

REGENERATIVE AGRICULTURAL DEVELOPMENT

Microbial application in corn cultivation

Two acres of corn treated with a **Bacillus** consortium and reduced NPK, set against adjacent control acres on standard fertiliser alone. 16S rRNA sequencing found the treated ground carrying a materially different microbial community, with **nitrogen cycling running several times faster**.

SITE

Prosper, Texas

2 acres treated, adjacent control

SAMPLED

13 August 2025

REPORT DATE

12 October 2025

PREPARED BY

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RAD Microbes

SEQUENCING

Environmental Genomics

16S rRNA

HEADLINE OUTCOMES

What the treated ground was doing that the control ground was not

133%More ammonia
oxidisers**786%**More nitrite
oxidisers**179%**More filamentous
bacteria**20–30%**Projected
fertiliser
reduction

133% & 786%

NITROGEN CYCLING

Ammonia oxidisers rose 133% and nitrite oxidisers 786% in the treated soil. Both steps of nitrification were running harder, which is what converts applied and mineralised nitrogen into a form the crop can take up. **This is the finding the rest of the trial rests on.**

179%

SOIL STRUCTURE

Filamentous bacteria rose 179%. These build aggregate structure and improve water retention. The population needs monitoring across seasons, but the direction is the one you want in a Texas summer.

~50%

PATHOGEN LOAD

Opportunistic pathogens appear roughly halved. Control soil carried *Streptococcus* and *Staphylococcus* among its enriched genera; treated soil did not.

5–15%

YIELD, PROJECTED

Enrichment of *Microvirga* and *Bacillus* points to a biofertiliser effect worth 20–30% off fertiliser cost and 5–15% on yield through better nutrient management. **These are projections from the microbial data, not measured harvest figures.**

EXECUTIVE SUMMARY

A comparative trial on working farmland, not a greenhouse

RAD Microbes ran a comparative field trial to assess what its microbial consortium does to corn ground. Two acres received the consortium plus NPK fertiliser at below standard rates. Adjacent control acres received standard NPK alone, with no microbes.

Soil samples analysed by 16S rRNA sequencing showed distinct microbial shifts in the treated soil, with improved nutrient cycling, functional diversity and resilience traits.

The treated ground carried higher levels of the bacteria that handle nitrogen and phosphorus, which is the mechanism behind reduced dependence on synthetic fertiliser and the environmental case that follows from it.

These findings support the company's work on bioinoculants for regenerative farming, and they were produced under real conditions on a real field rather than in a controlled environment.

BACKGROUND

Why this trial was run

RAD Microbes works on microbial solutions for regenerative agriculture, with an emphasis on bioinoculants that improve soil health, plant resilience and bioremediation while cutting synthetic chemical use.

This trial sits inside the company's research and development work, validating a **Bacillus**-based liquid culture consortium built on *Bacillus licheniformis*, *Bacillus megaterium* and *Bacillus subtilis*. Those strains were chosen for their ability to solubilise phosphates, break down organic matter and stimulate plant growth. The question the trial set out to answer was whether combining them with reduced fertiliser input would strengthen the soil microbial community enough to support efficient corn production in the field.

METHODOLOGY

How the trial was set up and sampled

LOCATION AND DESIGN

Two acres treated, adjacent acres held back

Corn fields in Prosper, Texas. Two acres were designated the treatment area and received the microbial consortium plus NPK applied at planting below standard rates. Adjacent control acres received only standard NPK per acre, with no microbes.

APPLICATION

Liquid inoculum at planting

The consortium was applied as a liquid inoculum during planting. Dosage and timing followed standard agricultural protocols so the application stayed compatible with corn growth stages.

SAMPLING AND ANALYSIS

16S rRNA sequencing, 13 August 2025

Soil samples were collected after treatment application and analysed by Environmental Genomics, covering bacterial taxa at 0.1% relative abundance or above. Functional traits, such as ammonia oxidation or phosphate accumulation, were inferred from established microbial databases.

On the strength of the evidence. This setup builds on earlier proof-of-concept work and provides evidence of microbial benefit under practical farming conditions. It is a single-season comparative trial on two acres. The microbial shifts are measured; the fertiliser and yield figures that follow from them are projections.

THE CONSORTIUM

Five microbial species, each doing a different job

The consortium is built so that the strains cover distinct functions rather than duplicating each other: enzyme production, mineral solubilisation, pathogen suppression, and the breakdown of chemistry the ground has already been exposed to.

Bacillus licheniformis

ORGANIC MATTER BREAKDOWN

Produces extracellular enzymes that degrade complex organic compounds, improving nutrient availability and soil fertility. This strengthens root systems and reduces reliance on chemical fertiliser.

Bacillus megaterium

PHOSPHATE SOLUBILISATION

Solubilises phosphate and trace minerals while producing extracellular polysaccharides that promote root colonisation and nutrient uptake. It supports plant development, higher yields and resilience in nutrient-deficient soils.

Bacillus subtilis

BIOCONTROL AND STRUCTURE

Secretes subtilisin enzymes and biosurfactants that suppress pathogenic fungi and bacteria, while improving soil structure and water infiltration through organic matter degradation. That dual role reduces pesticide need and builds natural soil resilience.

Pseudomonas protegens, P. fluorescens, P. chlororaphis

PESTICIDE DEGRADATION

Degrade recalcitrant pesticides and herbicides, supporting soil remediation and contaminant removal. These species restore soil health in chemically impacted ground, which is what makes low-residue agriculture possible on land with a history.

***Trametes* sp.**

WHITE-ROT FUNGI · BIOREMEDIATION

Degrades persistent pesticides and herbicides through ligninolytic enzymes. This detoxifies contaminated soils and aids ecosystem recovery, making the crop that follows a safer one.

RESULTS

Comparative bacterial traits

The sequencing data showed clear differences in microbial composition between the microbe-treated and fertiliser-only soils. Figures below are relative frequency percentages.

TRAIT	MICROBE-TREATED	FERTILISER-ONLY	NOTABLE DIFFERENCE
Ammonia oxidisers	1.00 	0.43 	133% higher, treated Improves nitrogen transformation.
Nitrite oxidisers	0.62 	0.07 	786% higher, treated Enhances the nitrification process.
Nitrite reducers	7.14 	8.21 	Slightly higher, control Indicates denitrification potential.
Phosphate accumulators	0.79 	0.28 	Higher, treated Boosts phosphorus availability
Glycogen accumulators	0.25 	0.00 	Treated soil only Aids biological phosphorus removal.
Filamentous bacteria	3.37 	1.29 	179% higher, treated Supports soil structure, needs monitoring.
Methylotrophs	0.24 	0.28 	Slightly higher, control Aids carbon cycling.

 Microbe-treated  Fertiliser-only

Bars are scaled against the highest single value in the table, 8.21% for nitrite reducers in the control soil, so the small traits read correctly against each other rather than each filling its own row.

RESULTS

Dominant genera at 0.1% abundance or above

MICROBE-TREATED

A spread of genera, none dominating

<i>Microvirga</i> Nitrogen fixing	5.6%
<i>Rubrobacter</i> Stress tolerant, arid soils	4.8%
<i>Ramlibacter</i> Nutrient cycling	3.6%
<i>Altererythrobacter</i> Organic matter turnover	2.9%
<i>Bacillus</i> Phosphate solubilising, nitrite reduction	2.6%

No single genus runs away with the population. That spread is the balanced, diverse community the consortium is meant to build.

FERTILISER-ONLY

Two genera taking most of the ground

<i>Ramlibacter</i>	11.4%
Much higher than treated	
<i>Altererythrobacter</i>	8.1%
Much higher than treated	
<i>Aquicella</i>	6.1%
Absent from treated soil	
<i>Sphingomonas</i>	4.0%
Heterotroph	
<i>Novosphingobium</i>	2.8%
Heterotroph	

A more uniform profile, with *Ramlibacter* and *Altererythrobacter* dominant. That pattern may signal nutrient imbalance and carries a longer-term risk of degradation.

ENRICHED, MICROBE-TREATED

What the consortium brought in

Microvirga, *Rubrobacter*, *Microlunatus*, *Gaiella*, *Tetrasphaera* (phosphate accumulator), *Nitrospira* (nitrite oxidiser), *Azospirillum*, *Defluviicoccus* (glycogen accumulator).

These drive nutrient cycling and plant growth. *Nitrospira* in particular is the organism behind the 786% nitrite oxidiser figure.

ENRICHED, FERTILISER-ONLY

What grew in its place

Aquicella, *Novosphingobium*, *Mucilaginibacter*, *Sphingobium*, *Streptococcus*, *Staphylococcus*.

A heavier heterotroph load, and the presence of *Streptococcus* and *Staphylococcus* is what sits behind the opportunistic pathogen reading.

DISCUSSION

What the profiles mean for the ground and for the farm

The consortium fosters a balanced, diverse community in the treated soil, against a more uniform profile in the control. The dramatic increases in nitrite oxidisers at 786% and ammonia oxidisers at 133% are the significant part: both raise nitrogen efficiency, which is what supports the projected 20–30% reduction in fertiliser need.

The 179% rise in filamentous bacteria supports better soil aggregation and water retention. The roughly 50% reduction in opportunistic pathogens points to better crop protection. Enriched genera such as *Microvirga*, which fixes nitrogen, and *Bacillus*, which solubilises phosphate, imply a biofertiliser effect leading to cost savings and yield gains of 5–15%.

In the control soil, dominance by *Ramlibacter* and *Altererythrobacter* may signal nutrient imbalance, which raises the long-term risk of degradation and the cost of farming that ground.

For a grower, the argument is three things. Land regenerates through organic matter buildup. Input cost falls. Profitability improves because the crop is more resilient. The trial is not an argument for abandoning fertiliser, it is evidence that microbes work as a complement to it.

CONCLUSIONS

Preliminary, and pointing in one direction

The trial confirms that the RAD Microbes consortium, integrated with reduced NPK, enhances soil microbial health and nutrient dynamics in corn ground. The changes suggest practical benefits in fertiliser savings, yield and environmental sustainability.

The results are preliminary. They come from one season, two acres and a single sampling date. What they establish is that the mechanism is real and measurable in the field, which is the point a trial of this size is meant to settle before a larger one is committed to.

WHAT HAPPENS NEXT

Already under way

50 acres

Expanded trial site

We are scaling from two acres to fifty, testing varying microbial doses against different NPK levels to find where the input reduction stops paying.

Multi-season

Long-term monitoring

We are tracking yield, soil nutrients and microbial stability across multiple seasons, which is the only way to know whether the filamentous population and the pathogen reduction hold.

REFERENCES AND ANALYSIS

Source data

MICROBE-ADDED SAMPLE

environmentalgenomics.com/data/sample/Px16QA7N/

FERTILISER-ONLY SAMPLE

environmentalgenomics.com/data/sample/AqkvYP8e/

SEQUENCING ANALYSIS

Environmental Genomics 16S rRNA sequencing analysis by Erik Rumbaugh, Microbiologist, RAD Microbes.

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Regenerative Agricultural Development. Living microbial consortia for soil biology, agriculture, and contaminated land and water.

THIS REPORT

Corn field trial, Prosper, Texas
Sampled 13 August 2025
Issued 12 October 2025
Bacillus consortium, reduced NPK

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Results are drawn from a single-season comparative trial on two treated acres with an adjacent control, sampled once on 13 August 2025. Microbial shifts are measured by 16S rRNA sequencing. Fertiliser reduction and yield figures are projections inferred from the microbial data, not measured harvest results. Outcomes vary with soil chemistry, contaminant profile and site conditions. Molecular diagnostics are delivered with our specialist United States microbiology partner.