rhizosphere.

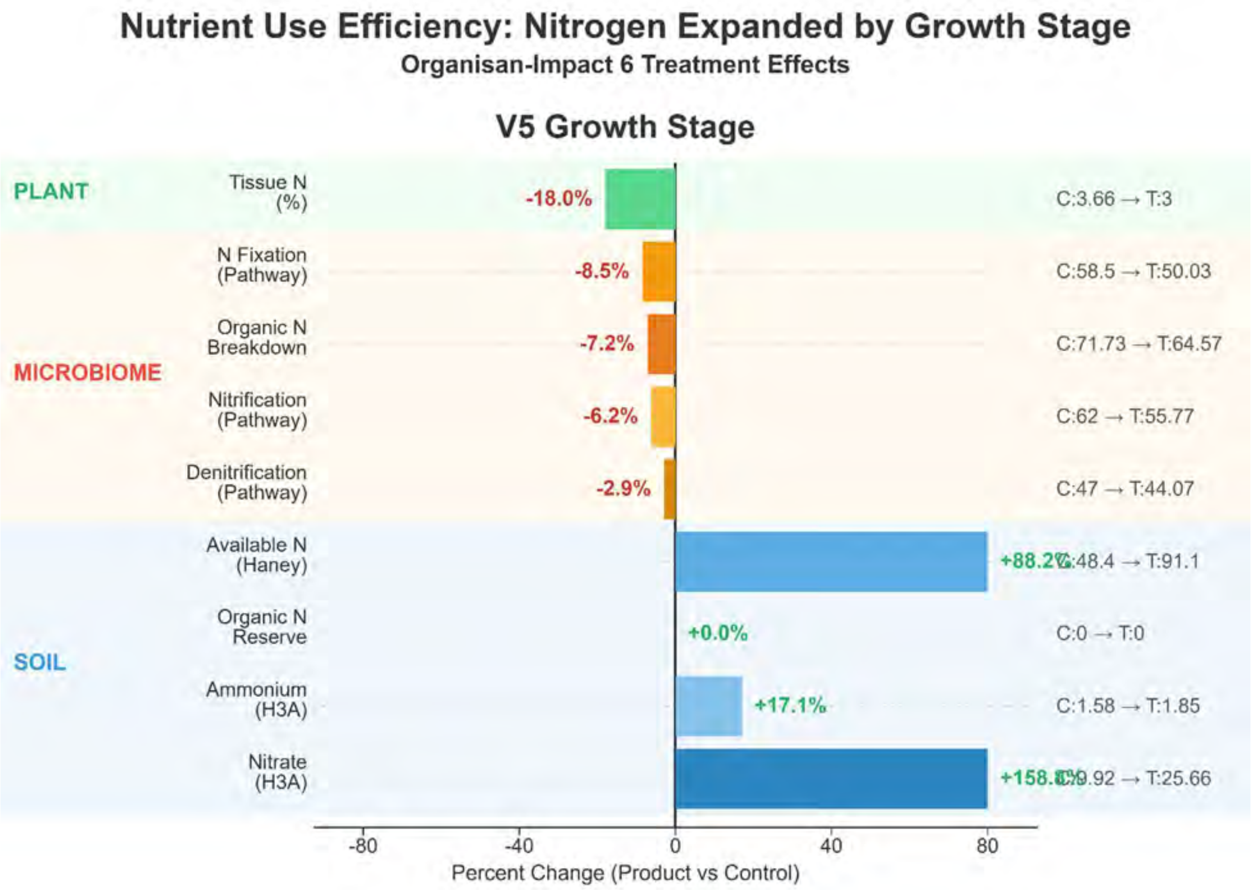

*Figure 8. Nitrogen Cycling Dynamics at V5 Stage*

By V5, nitrogen cycling demonstrated stability with some beneficial trends. Available nitrogen increased substantially (+88.2%), though this change did not reach statistical significance. Nitrogen fixation potential showed modest decline (-8.5 percentile points), while nitrification potential was slightly reduced (-6.2 percentile points). Tissue nitrogen declined moderately (-18.0%), although both sets of samples remained at sufficiency levels. The elevated nitrogen cycling potential observed at V2 did not persist through V5, but was replaced by increased in soil nitrogen pools in treated areas.

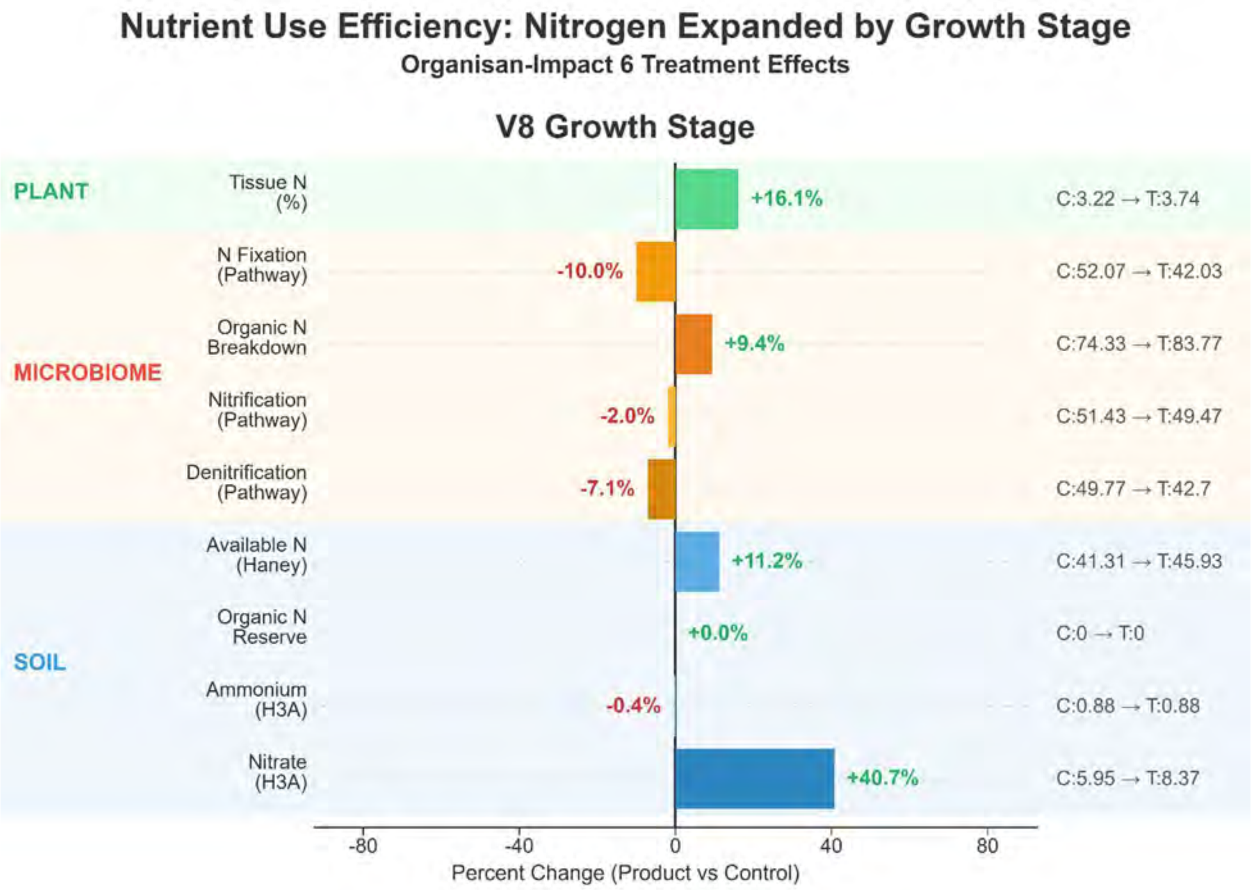

*Figure 9. Nitrogen Cycling Dynamics at V8 Stage*

At V8, treatment enhanced nitrogen cycling patterns in a manner that supported plant nutrition. Available nitrogen remained elevated (+11.2%) relative to controls, primarily due to increased nitrate. Organic nitrogen breakdown potential showed marginal enhancement (+9.4 percentile points, $p = 0.100$), supporting nutrient mineralization during active growth. Tissue nitrogen increased marginally (+16.1%, $p = 0.068$), suggesting improved nitrogen uptake or retention during late vegetative development, likely facilitated at least in part by the increased soil carbon pools observed at V5.

## General Nitrogen Summary

Nitrogen cycling demonstrated variable responses across stages, but resulting in increased tissue nitrogen in treated samples at the V2 and V8 stages, and significantly increased soil nitrogen at V5. These changes illustrate a trend of effective early mobilization following application, stabilization and buildup of soil N pools at V5, and efficient mobilization of Nitrogen into plant tissues at V8. The strong inverse correlation between organic matter and nitrification potential (r = -

0.913, p = 0.0006) indicates that treatment-induced organic matter accumulation coincided with modulated nitrification potential which supports nitrogen retention.

# 7. PHOSPHORUS CYCLING

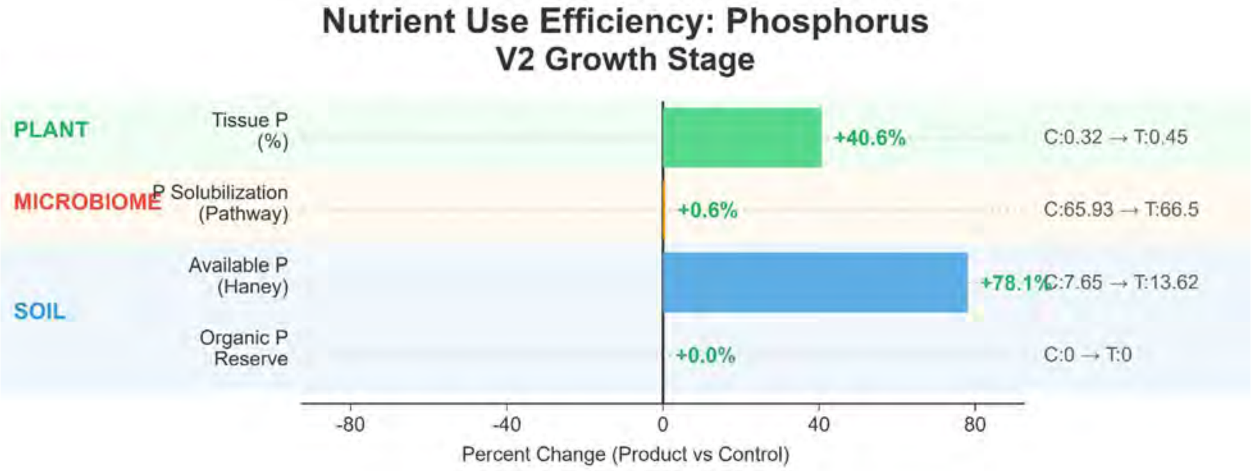

*Figure 10. Phosphorus Cycling Dynamics at V2 Stage*

Phosphorus cycling at V2 indicated favorable early-season dynamics. Available soil phosphorus was substantially elevated in treated soils (+78.1%), though high variability prevented statistical significance. Phosphorus solubilization pathway potential remained near control levels (+0.006), and tissue phosphorus showed notable elevation (+40.6%) based on single-replicate observation.

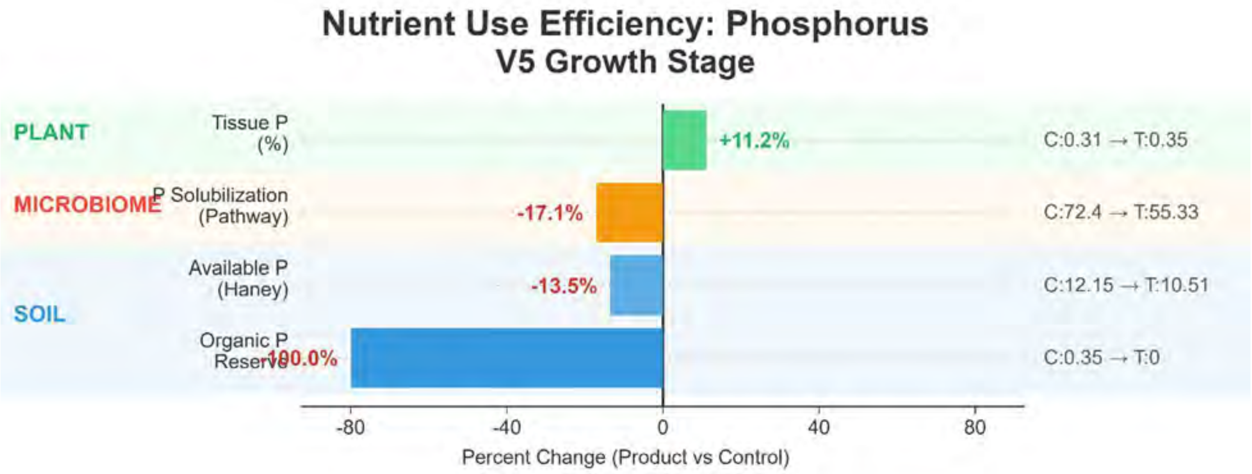

*Figure 11. Phosphorus Cycling Dynamics at V5 Stage*

By V5, phosphorus cycling shifted notably. Soil available phosphorus declined slightly (-11.0%) while phosphorus solubilization pathway potential decreased significantly (-0.171, p = 0.032). This reduction in microbial P-solubilization activity may reflect adequate phosphorus availability, reducing microbial investment in mobilization pathways. Tissue phosphorus maintained modest gains (+11.2%).

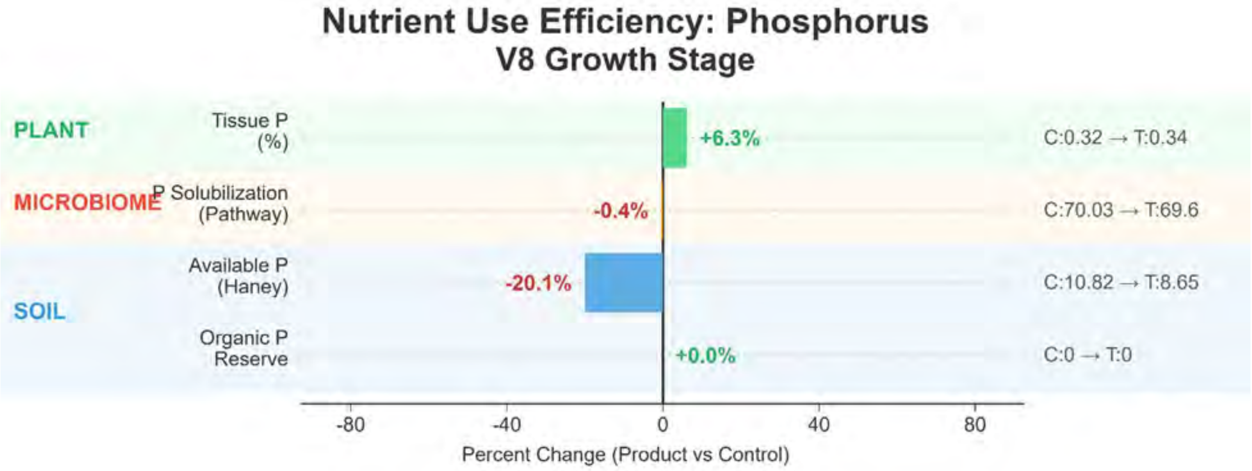

*Figure 12. Phosphorus Cycling Dynamics at V8 Stage*

At V8, available soil phosphorus further declined (-20.0%) while pathway potential remained stable (-0.4 percentile points). Tissue phosphorus maintained slight elevation (+6.3%). The declining soil pools alongside stable tissue concentrations suggest active phosphorus uptake from soil reserves established during earlier stages.

### General Phosphorus Summary

Phosphorus cycling demonstrated early-season pool enhancement followed by progressive drawdown, consistent with active plant uptake. The significant decline in P-solubilization potential at V5 likely reflects homeostatic regulation rather than functional impairment. Correlation analysis revealed a positive relationship between organic phosphorus pools and potassium solubilization potential (r = +0.698, p = 0.0365, Section 15), suggesting shared microbial drivers for organic acid production that simultaneously mobilize phosphorus and potassium. Additionally, the correlation between organic carbon breakdown and phosphorus dynamics suggests that carbon decomposition processes contribute to phosphorus availability through release of organically-bound phosphorus.

## 8. POTASSIUM CYCLING

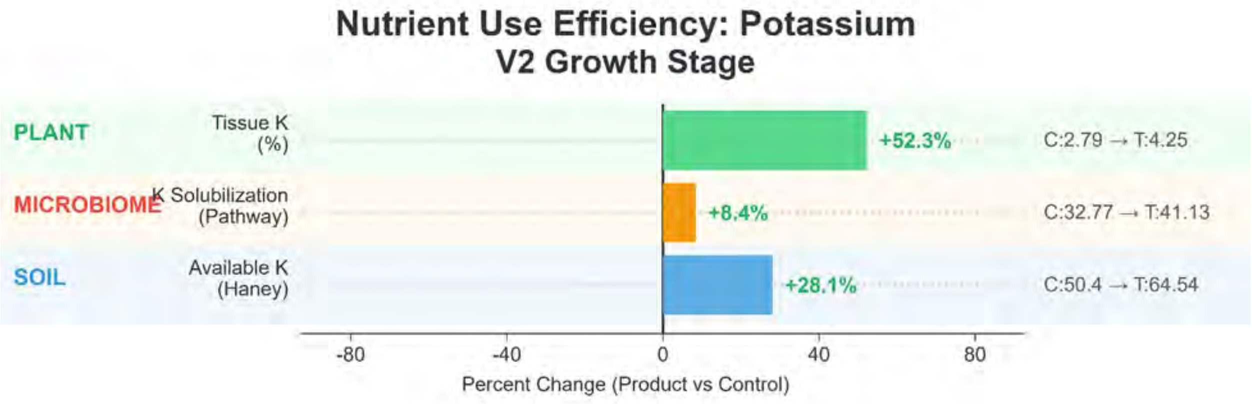

*Figure 13. Potassium Cycling Dynamics at V2 Stage*

Potassium cycling and uptake at V2 exhibited significant early-season enhancement in response to treatment. Potassium solubilization pathway potential increased significantly (+8.4 percentile points, p = 0.028), indicating improved microbial capacity for converting mineral-bound potassium to plant-available forms. Soil available potassium increased (+28.1%), and tissue potassium showed substantial elevation (+52.3%) based on single-replicate data. These patterns suggest effective coupling between microbial mobilization and plant uptake during early establishment.

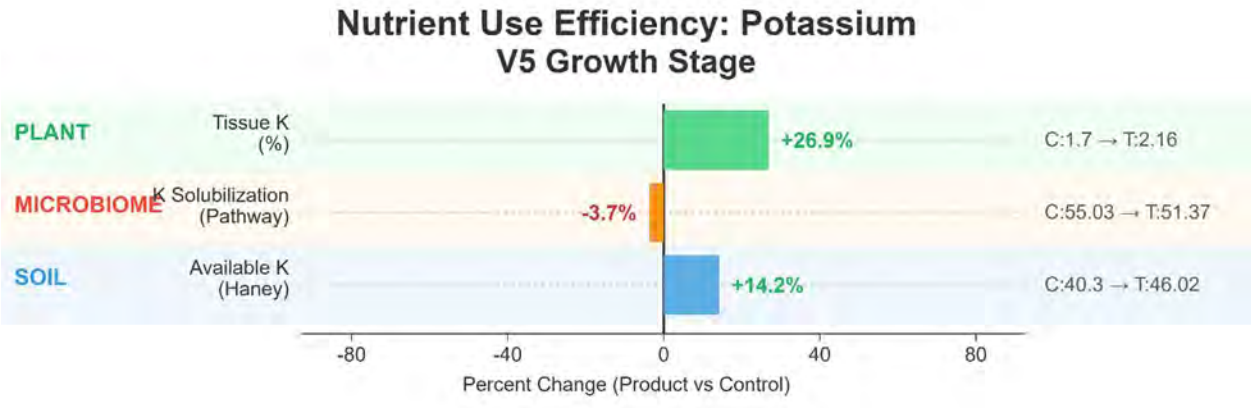

*Figure 14. Potassium Cycling Dynamics at V5 Stage*

By V5, potassium cycling transitioned to a stability pattern. Soil available potassium maintained positive trend (+14.2%) while K-solubilization potential returned to near-control levels (-3.7 percentile points). Tissue potassium remained elevated (+26.9%). This pattern is consistent with active potassium uptake during rapid vegetative growth, with earlier microbial priming reducing the need for continued pathway upregulation.

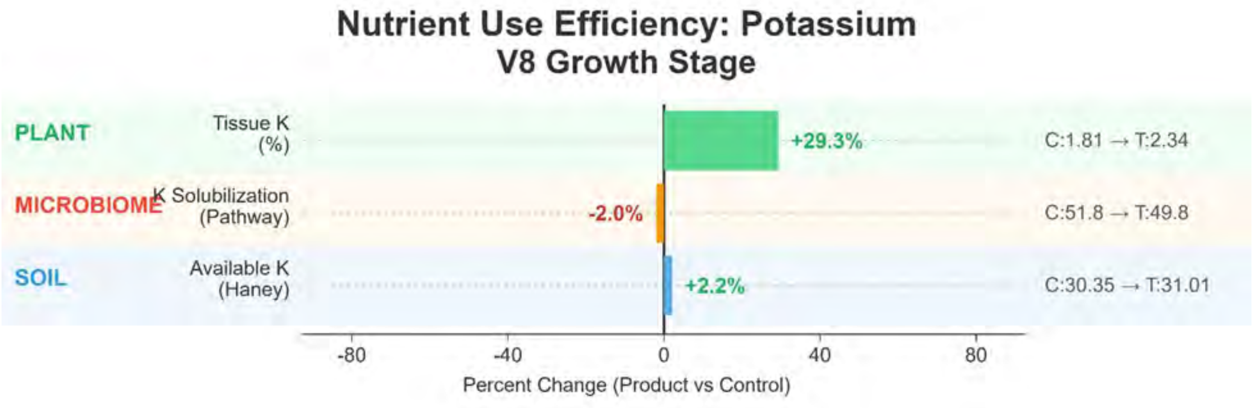

*Figure 15. Potassium Cycling Dynamics at V8 Stage*

At V8, potassium cycling remained stable, maintaining the improved tissue potassium that was observed at V2 and V5. Soil available potassium showed minimal change (+2.2%) while K-solubilization potential remained near baseline (-0.020). Tissue potassium maintained elevated concentrations (+29.3%), suggesting sustained nutritional benefit through late vegetative development.

## General Potassium Summary

Potassium cycling demonstrated a coherent treatment response: significant early-season enhancement of biological potassium mobilization coupled to improved plant potassium status that persisted through V8. The correlation between soil potassium and soil health metrics ($r = +0.905$, $p = 0.0008$) indicates integration between potassium availability and broader soil quality indicators. The transition from biologically-driven mobilization at V2 to plant-driven uptake at later stages reflects appropriate developmental progression.

# 9. SULFUR CYCLING

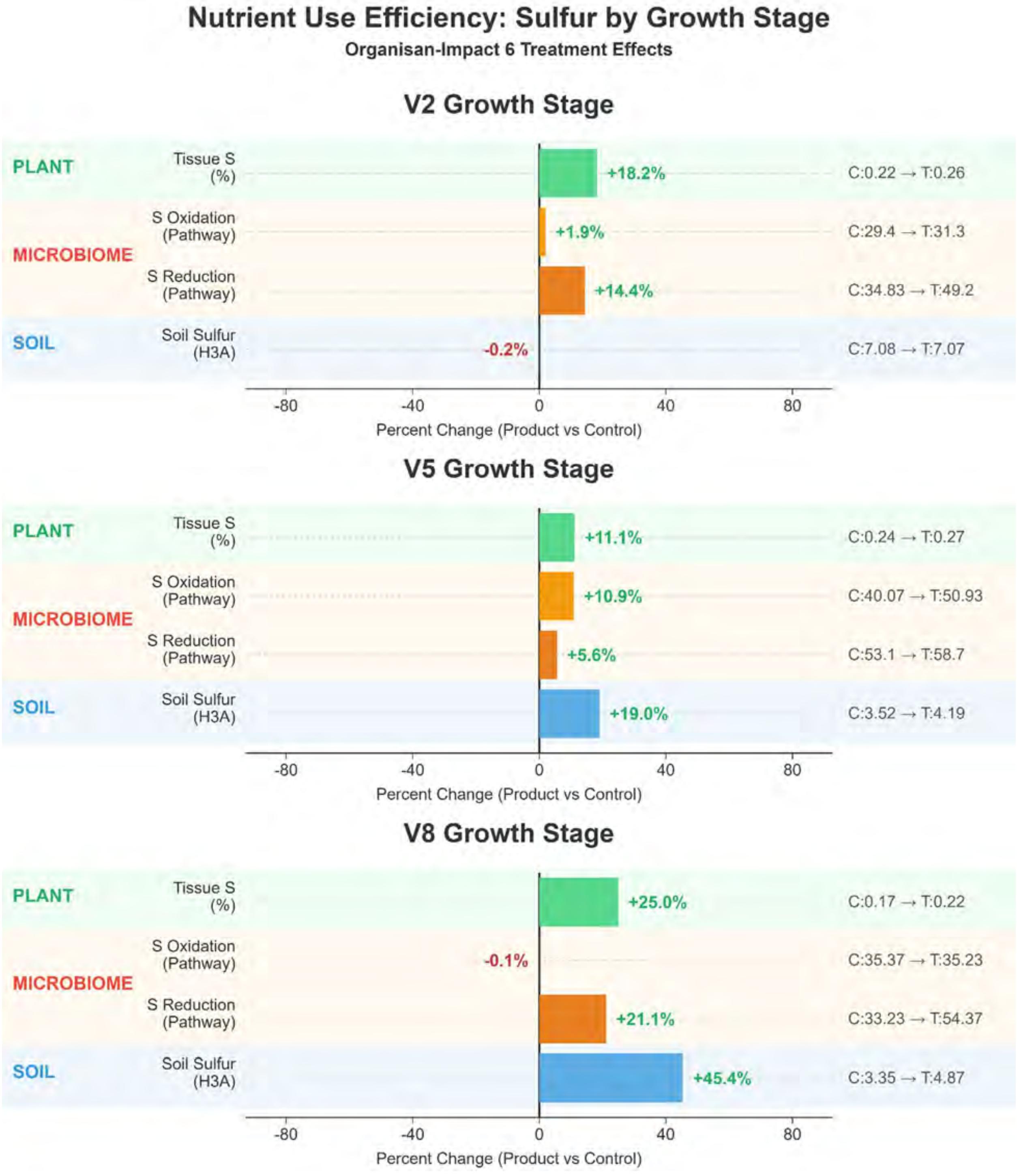

*Figure 16. Sulfur Cycling Dynamics Across Growth Stages*

Sulfur cycling exhibited persistent treatment effects across the growing season, representing one of the most consistent pathway responses observed. At V2, sulfur reduction potential demonstrated marginal elevation (+14.4 percentile points, p = 0.077) while soil sulfur remained essentially unchanged (-0.2%). Tissue sulfur increased modestly (+18.2%) based on single-replicate observation.

By V5, sulfur oxidation potential showed marginal elevation (+10.9 percentile points, p = 0.054), indicating activation of sulfur cycling in both oxidative and reductive directions. Soil sulfur increased (+19.0%) and tissue sulfur maintained gains (+11.1%). The sulfur reduction potential remained positive (+5.6) though non-significant.

At V8, sulfur reduction potential reached its strongest expression (+0.211, p = 0.002), representing the most significant late-season pathway finding. Soil sulfur increased substantially (+45.4%) and tissue sulfur showed marginal elevation (+25.0%, p = 0.076). The persistence of sulfur cycling enhancement through V8 indicates sustained treatment effects on sulfur metabolism.

# 10. CALCIUM CYCLING

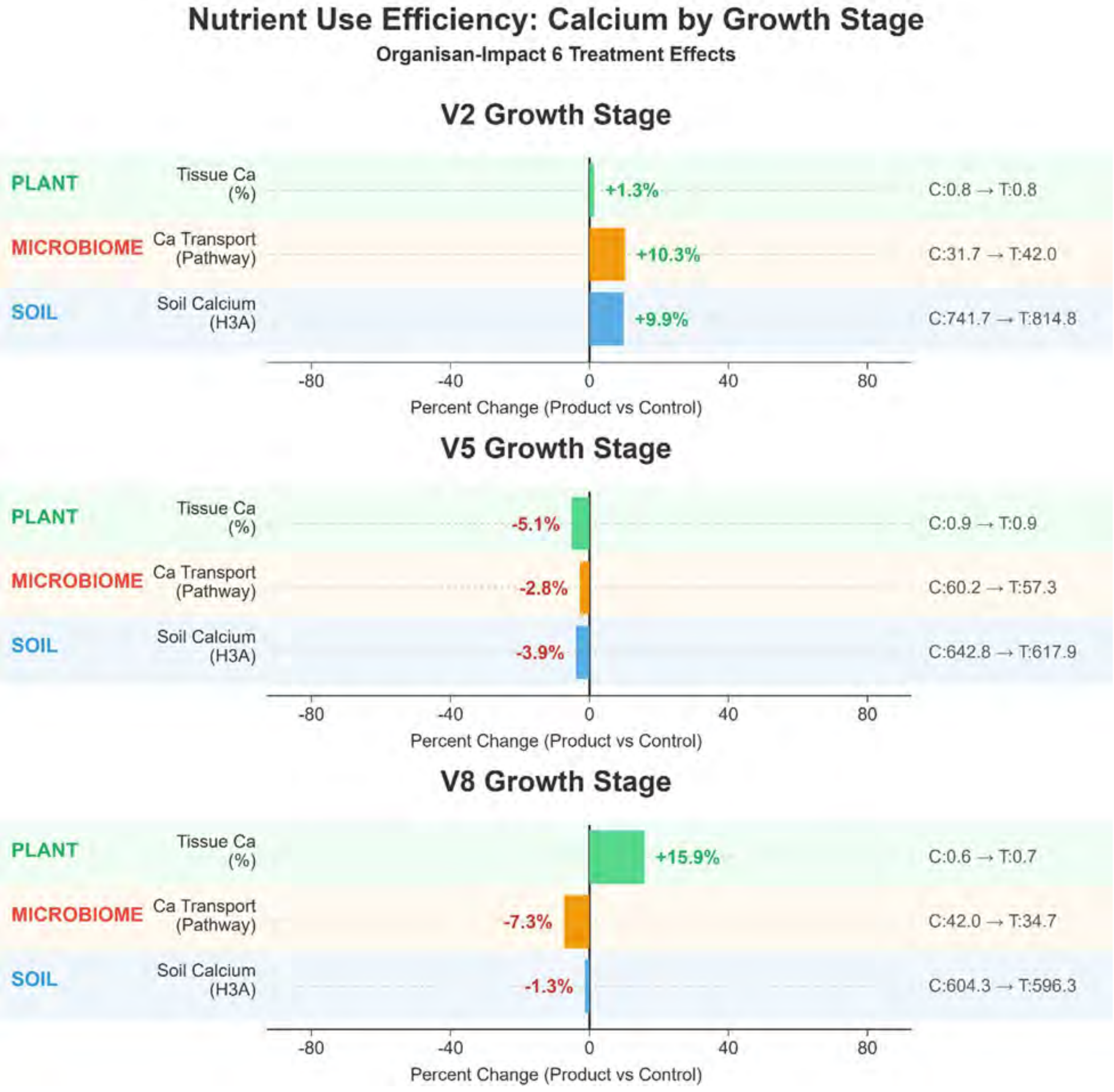

*Figure 17. Calcium Cycling Dynamics Across Growth Stages*

At V2, soil calcium availability increased significantly (+9.9%, $p = 0.043$) and calcium transport potential showed highly significant enhancement (+10.3 percentile points, $p = 0.003$). Tissue calcium showed a marginal improvement above control (+1.3%) based on single-replicate data.

By V5, calcium dynamics stabilized. Soil calcium  in treated areas was slightly below control (-3.9%) and calcium transport potential returned to near-control levels (-2.8 percentile points). Tissue calcium declined modestly (-5.1%). This mid-season pattern suggests calcium was being actively utilized during rapid vegetative growth.

At V8, Treated plants showed significantly higher tissue calcium (+15.9%, p = 0.044), despite calcium transport potential remaining below control (-7.3 percentile points).

Correlation analysis revealed positive relationships between soil calcium and plant stress adaptation pathway activity (r = +0.871, p = 0.0022), suggesting that adequate calcium availability enables microbial stress tolerance functions.

# 11. IRON CYCLING

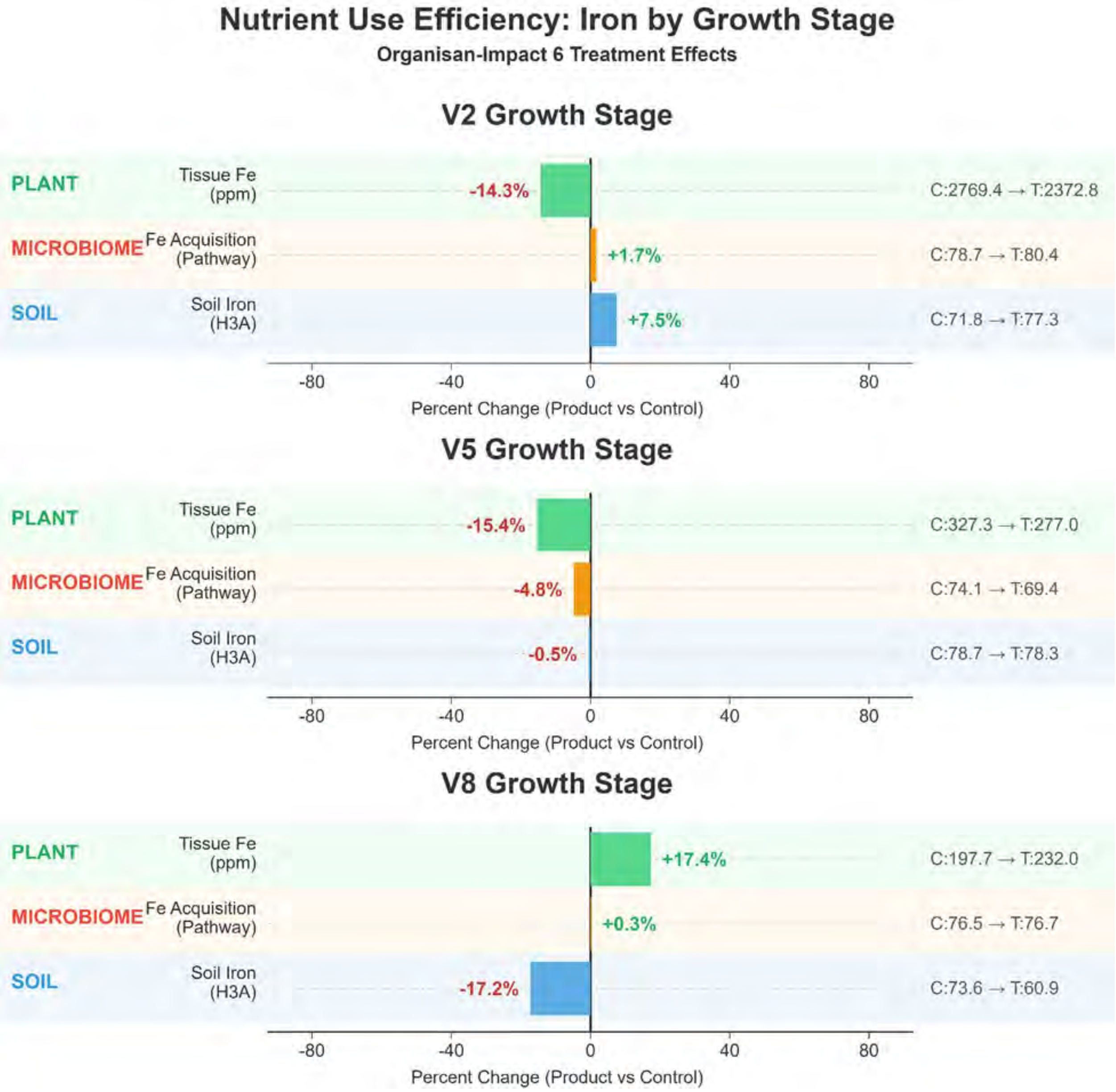

Figure 18. Iron Cycling Dynamics Across Growth Stages

Iron cycling demonstrated variable responses across growth stages. At V2, soil iron increased modestly (+7.5%) while iron acquisition pathway potential remained near control levels (+1.7 percentile points). Tissue iron showed decline (-14.3%) based on single-replicate observation, though this cannot be statistically evaluated.

By V5, soil iron remained stable (-0.5%) and iron acquisition potential showed non-significant decline (-4.8 percentile points). Tissue iron decreased (-15.4%), though without statistical significance. The mid-season iron patterns suggest complex dynamics that may relate to interactions with other nutrients.

At V8, soil iron declined notably (-17.2%), while iron acquisition potential remained stable (+0.3 percentile points). In addition, tissue iron increased (+17.4%), reversing the earlier declines. This pattern suggests successful iron mobilization from soil to plant tissue during late vegetative development.

Correlation analysis identified a strong inverse relationship between sulfur oxidation and tissue iron ($r = -0.911$, $p = 0.0044$), consistent with known rhizosphere interactions where sulfur metabolism can affect iron availability through pH and redox effects. This relationship suggests that sulfur cycling dynamics may have indirectly influenced iron nutrition.

# 12. NUTRIENT UPTAKE SUMMARY

V2 represented a period of substantial microbiome enhancement and pathway activation. Significant increases were observed for calcium transport potential (+10.3 percentile points, p = 0.003), potassium solubilization potential (+8.4 percentile points , p = 0.028), denitrification potential (+ 20.1 percentile points, p = 0.005), and plant stress adaptation potential (+9.0 percentile points , p = 0.007). Microbial community structure improved significantly with diversity (+25.0 percentile points , p = 0.021), evenness (+10.3 percentile points , p = 0.004), and mycorrhizae abundance (+22.0 percentile points , p = 0.007). The fungal to bacterial ratio shifted significantly toward fungal dominance (+16.0%, p = 0.001). Soil calcium was significantly elevated (+9.9%, p = 0.043). These early-stage rhizosphere microbiome changes suggest a positive foundation for later nutritional benefits.

V5 demonstrated homeostatic nutrient cycling with most parameters suggesting stability. The significant decline in phosphorus solubilization potential (-17.1 percentile points , p = 0.032) likely reflects adequate P availability reducing microbial investment in mobilization. Sulfur oxidation showed marginal elevation (+10.9 percentile points , p = 0.054). Community metrics remained positive but returned toward baseline levels. CO2-C respiration and organic matter continued to exceed control levels.

At V8, tissue calcium significantly elevated above control (+15.9%, p = 0.044). Sulfur reduction potential remained significantly elevated (+21.1 percentile points , p = 0.002), indicating persistent treatment effects on sulfur metabolism. Tissue nitrogen (+16.1%, p = 0.068) and sulfur (+25.0%, p = 0.076) showed marginal improvements. Community diversity declined marginally relative to controls (-66.3 percentile points , p = 0.083), suggesting community restructuring over the season.

Overall, Organisan-Impact SIX demonstrated a multi-phase response pattern: exceptional early-season microbiome enhancement (V2), mid-season stability and homeostatic cycling (V5), and late-season nutritional benefit realization (V8). The significant tissue calcium improvement at V8 represents the clearest evidence of treatment benefit translating from soil and microbiome effects to plant nutrition.

# 13. TAXONOMY SUMMARY

Taxonomic analysis of rhizosphere bacterial and fungal communities revealed treatment-induced shifts with distinct functional implications. The analysis examined the top 20 bacterial and fungal genera across all growth stages.

## Bacterial Community Response

The bacterial community shifted favorably toward beneficial functional groups. Nitrogen-fixing genera substantially increased: *Burkholderia* (+91.5%), *Bradyrhizobium* (+48.2%), and *Rhizobium* (+1.2%). These increases indicate enhanced biological nitrogen fixation capacity in treated plots. Biocontrol-associated genera also increased: *Streptomyces* (+75.6%) and *Priestia* (+45.6%). Nutrient cycling genera showed positive trends: *Nocardioides* (+37.6%), *Paenarthrobacter* (+40.8%), and *Arthrobacter* (+18.2%).

*Pseudomonas* abundance declined (-28.5%). This reduction reflects community rebalancing rather than loss of beneficial function, as *Pseudomonas* was disproportionately abundant in untreated plots. The decline was offset by increases in other biocontrol-associated genera.

**Table 13.1: Notable Bacterial Genera Changes**

| Bacterial Genus | Untreated (%) | Treated (%) | % Change | Function |
|---|---|---|---|---|
| Pseudomonas | 22.85 | 16.34 | -28.5% | Biocontrol |
| Burkholderia | 3.71 | 7.10 | +91.5% | N-fixation |
| Streptomyces | 3.43 | 6.03 | +75.6% | Biocontrol |
| Bradyrhizobium | 2.48 | 3.68 | +48.2% | N-fixation |
| Priestia | 3.56 | 5.19 | +45.6% | Biocontrol |
| Paenarthrobacter | 1.18 | 1.66 | +40.8% | Nutrient cycling |
| Nocardioides | 3.00 | 4.12 | +37.6% | Nutrient cycling |

## Bacterial Functional Guild Analysis

Functional guild analysis revealed substantial enhancement of nitrogen-fixing bacteria (+52.1%), representing a notable agronomic benefit that has the potential to improve nitrogen availability and reduce fertilizer requirements. Biocontrol bacteria showed modest gains (+8.5%), maintaining disease suppression capacity. Nutrient cycling bacteria increased (+17.6%), supporting improved nutrient availability.

## Fungal Community Response

The fungal community showed mixed responses at the taxonomic level. Biocontrol fungi *Trichoderma* was elevated above control (+48.9%), while *Clonostachys* (-72.4%) and *Pochonia* (-77.1%) were suppressed. Mycorrhizal fungi *Gigaspora* saw gains in treated areas (+7.0%). Saprophytic fungi increased substantially, including *Mucor* (+186.3%) and *Talaromyces* (+63.1%). *Fusarium* showed modest increase (+14.7%). Absolute fungal abundances were very low (<0.3%), limiting the biological significance of percentage changes.

**Table 13.2: Notable Fungal Genera Changes**

| Fungal Genus | Untreated (%) | Treated (%) | % Change | Category |
|---|---|---|---|---|
| Fusarium | 0.2314 | 0.2656 | +14.7% | Pathogen |
| Penicillium | 0.1966 | 0.2422 | +23.2% | Saprophyte |
| Clonostachys | 0.1550 | 0.0429 | -72.4% | Biocontrol |
| Trichoderma | 0.0448 | 0.0667 | +48.9% | Biocontrol |
| Gigaspora | 0.1183 | 0.1267 | +7.0% | Mycorrhizal |
| Mucor | 0.0432 | 0.1237 | +186.3% | Saprophyte |

## Fungal Functional Guild Analysis

Fungal biocontrol agents had a net decline (-57.8%) at the taxonomic level, though mycorrhizal fungi increased (+49.3%) and saprophytes had gains (+35.6%). Importantly, pathogen detection data (see Section 14) demonstrated -40.6% overall pathogen reduction despite the taxonomic shifts in biocontrol fungi, indicating the treatment's overall protective effect was maintained through alternative pathogen suppression mechanisms.

# 14. PATHOGEN ANALYSIS

Pathogen analysis revealed consistent suppression across all growth stages, with treated plots showing -40.6% overall reduction in pathogen occurrences above potential threat levels (101 untreated to 60 treated across all timepoints). The strongest suppression occurred at V5 (-56.7%), with sustained efficacy maintained through V8 (-25.0%).

**Table 14.1: Pathogen Pressure by Growth Stage**

| Growth Stage | Untreated (Avg) | Treated (Avg) | % Change | Assessment |
|---|---|---|---|---|
| V2 (Early) | 9.0 | 4.7 | -48.1% | Favorable |
| V5 (Mid) | 10.0 | 4.3 | -56.7% | Strongest |
| V8 (Late) | 14.7 | 11.0 | -25.0% | Sustained |
| **TOTAL** | **101** | **60** | **-40.6%** | **Favorable** |

## Pathogens Completely Eliminated

Eleven pathogen types saw complete suppression below threat thresholds in treated plots compared to control plots, representing 32 total pathogen occurrences reduced to zero. Completely suppressed pathogens included: Penicillium Ear Rot, Bacterial Leaf Streak, Fusarium Root Rot Complex, Sorghum Downy Mildew, Black Kernel Rot, Diplodia Ear Rot and Stalk Rot, Nigrospora Ear and Cob Rot, Storage Molds (*Aspergillus ochraceus*), Black Bundle Disease, Black Root Rot, and Root Dieback.

## Major Pathogen Reductions

Additional pathogens showed substantial reductions: Phoma Leaf Spot (-75.0%), Storage Molds (Aspergillus candidus, -75.0%), Pythium Root Rot Complex (-71.4%), Cladosporium Rot (-66.7%), Damping Off (-50.0%), and Rhizoctonia Ear Rot (-50.0%). Fungal disease suppression was particularly effective (-45.3% overall).

## Nematode Analysis

Soils treated with Impact SIX showed 42.6% fewer occurrences of plant-parasitic nematode populations, and 48.3% fewer cyst nematodes compared to controls. However, due to high variability between replicates that is common to nematode assays, these differences did not reach statistical significance. Cyst nematodes (*Heterodera* spp.) represented the dominant nematode pressure at this site, comprising over 90% of the total nematode load. The elevated populations detected exceed anticipated economic damage thresholds (Jagdale et al., 2013) for any subsequent soybean crops, making the observed 48.3% reduction biologically meaningful even without statistical significance.

Root lesion nematodes (*Pratylenchus* spp.) were completely absent from treated samples, with zero detections across all three treated replicates, although both sets of samples were below levels anticipated to significantly impact yields. Spiral nematodes (*Helicotylenchus* spp.) showed a 36.1% increase in treated plots, though populations in all samples again remained below the anticipated economic damage threshold. Thirteen additional nematode types were assayed but not detected in any sample, including important root-knot nematodes and highly pathogenic needle and sting nematodes, suggesting generally favorable baseline nematode community structure at this site.

**Table 14.2. Impact SIX Nematode Reduction Summary**

| Nematode Type | Check 11 (Mean ± SD) | Impact SIX (Mean ± SD) | % Change |
|---|---|---|---|
| Cyst (Eggs & Larvae) | 6,540 ± 5,572 | 3,380 ± 4,037 | -48.3% |
| Spiral (*Helicotylenchus*) | 480 ± 275 | 653 ± 682 | +36.1% |
| Root Lesion (*Pratylenchus*) | 7 ± 12 | 0 ± 0 | -100.0% |
| Pin (*Paratylenchus*) | 0 ± 0 | 0 ± 0 | N/A |
| Total Nematode Load | 7,027 ± 5,658 | 4,033 ± 3,719 | -42.6% |

*All counts per 500 cc soil; n = 3 replicates per treatment. No comparisons reached statistical significance ($p > 0.05$).*

# 15. INTEGRATED ANALYSIS

The integrated cross-domain correlation analysis examined relationships between soil chemistry, functional pathways, community structure, and plant tissue nutrients. Using paired treatment effects (n = 9 stage-replicate observations), the analysis identified 75 statistically significant correlations ($p < 0.05$), of which 27 represent cross-domain relationships linking different analytical platforms.

## Principal Mechanisms

The integrated analysis reveals a coherent treatment mechanism characterized by:

(1) initial community restructuring and activation of microbial respiration at V2;
(2) modulation of nitrogen cycling through nitrification dynamics through all growth stages;
(3) enhancement of mycorrhizal populations sustained across all growth stages; and
(4) translation of improved soil biology to enhanced plant calcium and potassium nutrition, particularly at later growth stages.

The relationship between soil ammonium and nitrification pathway potential showed near-perfect inverse correlation ($r = -0.913$, $p = 0.0006$), reflecting the direct mechanistic link between nitrifying microbial activity and ammonium consumption. Organic matter showed similar inverse correlation with nitrification potential ($r = -0.913$, $p = 0.0006$), indicating that treatment-induced organic matter accumulation coincided with suppressed nitrification potential, potentially supporting nitrogen retention.

**Table 15.1: Principal Cross-Domain Correlations**

| Correlation Pair | r | p-value | Interpretation |
|---|---|---|---|
| Sulfur Oxidation to Tissue S | -0.956 | 0.0007 | S oxidation inversely affected tissue S |
| Soil Ammonium to Nitrification | -0.913 | 0.0006 | Nitrification consume ammonium |
| Organic Matter to Nitrification | -0.913 | 0.0006 | OM accumulates when nitrification is low |
| Soil Ca to Stress Adaptation | +0.871 | 0.0022 | Ca availability enables stress functions |
| % MAC to Mycorrhizae | +0.775 | 0.0142 | Active carbon supports AMF |
| H2O Org C to Genera Count | +0.807 | 0.0085 | Labile C supports diversity |

*Note: Correlations computed using paired treatment effects (n = 8 stage-replicate pairs).*

## Temporal Response Patterns

Treatment effects showed distinct temporal trajectories. Early season (V2) responses were characterized by dramatic increases in microbial activity (CO2-C +136.9%) and community restructuring with diversity (+25 percentile points) and evenness (+10.3 percentile points) significantly increased. Mid-season (V5) showed sustained organic matter accumulation (+34.4%) and maintained positive community metrics. Late season (V8) effects culminated in tissue calcium improvement (+15.9%, p = 0.044) and sustained sulfur cycling enhancement (+21.1 percentile points, p = 0.002).

## Limitations

The sample size of n = 3 replicates per treatment per stage limits statistical power for detecting moderate effects. V2 tissue data was limited to n = 1 per treatment and is reported descriptively. The single-site design cannot separate treatment effects from site-specific factors. Several unexpected findings, including inverse relationships between soil health metrics and certain tissue cation concentrations, warrant further investigation across multiple sites and seasons.

# 16. CONCLUSION

The Organisan-Impact SIX biological treatment trial at the Reese Farm demonstrated coherent treatment responses across the Soil to Microbiome to Plant pathway, with several notable findings supported by statistical significance.

## Primary Treatment Benefits

The most clearly demonstrated benefit was enhanced calcium nutrition. Early-season improvements in soil calcium availability (+9.9%, $p = 0.043$) and calcium transport pathway potential (+10.3 percentile points, $p = 0.003$) at V2 translated to significantly elevated tissue calcium (+15.9%, $p = 0.044$) at V8. This coherent pathway response demonstrates effective integration between soil, microbial, and plant compartments.

Microbiome enhancement at V2 was substantial, with significant improvements in diversity (+25 percentile points, $p = 0.021$), evenness (+10.3 percentile poitns, $p = 0.004$), mycorrhizae abundance (+22 percentile points, $p = 0.007$), and fungal to bacterial ratio (+16.0%, $p = 0.001$). These changes indicate treatment-induced restructuring toward a more diverse, balanced microbial community in treated areas during early rhizosphere establishment.

Pathogen suppression was consistent across all growth stages, with -40.6% overall reduction in pathogen occurrences. Complete elimination of 11 pathogen types and peak efficacy at V5 (-56.7%) demonstrate reliable disease protection. The combination of nitrogen-fixing bacterial enhancement (+52.1%) and sustained pathogen suppression represents complementary agronomic benefits.

## Study Limitations and Future Directions

The single-site design and limited sample sizes constrain generalizability. V2 tissue data was limited to $n = 1$ per treatment. Multi-year, multi-site trials would strengthen conclusions about treatment consistency across environments. Integration with yield data would validate whether observed microbiome and tissue improvements translate to productivity benefits.

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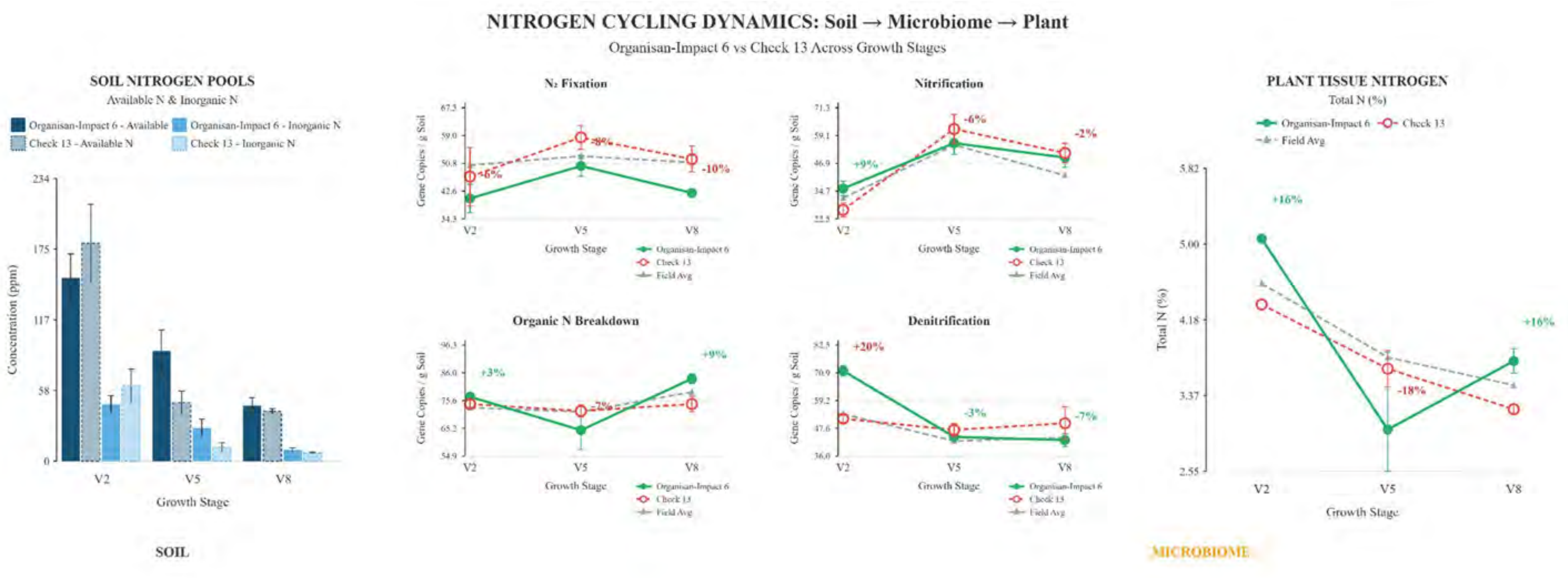
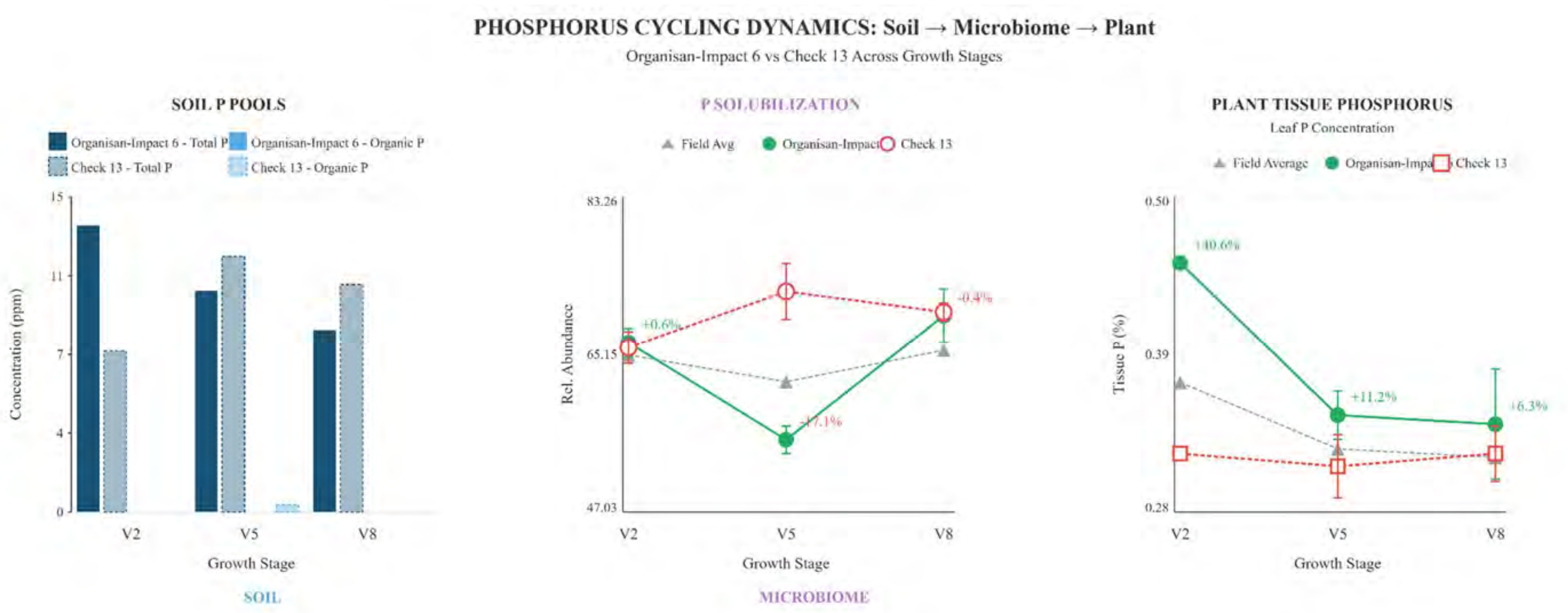
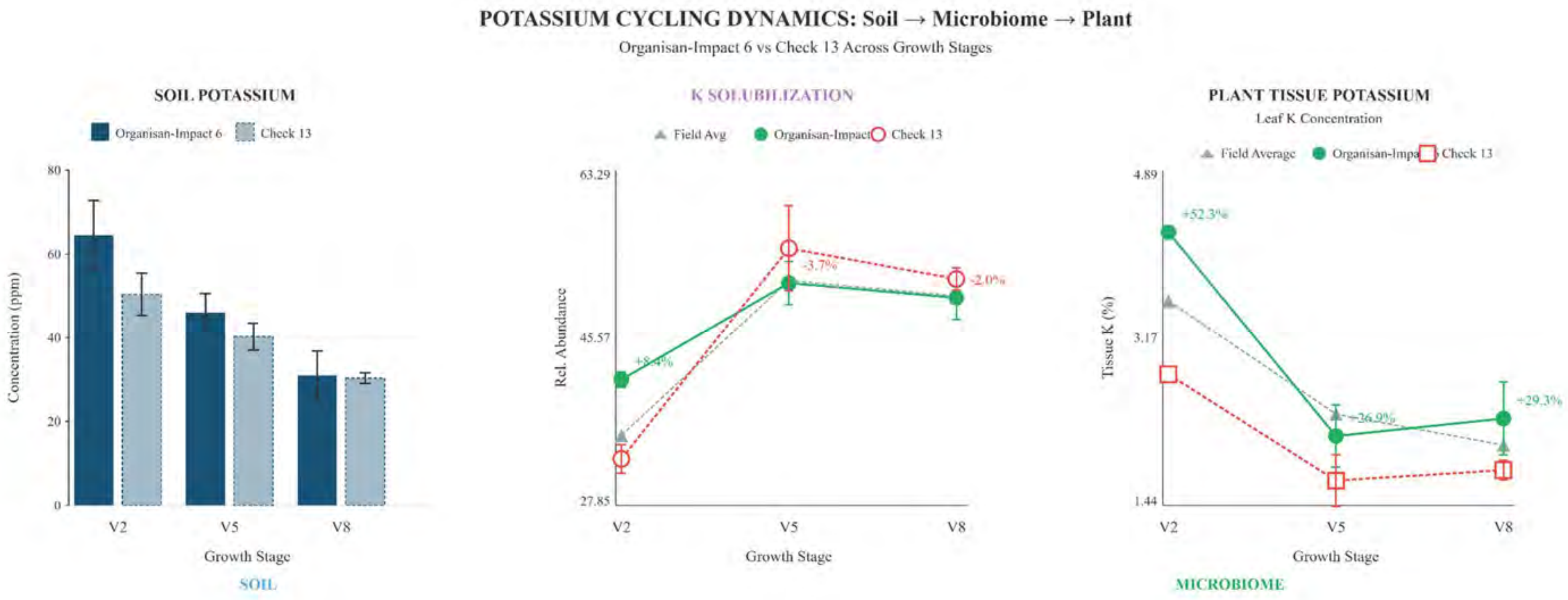
# Appendix 1 – Supplemental Figures



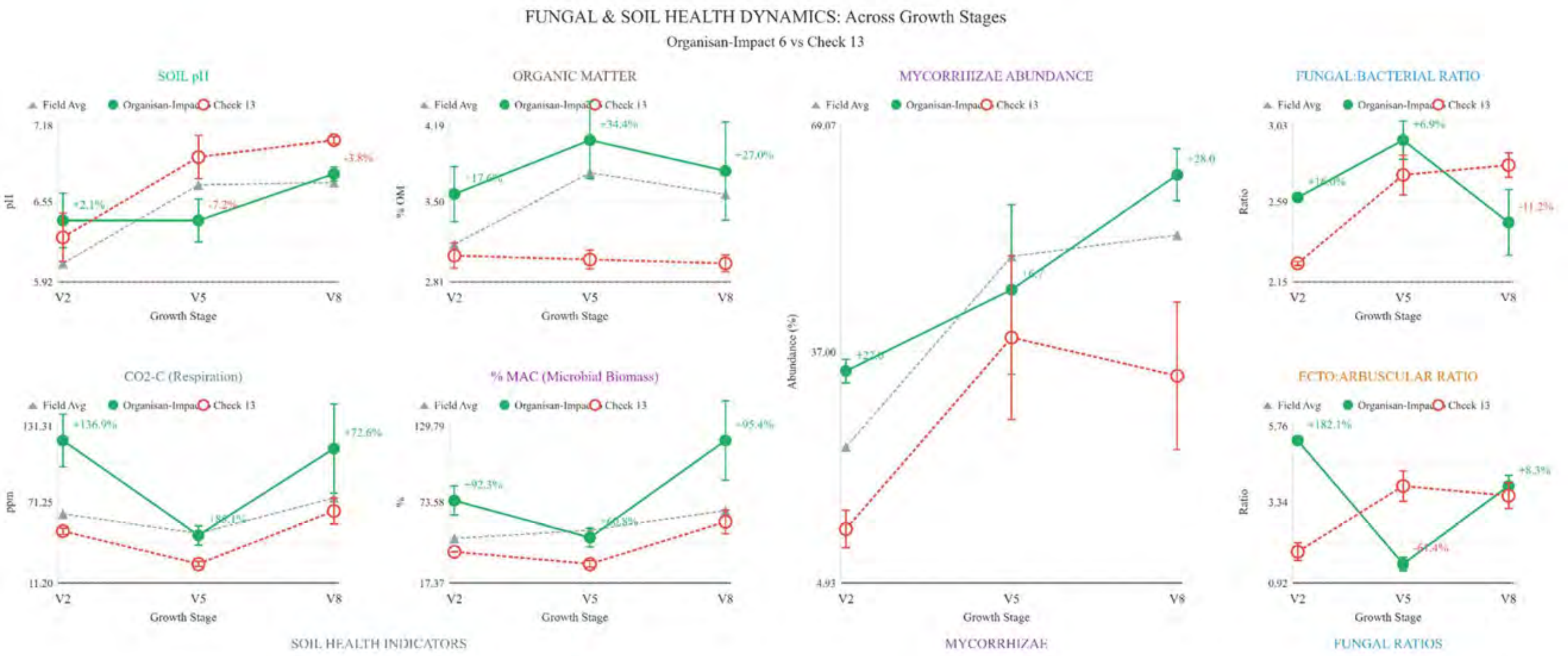
Supplemental Figure 1. Nitrogen Cycling Dynamics



<u>Supplemental Figure 2. Phosphorus Cycling Dynamics</u>



Supplemental Figure 3. Potassium Cycling Dynamics



Supplemental Figure 4. Soil Carbon Dynamics and Fungal Populations

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## Roots to Shoots Summary Report- Organisan-Impact 6 V2 Corn

| **Sample Type** | Untreated | | | Treated | | | % Change | | |
|---|---|---|---|---|---|---|---|---|---|
| | Haney | Rhize | Tissue | Haney | Rhize | Tissue | Haney | Rhize | Tissue |
| **Health Overview** | 8.8 | 47% | 57 | 14.9 | 51% | 31 | 69% | 8% | -25.92 |
| **Community Structure** | 8.8 | 54% | | 14.9 | 63% | | 69.4% | 18.0% | |
| **Respiration** | 49.6 | 68% | | 117.4 | 71% | | 136.9% | 3.7% | |
| **Environmental Stressors** | | 39% | | | 46% | | | 6.6% | |
| **Carbon** | 127.8 | 52% | | 155.0 | 49% | | 21.3% | -2.9% | |
| **Nitrogen** | 180.2 | 49% | 4.35 | 151.6 | 45% | 5.06 | -15.8% | -3.6% | 16.3% |
| **Phosphorus** | 17.6 | 66% | 0.32 | 31.3 | 67% | 0.45 | 78.1% | 0.6% | 40.6% |
| **Potassium** | 60.5 | 33% | 2.79 | 77.5 | 41% | 4.25 | 28.1% | 8.4% | 52.3% |
| **Sulfur** | 7.1 | 47% | 0.22 | 7.1 | 41% | 0.26 | -0.2% | -6.2% | 18.2% |
| **Calcium** | 741.7 | 32% | 0.75 | 814.8 | 42% | 0.76 | 9.9% | 10.3% | 1.3% |
| **Iron** | 71.8 | 79% | 2769.38 | 77.3 | 80% | 2372.85 | 7.5% | 1.7% | -14.3% |
| **Zinc** | 0.6 | | 36.59 | 0.7 | | 44.77 | 16.3% | | 22.4% |
| **Manganese** | 3.6 | | 74.59 | 1.3 | | 47.55 | -64.6% | | -36.3% |
| **Magnesium** | 133.1 | | 0.30 | 147.2 | | 0.27 | 10.6% | | -10.0% |
| **Sodium** | 7.5 | | 0.02 | 7.5 | | 0.02 | -0.9% | | 0.0% |
| **Copper** | 0.3 | | 15.16 | 0.4 | | 16.57 | 11.7% | | 9.3% |
| **Aluminum** | 146.0 | | 1160.77 | 145.7 | | 1051.13 | -0.2% | | -9.4% |
| **Molybdenum** | | | 1.06 | | | 1.36 | | | 28.3% |
| **Boron** | | | 12.46 | | | 11.13 | | | -10.7% |

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## Roots to Shoots Summary Report- Organisan-Impact 6  V2 Corn

| **Sample Type** | Untreated | | | Treated | | | % Change | | |
|---|---|---|---|---|---|---|---|---|---|
| | Haney | Rhize | Tissue | Haney | Rhize | Tissue | Haney | Rhize | Tissue |
| **Health Overview** | 8.8 | 47% | 57 | 14.9 | 51% | 31 | 69% | 8% | -25.92 |
| **Community Structure** | 8.8 | 54% | | 14.9 | 63% | | 69.4% | 18.0% | |
| Number of Genera | | 2477.3 | | | 2647.0 | | | 6.8% | |
| Diversity | | 8.3% | | | 33.3% | | | 300.0% | |
| Evenness | | 4.7% | | | 15.0% | | | 221.4% | |
| Mycorrhizae Abundance | | 12% | | | 34% | | | 22.0% | |
| Plant Stress Adaptation | | 68% | | | 77% | | | 9.0% | |
| Fungal to Bacterial Ratio | | | | | | | | | |
| Ectomycorrhizal to Arbuscular Ratio | | | | | | | | | |
| 1:1 Soil pH | 6.3 | | | 6.4 | | | 2.1% | | |
| Soil Health Calculation | 8.8 | | | 14.9 | | | 69.4% | | |
| Organic Matter | 3.0 | | | 3.6 | | | 17.6% | | |
| 1:1 Soluble Salt | 0.6 | | | 0.6 | | | -10.8% | | |
| Organic C:N | 9.9 | | | 9.7 | | | -1.9% | | |
| **Respiration** | 49.6 | 68% | | 117.4 | 71% | | 136.9% | 3.7% | |
| High Oxygen Environment | | 68% | | | 71% | | | 3.7% | |
| CO2-C | 49.6 | | | 117.4 | | | 136.9% | | |
| **Environmental Stressors** | | 39% | | | 46% | | | 6.6% | |
| Anoxic Environment | | 39% | | | 46% | | | 6.6% | |
| **Carbon** | 127.8 | 52% | | 155.0 | 49% | | 21.3% | -2.9% | |
| CO2-C | 49.6 | | | 117.4 | | | 136.9% | | |
| Organic Matter | 3.0 | | | 3.6 | | | 17.6% | | |
| Carbon Fixation | | 38% | | | 29% | | | -9.5% | |
| Organic Carbon Breakdown | | 56% | | | 57% | | | 0.9% | |
| Methanogenesis | | 39% | | | 39% | | | 0.2% | |
| H2O Total Organic C | 127.8 | | | 155.0 | | | 21.3% | | |
| % MAC | 38.8 | | | 74.6 | | | 92.3% | | |

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## Roots to Shoots Summary Report- Organisan-Impact 6 V2 Corn

| **Sample Type** | Untreated | | | Treated | | | % Change | | |
|---|---|---|---|---|---|---|---|---|---|
| | Haney | Rhize | Tissue | Haney | Rhize | Tissue | Haney | Rhize | Tissue |
| **Health Overview** | 8.8 | 47% | 57 | 14.9 | 51% | 31 | 69% | 8% | -25.92 |
| **Nitrogen** | 180.2 | 49% | 4.35 | 151.6 | 45% | 5.06 | -15.8% | -3.6% | 16.3% |
| Nitrogen Fixation | | 47% | | | 40% | | | -6.5% | |
| Nodulating Bacteria | | 51% | | | 49% | | | -1.6% | |
| Organic Nitrogen Breakdown | | 74% | | | 77% | | | 2.7% | |
| H3A Ammonium | 1.3 | | | 1.3 | | | -0.5% | | |
| Nitrification | | 27% | | | 36% | | | 9.3% | |
| H3A Nitrate | 60.9 | | | 45.8 | | | -24.7% | | |
| Denitrification | | 52% | | | 72% | | | 20.1% | |
| H2O Total N | 75.5 | | | 63.6 | | | -15.8% | | |
| H2O Organic N | 12.9 | | | 16.0 | | | 24.9% | | |
| H3A Inorganic Nitrogen | 62.2 | | | 47.1 | | | -24.2% | | |
| Organic N Release | 12.9 | | | 16.0 | | | 24.9% | | |
| Organic N Reserve | 0.0 | | | 0.0 | | | | | |
| Available N | 180.2 | | | 151.6 | | | -15.8% | | |
| Total Nitrogen, % N | | | 4.4 | | | 5.1 | | | 16.3% |
| **Phosphorus** | 17.6 | 66% | 0.32 | 31.3 | 67% | 0.45 | 78.1% | 0.6% | 40.6% |
| Phosphorus Solubilization | | 66% | | | 67% | | | 0.6% | |
| H3A Total Phosphorus | 7.6 | | | 13.6 | | | 78.1% | | |
| H3A Inorganic Phosphorus | 5.6 | | | 10.4 | | | 84.2% | | |
| H3A Organic Phosphorus | 2.0 | | | 3.3 | | | 60.9% | | |
| Organic P Release | 2.0 | | | 3.3 | | | 60.9% | | |
| Organic P Reserve | 0.0 | | | 0.0 | | | | | |
| Available P | 17.6 | | | 31.3 | | | 78.1% | | |
| Phosphorus, % P | | | 0.32 | | | 0.45 | | | 40.6% |

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## Roots to Shoots Summary Report- Organisan-Impact 6 V2 Corn

| **Sample Type** | Untreated | | | Treated | | | % Change | | |
|---|---|---|---|---|---|---|---|---|---|
| | Haney | Rhize | Tissue | Haney | Rhize | Tissue | Haney | Rhize | Tissue |
| **Health Overview** | 8.8 | 47% | 57 | 14.9 | 51% | 31 | 69% | 8% | -25.92 |
| **Potassium** | 60.5 | 33% | 2.79 | 77.5 | 41% | 4.25 | 28.1% | 8.4% | 52.3% |
| Potassium Solubilization | | 33% | | | 41% | | | 8.4% | |
| H3A ICAP Potassium | 50.4 | | | 64.5 | | | 28.1% | | |
| Available K | 60.5 | | | 77.5 | | | 28.1% | | |
| Potassium, % K | | | 2.79 | | | 4.25 | | | 52.3% |
| **Sulfur** | 7.1 | 47% | 0.22 | 7.1 | 41% | 0.26 | -0.2% | -6.2% | 18.2% |
| Sulfur Oxidation | | 29% | | | 31% | | | 1.9% | |
| Sulfur Reduction | | 35% | | | 49% | | | 14.4% | |
| H3A ICAP Sulfur | 7.1 | | | 7.1 | | | -0.2% | | |
| Sulfur, % S | | | 0.22 | | | 0.26 | | | 18.2% |
| **Calcium** | 741.7 | 32% | 0.75 | 814.8 | 42% | 0.76 | 9.9% | 10.3% | 1.3% |
| Calcium Transport | | 32% | | | 42% | | | 10.3% | |
| H3A ICAP Calcium | 741.7 | | | 814.8 | | | 9.9% | | |
| Calcium, % Ca | | | 0.75 | | | 0.76 | | | 1.3% |
| **Iron** | 71.8 | 79% | 2769.38 | 77.3 | 80% | 2372.85 | 7.5% | 1.7% | -14.3% |
| Iron Acquisition | | 79% | | | 80% | | | 1.7% | |
| H3A ICAP Iron | 71.8 | | | 77.3 | | | 7.5% | | |
| Iron, ppm Fe | | | 2769.38 | | | 2372.85 | | | -14.3% |
| **Zinc** | 0.6 | | 36.59 | 0.7 | | 44.77 | 16.3% | | 22.4% |
| H3A ICAP Zinc | 0.6 | | | 0.7 | | | 16.3% | | |
| Zinc, ppm Zn | | | 36.59 | | | 44.77 | | | 22.4% |
| **Manganese** | 3.6 | | 74.59 | 1.3 | | 47.55 | -64.6% | | -36.3% |
| H3A ICAP Manganese | 3.6 | | | 1.3 | | | -64.6% | | |
| Manganese, ppm Mn | | | 74.59 | | | 47.55 | | | -36.3% |

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## Roots to Shoots Summary Report- Organisan-Impact 6 V2 Corn

| **Sample Type** | Untreated | | | Treated | | | % Change | | |
|---|---|---|---|---|---|---|---|---|---|
| | Haney | Rhize | Tissue | Haney | Rhize | Tissue | Haney | Rhize | Tissue |
| **Health Overview** | 8.8 | 47% | 57 | 14.9 | 51% | 31 | 69% | 8% | -25.92 |
| **Magnesium** | 133.1 | | 0.30 | 147.2 | | 0.27 | 10.6% | | -10.0% |
| H3A ICAP Magnesium | 133.1 | | | 147.2 | | | 10.6% | | |
| Magnesium, % Mg | | | 0.30 | | | 0.27 | | | -10.0% |
| **Sodium** | 7.5 | | 0.02 | 7.5 | | 0.02 | -0.9% | | 0.0% |
| H3A ICAP Sodium | 7.5 | | | 7.5 | | | -0.9% | | |
| Sodium, % Na | | | 0.02 | | | 0.02 | | | 0.0% |
| **Copper** | 0.3 | | 15.16 | 0.4 | | 16.57 | 11.7% | | 9.3% |
| H3A ICAP Copper | 0.3 | | | 0.4 | | | 11.7% | | |
| Copper, ppm Cu | | | 15.16 | | | 16.57 | | | 9.3% |
| **Aluminum** | 146.0 | | 1160.77 | 145.7 | | 1051.13 | -0.2% | | -9.4% |
| H3A ICAP Aluminum | 146.0 | | | 145.7 | | | -0.2% | | |
| Aluminum, ppm Al | | | 1160.77 | | | 1051.13 | | | -9.4% |
| **Molybdenum** | | | 1.06 | | | 1.36 | | | 28.3% |
| Molybdenum, ppm Mo | | | 1.06 | | | 1.36 | | | 28.3% |
| **Boron** | | | 12.46 | | | 11.13 | | | -10.7% |
| Boron, ppm B | | | 12.46 | | | 11.13 | | | -10.7% |

| Report Date: | 1/16/2026 |
|---|---|

| CUSTOMER INFORMATION | | CUSTOMER INFORMATION | |
|---|---|---|---|
| **Name:** | Mark Nichols | **Grower Name:** | Mark Nichols |
| **Address:** | markn@organisancorp.com | **Field ID:** | Organisan-Impact SIX |
| **Phone:** | 678-935-8120 | **Crop Type:** | Corn |
| **Bill To:** | Organisan Corporation | **Crop Variety:** | Corn |

## Top 20 Bacterial Genera

AE = Aerobic AN = Anaerobic OA = Obligate Aerobic ON = Obligate Anaerobic F = Facultative MA = Microaerophilic ECM = Ecyomycorrhizal Fungi AMF = Arbuscular Mycorrhizal Fungi

| **Untreated** | | | **Treated** | | | **Response to Treatment** | | |
|---|---|---|---|---|---|---|---|---|
| Genera | Abundance | Metabolism | Genera | Abundance | Metabolism | Genera | Change in Abundance | Metabolism |
| Pseudomonas | 37.64% | aerobic | Pseudomonas | 23.92% | aerobic | Pseudomonas | ▼ -36.47% | aerobic |
| Arthrobacter | 8.24% | obligate_aerobic | Arthrobacter | 6.23% | obligate_aerobic | Arthrobacter | ▼ -24.40% | obligate_aerobic |
| Paenarthrobacter | 3.39% | aerobic | Priestia | 3.84% | obligate_aerobic | Paenarthrobacter | ▼ -22.32% | aerobic |
| Streptomyces | 3.35% | aerobic | Nocardioides | 3.83% | NA | Streptomyces | ▲ 1.49% | aerobic |
| Mesorhizobium | 2.97% | obligate_aerobic | Streptomyces | 3.40% | aerobic | Mesorhizobium | ▼ -52.41% | obligate_aerobic |
| Rhodococcus | 2.81% | aerobic | Paenarthrobacter | 2.63% | aerobic | Rhodococcus | ▼ -18.48% | aerobic |
| Nocardioides | 2.46% | obligate_aerobic | Rhodococcus | 2.29% | aerobic | Nocardioides | ▲ 55.56% | obligate_aerobic |
| Priestia | 2.45% | NA | Microbacterium | 2.23% | aerobic | Priestia | ▲ 56.66% | NA |
| Microbacterium | 1.80% | aerobic | Bradyrhizobium | 1.98% | aerobic | Microbacterium | ▲ 23.66% | aerobic |
| Bradyrhizobium | 1.45% | aerobic | Agromyces | 1.70% | aerobic | Bradyrhizobium | ▲ 36.01% | aerobic |
| Variovorax | 1.34% | aerobic | Mesorhizobium | 1.41% | obligate_aerobic | Variovorax | ▼ -14.43% | aerobic |
| Pseudarthrobacter | 1.26% | aerobic | Pseudarthrobacter | 1.36% | aerobic | Pseudarthrobacter | ▲ 7.65% | aerobic |
| Rhizobium | 1.08% | aerobic | Variovorax | 1.15% | aerobic | Rhizobium | ▼ -11.11% | aerobic |
| Pantoea | 0.96% | facultative | Rhizobium | 0.96% | aerobic | Pantoea | NA | facultative |
| Aquamicrobium | 0.86% | obligate_aerobic | Acinetobacter | 0.83% | aerobic | Aquamicrobium | NA | obligate_aerobic |
| Salmonella | 0.64% | facultative | Mycobacterium | 0.78% | aerobic | Salmonella | ▼ -69.11% | facultative |
| Sphingomonas | 0.60% | aerobic | Sphingomonas | 0.70% | aerobic | Sphingomonas | ▲ 17.22% | aerobic |
| Enterobacter | 0.55% | aerobic | Stenotrophomonas | 0.68% | | Enterobacter | ▼ -5.45% | aerobic |
| Telluria | 0.40% | aerobic | Enterobacter | 0.52% | aerobic | Telluria | NA | aerobic |
| Mycobacterium | 0.37% | aerobic | Kribbella | 0.43% | obligate aerobic | Mycobacterium | ▲ 108.93% | aerobic |

## Top 20 Fungal Genera

AE = Aerobic AN = Anaerobic OA = Obligate Aerobic ON = Obligate Anaerobic F = Facultative MA = Microaerophilic ECM = Ecyomycorrhizal Fungi AMF = Arbuscular Mycorrhizal Fungi

| **Untreated** | | | **Treated** | | | **Response to Treatment** | | |
|---|---|---|---|---|---|---|---|---|
| Genera | Abundance | Metabolism | Genera | Abundance | Metabolism | Genera | Change in Abundance | Metabolism |
| Microdochium | 0.78% | NA | Epicoccum | 0.27% | facultative | Microdochium | ▼ -89.27% | NA |
| Alternaria | 0.39% | NA | Alternaria | 0.10% | NA | Alternaria | ▼ -73.50% | NA |
| Fusarium | 0.38% | NA | Microdochium | 0.08% | NA | Fusarium | NA | NA |
| Mortierella | 0.13% | NA | Cladosporium | 0.05% | NA | Mortierella | ▼ -85.00% | NA |
| Chaetomium | 0.09% | NA | Furcasterigmium | 0.04% | NA | Chaetomium | ▼ -67.86% | NA |
| Linnemannia | 0.08% | NA | Diaporthe | 0.04% | NA | Linnemannia | ▼ -80.00% | NA |
| Epicoccum | 0.07% | facultative | Metarhizium | 0.03% | NA | Epicoccum | ▲ 263.64% | facultative |
| Penicillium | 0.06% | NA | Mucor | 0.03% | NA | Penicillium | NA | NA |
| Periconia | 0.04% | NA | Chaetomium | 0.03% | NA | Periconia | ▼ -38.46% | NA |
| Rhizopus | 0.03% | aerobic | Colletotrichum | 0.03% | aerobic | Rhizopus | ▼ -40.00% | aerobic |
| Furcasterigmium | 0.03% | NA | Periconia | 0.03% | NA | Furcasterigmium | ▲ 22.22% | NA |
| Staphylotrichum | 0.03% | NA | Staphylotrichum | 0.03% | NA | Staphylotrichum | ▼ -11.11% | NA |
| Metarhizium | 0.03% | NA | Mortierella | 0.02% | NA | Metarhizium | ▲ 11.11% | NA |
| Didymella | 0.03% | NA | Didymella | 0.02% | aerobic | Didymella | ▼ -33.33% | NA |
| Plectosphaerella | 0.02% | NA | Rhizopus | 0.02% | NA | Plectosphaerella | NA | NA |
| Colletotrichum | 0.02% | aerobic | Trichoderma | 0.02% | NA | Colletotrichum | ▲ 28.57% | aerobic |
| Aspergillus | 0.02% | NA | Podila | 0.02% | NA | Aspergillus | NA | NA |
| Trichoderma | 0.02% | NA | Linnemannia | 0.02% | NA | Trichoderma | ▲ 0.00% | NA |
| Cladosporium | 0.02% | NA | Fusarium | 0.00% | NA | Cladosporium | ▲ 166.67% | NA |
| Diaporthe | 0.01% | NA | Penicillium | 0.00% | NA | Diaporthe | ▲ 175.00% | NA |

# Roots to Shoots Summary Report- Organisan-Impact SIX V2 Corn

## Pathogen Screening

| | Untreated | | Treated | |
|---|---|---|---|---|
| | Average Number of Abundant Pathogens Identified: 4 | | Average Number of Abundant Pathogens Identified: 4.7 | |
| | **Pathogen Species** | **Disease Common Name** | **Pathogen Species** | **Disease Common Name** |
| **Replicate 1** | Globisporangium ultimum | Pythium Root Rot | Alternaria spp. | Black Point |
| | Pythium spp. | Damping Off | Pseudomonas syringae pv. syringae | Bacterial Kernel Blight |
| | Pythium spp. | Damping Off | Puccinia polysora | Southern Rust |
| | Pythium spp. | Damping Off | Meloidogyne arenaria | Root Knot Nematode |
| | Puccinia polysora | Southern Rust | | |
| | Pratylenchus spp. | Root Lesion Nematode | | |
| | Colletotrichum graminicola | Anthracnose | | |
| **Replicate 2** | Globisporangium paroecandrum | Pythium Root Rot Complex | Sclerospora graminicola | Graminicola Downy Mildew |
| | Pratylenchus spp. | Root Lesion Nematode | Aspergillus candidus | Storage Molds |
| | | | Pseudomonas syringae pv. syringae | Bacterial Kernel Blight |
| | | | Globisporangium paroecandrum | Pythium Root Rot Complex |
| | | | Cercospora spp. | Gray Leaf Spot |
| | | | Meloidogyne arenaria | Root Knot Nematode |
| | | | Diabrotica virgifera | Western Corn Rootworm |
| **Replicate 3** | Hoplolaimus galeatus | Lance Nematode | Hoplolaimus galeatus | Lance Nematode |
| | Hoplolaimus columbus | Lance Nematode | Hoplolaimus columbus | Lance Nematode |
| | Pseudomonas syringae pv. syringae | Bacterial Kernel Blight | Pseudomonas syringae pv. syringae | Bacterial Kernel Blight |

| CUSTOMER INFORMATION | | | |
|---|---|---|---|
| **Name:** | Mark Nichols | **Bill To:** | Mark Nichols |
| **Email** | markn@organisancorp.com | **Phone** | 678-935-8120 |

## Roots to Shoots Summary Report- Organisan-Impact SIX  V5 Corn

| **Sample Type** | Untreated | | | Treated | | | % Change | | |
|---|---|---|---|---|---|---|---|---|---|
| | Haney | Rhize | Tissue | Haney | Rhize | Tissue | Haney | Rhize | Tissue |
| **Health Overview** | 5.0 | 57% | 20 | 7.6 | 58% | 28 | 50% | 2% | 8.10 |
| **Community Structure** | 5.0 | 61% | | 7.6 | 61% | | 50.5% | 0.1% | |
| **Respiration** | 25.1 | 45% | | 46.4 | 46% | | 85.1% | 0.8% | |
| **Environmental Stressors** | | 50% | | | 41% | | | -9.2% | |
| **Carbon** | 83.0 | 52% | | 94.6 | 55% | | 13.9% | 3.4% | |
| **Nitrogen** | 48.4 | 61% | 3.66 | 91.1 | 57% | 3.00 | 88.2% | -4.7% | -18.0% |
| **Phosphorus** | 27.1 | 72% | 0.31 | 24.2 | 55% | 0.35 | -11.0% | -17.1% | 11.2% |
| **Potassium** | 48.4 | 55% | 1.70 | 55.2 | 51% | 2.16 | 14.2% | -3.7% | 26.9% |
| **Sulfur** | 3.5 | 43% | 0.24 | 4.2 | 46% | 0.27 | 19.0% | 2.6% | 11.1% |
| **Calcium** | 642.8 | 60% | 0.91 | 617.9 | 57% | 0.86 | -3.9% | -2.8% | -5.1% |
| **Iron** | 78.7 | 74% | 327.31 | 78.3 | 69% | 277.02 | -0.5% | -4.8% | -15.4% |
| **Zinc** | 0.6 | | 33.37 | 0.7 | | 40.20 | 23.7% | | 20.4% |
| **Manganese** | 2.6 | | 29.79 | 3.1 | | 38.97 | 16.9% | | 30.8% |
| **Magnesium** | 132.2 | | 0.63 | 115.4 | | 0.57 | -12.6% | | -9.5% |
| **Sodium** | 7.1 | | 0.02 | 6.7 | | 0.02 | -5.6% | | -14.3% |
| **Copper** | 0.3 | | 19.28 | 0.3 | | 22.17 | 8.6% | | 15.0% |
| **Aluminum** | 155.3 | | 183.28 | 135.7 | | 113.93 | -12.6% | | -37.8% |
| **Molybdenum** | | | 4.38 | | | 2.61 | | | -40.3% |
| **Boron** | | | 14.82 | | | 18.10 | | | 22.1% |

## CUSTOMER INFORMATION

| | | | |
|---|---|---|---|
| **Name:** | Mark Nichols | **Bill To:** | Mark Nichols |
| **Email** | markn@organisancorp.com | **Phone** | 678-935-8120 |

## Roots to Shoots Summary Report- Organisan-Impact SIX V5 Corn

| **Sample Type** | Untreated | | | Treated | | | % Change | | |
|---|---|---|---|---|---|---|---|---|---|
| | Haney | Rhize | Tissue | Haney | Rhize | Tissue | Haney | Rhize | Tissue |
| **Health Overview** | 5.0 | 57% | 20 | 7.6 | 58% | 28 | 50% | 2% | 8.10 |
| **Community Structure** | 5.0 | 61% | | 7.6 | 61% | | 50.5% | 0.1% | |
| Number of Genera | | 2890.3 | | | 2944.0 | | | 1.9% | |
| Diversity | | 54.0% | | | 62.0% | | | 14.8% | |
| Evenness | | 30.3% | | | 45.7% | | | 50.5% | |
| Mycorrhizae Abundance | | 39% | | | 46% | | | 6.7% | |
| Plant Stress Adaptation | | 74% | | | 73% | | | -0.4% | |
| Fungal to Bacterial Ratio | | | | | | | | | |
| Ectomycorrhizal to Arbuscular Ratio | | | | | | | | | |
| 1:1 Soil pH | 6.9 | | | 6.4 | | | -7.2% | | |
| Soil Health Calculation | 5.0 | | | 7.6 | | | 50.5% | | |
| Organic Matter | 3.0 | | | 4.0 | | | 34.4% | | |
| 1:1 Soluble Salt | 0.2 | | | 0.3 | | | 64.9% | | |
| Organic C:N | 9.6 | | | 9.1 | | | -5.7% | | |
| **Respiration** | 25.1 | 45% | | 46.4 | 46% | | 85.1% | 0.8% | |
| High Oxygen Environment | | 45% | | | 46% | | | 0.8% | |
| CO2-C | 25.1 | | | 46.4 | | | 85.1% | | |
| **Environmental Stressors** | | 50% | | | 41% | | | -9.2% | |
| Anoxic Environment | | 50% | | | 41% | | | -9.2% | |
| **Carbon** | 83.0 | 52% | | 94.6 | 55% | | 13.9% | 3.4% | |
| CO2-C | 25.1 | | | 46.4 | | | 85.1% | | |
| Organic Matter | 3.0 | | | 4.0 | | | 34.4% | | |
| Carbon Fixation | | 43% | | | 51% | | | 7.4% | |
| Organic Carbon Breakdown | | 65% | | | 64% | | | -1.6% | |
| Methanogenesis | | 53% | | | 49% | | | -4.4% | |
| H2O Total Organic C | 83.0 | | | 94.6 | | | 13.9% | | |
| % MAC | 30.3 | | | 48.8 | | | 60.8% | | |

## CUSTOMER INFORMATION

| | | | |
|---|---|---|---|
| **Name:** | Mark Nichols | **Bill To:** | Mark Nichols |
| **Email** | markn@organisancorp.com | **Phone** | 678-935-8120 |

## Roots to Shoots Summary Report- Organisan-Impact SIX V5 Corn

| **Sample Type** | Untreated | | | Treated | | | % Change | | |
|---|---|---|---|---|---|---|---|---|---|
| | Haney | Rhize | Tissue | Haney | Rhize | Tissue | Haney | Rhize | Tissue |
| **Health Overview** | 5.0 | 57% | 20 | 7.6 | 58% | 28 | 50% | 2% | 8.10 |
| **Nitrogen** | 48.4 | 61% | 3.66 | 91.1 | 57% | 3.00 | 88.2% | -4.7% | -18.0% |
| Nitrogen Fixation | | 59% | | | 50% | | | -8.5% | |
| Nodulating Bacteria | | 35% | | | 37% | | | 1.1% | |
| Organic Nitrogen Breakdown | | 72% | | | 65% | | | -7.2% | |
| H3A Ammonium | 1.6 | | | 1.9 | | | 17.1% | | |
| Nitrification | | 62% | | | 56% | | | -6.2% | |
| H3A Nitrate | 9.9 | | | 25.7 | | | 158.8% | | |
| Denitrification | | 47% | | | 44% | | | -2.9% | |
| H2O Total N | 19.6 | | | 37.3 | | | 90.2% | | |
| H2O Organic N | 8.7 | | | 10.4 | | | 20.5% | | |
| H3A Inorganic Nitrogen | 11.5 | | | 27.5 | | | 139.3% | | |
| Organic N Release | 8.7 | | | 10.4 | | | 20.5% | | |
| Organic N Reserve | 0.0 | | | 0.0 | | | | | |
| Available N | 48.4 | | | 91.1 | | | 88.2% | | |
| Total Nitrogen, % N | | | 3.7 | | | 3.0 | | | -18.0% |
| **Phosphorus** | 27.1 | 72% | 0.31 | 24.2 | 55% | 0.35 | -11.0% | -17.1% | 11.2% |
| Phosphorus Solubilization | | 72% | | | 55% | | | -17.1% | |
| H3A Total Phosphorus | 12.2 | | | 10.5 | | | -13.5% | | |
| H3A Inorganic Phosphorus | 9.2 | | | 7.4 | | | -19.6% | | |
| H3A Organic Phosphorus | 3.0 | | | 3.1 | | | 5.5% | | |
| Organic P Release | 2.6 | | | 3.1 | | | 19.7% | | |
| Organic P Reserve | 0.4 | | | 0.0 | | | -100.0% | | |
| Available P | 27.1 | | | 24.2 | | | -11.0% | | |
| Phosphorus, % P | | | 0.31 | | | 0.35 | | | 11.2% |

Contact RhizeBio:
Phone: 919-351-2038
Email: support@rhizebio.com

| CUSTOMER INFORMATION | | | |
|---|---|---|---|
| Name: | Mark Nichols | Bill To: | Mark Nichols |
| Email | markn@organisancorp.com | Phone | 678-935-8120 |

## Roots to Shoots Summary Report- Organisan-Impact SIX V5 Corn

| Sample Type | Untreated | | | Treated | | | % Change | | |
|---|---|---|---|---|---|---|---|---|---|
| | Haney | Rhize | Tissue | Haney | Rhize | Tissue | Haney | Rhize | Tissue |
| **Health Overview** | 5.0 | 57% | 20 | 7.6 | 58% | 28 | 50% | 2% | 8.10 |
| **Potassium** | 48.4 | 55% | 1.70 | 55.2 | 51% | 2.16 | 14.2% | -3.7% | 26.9% |
| Potassium Solubilization | | 55% | | | 51% | | | -3.7% | |
| H3A ICAP Potassium | 40.3 | | | 46.0 | | | 14.2% | | |
| Available K | 48.4 | | | 55.2 | | | 14.2% | | |
| Potassium, % K | | | 1.70 | | | 2.16 | | | 26.9% |
| **Sulfur** | 3.5 | 43% | 0.24 | 4.2 | 46% | 0.27 | 19.0% | 2.6% | 11.1% |
| Sulfur Oxidation | | 40% | | | 51% | | | 10.9% | |
| Sulfur Reduction | | 53% | | | 59% | | | 5.6% | |
| H3A ICAP Sulfur | 3.5 | | | 4.2 | | | 19.0% | | |
| Sulfur, % S | | | 0.24 | | | 0.27 | | | 11.1% |
| **Calcium** | 642.8 | 60% | 0.91 | 617.9 | 57% | 0.86 | -3.9% | -2.8% | -5.1% |
| Calcium Transport | | 60% | | | 57% | | | -2.8% | |
| H3A ICAP Calcium | 642.8 | | | 617.9 | | | -3.9% | | |
| Calcium, % Ca | | | 0.91 | | | 0.86 | | | -5.1% |
| **Iron** | 78.7 | 74% | 327.31 | 78.3 | 69% | 277.02 | -0.5% | -4.8% | -15.4% |
| Iron Acquisition | | 74% | | | 69% | | | -4.8% | |
| H3A ICAP Iron | 78.7 | | | 78.3 | | | -0.5% | | |
| Iron, ppm Fe | | | 327.31 | | | 277.02 | | | -15.4% |
| **Zinc** | 0.6 | | 33.37 | 0.7 | | 40.20 | 23.7% | | 20.4% |
| H3A ICAP Zinc | 0.6 | | | 0.7 | | | 23.7% | | |
| Zinc, ppm Zn | | | 33.37 | | | 40.20 | | | 20.4% |
| **Manganese** | 2.6 | | 29.79 | 3.1 | | 38.97 | 16.9% | | 30.8% |
| H3A ICAP Manganese | 2.6 | | | 3.1 | | | 16.9% | | |
| Manganese, ppm Mn | | | 29.79 | | | 38.97 | | | 30.8% |

## CUSTOMER INFORMATION

| | | | |
|---|---|---|---|
| **Name:** | Mark Nichols | **Bill To:** | Mark Nichols |
| **Email** | markn@organisancorp.com | **Phone** | 678-935-8120 |

## Roots to Shoots Summary Report- Organisan-Impact SIX V5 Corn

| **Sample Type** | Untreated | | | Treated | | | % Change | | |
|---|---|---|---|---|---|---|---|---|---|
| | Haney | Rhize | Tissue | Haney | Rhize | Tissue | Haney | Rhize | Tissue |
| **Health Overview** | 5.0 | 57% | 20 | 7.6 | 58% | 28 | 50% | 2% | 8.10 |
| **Magnesium** | 132.2 | | 0.63 | 115.4 | | 0.57 | -12.6% | | -9.5% |
| H3A ICAP Magnesium | 132.2 | | | 115.4 | | | -12.6% | | |
| Magnesium, % Mg | | | 0.63 | | | 0.57 | | | -9.5% |
| **Sodium** | 7.1 | | 0.02 | 6.7 | | 0.02 | -5.6% | | -14.3% |
| H3A ICAP Sodium | 7.1 | | | 6.7 | | | -5.6% | | |
| Sodium, % Na | | | 0.02 | | | 0.02 | | | -14.3% |
| **Copper** | 0.3 | | 19.28 | 0.3 | | 22.17 | 8.6% | | 15.0% |
| H3A ICAP Copper | 0.3 | | | 0.3 | | | 8.6% | | |
| Copper, ppm Cu | | | 19.28 | | | 22.17 | | | 15.0% |
| **Aluminum** | 155.3 | | 183.28 | 135.7 | | 113.93 | -12.6% | | -37.8% |
| H3A ICAP Aluminum | 155.3 | | | 135.7 | | | -12.6% | | |
| Aluminum, ppm Al | | | 183.28 | | | 113.93 | | | -37.8% |
| **Molybdenum** | | | 4.38 | | | 2.61 | | | -40.3% |
| Molybdenum, ppm Mo | | | 4.38 | | | 2.61 | | | -40.3% |
| **Boron** | | | 14.82 | | | 18.10 | | | 22.1% |
| Boron, ppm B | | | 14.82 | | | 18.10 | | | 22.1% |

Contact RhizeBio:
Phone: 919-351-2038
Email: support@rhizebio.com

| Report Date: | 1/16/2026 |
|---|---|

| CUSTOMER INFORMATION | | CUSTOMER INFORMATION | |
|---|---|---|---|
| **Name:** | Mark Nichols | **Grower Name:** | Mark Nichols |
| **Address:** | markn@organisancorp.com | **Field ID:** | Organisan-Impact SIX |
| **Phone:** | 678-935-8120 | **Crop Type:** | Corn |
| **Bill To:** | Organisan Corporation | **Crop Variety:** | Corn |

## Top 20 Bacterial Genera

AE = Aerobic   AN = Anaerobic   OA = Obligate Aerobic   ON = Obligate Anaerobic   F = Facultative   MA = Microaerophilic   ECM = Ecyomycorrhizal Fungi   AMF = Arbuscular Mycorrhizal Fungi

| Untreated | | | Treated | | | Response to Treatment | | |
|---|---|---|---|---|---|---|---|---|
| Genera | Abundance | Metabolism | Genera | Abundance | Metabolism | Genera | Change in Abundance | Metabolism |
| Streptomyces | 17.45% | aerobic | Streptomyces | 10.51% | aerobic | Streptomyces | ▼ -39.80% | aerobic |
| Enterobacter | 8.23% | aerobic | Nocardioides | 6.43% | obligate_aerobic | Enterobacter | ▼ -53.20% | aerobic |
| Nocardioides | 5.24% | obligate_aerobic | Priestia | 4.27% | NA | Nocardioides | ▲ 22.63% | obligate_aerobic |
| Priestia | 4.28% | NA | Enterobacter | 3.85% | aerobic | Priestia | ▼ -0.39% | NA |
| Bradyrhizobium | 3.94% | aerobic | Sphingomonas | 3.56% | aerobic | Bradyrhizobium | ▼ -9.97% | aerobic |
| Pseudomonas | 2.97% | aerobic | Bradyrhizobium | 3.55% | aerobic | Pseudomonas | ▼ -66.18% | aerobic |
| Kribbella | 2.20% | obligate_aerobic | Burkholderia | 2.28% | aerobic | Kribbella | ▼ -34.34% | obligate_aerobic |
| Microbacterium | 1.92% | aerobic | Rhizobium | 1.93% | obligate_aerobic | Microbacterium | ▼ -5.21% | aerobic |
| Mycobacterium | 1.87% | aerobic | Microbacterium | 1.82% | aerobic | Mycobacterium | ▼ -7.65% | aerobic |
| Glycomyces | 1.82% | obligate_aerobic | Mesorhizobium | 1.75% | obligate_aerobic | Glycomyces | ▼ -15.75% | obligate_aerobic |
| Rhizobium | 1.71% | aerobic | Mycobacterium | 1.73% | aerobic | Rhizobium | ▲ 13.28% | aerobic |
| Arthrobacter | 1.67% | obligate_aerobic | Glycomyces | 1.53% | obligate_aerobic | Arthrobacter | ▼ -18.56% | obligate_aerobic |
| Mesorhizobium | 1.47% | obligate_aerobic | Kribbella | 1.45% | aerobic | Mesorhizobium | ▲ 18.78% | obligate_aerobic |
| Mycolicibacterium | 1.04% | NA | Arthrobacter | 1.36% | obligate_aerobic | Mycolicibacterium | ▼ -9.58% | NA |
| Sphingomonas | 1.03% | aerobic | Pseudomonas | 1.00% | aerobic | Sphingomonas | ▲ 246.75% | aerobic |
| Burkholderia | 0.74% | aerobic | Mycolicibacterium | 0.94% | NA | Burkholderia | ▲ 208.56% | aerobic |
| Variovorax | 0.69% | aerobic | Micromonospora | 0.69% | obligate_aerobic | Variovorax | ▼ -58.74% | aerobic |
| Amycolatopsis | 0.63% | aerobic | Amycolatopsis | 0.61% | aerobic | Amycolatopsis | ▼ -3.68% | aerobic |
| Micromonospora | 0.58% | obligate_aerobic | Paraburkholderia | 0.52% | obligate aerobic | Micromonospora | ▲ 17.71% | obligate_aerobic |
| Lentzea | 0.54% | aerobic | Terrabacter | 0.49% | aerobic | Lentzea | NA | aerobic |

## Top 20 Fungal Genera

AE = Aerobic   AN = Anaerobic   OA = Obligate Aerobic   ON = Obligate Anaerobic   F = Facultative   MA = Microaerophilic   ECM = Ecyomycorrhizal Fungi   AMF = Arbuscular Mycorrhizal Fungi

| Untreated | | | Treated | | | Response to Treatment | | |
|---|---|---|---|---|---|---|---|---|
| Genera | Abundance | Metabolism | Genera | Abundance | Metabolism | Genera | Change in Abundance | Metabolism |
| Fusarium | 0.45% | facultative | Aspergillus | 0.50% | aerobic | Fusarium | ▼ -34.56% | facultative |
| Penicillium | 0.29% | aerobic | Fusarium | 0.30% | facultative | Penicillium | ▼ -81.61% | aerobic |
| Talaromyces | 0.29% | aerobic | Talaromyces | 0.25% | aerobic | Talaromyces | ▼ -13.95% | aerobic |
| Rhizopus | 0.13% | NA | Gigaspora | 0.17% | NA | Rhizopus | ▼ -69.23% | NA |
| Trichoderma | 0.09% | aerobic | Rhodotorula | 0.13% | NA | Trichoderma | ▼ -14.29% | aerobic |
| Alternaria | 0.08% | aerobic | Trichoderma | 0.08% | aerobic | Alternaria | ▼ -44.00% | aerobic |
| Staphylotrichum | 0.07% | NA | Rhizophagus | 0.07% | NA | Staphylotrichum | ▼ -76.19% | NA |
| Gigaspora | 0.04% | NA | Furcasterigmium | 0.05% | NA | Gigaspora | ▲ 284.62% | NA |
| Aspergillus | 0.04% | aerobic | Penicillium | 0.05% | aerobic | Aspergillus | ▲ 1061.54% | aerobic |
| Colletotrichum | 0.04% | NA | Alternaria | 0.05% | aerobic | Colletotrichum | ▼ -15.38% | NA |
| Rhodotorula | 0.03% | NA | Cantharellus | 0.05% | NA | Rhodotorula | ▲ 280.00% | NA |
| Mycena | 0.03% | NA | Cutaneotrichosporon | 0.05% | NA | Mycena | ▼ -80.00% | NA |
| Diaporthe | 0.03% | NA | Sporothrix | 0.04% | NA | Diaporthe | ▲ 33.33% | NA |
| Cutaneotrichosporon | 0.02% | NA | Diaporthe | 0.04% | NA | Cutaneotrichosporon | ▲ 100.00% | NA |
| Chaetomium | 0.02% | NA | Rhizopus | 0.04% | NA | Chaetomium | NA | NA |
| Cantharellus | 0.02% | NA | Colletotrichum | 0.04% | NA | Cantharellus | ▲ 180.00% | NA |
| Clonostachys | 0.02% | NA | Xylaria | 0.03% | NA | Clonostachys | NA | NA |
| Exophiala | 0.02% | NA | Lecanicillium | 0.02% | NA | Exophiala | ▼ -60.00% | NA |
| Coemansia | 0.01% | NA | Staphylotrichum | 0.02% | NA | Coemansia | NA | NA |
| Xylaria | 0.01% | NA | Purpureocillium | 0.02% | NA | Xylaria | ▲ 150.00% | NA |

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# Roots to Shoots Summary Report- Organisan-Impact SIX  V5 Corn

## Pathogen Screening

| | Untreated | | Treated | |
|---|---|---|---|---|
| | Average Number of Abundant Pathogens Identified: 4 | | Average Number of Abundant Pathogens Identified: 4.3 | |
| | Pathogen Species | Disease Common Name | Pathogen Species | Disease Common Name |
| **Replicate 1** | Hoplolaimus columbus | Lance Nematode | Globisporangium ultimum | Pythium Root Rot |
| | Pseudomonas syringae pv. syringae | Bacterial Kernel Blight | Sclerospora graminicola | Graminicola Downy Mildew |
| | Puccinia polysora | Southern Rust | Alternaria spp. | Black Point |
| | Meloidogyne arenaria | Root Knot Nematode | Hoplolaimus columbus | Lance Nematode |
| | Septoria spp. | Septoria Leaf Blotch | Pratylenchus spp. | Root Lesion Nematode |
| | | | Cladosporium spp. | Storage Molds |
| | | | Diabrotica virgifera | Western Corn Rootworm |
| **Replicate 2** | Penicillium oxalicum | Penicillium Ear Rot | Sclerospora graminicola | Graminicola Downy Mildew |
| | Penicillium oxalicum | Penicillium Ear Rot | Pratylenchus spp. | Root Lesion Nematode |
| | Penicillium oxalicum | Penicillium Ear Rot | Meloidogyne arenaria | Root Knot Nematode |
| | Cladosporium cladosporioides | Cladosporium Rot | Diabrotica virgifera | Western Corn Rootworm |
| | Pratylenchus spp. | Root Lesion Nematode | | |
| | Diabrotica virgifera | Western Corn Rootworm | | |
| **Replicate 3** | Puccinia polysora | Southern Rust | Cercospora zeae maydis | Gray Leaf Spot |
| | | | Pratylenchus spp. | Root Lesion Nematode |

| CUSTOMER INFORMATION | | | |
|---|---|---|---|
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## Roots to Shoots Summary Report- Organisan-Impact SIX  V8 Corn

| **Sample Type** | Untreated | | | Treated | | | % Change | | |
|---|---|---|---|---|---|---|---|---|---|
| | Haney | Rhize | Tissue | Haney | Rhize | Tissue | Haney | Rhize | Tissue |
| **Health Overview** | 9.6 | 55% | 30 | 12.3 | 55% | 34 | 28% | 0% | 4.09 |
| **Community Structure** | 9.6 | 59% | | 12.3 | 61% | | 28.0% | 3.0% | |
| **Respiration** | 64.5 | 58% | | 111.4 | 64% | | 72.6% | 6.1% | |
| **Environmental Stressors** | | 51% | | | 36% | | | -14.3% | |
| **Carbon** | 107.4 | 49% | | 91.3 | 57% | | -15.0% | 8.2% | |
| **Nitrogen** | 41.3 | 57% | 3.22 | 45.9 | 58% | 3.74 | 11.2% | 1.1% | 16.1% |
| **Phosphorus** | 24.9 | 70% | 0.32 | 19.9 | 70% | 0.34 | -20.0% | -0.4% | 6.3% |
| **Potassium** | 36.4 | 52% | 1.81 | 37.2 | 50% | 2.34 | 2.2% | -2.0% | 29.3% |
| **Sulfur** | 3.4 | 51% | 0.17 | 4.9 | 40% | 0.22 | 45.4% | -10.6% | 25.0% |
| **Calcium** | 604.3 | 42% | 0.63 | 596.3 | 35% | 0.73 | -1.3% | -7.3% | 15.9% |
| **Iron** | 73.6 | 76% | 197.67 | 60.9 | 77% | 232.05 | -17.2% | 0.3% | 17.4% |
| **Zinc** | 0.7 | | 34.97 | 0.8 | | 29.17 | 13.3% | | -16.6% |
| **Manganese** | 3.4 | | 28.76 | 3.8 | | 46.35 | 10.5% | | 61.1% |
| **Magnesium** | 110.3 | | 0.29 | 115.4 | | 0.39 | 4.6% | | 37.2% |
| **Sodium** | 6.0 | | 0.01 | 4.7 | | 0.01 | -21.9% | | 0.0% |
| **Copper** | 0.4 | | 10.79 | 0.4 | | 13.35 | 14.8% | | 23.7% |
| **Aluminum** | 111.6 | | 53.41 | 112.9 | | 98.77 | 1.2% | | 84.9% |
| **Molybdenum** | | | 2.74 | | | 2.93 | | | 6.9% |
| **Boron** | | | 16.76 | | | 21.60 | | | 28.9% |

| CUSTOMER INFORMATION | | | |
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## Roots to Shoots Summary Report- Organisan-Impact SIX V8 Corn

| **Sample Type** | Untreated | | | Treated | | | % Change | | |
|---|---|---|---|---|---|---|---|---|---|
| | Haney | Rhize | Tissue | Haney | Rhize | Tissue | Haney | Rhize | Tissue |
| **Health Overview** | 9.6 | 55% | 30 | 12.3 | 55% | 34 | 28% | 0% | 4.09 |
| **Community Structure** | 9.6 | 59% | | 12.3 | 61% | | 28.0% | 3.0% | |
| Number of Genera | | 3262.3 | | | 2886.7 | | | -11.5% | |
| Diversity | | 78.3% | | | 12.0% | | | -84.7% | |
| Evenness | | 33.3% | | | 5.3% | | | -84.0% | |
| Mycorrhizae Abundance | | 34% | | | 62% | | | 28.0% | |
| Plant Stress Adaptation | | 72% | | | 72% | | | 0.3% | |
| Fungal to Bacterial Ratio | | | | | | | | | |
| Ectomycorrhizal to Arbuscular Ratio | | | | | | | | | |
| 1:1 Soil pH | 7.0 | | | 6.8 | | | -3.8% | | |
| Soil Health Calculation | 9.6 | | | 12.3 | | | 28.0% | | |
| Organic Matter | 3.0 | | | 3.8 | | | 27.0% | | |
| 1:1 Soluble Salt | 0.1 | | | 0.2 | | | 23.8% | | |
| Organic C:N | 10.4 | | | 9.3 | | | -10.7% | | |
| **Respiration** | 64.5 | 58% | | 111.4 | 64% | | 72.6% | 6.1% | |
| High Oxygen Environment | | 58% | | | 64% | | | 6.1% | |
| CO2-C | 64.5 | | | 111.4 | | | 72.6% | | |
| **Environmental Stressors** | | 51% | | | 36% | | | -14.3% | |
| Anoxic Environment | | 51% | | | 36% | | | -14.3% | |
| **Carbon** | 107.4 | 49% | | 91.3 | 57% | | -15.0% | 8.2% | |
| CO2-C | 64.5 | | | 111.4 | | | 72.6% | | |
| Organic Matter | 3.0 | | | 3.8 | | | 27.0% | | |
| Carbon Fixation | | 41% | | | 42% | | | 0.7% | |
| Organic Carbon Breakdown | | 57% | | | 60% | | | 3.5% | |
| Methanogenesis | | 52% | | | 32% | | | -20.4% | |
| H2O Total Organic C | 107.4 | | | 91.3 | | | -15.0% | | |
| % MAC | 59.8 | | | 116.8 | | | 95.4% | | |

| CUSTOMER INFORMATION | | | |
|---|---|---|---|
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## Roots to Shoots Summary Report- Organisan-Impact SIX V8 Corn

| **Sample Type** | Untreated | | | Treated | | | % Change | | |
|---|---|---|---|---|---|---|---|---|---|
| | Haney | Rhize | Tissue | Haney | Rhize | Tissue | Haney | Rhize | Tissue |
| **Health Overview** | 9.6 | 55% | 30 | 12.3 | 55% | 34 | 28% | 0% | 4.09 |
| **Nitrogen** | 41.3 | 57% | 3.22 | 45.9 | 58% | 3.74 | 11.2% | 1.1% | 16.1% |
| Nitrogen Fixation | | 52% | | | 42% | | | -10.0% | |
| Nodulating Bacteria | | 42% | | | 48% | | | 6.1% | |
| Organic Nitrogen Breakdown | | 74% | | | 84% | | | 9.4% | |
| H3A Ammonium | 0.9 | | | 0.9 | | | -0.4% | | |
| Nitrification | | 51% | | | 49% | | | -2.0% | |
| H3A Nitrate | 6.0 | | | 8.4 | | | 40.7% | | |
| Denitrification | | 50% | | | 43% | | | -7.1% | |
| H2O Total N | 18.2 | | | 20.2 | | | 10.7% | | |
| H2O Organic N | 10.4 | | | 9.9 | | | -4.8% | | |
| H3A Inorganic Nitrogen | 6.8 | | | 9.3 | | | 35.4% | | |
| Organic N Release | 10.4 | | | 9.9 | | | -4.8% | | |
| Organic N Reserve | 0.0 | | | 0.0 | | | | | |
| Available N | 41.3 | | | 45.9 | | | 11.2% | | |
| Total Nitrogen, % N | | | 3.2 | | | 3.7 | | | 16.1% |
| **Phosphorus** | 24.9 | 70% | 0.32 | 19.9 | 70% | 0.34 | -20.0% | -0.4% | 6.3% |
| Phosphorus Solubilization | | 70% | | | 70% | | | -0.4% | |
| H3A Total Phosphorus | 10.8 | | | 8.7 | | | -20.1% | | |
| H3A Inorganic Phosphorus | 8.1 | | | 6.2 | | | -23.9% | | |
| H3A Organic Phosphorus | 2.7 | | | 2.5 | | | -8.6% | | |
| Organic P Release | 2.7 | | | 2.5 | | | -8.6% | | |
| Organic P Reserve | 0.0 | | | 0.0 | | | | | |
| Available P | 24.9 | | | 19.9 | | | -20.0% | | |
| Phosphorus, % P | | | 0.32 | | | 0.34 | | | 6.3% |

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| CUSTOMER INFORMATION | | | |
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## Roots to Shoots Summary Report- Organisan-Impact SIX V8 Corn

| **Sample Type** | Untreated | | | Treated | | | % Change | | |
|---|---|---|---|---|---|---|---|---|---|
| | Haney | Rhize | Tissue | Haney | Rhize | Tissue | Haney | Rhize | Tissue |
| **Health Overview** | 9.6 | 55% | 30 | 12.3 | 55% | 34 | 28% | 0% | 4.09 |
| **Potassium** | 36.4 | 52% | 1.81 | 37.2 | 50% | 2.34 | 2.2% | -2.0% | 29.3% |
| Potassium Solubilization | | 52% | | | 50% | | | -2.0% | |
| H3A ICAP Potassium | 30.4 | | | 31.0 | | | 2.2% | | |
| Available K | 36.4 | | | 37.2 | | | 2.2% | | |
| Potassium, % K | | | 1.81 | | | 2.34 | | | 29.3% |
| **Sulfur** | 3.4 | 51% | 0.17 | 4.9 | 40% | 0.22 | 45.4% | -10.6% | 25.0% |
| Sulfur Oxidation | | 35% | | | 35% | | | -0.1% | |
| Sulfur Reduction | | 33% | | | 54% | | | 21.1% | |
| H3A ICAP Sulfur | 3.4 | | | 4.9 | | | 45.4% | | |
| Sulfur, % S | | | 0.17 | | | 0.22 | | | 25.0% |
| **Calcium** | 604.3 | 42% | 0.63 | 596.3 | 35% | 0.73 | -1.3% | -7.3% | 15.9% |
| Calcium Transport | | 42% | | | 35% | | | -7.3% | |
| H3A ICAP Calcium | 604.3 | | | 596.3 | | | -1.3% | | |
| Calcium, % Ca | | | 0.63 | | | 0.73 | | | 15.9% |
| **Iron** | 73.6 | 76% | 197.67 | 60.9 | 77% | 232.05 | -17.2% | 0.3% | 17.4% |
| Iron Acquisition | | 76% | | | 77% | | | 0.3% | |
| H3A ICAP Iron | 73.6 | | | 60.9 | | | -17.2% | | |
| Iron, ppm Fe | | | 197.67 | | | 232.05 | | | 17.4% |
| **Zinc** | 0.7 | | 34.97 | 0.8 | | 29.17 | 13.3% | | -16.6% |
| H3A ICAP Zinc | 0.7 | | | 0.8 | | | 13.3% | | |
| Zinc, ppm Zn | | | 34.97 | | | 29.17 | | | -16.6% |
| **Manganese** | 3.4 | | 28.76 | 3.8 | | 46.35 | 10.5% | | 61.1% |
| H3A ICAP Manganese | 3.4 | | | 3.8 | | | 10.5% | | |
| Manganese, ppm Mn | | | 28.76 | | | 46.35 | | | 61.1% |

## CUSTOMER INFORMATION

| | | | |
|---|---|---|---|
| **Name:** | Mark Nichols | **Bill To:** | Mark Nichols |
| **Email** | markn@organisancorp.com | **Phone** | 678-935-8120 |

## Roots to Shoots Summary Report- Organisan-Impact SIX V8 Corn

| **Sample Type** | Untreated | | | Treated | | | % Change | | |
|---|---|---|---|---|---|---|---|---|---|
| | Haney | Rhize | Tissue | Haney | Rhize | Tissue | Haney | Rhize | Tissue |
| **Health Overview** | 9.6 | 55% | 30 | 12.3 | 55% | 34 | 28% | 0% | 4.09 |
| **Magnesium** | 110.3 | | 0.29 | 115.4 | | 0.39 | 4.6% | | 37.2% |
| H3A ICAP Magnesium | 110.3 | | | 115.4 | | | 4.6% | | |
| Magnesium, % Mg | | | 0.29 | | | 0.39 | | | 37.2% |
| **Sodium** | 6.0 | | 0.01 | 4.7 | | 0.01 | -21.9% | | 0.0% |
| H3A ICAP Sodium | 6.0 | | | 4.7 | | | -21.9% | | |
| Sodium, % Na | | | 0.01 | | | 0.01 | | | 0.0% |
| **Copper** | 0.4 | | 10.79 | 0.4 | | 13.35 | 14.8% | | 23.7% |
| H3A ICAP Copper | 0.4 | | | 0.4 | | | 14.8% | | |
| Copper, ppm Cu | | | 10.79 | | | 13.35 | | | 23.7% |
| **Aluminum** | 111.6 | | 53.41 | 112.9 | | 98.77 | 1.2% | | 84.9% |
| H3A ICAP Aluminum | 111.6 | | | 112.9 | | | 1.2% | | |
| Aluminum, ppm Al | | | 53.41 | | | 98.77 | | | 84.9% |
| **Molybdenum** | | | 2.74 | | | 2.93 | | | 6.9% |
| Molybdenum, ppm Mo | | | 2.74 | | | 2.93 | | | 6.9% |
| **Boron** | | | 16.76 | | | 21.60 | | | 28.9% |
| Boron, ppm B | | | 16.76 | | | 21.60 | | | 28.9% |

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RHIZE BIO

| Report Date: | 1/16/2026 |
|---|---|

| CUSTOMER INFORMATION | | CUSTOMER INFORMATION | |
|---|---|---|---|
| **Name:** | Mark Nichols | **Grower Name:** | Mark Nichols |
| **Address:** | markn@organisancorp.com | **Field ID:** | Organisan-Impact SIX |
| **Phone:** | 678-935-8120 | **Crop Type:** | Corn |
| **Bill To:** | Organisan Corporation | **Crop Variety:** | Corn |

## Top 20 Bacterial Genera

AE = Aerobic AN = Anaerobic OA = Obligate Aerobic ON = Obligate Anaerobic F = Facultative MA = Microaerophilic ECM = Ecyomycorrhizal Fungi AMF = Arbuscular Mycorrhizal Fungi

| **Untreated** | | | **Treated** | | | **Response to Treatment** | | |
|---|---|---|---|---|---|---|---|---|
| Genera | Abundance | Metabolism | Genera | Abundance | Metabolism | Genera | Change in Abundance | Metabolism |
| Pseudomonas | 13.70% | aerobic | Pseudomonas | 11.58% | aerobic | Pseudomonas | ▼ -15.47% | aerobic |
| Streptomyces | 8.03% | aerobic | Enterobacter | 7.14% | aerobic | Streptomyces | ▼ -25.71% | aerobic |
| Nocardioides | 5.40% | obligate_aerobic | Priestia | 6.43% | NA | Nocardioides | ▼ -56.82% | obligate_aerobic |
| Arthrobacter | 4.10% | obligate_aerobic | Burkholderia | 6.38% | obligate_aerobic | Arthrobacter | ▼ -2.52% | obligate_aerobic |
| Priestia | 4.09% | NA | Streptomyces | 5.96% | aerobic | Priestia | ▲ 57.08% | NA |
| Enterobacter | 3.65% | aerobic | Microbacterium | 4.09% | aerobic | Enterobacter | ▲ 95.53% | aerobic |
| Bradyrhizobium | 3.38% | aerobic | Arthrobacter | 4.00% | obligate_aerobic | Bradyrhizobium | ▼ -19.13% | aerobic |
| Rhizobium | 2.71% | aerobic | Micromonospora | 3.16% | aerobic | Rhizobium | ▼ -56.40% | aerobic |
| Microbacterium | 2.10% | aerobic | Bradyrhizobium | 2.73% | aerobic | Microbacterium | ▲ 94.61% | aerobic |
| Sphingobium | 1.88% | obligate_aerobic | Nocardioides | 2.33% | obligate_aerobic | Sphingobium | ▼ -83.89% | obligate_aerobic |
| Acinetobacter | 1.74% | aerobic | Pantoea | 1.48% | aerobic | Acinetobacter | NA | aerobic |
| Variovorax | 1.64% | aerobic | Rhizobium | 1.18% | aerobic | Variovorax | ▼ -61.71% | aerobic |
| Mesorhizobium | 1.42% | obligate_aerobic | Mesorhizobium | 1.13% | obligate_aerobic | Mesorhizobium | ▼ -20.37% | obligate_aerobic |
| Mycobacterium | 1.31% | aerobic | Paraburkholderia | 1.05% | aerobic | Mycobacterium | ▼ -23.86% | aerobic |
| Sphingomonas | 1.18% | aerobic | Mycobacterium | 1.00% | aerobic | Sphingomonas | ▼ -58.31% | aerobic |
| Burkholderia | 1.04% | obligate_aerobic | Glycomyces | 0.96% | aerobic | Burkholderia | ▲ 513.78% | obligate_aerobic |
| Mycolicibacterium | 1.03% | NA | Telluria | 0.70% | | Mycolicibacterium | ▼ -38.83% | NA |
| Phycicoccus | 0.93% | obligate_aerobic | Ralstonia | 0.67% | | Phycicoccus | ▼ -53.21% | obligate_aerobic |
| Kribbella | 0.79% | obligate_aerobic | Mycolicibacterium | 0.63% | NA | Kribbella | ▼ -67.65% | obligate_aerobic |
| Agrobacterium | 0.60% | aerobic | Variovorax | 0.63% | aerobic | Agrobacterium | NA | aerobic |

## Top 20 Fungal Genera

AE = Aerobic AN = Anaerobic OA = Obligate Aerobic ON = Obligate Anaerobic F = Facultative MA = Microaerophilic ECM = Ecyomycorrhizal Fungi AMF = Arbuscular Mycorrhizal Fungi

| **Untreated** | | | **Treated** | | | **Response to Treatment** | | |
|---|---|---|---|---|---|---|---|---|
| Genera | Abundance | Metabolism | Genera | Abundance | Metabolism | Genera | Change in Abundance | Metabolism |
| Fusarium | 0.20% | facultative | Pochonia | 0.23% | NA | Fusarium | ▲ 14.75% | facultative |
| Talaromyces | 0.11% | aerobic | Fusarium | 0.23% | facultative | Talaromyces | ▼ -73.53% | aerobic |
| Alternaria | 0.10% | NA | Colletotrichum | 0.19% | aerobic | Alternaria | ▼ -12.90% | NA |
| Gigaspora | 0.05% | aerobic | Sporothrix | 0.19% | aerobic | Gigaspora | ▲ 100.00% | aerobic |
| Penicillium | 0.04% | NA | Gigaspora | 0.10% | aerobic | Penicillium | NA | NA |
| Epicoccum | 0.04% | NA | Alternaria | 0.09% | NA | Epicoccum | ▼ -50.00% | NA |
| Aspergillus | 0.04% | aerobic | Rhodotorula | 0.09% | NA | Aspergillus | ▲ 9.09% | aerobic |
| Colletotrichum | 0.04% | aerobic | Chaetomium | 0.08% | NA | Colletotrichum | ▲ 418.18% | aerobic |
| Mucor | 0.04% | NA | Aspergillus | 0.04% | aerobic | Mucor | NA | NA |
| Gongronella | 0.04% | NA | Staphylotrichum | 0.03% | NA | Gongronella | ▼ -18.18% | NA |
| Chaetomium | 0.03% | NA | Talaromyces | 0.03% | aerobic | Chaetomium | ▲ 130.00% | NA |
| Diaporthe | 0.03% | NA | Gongronella | 0.03% | NA | Diaporthe | ▼ -33.33% | NA |
| Trichoderma | 0.03% | NA | Metarhizium | 0.03% | NA | Trichoderma | NA | NA |
| Mycena | 0.03% | NA | Cantharellus | 0.03% | NA | Mycena | ▼ -50.00% | NA |
| Rhodotorula | 0.03% | NA | Solicoccozyma | 0.02% | facultative | Rhodotorula | ▲ 225.00% | NA |
| Cladosporium | 0.03% | NA | Diaporthe | 0.02% | NA | Cladosporium | ▼ -75.00% | NA |
| Cutaneotrichosporon | 0.02% | NA | Epicoccum | 0.02% | NA | Cutaneotrichosporon | ▼ -40.00% | NA |
| Pochonia | 0.01% | NA | Mycena | 0.01% | NA | Pochonia | ▲ 1650.00% | NA |
| Metarhizium | 0.01% | NA | Moesziomyces | 0.01% | NA | Metarhizium | ▲ 125.00% | NA |
| Clonostachys | 0.01% | NA | Furcasterigmium | 0.01% | NA | Clonostachys | NA | NA |

# Roots to Shoots Summary Report- Organisan-Impact SIX  V8 Corn

## Pathogen Screening

### Untreated

| | Average Number of Abundant Pathogens Identified: 11.3 | |
|---|---|---|
| | **Pathogen Species** | **Disease Common Name** |
| **Replicate 1** | Phoma spp. | Phoma Leaf Spot |
| | Alternaria spp. | Black Point |
| | Hoplolaimus columbus | Lance Nematode |
| | Pseudomonas syringae pv. syringae | Bacterial Kernel Blight |
| | Exserohilum rostratum | Rostratum Leaf Spot |
| | Pratylenchus spp. | Root Lesion Nematode |
| | Robbsia andropogonis | Bacterial Stripe and Leaf Spot |
| | Waitea circinata | Rhizoctonia Ear Rot |
| | Diabrotica virgifera | Western Corn Rootworm |
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| **Replicate 2** | Hoplolaimus columbus | Lance Nematode |
| | Pseudomonas syringae pv. syringae | Bacterial Kernel Blight |
| | Puccinia polysora | Southern Rust |
| | Pratylenchus spp. | Root Lesion Nematode |
| | Fusarium acuminatum | Fusarium Root Rot Complex |
| | Fusarium acuminatum | Fusarium Root Rot Complex |
| | Diabrotica virgifera | Western Corn Rootworm |
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### Treated

| | Average Number of Abundant Pathogens Identified: 11 | |
|---|---|---|
| | **Pathogen Species** | **Disease Common Name** |
| **Replicate 1** | Globisporangium ultimum | Pythium Root Rot |
| | Sclerospora graminicola | Graminicola Downy Mildew |
| | Pythium spp. | Damping Off |
| | Pythium spp. | Damping Off |
| | Pythium spp. | Damping Off |
| | Hoplolaimus columbus | Lance Nematode |
| | Pseudomonas syringae pv. syringae | Bacterial Kernel Blight |
| | Puccinia polysora | Southern Rust |
| | Pratylenchus spp. | Root Lesion Nematode |
| | Robbsia andropogonis | Bacterial Stripe and Leaf Spot |
| | Meloidogyne arenaria | Root Knot Nematode |
| | Waitea circinata | Rhizoctonia Ear Rot |
| | Diabrotica virgifera | Western Corn Rootworm |
| **Replicate 2** | Globisporangium ultimum | Pythium Root Rot |
| | Phoma spp. | Phoma Leaf Spot |
| | Sclerospora graminicola | Graminicola Downy Mildew |
| | Cladosporium cladosporioides | Cladosporium Rot |
| | Hoplolaimus columbus | Lance Nematode |
| | Pseudomonas syringae pv. syringae | Bacterial Kernel Blight |
| | Globisporangium paroecandrum | Pythium Root Rot Complex |
| | Globisporangium debaryanum | Damping Off Complex |
| | Puccinia polysora | Southern Rust |
| | Pratylenchus spp. | Root Lesion Nematode |
| | Robbsia andropogonis | Bacterial Stripe and Leaf Spot |
| | Meloidogyne arenaria | Root Knot Nematode |
| | Diabrotica virgifera | Western Corn Rootworm |

| | | |
|---|---|---|
| **Replicate 3** | Sclerospora graminicola | Graminicola Downy Mildew |
| | Aspergillus versicolor | Storage Molds |
| | Aspergillus candidus | Storage Molds |
| | Cladosporium cladosporioides | Cladosporium Rot |
| | Alternaria spp. | Black Point |
| | Aspergillus ochraceus | Storage Molds |
| | Hoplolaimus columbus | Lance Nematode |
| | Pseudomonas syringae pv. syringae | Bacterial Kernel Blight |
| | Globisporangium paroecandrum | Pythium Root Rot Complex |
| | Puccinia polysora | Southern Rust |
| | Peronosclerospora sorghi | Sorghum Downy Mildew |
| | Pratylenchus spp. | Root Lesion Nematode |
| | Sarocladium strictum | Black Bundle Disease |
| | Robbsia andropogonis | Bacterial Stripe and Leaf Spot |
| | Meloidogyne arenaria | Root Knot Nematode |
| | Globisporangium irregulare | Root Dieback |
| | Fusarium proliferatum | Fusarium Wilt And Rot |
| | Diabrotica virgifera | Western Corn Rootworm |

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|---|---|
| Sclerospora graminicola | Graminicola Downy Mildew |
| Pseudomonas syringae pv. syringae | Bacterial Kernel Blight |
| Puccinia polysora | Southern Rust |
| Pratylenchus spp. | Root Lesion Nematode |
| Robbsia andropogonis | Bacterial Stripe and Leaf Spot |
| Meloidogyne arenaria | Root Knot Nematode |
| Diabrotica virgifera | Western Corn Rootworm |
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