The Bacterial *Methylorubrum extorquens* Product TS201 Induces Multiple Modes

of Action to Reduce Insect Feeding Damage on Maize

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ABSTRACT

Pink-pigmented facultative methylotrophs (PPFMs) are known to promote plant growth and enhance pathogen resistance, but their role in insect defense remains largely unexplored. Here, we report that TS201, a U.S. EPA-registered bioinsecticide composed of *Methylorubrum extorquens*, enhances maize defense against corn rootworms (CRW) and improves yield through plant-mediated mechanisms. Over seven years of small-plot trials at 22 U.S. Midwest locations, TS201 increased yield by 220 kg/ha under moderate to high CRW pressure. Additional trials demonstrated rooting and lodging benefits. Large-scale trials across 81 sites in eight U.S. states (2023–2024) validated its agronomic benefit. Transcriptomic and metabolomic analyses revealed activation of anthranilate production and increased accumulation of methyl anthranilate, a volatile CRW-repellent compound. Insect assays indicated significant larval avoidance of TS201-treated roots. These findings reveal a novel mode of action for PPFM-induced plant defense and demonstrate TS201 as a strategic microbial tool for integration into broad-spectrum integrated pest management programs.

Keywords: Pink-pigmented facultative methylotrophs, corn rootworm, pests, microbial product, methyl anthranilate, repellent, IPM.

INTRODUCTION

Plant-associated microbiomes host diverse microflora that often establish symbiotic relationships with their host plants, thereby conferring health benefits and

protective effects[1]. Bacteria within the *Methylobacterium* and *Methylorubrum* genera

constitute a significant component of the above-ground microbial community in the

phyllosphere and are also prevalent in the rhizosphere, the soil region surrounding plant

roots[2-5]. They are characterized as aerobic, Gram-negative, α-proteobacteria. These rod-

shaped organisms primarily metabolize one-carbon compounds such as methanol as

their principal energy source for growth and propagation[6,7]. Many *Methylobacterium* and

Methylorubrum species synthesize carotenoids, which impart a distinctive red to pink

coloration, designating them as pink-pigmented facultative methylotrophs (PPFMs)[8].

These bacteria are ubiquitous in nature, having been isolated from diverse habitats

including soil, freshwater, and various plant species[4,9].

Several PPFMs have been documented to promote plant growth by supplying

essential nutrients and modulating phytohormone levels[3]. These beneficial bacteria have

also been reported to offer protection against pathogens by inducing the plant defense

response including induced systemic resistance (ISR) against fungal rot pathogens in a

variety of crops[10-12]. ISR is characterized by a lag time between when the elicitor (in this

case, PPFMs) is applied and when the plant defense response is primed. After priming

occurs, the plant grows as normal. If a pest/pathogen attacks the plant later in the season,

then a potentiated defense response is activated and rapidly expressed throughout the

entire plant[13]. This increased response in both timing and magnitude results in reduced

damage to the host plant, and helps the plant efficiently balance growth and defense.

Additionally, ISR plant defense is considered to have low resistance capacity as part of

an integrated pest management (IPM) strategy[14]. Nevertheless, the potential role of these

bacteria in enhancing plants against insect herbivores remains largely unexplored,

despite evidence that many other microbial taxa can induce plant responses which reduce

herbivore damage and improve yield[15].

Corn rootworms (CRW) mainly comprising western corn rootworm (WCRW,

Diabrotica virgifera virgifera) and northern corn rootworm (NCRW, *Diabrotica barberi*) are

devastating pests of maize (*Zea mays*). Within the CRW complex, WCRW is the most

invasive and economically damaging species, with established populations across the

Americas and parts of Europe, whereas NCRW remains restricted to North America[16,17].

These pests are responsible for annual losses exceeding 2 billion USD, stemming from

both the cost of control measures and yield reductions due to larval root feeding

damage[18-20]. Larval feeding injures the root system and disrupts the plant's ability to

efficiently absorb water and nutrients from the soil, thereby compromising overall plant

vigor and structural stability[17,21]. In the presence of environmental stressors such as wind

and rainfall, even moderate levels of root damage can cause plants to lodge or topple in

the field[21]. Lodged plants exhibit reduced light interception and diminished photosynthetic

capacity, resulting in lower biomass accumulation and grain yield, while also complicating

mechanical harvesting and contributing to further losses through unharvested grain[19].

Furthermore, adult feeding on silks, pollen, kernels and foliage can occasionally result in

yield loss, particularly when populations reach high densities prior to anthesis[22].

Management of CRW in maize continues to be a challenge for current producers

since nearly all management strategies developed for controlling WCRW and NCRW

have faltered due to the adaptation of these pests. Resistance in WCRW and NCRW has

been documented to almost every management practice currently available to growers

including cultural control techniques (e.g., crop rotation)[23-25], chemical insecticides[26-29],

and transgenic maize hybrids expressing at least one of the four currently available

insecticidal toxins from *Bacillus thuringiensis* (Bt)[30-35], as well as innate plant resistance

factors[36] and double-stranded RNA (dsRNA) targeting WCRW essential genes[37,38].

Therefore, additional control tools need to be developed and implemented for sustainable

management programs of CRW[39].

Novel biological products which are among the fastest growing categories being

adopted by growers to date[40] provide additional management tools to mitigate corn

rootworm damage. However, biological control agents will only be commercially viable if

their cost and efficacy are comparable to commonly used chemical control strategies[41].

A variety of biological control agents including entomopathogenic fungi, bacteria and

nematodes, as well as a parasitoid and a predator have been investigated for managing

WCRW in the United States and Europe[42-47]. Additionally, several microbial plant

biostimulants including bacteria, fungi, and algae have been evaluated for their potential

to control WCRW[46,48]. Despite promising results in some laboratory and field trials, none

of the examined agents have yet been proven to be economically practical for large-scale

applications.

In this study, we report a PPFM isolate, *Methylorubrum extorquens* that mitigates

CRW damage in maize and improves yield. Initially, various PPFMs were evaluated as

biological inoculants (biostimulants) to enhance maize yield in contract research

organization (CRO) field trials across the U.S. Midwest. During one such trial, a field

experiencing high CRW pressure was subsequently impacted by a wind event, resulting

in widespread lodging in control plots without PPFM treatments. Notably, plots treated

with selective PPFM strains exhibited no lodging, leading to further investigation into their

potential activity for controlling CRW in maize. This observation initiated multiple years of

field trials to determine the most effective PPFM strain capable of both enhancing yield

and reducing CRW damage. Through this screening process, *M. extorquens* strain

NLS0042 designated TS201 was selected and further developed into a commercial

product. Due to its demonstrated biopesticidal properties, TS201 was registered as a

biological insecticide (TS201**™**, EPA Reg. No 95699-2, Terrasym®, NewLeaf Symbiotics,

St. Louis, MO) with the U.S. Environmental Protection Agency (EPA) in 2022, under the

regulatory framework of the Federal Insecticide, Fungicide, and Rodenticide Act

(FIFRA)[49].

Here, we evaluated the efficacy of TS201 in protecting and enhancing maize yield

under low to high CRW pressure in small-plot field trials conducted at 22 locations across

the U.S. Midwest over seven years. Subsequently, large-scale on-farm evaluations were

conducted across 81 locations in eight U.S. states over two years to assess yield

improvement under a diverse range of agronomic conditions. To elucidate the underlying

mode of action of TS201-induced maize defense against CRW, root phenotyping,

transcriptomic and GC-MS analyses combined with insect choice assays were performed.

RESULTS

Field trials demonstrated TS201 treatment increased root growth, reduced lodging,

and increased yield

Extensive field trials were conducted to evaluate the efficacy of TS201 in mitigating

CRW feeding damage and improving maize yield and overall agronomic performance.

Prior to its registration by the U.S. EPA in 2022, TS201 was restricted to small-scale evaluations, with testing restricted to a maximum of ~4.05 ha (10 acres) per year in accordance with EPA and USDA-APHIS guidelines. Following its registration, this acreage limitation was removed, enabling large-scale evaluations of TS201 in commercial scale field trials, i.e. over 4.05 ha per location, during the 2023 and 2024 growing seasons.

From 2016 to 2022, small-plot field trials conducted at 22 locations across the U.S. Midwest with low to high CRW pressure demonstrated that TS201 treatment significantly increased maize yield, with an average gain of 220 kg/ha (3.5 bushels/acre (bu/A)) (Table 1, Suppl. Tables 1-2) compared to the untreated control. These trials included locations where CRW pressure was confirmed and was greater than the economic injury threshold, as indicated by a minimum nodal injury score (NIS) of 0.25[50,51] in control plots, based on the Iowa State University 0–3 root damage rating scale[50]. Across all trial sites over seven years, TS201 treatment consistently and significantly reduced NIS by an average of 0.11, revealing improved root protection under CRW pressure (Table 1, Suppl. Table 1). This reduction in NIS was observed consistently in both corn hybrids with and without insecticidal traits targeting CRW such as Bt toxins and lethal dsRNA constructs (Suppl. Table 2).

Table 1. TS201 improves maize yield and root protection in small-plot field trials under corn rootworm pressure. Field trials were conducted over seven growing seasons (2016-2022) at 22 locations across the U.S. Midwest. Data represent phenotypic responses in TS201 treatment relative to untreated control. Values summarize key agronomic and root protection traits observed in replicated small-plot trials. NIS= Nodal injury score.

Metric	TS201 treatment compared to control	P-value	Trialing scale

Performance	Yield	+220 kg/ha 11,706 kg/ha (control) vs. 11,926 kg/ha (TS201)	0.0108	22 locations over 7 years
Root damage	Nodal injury score (NIS)	-0.11 NIS 1.34 (control) vs. 1.23 (TS201)	0.0007	22 locations over 7 years
	Lodging	-20% at moderate CRW pressure; -36% at high CRW pressure	NA*	2 locations over 1 year
Root enhancement (TS201 + biostimulant)	Root phenotyping	+25% increase in total root length in nodes 1–3	0.0376	1 location over 1 year

*The lodging experiment was conducted in nine replicates (locations) across distinct locations in four U.S states (i.e., Colorado, Illinois, Iowa, and Minnesota); however, only two sites exhibited larval root injury above the economic threshold (NIS > 0.25) and were subsequently included in lodging analysis, thereby precluding statistical analysis.

Lodging incidence was measured in two 0.1 ha (quarter-acre) on-farm strip field trials in 2020. Lodging is one of the most visible and economically consequential outcomes of CRW damage recognized by growers. At the site with moderate CRW pressure of 1.2 NIS, TS201 treatment resulted in a 20% reduction in lodging, from 59% lodging in control to 39% lodging in TS201-treated (Table 1). At the site under high CRW pressure of 2.7 NIS, lodging was reduced by 36%, from 65% in control to 29% in TS201-treated (Table 1).

Based on prior observations of reduced CRW feeding damage and plant lodging, a small-plot field trial was conducted in 2024 to evaluate the effects of TS201 on maize root system architecture when applied in combination with Terrasym 450, a maize biostimulant containing *Methylobacterium gregans*. The single location trial was conducted in low but economically relevant CRW pressure, with a mean NIS of 0.26, slightly above the economic threshold of 0.25[50,51]. Application of TS201 + Terrasym 450

resulted in consistent numerical increases in total root volume, surface area, cumulative

root length, and root tip number relative to the untreated control, independent of visible

feeding damage (Fig. 1, Table 1, Suppl. Tables 3 & 4). The most pronounced and

statistically significant enhancements were observed in nodal positions 1 through 3,

where total root length increased by 25%, primarily driven by a 39% increase in fine root

length (≤0.5 mm diameter) (Suppl. Table 4).

Figure 1. Enhanced maize root development observed under TS201 + Terrasym 450 treatment

compared to untreated control. Root systems were collected from a small-plot field trial conducted

in 2024 (10 plants per plot per replicate, four replicates per treatment). Following excavation and

pressure washing, roots were imaged through a structured phenotyping workflow: intact root

crowns imaged from below (top panel), then nodal segments were dissected and imaged (bottom

panel). Images shown are representative of each treatment.

In 2023 and 2024, yield performance by TS201 was evaluated in large-scale on-

farm evaluations in combination with Terrasym 450. Since these were commercial scale

evaluations, they were tested with grower standard practice (GSP) including a range of

corn hybrids, management practices, and insecticides as determined by the grower.

These trials were conducted across 81 locations in eight U.S. states, representing a

diverse range of agronomic conditions (Fig. 2a). The combined treatment with GSP

resulted in a significant yield increase of +351 kg/ha (5.6 bu/A, $P < 0.001$) and achieved

a 72% win rate compared to GSP alone ($P < 0.001$, Fig. 2b). Importantly, these trials were

included in the analysis regardless of actual CRW pressure to assess the agronomic

performance and economic return of the TS201-biostimulant combination under real-

world field conditions.

Figure 2. Large-scale on-farm evaluation of TS201 + Terrasym 450 in maize during 2023 and

2024 growing seasons across eight U.S. states. a) Geographic distribution of 81 commercial

evaluation sites within eight U.S. states: Colorado (CO), Iowa (IA), Illinois (IL), Indiana (IN),

Maryland (MD), Minnesota (MN), Nebraska (NE), and Wisconsin (WI). Trials were conducted

regardless of corn rootworm pressure to assess real-world agronomic performance. Map

background adapted from Google Maps (Map data ©2025 Google) with markers indicating county-level trial locations. b) Piano chart showing yield improvement of TS201 + Terrasym 450 + grower standard practice (GSP) as compared to GSP alone across large-scale on-farm trials (ranging from 4.05 to 40.5 ha per site, n=81).

Transcriptomic analysis revealed the upregulation of defense-related genes associated with WCRW repellent in TS201-treated maize roots.

To elucidate the molecular mechanisms by which TS201 influences maize physiology under CRW pressure, an RNA-Seq analysis was conducted using root tissue collected from a field trial in Illinois. In this study, maize was planted and treated with TS201 in April, and root samples were harvested in mid-July, coinciding with root digs conducted to determine CRW feeding damage on maize roots. TS201-treated root samples collected from their corresponding plots that exhibited both a reduction in NIS and an increase in grain yield compared to UTC plots were utilized in the differential gene expression analysis (Suppl. Table 5).

Five genes were significantly upregulated at $P<0.05$ and four additional genes were upregulated at $P<0.1$ in TS201-treated maize roots compared to those roots from control plots (Table 2), with several annotated as being involved in stress response and/or defense mechanisms based on the B73 maize reference genome. An additional 18 genes were identified as downregulated and are shown in Supplementary Table 6. Notably, two of the upregulated genes were annotated as components of the anthranilate biosynthetic pathway. This result led to the hypothesis that TS201-treated roots may produce methyl anthranilate, a volatile compound previously demonstrated to repel WCRW[52].

221 **Table 2.** Up-regulated genes in TS201-treated maize roots relative to untreated control roots.

222 TF= transcription factor, ROS=reactive oxygen species, ET=ethylene.

v4 Gene Model ID	Gene Symbol	Full Name	Putative Function	log2 Fold Change	Adjusted P-value
Zm00001d050455	pco096884	anthranilate N-benzoyltransferase protein 1	Anthranilate synthesis	1.63	0.0147
Zm00001d003395	ans1	anthranilate synthase homolog1	Anthranilate synthesis	1.55	0.0957
Zm00001d002799	hb66	Homeobox-transcription factor 66	TF in development	2.07	0.0995
Zm00001d049860	nactf75	NAC-transcription factor 75	TF in drought stress tolerance	1.73	0.0957
Zm00001d023617	lac23	laccase23	Enzyme in lignification/ defense	2.18	0.0957
Zm00001d024852	acco3	1-aminocyclopropane-1-carboxylate oxidase3	Enzyme in ET production	2.07	0.0408
Zm00001d002434	aox3	alternative oxidase3	Enzyme in ROS stress tolerance/ defense	1.85	0.0578
Zm00001d002052	NA	Probable isoaspartyl peptidase/ L-asparaginase 2	Nitrogen metabolism/ defense	2.48	<0.0001
Zm00001d011319	ZmABCG48	Probable ABCG Transporter 48	Transport	1.78	0.0408

Insect choice assays indicated that TS201-treated maize roots enhance the

production of volatile compound(s) that repel WCRW larvae.

To determine whether TS201 induces the release of CRW-repellent volatiles,

insect choice assays were conducted using a two-choice olfactometer system previously

used for WCRW behavioral studies[53]. Western corn rootworm, the most destructive and

economically significant species within the CRW complex, was selected as the insect

model for this study. Initial assays conducted three days post-treatment showed no

significant differences in larval behavior between TS201-treated and control roots (data

not shown). However, when assays were performed 10 days after seed treatment,

TS201-treated roots exhibited significant repellency effects on WCRW larvae compared

to the control.

Significantly fewer WCRW larvae were observed in all TS201-treated seed

treatments, both with and without WCRW infestation compared to untreated controls and

the infested arena (Figs. 3a, c–f). Notably, a significantly greater number of larvae were

recovered from the TS201-treated seed without WCRW infestation than from the

corresponding treatment with WCRW infestation (Fig. 3e), suggesting that prior herbivory

feeding may modulate volatile production or impose fitness cost in maize. Similarly, a

significantly higher proportion of larvae was found in the untreated seed with WCRW

infestation compared to those without infestation (Fig. 3b).

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Figure 3. Percentage of larvae approaching experimental treatments in two-choice bioassays.

Control: untreated seed without western corn rootworm (WCRW) infestation; TS201: TS201-

treated seed without WCRW infestation; WCRW: untreated seed with WCRW infestation; TS201

+ WCRW: TS201-treated seed with WCRW infestation. Bars with different letters are significantly

different (P < 0.05). Mean ± SEM (n=12 independent choice assays).

These results indicate that TS201 induces maize plants to increase the release of

volatile compounds that are strongly repellent to WCRW larvae. This defense response,

mediated by ISR[13], requires a characteristic lag period, typically 5 to 10 days, for priming

to become effective. Interestingly, larval feeding was not required under the assay

conditions to trigger the production of repellent volatiles, revealing that this effect was part

of the initial ISR priming defense response induced by TS201.

Enhanced methyl anthranilate emission in maize was uniquely induced TS201

To identify WCRW-repellent volatiles, volatile organic compounds (VOCs) from

TS201-treated maize plants and control plants were collected and analyzed using gas

chromatography coupled to quadrupole time-of-flight mass spectrometry (GC-QTOF-

MS). Among the 18 VOCs detected, methyl anthranilate was uniquely and markedly

induced by TS201 treatment (Fig. 4). TS201-treated plants exhibited a significantly higher

relative abundance of methyl anthranilate compared to untreated controls, whereas the

remaining 17 VOCs showed smaller magnitude or non-significant differences between

treatment groups (Fig. 4, Suppl. Tables 7 & 8). The elevated emission of methyl

anthranilate was not attributed to differences in plant size, as VOC levels were normalized

to plant biomass. Notably, the increase in methyl anthranilate production was

independent of WCRW herbivory, with higher levels detected in TS201-treated plants not

exposed to insect feeding. The emission pattern of this repellent compound corresponded

with results from insect choice assays conducted on the same set of plants, in which

significantly fewer WCRW larvae were found in TS201-treated plants compared to

controls (Suppl. Fig. 1).

Figure 4. TS201 induces methyl anthranilate emission in maize. A list of all detected volatiles is

available at Supplementary Table 7. Mean ± SEM (n ≥ 4). Untransformed data were presented,

whereas analyses were performed with log10 transformed data. Signficant differences between

the control and treated plants are indicated by *($P < 0.05$), **($P<0.01$), and ***($P<0.001$).

Methyl anthranilate repels WCRW larvae

To validate the repellent effects of methyl anthranilate, insect choice assays were

conducted using purified methyl anthranilate at varying concentrations. Across all assays,

the percentage of WCRW larvae approaching methyl anthranilate treatments either alone

or in combination with untreated maize plants was significantly lower than that observed

for untreated plants and the infested arena (Fig. 5). Methyl anthranilate exhibited a strong,

dose-dependent repellent effect against WCRW larvae, with few or no larvae found in its

treatments. Specifically, only 4.0 ± 2.5% of larvae approached the 0.1 µL methyl

anthranilate treatment (Fig. 5d), which was significantly higher than the responses to the

1 µL (0.8 ± 0.8%) and 10 µL (0%) (Figs. 5b, c, e, and f). No significant difference was

observed between untreated seed (40.9 ± 4.6%) and those with the solvent blank added

(38.7 ± 3.4%) (Fig. 5a).

Figure 5. Percentage of larvae approaching experimental treatments in two-choice bioassays.

Bars with different letters are significantly different (*P* < 0.05). Mean ± SEM (n=10 independent

choice assays). MA: methyl anthranilate.

DISCUSSION

By bridging molecular mechanisms with ecological outcomes, this study provides

a robust model for investigations into cross-kingdom signaling in agricultural ecosystems.

Our study establishes that the PPFM species, *M. extorquens*, formulated as TS201, offers

a novel and ecologically sound strategy for CRW management in maize. These findings

advance the current understanding of plant-microbe-insect interactions by revealing how

a naturally occurring rhizobacterium, originally isolated from the phyllosphere, can trigger

endogenous plant defense pathways to mitigate belowground herbivory. To our

knowledge, this is the first report demonstrating that a PPFM strain elicits ISR in plants

against a subterranean insect pest, while simultaneously enhancing crop vigor and yield.

Through an integrative approach combining multi-year field trials, root phenotyping,

transcriptomic profiling, metabolomic analysis, and insect behavioral assays, this work

presents a systems biology framework for harnessing microbially mediated plant defense

responses toward effective and sustainable crop protection. Mechanistically, we show

that TS201 modulates host transcriptional networks to activate volatile biosynthetic

pathways, illustrating a functional convergence between microbial colonization, host gene

expression, and volatile-mediated insect repellency (Fig. 6).

Figure 6. Schematic of TS201-induced enhancement of maize defense against western corn rootworm.

Our data provide compelling evidence that TS201 induces the biosynthesis of methyl anthranilate, a volatile compound previously documented to repel WCRW[52], through transcriptional activation of genes within the anthranilate biosynthetic pathway. Notably, this volatile-mediated repellency was elicited with and without herbivory, indicating that the TS201-induced systemic resistance mechanism was preemptively activated through microbial priming that requires a lag phase of more than three days post-application. ISR is characterized by the sensitization of the plant's defense machinery in the absence of immediate threat, enabling a faster and more robust activation of defensive responses upon biotic challenge. In contrast to systemic acquired resistance (SAR), which is primarily mediated by salicylic acid and is pathogen-specific, ISR typically engages jasmonic acid and ethylene signaling pathways and is triggered by beneficial rhizobacteria such as PPFMs[13,54,55]. Importantly, ISR does not constitutively activate defense genes but primes them for potentiated expression, conserving metabolic

resources while ensuring rapid deployment upon stress[56]. Furthermore, recent reports

suggest that ISR can coordinate systemic metabolic reprogramming, hormone crosstalk,

and oxidative signaling networks to strengthen plant resilience[57].

Across ecosystems, beneficial microbes are increasingly recognized as pivotal

architects of plant resilience against biotic stressors. Our study provides experimental

validation for the regulatory role of beneficial microbes in modulating plant-insect

interactions. Shikano, et al. [15] reviewed how beneficial microbes can influence insect

herbivores both directly and indirectly by altering plant defenses, nutritional quality, and

volatile profiles, building upon earlier foundational concepts of microbe-mediated

systemic resistance[13]. Here, we demonstrate that a naturally occurring PPFM species

activates a primed defense state in maize, significantly enhancing the production of

WCRW-repellent volatiles such as methyl anthranilate. Recent advances have expanded

the understanding of microbe-induced volatile signaling in shaping herbivore behaviors

both above- and below-ground[58,59]. Microbial modulation of root exudates has been

shown to influence herbivore foraging patterns[58], while herbivore-induced restructuring of

plant exudates can alter rhizosphere microbial communities with cascading effects on

insect performance[60]. Furthermore, overlapping microbiome functions across root and

shoot tissues have been shown to orchestrate systemic plant defenses against

herbivores[59]. Beneficial microbes also serve as chemical brokers, modulating

phytohormone signaling networks and orchestrating ISR-linked metabolic reprogramming

under multi-stressor environments[61]. Collectively, our findings indicate TS201 as a vital

integrator within this emerging paradigm, linking microbial application, volatile-mediated

defense priming, and pest deterrence, with direct translational relevance for advancing

sustainable and resilient agricultural systems.

Our results reveal TS201 as a major advancement in IPM strategies for CRW, a

pest complex that has evolved resistance to nearly all management tactics developed to

its control[30,39]. Unlike conventional insecticides and Bt traits that impose direct lethal

pressure and drive rapid resistance evolution, TS201 primes plant defenses through ISR,

activating endogenous pathways without direct toxicity, thereby minimizing selection

pressure and potentially preserving non-target organisms[14,62,63]. Whereas biological

control agents such as *Heterorhabditis bacteriophora* and microbial biostimulants have

demonstrated variable efficacy and inconsistent field performance[42,45,46,48], TS201

consistently enhances maize protection across diverse agroecosystems, independent of

pest pressure or environmental variability. These findings position TS201 as an

ecologically rational and needed addition to sustainable CRW management frameworks.

Beyond mitigating pest damage, TS201 significantly enhances agronomic

performance by enhancing maize root development, reducing lodging, and improving

yield under real-world production conditions. Over seven years of small-plot field trials

conducted at 22 locations across the U.S. Midwest under low to high CRW pressure,

TS201-treated maize consistently achieved a yield increase of 220 kg/ha relative to the

untreated control. When applied in combination with a biostimulant product Terrasym 450,

TS201 also improved maize root architecture, including increases in total root length and

the number of root tips, which is likely associated with reduced lodging. The greatest

effects were observed in the basal nodal zones, particularly among fine roots (0–0.5 mm

diameter). Taken together, these findings suggest that TS201 may provide early

protection by preserving finer, actively growing roots that are preferentially targeted by

CRW larvae[17,64]. Further studies at higher CRW pressure are needed to validate these

hypotheses.

Following U.S. EPA registration, large-scale on-farm evaluations during the 2023

and 2024 seasons across 81 geographically and agronomically diverse environments

further validated TS201's efficacy, with a yield gain of 351 kg/ha when applied in

combination with Terrasym 450. These findings demonstrate that TS201 promotes

scalable yield enhancement across diverse genotypes, soil microbiomes, and climatic

conditions. The ability of TS201 to stably induce plant-mediated defenses and metabolic

priming without reliance on pest pressure or chemical inputs aligns with emerging

paradigms advocating for microbiome-assisted crop improvement[65,66]. Moreover, the

integration of TS201 into production systems complements sustainable IPM frameworks,

which emphasize resilience, nutrient use efficiency, and reduced ecological footprint[67].

By leveraging plant-microbe signaling networks to CRW, TS201 addresses a critical need

in sustainable CRW management and promotes strategies for resilient agriculture[68].

This study highlights the transformative potential of harnessing beneficial microbes

to reengineer plant resilience for sustainable agriculture. By activating ISR and promoting

volatile-mediated defense, TS201 adds a fundamentally distinct mechanism to mitigate

CRW damage. Unlike conventional methods challenged to CRW resistance evolution,

TS201 strengthens innate plant defenses, while enhancing agronomic performance

across diverse environmental conditions. These findings bridge molecular insights with

ecological outcomes, demonstrating that microbe-induced priming strategies can achieve

both pest management and yield enhancement. Additionally, ISR is effective in many

plants and against many pests/pathogens, suggesting that TS201 would be effective

against other pests as well, an area that is under active investigation. As global agriculture

faces escalating biotic and abiotic pressures, TS201 exemplifies a next-generation

biopesticide that addresses the urgent need for resilient crop management strategies

leveraging plant-microbe interactions, delivering scalable efficacy across geographies,

ecological sustainability, and strategic compatibility with current IPM frameworks.

MATERIALS AND METHODS

Biological materials

The EPA registered biopesticide product TS201, containing *M. extorquens* strain

NLS0042 (2.0%, 1×10^9 CFU/g) as an active ingredient, was provided by NewLeaf

Symbiotics (St. Louis, MO). This bacterial strain was originally sourced from a soybean

plant in Saint Louis County, MO. Maize hybrids (P1197, Pioneer, Johnston, IA) were

purchased from local seed suppliers unless otherwise indicated.

Western corn rootworm neonates were obtained from a non-diapausing colony

maintained at the Plant Genetics Research Unit-USDA-ARS in Columbia, MO[32,69]. The

eggs were obtained in Petri dishes consisting of eggs and soil and were incubated at 25

± 1 °C in darkness in an incubator (Percival, Perry, IA). Neonates that hatched within 24

h were used for insect assays.

Field experiments

From 2016 to 2022, a series of 22 small-plot field trials were conducted across multiple locations in the U.S. Midwest with documented histories of elevated WCRW and NCRW damage, capturing variability in climate, soil type, and pest pressure. TS201 was evaluated as a standalone treatment to establish proof of concept under diverse field environments. During this pre-registration phase, trials were conducted under USDA-APHIS jurisdiction, with testing limited to a maximum of 4.05 ha (10 acres) per year in compliance with U.S. federal guidelines while EPA registration was in process.

The small-plot field experiments were designed as a randomized complete block design (RCBD) with four row plots 12 m (40 ft) in length and 4 to 6 replicates per location. TS201 was applied via multiple delivery methods to evaluate its efficacy and consistency under agronomically relevant deployment applications, including in furrow (309 g/ha, 1×10^9 CFU/g wettable powder), liquid seed treatment (1×10^6 CFU/seed application rate, 1×10^9 CFU/g wettable powder) or planter box application (0.5 oz/ unit seed or 14 g/ 8×10^4 maize seed, 1×10^9 CFU/g powder with seed lubricity agent). In each trial, the cooperating contract researcher selected the maize hybrid and agronomic management practices with base insecticide treatments specifically excluded, and these plots served as the untreated control. TS201 application was the sole treatment variable distinguishing the treated plots from the untreated control. In a subset of these trials, the same maize hybrids were evaluated with and without belowground CRW protection traits such as Bt traits, with TS201 application was the only difference from the untreated control. Trials were conducted under continuous maize cultivation (corn-on-corn rotations) with select sites incorporating squash trap crops to facilitate consistent CRW feeding pressure. Root damage was evaluated in mid-July to early August, corresponding with the observed

emergence of adult CRW beetles on maize plants, using the Iowa State University NIS system as described previously[50]. To determine the efficacy of TS201 under CRW pressure, only field trials in which untreated control plots exhibited an NIS score greater than 0.25, a common economic damage threshold[50,51], were analyzed. Grain yield data were collected as bu/A and converted to kg/ha using the conversion of 1 bushel as 25.4 kg[70].

In 2020, an on-farm experiment was carried out to evaluate the impact of TS201 on maize lodging under CRW pressure. The trial included nine replicates in distinct locations in IA, IL, MN, and CO. At each site, 0.1 ha (¼-acre) strips were assigned to compare the untreated control with an in-furrow application of TS201 (309 g/ha, 1×10^9 CFU/g). TS201 was applied to a corn hybrid without CRW protection traits. Roots were sampled along two defined transects (37 m) in each treatment, 20 roots total per treatment, pressure washed and rated using the NIS system. Out of nine locations, two in IA exhibited larval root injury exceeding the economic threshold (NIS > 0.25) and were included in lodging analysis. Based on NIS values, trial sites were categorized into low (0.25–1), moderate (1–2), or high (2–3) levels of CRW pressure levels. Lodging was quantified as the percentage of lodged plants within two, 37 m predefined transects for each treatment.

In 2024, building on prior observations of reduced CRW feeding damage and plant lodging, a small-plot field trial was conducted to evaluate the impact of TS201 on maize root system architecture when applied in combination with Terrasym 450. The trial was designed as a RCBD with four replicates. To determine baseline CRW pressure, roots from untreated control plots were sampled, pressure washed, and scored using the NIS

system[50]. Three weeks later, 10 root crowns per replicate were collected from both TS201

and Terrasym 450 treated and control plots to assess root architecture under CRW

pressure. Roots were imaged using a structured phenotyping workflow: intact crowns

imaged from below in the transverse plane and dissected nodal segments imaged per

individual crown to enable accurate imaging of total root length, root size classes, and

numbers of root tips. Root phenotyping images were analyzed using RhizoVision Explorer

v2.0.3[71]. All images included a size marker for normalization and to convert pixel

dimensions to metric units (mm). Dissected roots were grouped by node: 1-3, 4, 5, and

6. No node 7 roots were present in this study. Yield data were not collected, as the trial

employed destructive sampling for detailed root phenotyping.

Following EPA registration, field evaluations of TS201 shifted from small-plot

studies to large-scale, on-farm evaluations under commercial production conditions

during the 2023 and 2024 growing seasons. The large-scale field experiment included 81

replicates, each representing a maize field at different locations within eight U.S. states

(Fig. 2a). Across 81 trials (≥ 4.05 ha each), conducted in collaboration with contract

researchers and commercial growers, TS201 was applied in combination with Terrasym

450 as a planter box treatment (0.5 oz per unit of seed of each PPFM isolate at 1×10^9

CFU/g with seed lubricity agent) as an addition to the grower standard practice (GSP)

and evaluated in comparison to GSP alone for CRW management. GSP reflected real-

world production systems incorporating diverse IPM strategies, including combinations of

belowground CRW protection traits (e.g., Bt, RNAi), in-furrow insecticides, crop rotation,

and prior-season aerial applications targeting adult beetles. Trials were primarily

conducted in corn-on-corn systems in regions with a reported history of CRW pressure.

Experimental designs included full-field side-by-sides, split-planter setups, and replicated

strips ranging from 4.05 ha to over 40.5 ha. Win rate was determined by dividing the

number of trials with a positive yield over GSP by the total number of trials and converting

to a percentage. Yield data were collected using precision monitors or weigh wagons and

converted from bu/A to kg/ha as described above. Data were expressed as differences

relative to the GSP control.

Transcriptomic analysis

Root tissue samples from untreated and TS201-treated maize plants (one sample

per plot; six replicates per treatment) were collected from different RCBD plots in a field

trial. Total RNA was extracted using RNeasy Plant Mini Kits (74104, Qiagen,

Germantown, MD), treated with DNase using the RNase-Free DNase Set (Catalog

#15200, Qiagen), and assessed for RNA quality using an Agilent 2100 Bioanalyzer with

RNA 6000 Nano Kits (5067-1511, Agilent Technologies, Santa Clara, CA).

Root samples from TS201-treated plots that exhibited both increased yield and

reduced nodal injury scores (NIS) compared to control plots (three plots total) were used

for gene expression profiling using QuantSeq FWD 3′ mRNA-Seq using 75bp reads with

V2 Illumina chemistry (Lexogen, Vienna, Austria). QuantSeq is a tag-based sequencing

method that captures and sequences the 3′ end of polyadenylated transcripts, allowing

accurate gene expression quantification via read counting[72]. The B73 v.4 maize reference

genome was used for read alignment. Differential gene expression analysis was

performed using the BlueBee Genomics platform which utilizes DESeq2; genes were

considered differentially expressed if the $\log_2$ (fold change) was greater than 1.5 and the

adjusted *P*-value was less than 0.1[73]. All raw sequencing data have been deposited in

the NCBI Sequence Read Archive database with BioProject accession number

PRJNA1260573.

Insect choice assays

Untreated maize seeds were rinsed and incubated in distilled water overnight in a

Percival incubator maintained at $25 \pm 1°C$ to promote germination. After incubation, seeds

were dried out and treated with TS201 at a concentration of 1×10^6 CFU/seed, or with

sterile distilled water (0.01 mL/seed, untreated seed). Subsequently, 3 kernels were

planted per 50-mL conical tube and grown in the Percival incubator for 10 days. Plants

were watered with 2 mL of distilled water every other day. The experiment included four

treatment groups: untreated seed without WCRW infestation (control), serving as the

control, TS201-treated seed without WCRW infestation, untreated seed with WCRW

infestation, and TS201-treated seed with WCRW infestation. To allow for ISR priming to

occur, seeds were allowed to germinate and grow for 7 days prior to insect infestation.

Insect feeding was designed for 3-days to allow the potentiated ISR mediated-defense

response to occur, if required. On day 7, 8 WCRW neonates (<24 h old) were transferred

to plants assigned to infestation treatments. On day 10, plants were removed from the

soil using a fine paintbrush and used for insect choice assays.

Insect choice assays were conducted using a modified olfactometer system

adapted from Branson and Ortman[53]. The olfactometer consisted of three 50×15 mm

Petri dishes connected in a linear arrangement via 12 mm segments of Teflon tubing (8

mm I.D. $\times$ 10 mm O.D.). The bioassays were designed as a completely randomized

experiment. Ten WCRW neonates were introduced into the central arena, while treatment

and control plants were randomly assigned to the terminal arenas at either end of the

olfactometer. The experiment was conducted in complete darkness in the Percival

incubator, and larval positions were recorded after 30 minutes to assess behavioral

responses. The experiment was run in three cohorts at different times, with each cohort

consisting of four replicates, for a total of 12 replicates. Each replicate used unexposed

larvae and freshly prepared plant seedlings.

Larval behavioral response was quantified by calculating the proportion of larvae

that responded (PLR), using the formula: $PLR = Nr / Nt$, where Nr is the number of larvae

found in each zone (treatment side, control side, or infested center) at the end of the

assay (30 min), and Nt is the total number of larvae introduced[52].

GC-MS analysis

Volatile organic compounds from control and TS201-treated maize plants were

collected using a modified headspace sampling system based on the method described

previously[74]. Briefly, maize seeds were treated with TS201 or sterile water, and the

treated seeds were planted without WCRW infestation in 50-mL conical tubes as

previously described. At 10 days post-germination, seedlings were gently removed from

the soil using a fine paintbrush. Maize seedlings were transferred into a 50-mL collection

chamber (5 seedlings per chamber) fitted with Teflon tubing at both ends. One end of

each chamber was connected to a flow meter (B07B6HQDDW, Wuhan, China), which

was linked to a Whatman® carbon/HEPA filter capsule (WHA67041500, Sigma-Aldrich,

St. Louis, MO) and a 6-arm air delivery pump. The opposite end was connected to a

Tenax® TA thermal desorption tube (35/60 mesh, 0.25 in. O.D. × 3.5 in. length, Tenax®

TA, 29747-U, Sigma-Aldrich) for VOC trapping. Air was drawn through the chamber at a

flow rate of 2 mL/min for 90 minutes to collect volatiles. VOCs from blank chambers

containing sterile water and purified methyl anthranilate (≥98% purity, W268224, Sigma-

Aldrich) were used as negative and positive controls, respectively. Adsorbed compounds

were eluted from the Tenax tubes with 2 mL of methanol (Optima™ LC/MS Grade, A456,

Fisher Chemical, Waltham, MA) for GC-MS analysis. The volatile assay was conducted

as a completely randomized experiment with more than 4 replicates. Each replicate

consisted of freshly prepared, unexposed maize seedlings randomly assigned to

individual chambers within the headspace sampling system.

Headspace volatiles were analyzed using an Agilent 7890B gas chromatograph

(GC, Agilent Technologies, Santa Clara, CA) coupled to an Agilent 7250 quadrupole time-

of-flight mass spectrometer (QTOF-MS). Sample injection was performed using a Gerstel

multipurpose sampler. The GC-MS operating conditions were as follows: helium was

used as the carrier gas at a constant flow rate of 1 mL/min; injection volume was 1 µL

with a split ratio of 5:1; and the inlet temperature was maintained at 280 °C. The oven

temperature program began at 50 °C (held for 2 minutes), ramped at 6 °C/min to 215 °C,

then increased at 5 °C/min to 315 °C, where it was held for 12 minutes before cooling

back to 50 °C. Separation was performed using an Agilent DB-5MS capillary column (60

m × 250 µm i.d. × 0.25 µm film thickness). The MS transfer line was maintained at 250 °C,

and electron ionization (EI) was conducted at 70 eV. Mass spectra were acquired in full-

scan mode over a mass range of 40-650 m/z.

Data processing, including deconvolution, alignment, and compound identification,

was performed using MS-DIAL software, with spectral matching against an in-house

mass spectral library. The peak areas of identified compounds were integrated using

Agilent MassHunter Qualitative Analysis 10.0 and normalized to plant biomass (mg) to

determine their relative concentrations.

Insect choice assays with methyl anthranilate

To determine the behavioral response of WCRW larvae to methyl anthranilate

(MA), insect choice assays were conducted using the olfactometer system described

above. In each assay, purified methyl anthranilate (≥98% purity; Sigma-Aldrich) was

applied to one side of the olfactometer arena at concentrations of 0 (solvent control,

methanol), 0.1, 1, or 10 µg with and without untreated maize seedlings, while the opposite

side contained untreated maize seedlings. Ten neonate WCRW larvae (<24 h old) were

introduced into the central arena of the olfactometer, and larval distribution was recorded

after 30 minutes in complete darkness. Each treatment was replicated at least five times.

The proportion of larvae responding was calculated as described above to determine the

repellent effect of methyl anthranilate at each concentration.

Statistical analysis

The VOC data were analyzed using Student's unpaired t-test (PROC TTEST, SAS

9.4, SAS Institute, Cary, NC). Compounds were considered significantly induced when P

< 0.05 and $\log_{10}$(fold change) > 1. Other data (i.e., small-plot field trial, root phenotyping,

large-scale field trial, insect choice data) were analyzed using analysis of variance

(ANOVA) followed by pairwise comparisons of least squares means (LSMEANs) or

Fisher's least significant difference (LSD) for multiple comparisons. Analyses were

conducted using a generalized linear mixed model in PROC GLIMMIX (SAS 9.4) or JMP

v18.1.1 (JMP Statistical Discovery LLC, Cary, NC), with treatment specified as a fixed

effect and year, location, block, or replication as random effects. For win rate analysis,

trial-level outcomes were treated as binary responses (win = 1, loss = 0) and modeled

using a binomial distribution. Normality and homogeneity of variance were evaluated

using univariate analysis in PROC UNIVARIATE (SAS 9.4). Datasets that did not meet

these assumptions were transformed prior to analysis: percentage variables were arcsine

square-root transformed, and numeric variables were square-root transformed, to meet

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AUTHOR CONTRUBUTIONS

M.P.H. and N.W.B. wrote the first draft of the manuscript. M.P.H., B.E.H., and

N.W.B. designed and supervised the project. M.P.H., K-V.H., A.Z.P., A.F.E., A.J., and

N.W.B. performed the experiments. M.P.H., K.V.H., A.Z.P., Z.L., A.J., and N.W.B.

performed the analyses and provided the visualization. D.C.L., B.E.H., D.F., and N.W.B.

provided materials required for the experiments. All authors read and approved the final

version.

DATA AVAILABILITY

All raw transcriptomic sequencing data has been deposited in the Sequence Read

Archive database on NCBI with BioSample Accessions SAMN48399254,

SAMN48399255, SAMN48399256, SAMN48399257, SAMN48399258, SAMN48399259

under BioProject accession number PRJNA1260573. All other pertinent data are found

in the figures and tables. Request for data and additional information should be submitted

to the corresponding author.

COMPETING INTEREST

Anne Phillips, Allison Jack and Natalie Breakfield are employees of NewLeaf

Symbiotics, St. Louis, MO, USA. All other authors declare no competing interests.

REFERENCES

REFERENCES

1   del Carmen Orozco-Mosqueda, M., del Carmen Rocha-Granados, M., Glick, B.

R. & Santoyo, G. Microbiome engineering to improve biocontrol and plant

growth-promoting mechanisms. *Microbiol. Res.* **208**, 25-31 (2018).

2   Vorholt, J. A. Microbial life in the phyllosphere. *Nat. Rev. Microbiol.* **10**, 828-840

(2012).

3   Zhang, C., Wang, M.-Y., Khan, N., Tan, L.-L. & Yang, S. Potentials, utilization,

and bioengineering of plant growth-Promoting Methylobacterium for sustainable

agriculture. *Sustainability* **13**, 3941 (2021).

4   Lindow, S. E. & Brandl, M. T. Microbiology of the phyllosphere. *Appl. Environ.*

Microbiol. **69**, 1875-1883 (2003).

5   McNear Jr, D. H. The rhizosphere-roots, soil and everything in between. *Nat. Ed.*

Know. **4**, 1 (2013).

6   Green, P. N. & Ardley, J. K. Review of the genus *Methylobacterium* and closely

related organisms: a proposal that some *Methylobacterium* species be

reclassified into a new genus, *Methylorubrum* gen. nov. *Int. J. Syst. Evol* **68**,

2727-2748 (2018).

7   Schauer, S. & Kutschera, U. Methylotrophic bacteria on the surfaces of field-

grown sunflower plants: a biogeographic perspective. *Theory Biosci.* **127**, 23-29

(2008).

8   Green, P. N. & Bousfield, I. J. A taxonomic study of some Gram-negative

facultatively methylotrophic bacteria. *Microbiology* **128**, 623-638 (1982).

9   Kutschera, U. Plant-associated methylobacteria as co-evolved phytosymbionts: a

hypothesis. *Plant Signal. Behav.* **2**, 74-78 (2007).

10   Madhaiyan, M. *et al.* Plant growth–promoting *Methylobacterium* induces defense

responses in groundnut (*Arachis hypogaea* L.) compared with rot pathogens.

Curr. Microbiol. **53**, 270-276 (2006).

11   Madhaiyan, M. *et al.* Growth promotion and induction of systemic resistance in

rice cultivar Co-47 (*Oryza sativa* L.) by *Methylobacterium* spp. *Bot. Bull. Acad.*

Sin. **45** (2004).

12   Poorniammal, R., Sundaram, S. & Kumutha, K. *In vitro* biocontrol activity of

Methylobacterium extorquens against fungal pathogens. *Int. J. Plant Prot.* **2**, 59-

62 (2009).

13   Pieterse, C. M. *et al.* Induced systemic resistance by beneficial microbes. *Annu.*

Rev. Phytopathol. **52**, 347-375 (2014).

14   Köhl, J., Kolnaar, R. & Ravensberg, W. J. Mode of action of microbial biological

control agents against plant diseases: relevance beyond efficacy. *Front. Plant*

Sci. **10**, 845 (2019).

15   Shikano, I., Rosa, C., Tan, C.-W. & Felton, G. W. Tritrophic interactions: microbe-

mediated plant effects on insect herbivores. *Annu. Rev. Phytopathol.* **55**, 313-331

(2017).

16   Eben, A. Ecology and evolutionary history of *Diabrotica* beetles-overview and

update. *Insects* **13**, 156 (2022).

17   Chiang, H. C. Bionomics of the northern and western corn rootworms. *Annu.*

Rev. Entomol. **18**, 47-72 (1973).

18 Kahler, A. L., Olness, A. E., Sutter, G. R., Dybing, C. D. & Devine, O. J. Root

damage by western corn rootworm and nutrient content in maize. *Agron. J.* **77**,

769-774 (1985).

19 Spike, B. P. & Tollefson, J. J. Yield response of corn subjected to western corn

root worm (Coleoptera: Chrysomelidae) infestation and lodging. *J. Econ.*

Entomol. **84**, 1585-1590 (1991).

20 Wechsler, S. & Smith, D. Has resistance taken root in US corn fields? Demand

for insect control. *Amer. J. Agr. Econ.* **100**, 1136-1150 (2018).

21 Levine, E. & Oloumi-Sadeghi, H. Management of *diabroticite* rootworms in corn.

Annu. Rev. Entomol. **36**, 229-255 (1991).

22 Culy, M. D., Edwards, C. R. & Cornelius, J. R. Effect of silk feeding by western

corn rootworm (Coleoptera: Chrysomelidae) on yield and quality of inbred corn in

seed corn production fields. *J. Econ. Entomol.* **85**, 2440-2446 (1992).

23 Gray, M. E., Sappington, T. W., Miller, N. J., Moeser, J. & Bohn, M. O.

Adaptation and invasiveness of western corn rootworm: intensifying research on

a worsening pest. *Ann. Rev. Entomol.* **54**, 303-321 (2009).

24 Levine, E., Spencer, J. L., Isard, S. A., Onstad, D. W. & Gray, M. E. Adaptation of

the western corn rootworm to crop rotation: evolution of a new strain in response

to a management practice. *Am. Entomol.* **48**, 94-117 (2002).

25 Krysan, J., Jackson, J. & Lew, A. C. Field termination of egg diapause in

Diabrotica with new evidence of extended diapause in *D. barberi* (Coleoptera:

Chrysomelidae). *Environ. Entomol.* **13**, 1237-1240 (1984).

26   Ball, H. J. & Weekman, G. T. Insecticide resistance in the adult western corn

rootworm in Nebraska. *J. Econ. Entomol.* **55**, 439-441 (1962).

27   Meinke, L. J., Siegfried, B. D., Wright, R. J. & Chandler, L. D. Adult susceptibility

of Nebraska western corn rootworm (Coleoptera: Chrysomelidae) populations to

selected insecticides. *J. Econ. Entomol.* **91**, 594-600 (1998).

28   Pereira, A. E. *et al.* Evidence of field-evolved resistance to Bifenthrin in western

corn rootworm (*Diabrotica virgifera virgifera* LeConte) populations in Western

Nebraska and Kansas. *PLos one* **10**, e0142299 (2015).

29   Meinke, L. J., Souza, D. & Siegfried, B. D. The use of insecticides to manage the

western corn rootworm, *Diabrotica virgifera virgifera*, LeConte: history, field-

evolved resistance, and associated mechanisms. *Insects* **12**, 112 (2021).

30   Gassmann, A. J. Resistance to Bt maize by western corn rootworm: Effects of

pest biology, the pest–crop interaction and the agricultural landscape on

resistance. *Insects* **12**, 136 (2021).

31   Gassmann, A. J. *et al.* Sequential evolution of resistance by western corn

rootworm to multiple *Bacillus thuringiensis* traits in transgenic maize. *Proc. Natl.*

Acad. Sci. **122**, e2422337122 (2025).

32   Meihls, L. N. *et al.* Increased survival of western corn rootworm on transgenic

corn within three generations of on-plant greenhouse selection. *Proc. Natl. Acad.*

Sci. **105**, 19177-19182 (2008).

33   Gassmann, A. J., Petzold-Maxwell, J. L., Keweshan, R. S. & Dunbar, M. W.

Field-evolved resistance to Bt maize by western corn rootworm. *PLoS one* **6**,

e22629 (2011).

34 Zukoff, S. N. *et al.* Multiple assays indicate varying levels of cross resistance in

Cry3Bb1-selected field populations of the western corn rootworm to mCry3A,

eCry3.1Ab, and Cry34/35Ab1. *J. Econ. Entomol.* **109(3)**, 1387-1398 (2016).

35 Calles-Torrez, V. *et al.* Field-evolved resistance of northern and western corn

rootworm (Coleoptera: Chrysomelidae) populations to corn hybrids expressing

single and pyramided Cry3Bb1 and Cry34/35Ab1 Bt proteins in North Dakota. *J.*

Econ. Entomol. **112**, 1875-1886 (2019).

36 Robert, C. A. *et al.* A specialist root herbivore exploits defensive metabolites to

locate nutritious tissues. *Ecol. Lett.* **15**, 55-64 (2012).

37 Khajuria, C. *et al.* Development and characterization of the first dsRNA-resistant

insect population from western corn rootworm, *Diabrotica virgifera virgifera*

LeConte. *PLoS one* **13**, e0197059 (2018).

38 Darlington, M. *et al.* RNAi for western corn rootworm management: Lessons

learned, challenges, and future directions. *Insects* **13**, 57 (2022).

39 Paddock, K. J., Robert, C. A., Erb, M. & Hibbard, B. E. Western corn rootworm,

plant and microbe interactions: a review and prospects for new management

tools. *Insects* **12**, 171 (2021).

40 Jones, R. 4 ways to create next-generation messaging for biologicals. *CropLife*

News, Accessed May 14, 2025. www.agribusinessglobal.com/biologicals/2024-

ways-to-create-next-generation-messaging-for-biologicals/ (2021).

41 Van Rozen, K. & Ester, A. Chemical control against *Diabrotica v. virgifera*

LeConte: a review of the historical and current pest control strategies.

IOBC/IWGO Newsletter **28**, 7-11 (2007).

42 Toepfer, S. *et al.* A critical evaluation of host ranges of parasitoids of the subtribe

Diabroticina (Coleoptera: Chrysomelidae: Galerucinae: Luperini) using field and

laboratory host records. *Biocontrol Sci. Technol.* **18**, 483-504 (2008).

43 Pasquier, A. *et al.* A promising predator-in-first strategy to control western corn

rootworm population in maize fields. *Agronomy* **11**, 1984 (2021).

44 Pilz, C., Keller, S., Kuhlmann, U. & Toepfer, S. Comparative efficacy assessment

of fungi, nematodes and insecticides to control western corn rootworm larvae in

maize. *BioControl* **54**, 671-684 (2009).

45 Modic, Š., Žigon, P., Kolmanič, A., Trdan, S. & Razinger, J. Evaluation of the field

efficacy of *Heterorhabditis bacteriophora* Poinar (Rhabditida: Heterorhabditidae)

and synthetic insecticides for the control of western corn rootworm larvae.

Insects **11**, 202 (2020).

46 Jaffuel, G. *et al.* Protecting maize from rootworm damage with the combined

application of arbuscular mycorrhizal fungi, *Pseudomonas* bacteria and

entomopathogenic nematodes. *Scientific reports* **9**, 3127 (2019).

47 Journey, A. & Ostlie, K. Biological control of the western corn rootworm

(Coleoptera: Chrysomelidae) using the entomopathogenic nematode,

Steinernema carpocapsae. *Environ. Entomol.* **29**, 822-831 (2000).

48 Tarigan, S. I., Kiss, J., György, T., Doan, N. P. Y. & Toepfer, S. Effects of

microbial biostimulants on maize and its pest, the western corn rootworm,

Diabrotica virgifera virgifera. *Agronomy* **14**, 2239 (2024).

49 EPA. Summary of the Federal Insecticide, Fungicide, and Rodenticide Act.

Washington, D.C., United States: U. S. Environmental Protection Agency.

www.epa.gov/laws-regulations/summary-federal-insecticide-fungicide-and-

rodenticide-act (accessed on April 18, 2025). (1996).

50 Oleson, J. D., Park, Y.-L., Nowatzki, T. M. & Tollefson, J. J. Node-injury scale to

evaluate root injury by corn rootworms (Coleoptera: Chrysomelidae). *J. Econ.*

Entomol. **98**, 1-8 (2005).

51 Wright, B. Dig and rate roots to evaluate corn rootworm control. University of

Nebraska-Lincoln Extension. https://cropwatch.unl.edu/dig-and-rate-roots-

evaluate-corn-rootworm-control-0/ (accessed on May 5, 2025). (2008).

52 Bernklau, E. J., Hibbard, B. E., Norton, A. P. & Bjostad, L. B. Methyl anthranilate

as a repellent for western corn rootworm larvae (Coleoptera: Chrysomelidae). *J.*

Econ. Entomol. **109**, 1683-1690 (2016).

53 Branson, T. F. & Ortman, E. E. Feeding behavior of larvae of the western corn

rootworm: normal larvae and larvae maxillectomized with laser radiation. *Ann.*

Entomol. Soc. Am. **62**, 808-812 (1969).

54 Van der Ent, S. *et al.* Priming of plant innate immunity by rhizobacteria and β-

aminobutyric acid: differences and similarities in regulation. *New Phytologist* **183**,

419-431 (2009).

55 Durrant, W. E. & Dong, X. Systemic acquired resistance. *Annu. Rev.*

Phytopathol. **42**, 185-209 (2004).

56 Martinez-Medina, A. *et al.* Recognizing plant defense priming. *Trends Plant Sci.*

21, 818-822 (2016).

57 Yu, Y. *et al.* Induced systemic resistance for improving plant immunity by

beneficial microbes. *Plants* **11**, 386 (2022).

58   Erb, M. & Reymond, P. Molecular interactions between plants and insect

herbivores. *Annu. Rev. Plant Biol.* **70**, 527-557 (2019).

59   Bai, Y. *et al.* Functional overlap of the Arabidopsis leaf and root microbiota.

Nature **528**, 364-369 (2015).

60   Hu, L. *et al.* Root exudate metabolites drive plant-soil feedbacks on growth and

defense by shaping the rhizosphere microbiota. *Nat. Commun.* **9**, 2738 (2018).

61   Kolanchi, P. *et al.* Phytohormonal signaling network and immune priming

pertinence in plants to defend against insect herbivory. *Plant Stress*, 100850

(2025).

62   Bonanomi, G., Lorito, M., Vinale, F. & Woo, S. L. Organic amendments,

beneficial microbes, and soil microbiota: toward a unified framework for disease

suppression. *Annu. Rev. Phytopathol.* **56**, 1-20 (2018).

63   Timmusk, S., Behers, L., Muthoni, J., Muraya, A. & Aronsson, A.-C. Perspectives

and challenges of microbial application for crop improvement. *Front. Plant Sci.* **8**,

49 (2017).

64   Strnad, S. & Bergman, M. Distribution and orientation of western corn rootworm

(Coleoptera: Chrysomelidae) larvae in corn roots. *Environ. Entomol.* **16**, 1193-

1198 (1987).

65   Fitzpatrick, C. R. *et al.* The plant microbiome: from ecology to reductionism and

beyond. *Annu. Rev. Plant Biol.* **74**, 81-100 (2020).

66   Toju, H. *et al.* Core microbiomes for sustainable agroecosystems. *Nat. Plants* **4**,

247-257 (2018).

67   Mitter, E. K., Tosi, M., Obregón, D., Dunfield, K. E. & Germida, J. J. Rethinking

crop nutrition in times of modern microbiology: innovative biofertilizer

technologies. *Front. Sustain. Food Syst.* **5**, 606815 (2021).

68   Trivedi, P., Leach, J. E., Tringe, S. G., Sa, T. & Singh, B. K. Plant–microbiome

interactions: from community assembly to plant health. *Nat. Rev. Microbiol.* **18**,

607-621 (2020).

69   Huynh, M. P., Hibbard, B. E., Ho, K.-V. & Shelby, K. S. Toxicometabolomic

profiling of resistant and susceptible western corn rootworm larvae feeding on Bt

maize seedlings. *Scientific reports* **12**, 1-13 (2022).

70   Johanns, A. Metric conversions. Iowa State University Extension and Outreach.

https://www.extension.iastate.edu/AGDm/wholefarm/html/c6-80.html (accessed

on May 22, 2025). (2024).

71   Seethepalli, A. *et al.* RhizoVision Explorer: open-source software for root image

analysis and measurement standardization. *AoB Plants* **13**, plab056 (2021).

72   Ma, F. *et al.* A comparison between whole transcript and 3'RNA sequencing

methods using Kapa and Lexogen library preparation methods. *BMC Genomics*

20, 1-12 (2019).

73   Love, M. I., Huber, W. & Anders, S. Moderated estimation of fold change and

dispersion for RNA-seq data with DESeq2. *Genome Biol.* **15**, 1-21 (2014).

74   Som, S., Willett, D. S. & Alborn, H. T. Dynamics of belowground volatile diffusion

and degradation. *Rhizosphere* **4**, 70-74 (2017).