Supporting Information for

Nanosilica supplementation in tomato increases oviposition on stems and caterpillar mortality in the tomato pinworm

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Supporting Information Text

SI Methods.

Pilot Study to Determine Optimal Mesoporous Silica Nanoparticle (MSN) Amendment Rate

The planting substrate utilized in this study was composed of a 5:2 sand-to-manure (composted cattle manure) ratio, sterilized via autoclaving at 121°C under 15 psi pressure for 16 h. Mesoporous silica nanoparticles (MSN; ≥99.9% purity, particle size 50–80 nm; Chemazone Inc., Canada) were incorporated into the substrate at five concentrations: 0.2, 0.4, 0.6, 0.8, and 1.0 g/kg, alongside a control treatment devoid of nanosilica.

Tomato seeds (*Solanum lycopersicum*, cv. Nova F1), a widely cultivated variety in Kenya, were germinated in sterile seedling trays containing a standard seed mix. Seedlings were maintained under greenhouse conditions (22 ± 3°C day, 17 ± 3°C night, 60–80% relative humidity, and a 12-h light/dark cycle) until they reached 18 days post-germination. Subsequently, seedlings were transplanted into 13.5 cm × 16.0 cm pots containing substrate amended with the respective MSN concentrations.

Plant growth parameters were assessed at 4, 6, and 8 weeks after transplanting. Stem diameter was measured from 15 plants per treatment as biological replicates using a digital caliper to determine structural development. Leaf chlorophyll content was assessed using a Chlorophyll Meter SPAD-502Plus (Konica Minolta, Japan) to evaluate photosynthetic capacity. For each plant, measurements were taken from by gently placing the SPAD meter's sensor on three fully expanded leaves per plant, ensuring consistent positioning on the midrib of each leaf to avoid interference from veins (1). The average SPAD value was calculated for each plant, providing an estimate of chlorophyll content at 4, 6, and 8 weeks after transplanting. Based on consistent superior performance on stem diameter and moderate impact on SPAD chlorophyll concentration (see Fig. S1), the MSN concentration of 0.4 g/kg was selected for further experimentation.

Oviposition Experiments

Time-Dependent Oviposition Patterns

To evaluate the impact of MSN supplementation on the oviposition behavior of the tomato pinworm (*Phthorimaea absoluta*, TPW), a time-dependent oviposition experiment was conducted. Eight-week-old tomato plants from both +Si and –Si groups were randomly assigned to aerated cages (60 × 50 × 60 cm) under controlled environmental conditions (25 ± 1 °C, 65–70% relative humidity, and a 12-h light/dark cycle with red light (660 nm) to simulate crepuscular activity). The experimental cages were constructed from acrylic glass (5 mm thick) and insect-proof netting (mesh size 160 µm) to maintain ventilation while preventing insect escape.

TPW moths, with a 1:1 sex ratio, were sourced from the ICIPE-Nairobi, Kenya, mass rearing facility, where they were maintained under controlled conditions (25 ± 1 °C, 65–70% relative humidity, and a 06:45–18:45 h photoperiod). Each cage contained five seven-day-old gravid TPW moths, and the experiment was conducted over two intervals: 18 and 48 h. At the end of each exposure period, eggs laid on leaves and stem-petioles were counted using a 45× magnification LED magnifier. Ten to twelve plants were used as biological replicates for each oviposition period.

Sequential Oviposition

A sequential oviposition experiment was performed to determine how initial oviposition (iOVIP) influenced subsequent egg-laying behavior. Plants were exposed to initial oviposition durations of 18, 36, 48, or 72 h, during which gravid moths laid eggs. After each iOVIP period, the moths were carefully removed, and the eggs were counted and cleared to prevent density-dependent effects. The same moths were then reintroduced to the plants for an additional 18-h oviposition period under identical conditions. Eggs laid during this subsequent period were recorded. Six to nine biological replicates were used for each treatment group, and to ensure consistency, plants and moths were rotated between cages to minimize positional bias.

Chemical Analysis of Trichomes

Analysis of Sugars

Approximately 80 glandular trichomes were collected from the mid-stem region of each plant, with ~20 trichomes per plant pooled from four plants to ensure sufficient sample mass (~10 ± 0.04 µg). Trichomes were carefully excised using fine forceps under a dissecting microscope to ensure precision and avoid sampling stem surface tissues. Samples were homogenized in 100 µL of 80% methanol containing 0.1% formic acid using a FastPrep Tissue Homogenizer (MP Biomedicals, USA) at 6 m/s for 90 s. The homogenized extract was centrifuged at 10,000 rpm for 10 min at 4 °C, and the resulting supernatant (aqueous fraction) was carefully separated and oven-dried at 50 °C to remove residual solvents.

The dried fraction was derivatized with 75 µL of BSTFA N,O-bis(trimethylsilyl)trifluoroacetamide (Sigma-Aldrich, Germany). The vials were sealed, vortexed, and heated to 60 °C for 15 min to produce trimethylsilyl (TMS) derivatives for GC-MS analysis. A 2 µL aliquot of the derivatized sample was injected into a GC-MS system (Agilent 7890) equipped with an HP-5MS column. The system operated in splitless mode, with helium as the carrier gas at a constant flow rate of 1.25 mL/min. The temperature program for the GC oven started at 35 °C, ramped to 285 °C at 10 °C/min, and was held at the final temperature for 20.4 min. GC-MS data were processed using the Agilent Data Analysis Application. Sugars were identified by comparing the mass spectra of TMS derivatives with authentic standards where available, using the NIST spectral libraries as a secondary reference. Experiment-specific retention indices (RIs) were calculated relative to C5–C32 *n*-alkanes. Quantification was performed using a calibration curve for D-(−)-Fructose ($y = 5578.4x - 39{,}094$, $R^2 = 0.9990$). Data were expressed as nanograms of sugar per gram of trichome material. Five biological replicates were analyzed for each treatment group (+Si and –Si).

Analysis of Hydrocarbons

GT-I tissue (~10 µg) was collected from the mid-stem region of plants using fine forceps under a dissecting microscope, pooling ~20 trichomes from four plants per replicate, as described for sugar analysis. Samples were washed in 1.5 mL Eppendorf tubes with 200 µL of 80% cold methanol containing 0.1% formic acid, followed by three rinses with distilled water. Each wash involved gentle vortexing for 10 sec to ensure complete removal of surface metabolites. The washed trichome pellets were homogenized in 100 µL of methanol-formic acid (99:1, v/v) following the same procedure outlined in Sugar Analysis. After centrifugation at 10,000 rpm for 10 min at 4 °C, the supernatant was dried under a gentle nitrogen stream at room temperature and reconstituted in 100 µL of hexane. A 1 µL aliquot of the hexane extract was analyzed by GC-MS (Agilent 7890) equipped with an HP-5MS column. Instrument conditions, including the splitless injection mode, helium as the carrier gas at 1.25 mL/min, and the temperature ramp (40 °C to 310 °C, with a final hold of 5 min).

Hydrocarbons were identified by comparing their retention times and mass spectra with an alkane standard mixture (C_{10}–C_{40}, MilliporeSigma, USA) and validated using NIST spectral libraries. Quantification was performed using a calibration curve for tricosane (C23), with the equation $y = 9.5E + 05x - 9E + 07$ ($R^2 = 0.9877$). Results were expressed as nanograms of hydrocarbons per gram of trichome tissue. Six biological replicates were analyzed for each treatment group (+Si and –Si).

16S rRNA Sequencing of Microbial Communities in TPW Caterpillar Frass

Frass samples were collected in glass vials and pooled by caterpillar cohort (clip cage) as previously described. Each pooled sample weighed approximately 1 g, representing a single treatment group. A total of six pooled samples were analyzed as biological replicates. To ensure the preservation of microbial integrity, all frass samples were immediately stored at −80 °C. Mock samples were included during both DNA extraction and PCR amplification to monitor potential contamination.

DNA extraction from the pooled frass samples was performed using the DNeasy PowerSoil Kit (Qiagen) with protocol modifications, including an extended bead-beating step at 65 °C for 10 min to enhance microbial cell lysis. The purity and concentration of the extracted DNA were evaluated using a Nanodrop 2000 spectrophotometer (Thermo Fisher Scientific, Wilmington, USA). Library preparation followed the 16S Barcoding Kit (SQK-16S024; Oxford Nanopore Technologies, Oxford, UK) manufacturer's protocol. The PCR amplification process included an initial denaturation at 95 °C for 2 min, followed by 40 cycles of denaturation at 95 °C for 30 s, annealing at 55 °C for 45 s, and extension at 72 °C for 1 min, concluding with a final extension at 72 °C for 10 min. PCR reactions were performed using an Eppendorf Mastercycler™ Nexus Gradient thermal cycler (Eppendorf, Hamburg, Germany).

The resulting libraries were purified and loaded onto an ONT R9.4 flow cell (FLO-MIN106). Sequencing was conducted on a MinION Mk1C device (Oxford Nanopore Technologies) for 4 h, with real-time base calling carried out using MinKNOW software (v. 21.11.6) and MinKNOW Core (v. 4.5.4). The raw sequencing data were analyzed using the EPI2ME platform (version 2021.11.26). Taxonomic classification was performed using the 'What's In My Pot (WIMP)' workflow by Oxford Nanopore Technologies, enabling rapid species identification and quantification. Alpha diversity metrics (AEC, Chao1, and Shannon, indices) (2) were calculated to assess bacterial diversity across samples.

Differences in microbial communities were illustrated through Principal Coordinate Analysis (PCoA) employing non-metric multidimensional scaling (NMDS), implemented in R using the vegan package (v.2.43). Additionally, a chord diagram was used to depict relationships between bacterial phyla and treatment groups. All sequences generated in this study were deposited in GenBank database (www.ncbi.nlm.nih.gov/genbank) under BioProject PRJNA1214729.

Frass VOC Analysis and Natural Enemy Responses to Caterpillar Frass Volatiles

Frass samples (3 g per replicate) were pooled by caterpillar cohort and prepared for VOC trapping using methods described in plant volatile trapping. A total of seven replicates were analyzed. VOCs were collected from frass headspace for 3 h using Porapak Q adsorbents, with airflow maintained at 260 mL/min via a flow meter (AALBORG, USA). Trapped VOCs were eluted with 100 µL of DCM and stored at −80 °C until analysis. VOCs were analyzed using an Agilent 7890A GC coupled to a 5975C MS, with parameters identical to those used for plant VOC analysis. Identification was based on retention times and mass spectra compared against the NIST database, with synthetic standards used where available. VOC quantification was expressed as nanograms per gram of frass per h (ng/g/h) relative to fresh weight.

Behavioral responses of natural enemies to frass volatiles were tested using a glassware Y-tube olfactometer (0.5 cm i.d.; 6 cm stem; two 6 cm side arms at a 60° angle). Airflow was maintained at 120 mL/min using purified air delivered through activated charcoal. VOCs were applied to 3 cm diameter filter paper, allowing solvent evaporation for 60 sec before placement in one olfactometer arm. Fifth-instar nymphs of the predator *Nesidiocoris tenuis* and 2-day-old mated adult females of the parasitoid *Neochrysocharis formosa* were used. Before testing, insects were exposed to clean air for an hour to acclimate. Each test condition included 80 insects, with 10 insects tested per day across 8 experimental days. Individual insects were observed for 10 min, with responsiveness defined as spending at least 30 sec in one olfactometer arm.

Three test conditions were evaluated: clean air versus crude frass VOCs, clean air versus individual synthetic VOCs applied at natural release rate by 3 g frass (see Table S3), and crude VOCs versus synthetic VOCs.

SI Results

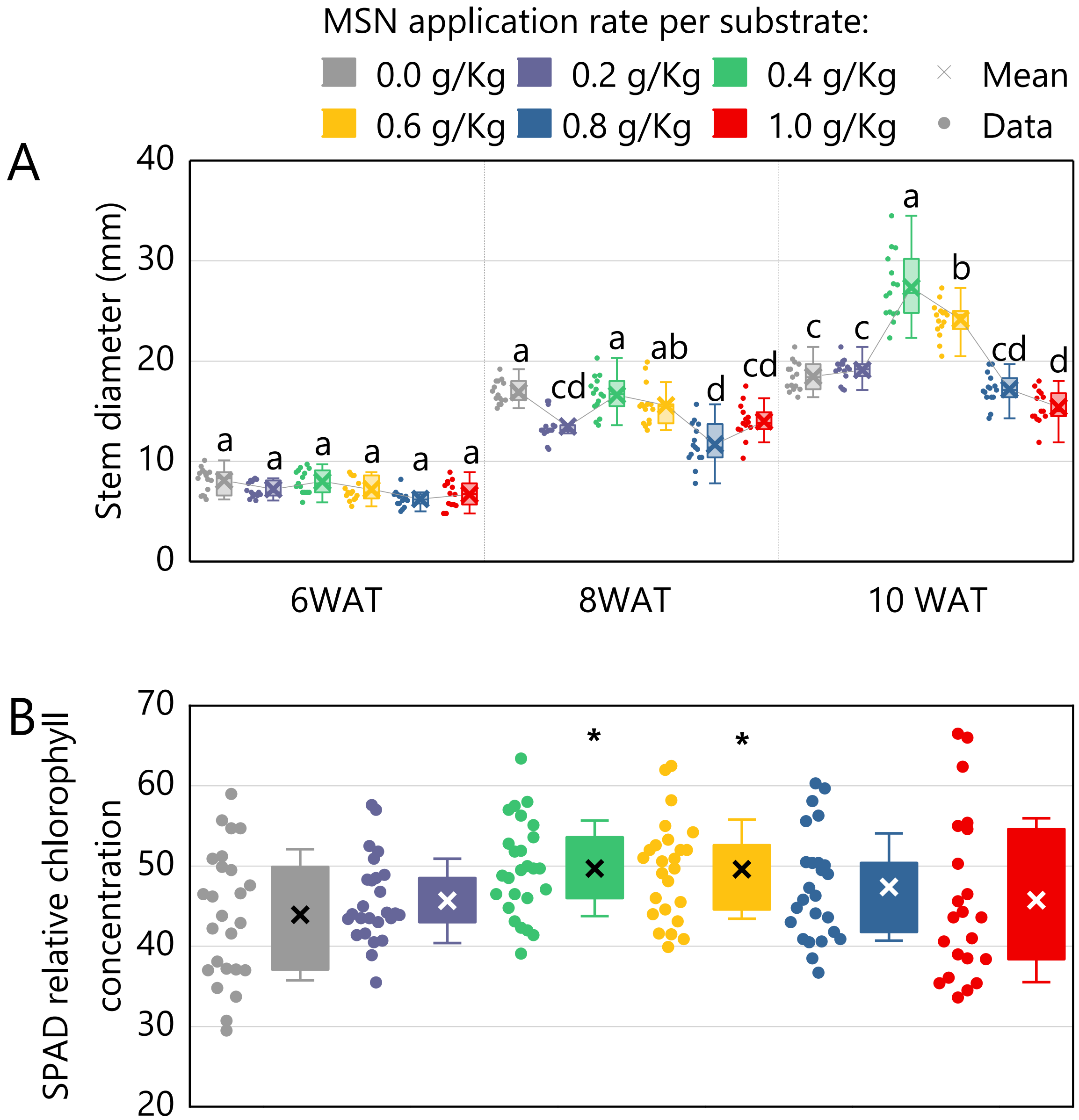

Fig. S1. Effects of MSN supplementation on tomato stem diameter (mm) and leaf chlorophyll concentration (SPAD values). (A) Stem diameter (mm) of tomato plants measured at 6, 8, and 10 weeks after transplanting (WAT) under different MSN application rates (g/kg substrate). Data are presented as box plots with means calculated from 15 plants per treatment. Different letters above the boxes indicate significant differences ($p < 0.05$) based on Tukey's post hoc test. Exact p-values are 6 WAT ($p = 0.38$ (6 WAT), 8 WAT ($p < 0.0001$), and 10 WAT ($p < 0.0001$). (B) SPAD chlorophyll concentration in tomato leaves under different MSN application rates (g/kg substrate). Bars represent means calculated from 15 plants per treatment, with asterisks (*) denoting significant differences compared to the control ($p < 0.05$). Exact p-values are 0 vs 0.2 ($p = 0.86$), 0 vs 0.4 ($p = 0.02$), 0 vs 0.6 ($p = 0.02$), 0 vs 0.8 ($p = 0.30$), and 0 vs 1 ($p = 0.86$). Overall, the 0.4 and 0.6 g/kg MSN rates resulted in the highest stem diameter and SPAD chlorophyll concentrations, indicating optimal plant growth parameters.

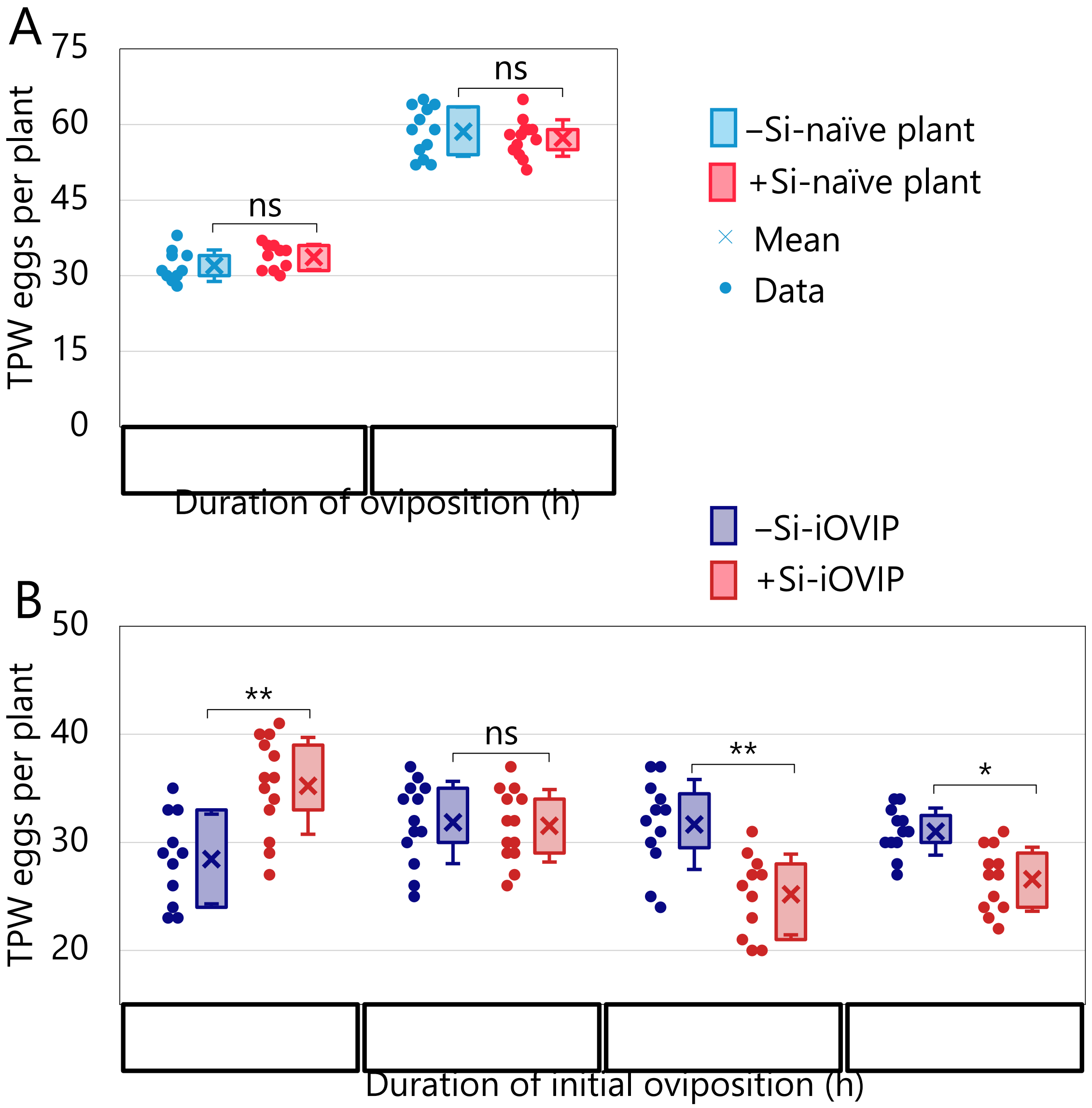

Fig. S2. Effects of Prior Oviposition Exposure on Subsequent Oviposition Patterns of TPW on Tomato Plants. (A) Total eggs laid by TPW on naïve tomato plants after 18-h and 48-h exposure. No significant differences were observed between treatments at either time point ($\chi^2 = 0.44$, $p = 0.51$ at 18 h; $\chi^2 = 0.07$, $p = 0.79$ at 48 h). (B) Oviposition responses of TPW on +Si-iOVIP and −Si-iOVIP plants at 18 h, 36 h, 48 h, and 72 h. Significant differences were observed at 18 h ($\chi^2 = 8.58$, $p = 0.003$), 48 h ($\chi^2 = 8.49$, $p = 0.004$), and 72 h ($\chi^2 = 4.07$, $p = 0.04$), while no significant differences were found at 36 h ($\chi^2 = 0.02$, $p = 0.89$). Box plots represent mean ± SD, and dots indicate individual data points. Statistical significance is denoted as ns (not significant), * ($p < 0.05$), and ** ($p < 0.01$).

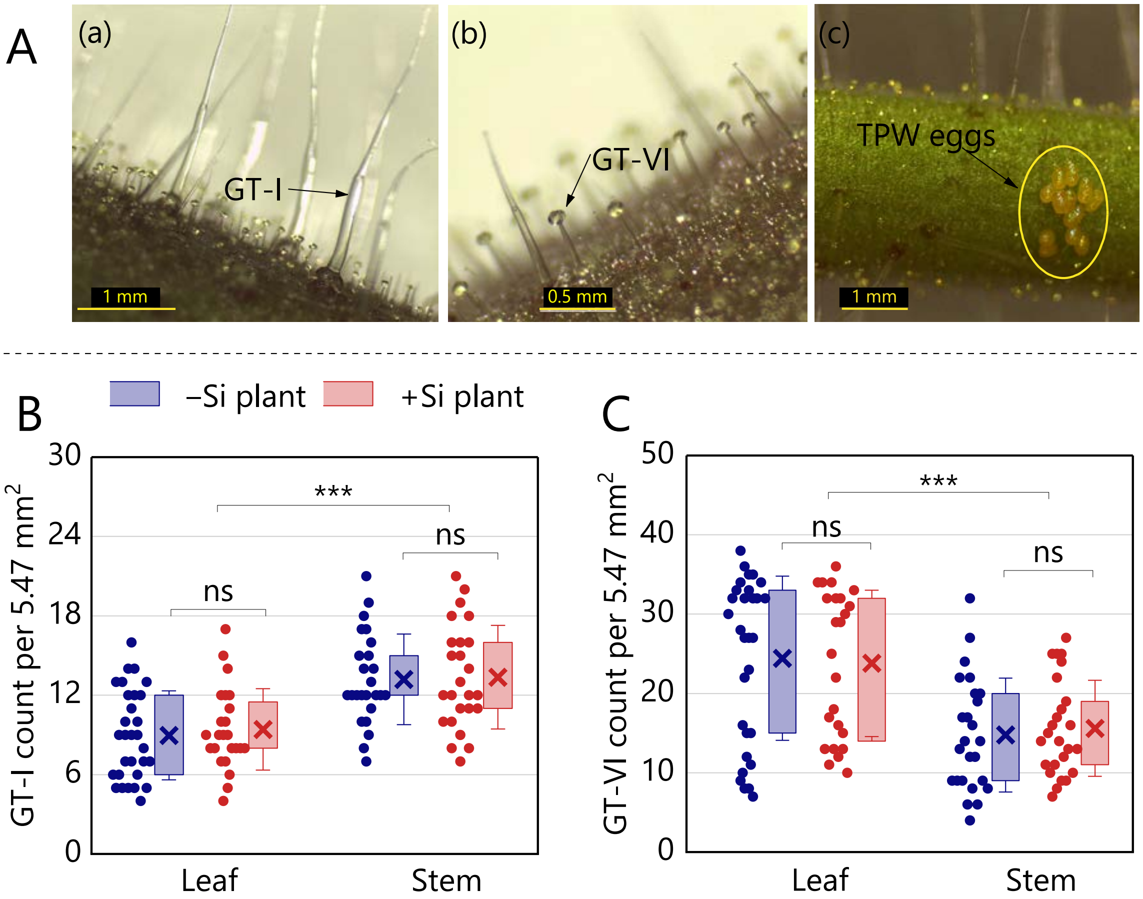

Fig. S3. Effects of MSN Supplementation on Trichome Density and TPW Oviposition on Tomato Plants. (A) Representative images of glandular trichome type I (GT-I) (a) and glandular trichome type VI (GT-VI) (b) on leaves and stems of +Si and –Si plants. Inset (c) shows TPW eggs laid on stems. Scale bars: GT-I = 0.5 mm, GT-VI = 1 mm, TPW eggs = 1 mm. (B) GT-I trichome density (count per 5.47 mm^2) on leaves and stems of +Si and –Si plants. Regardless of MSN supplementation, GT-I density was significantly higher on stems than leaves ($\chi^2 = 39.45$, $p < 0.0001$). However, MSN supplementation had no significant effect on trichome density on either leaves ($\chi^2 = 0.2940$, $p = 0.59$) or stems ($\chi^2 = 0.02$, $p = 0.88$). (C) GT-VI trichome density (count per 5.47 mm^2) on leaves and stems of +Si and –Si plants. GT-VI density was significantly higher on leaves than stems ($\chi^2 = 106.81$, $p < 0.0001$), but MSN supplementation had no significant effect, with similar trichome densities observed on leaves ($\chi^2 = 0.23$, $p = 0.63$) and stems ($\chi^2 = 0.58$, $p = 0.44$). Box plots show mean ± SD, with individual data points represented by dots. Statistical significance is indicated as ns (not significant) and *** ($p < 0.001$).

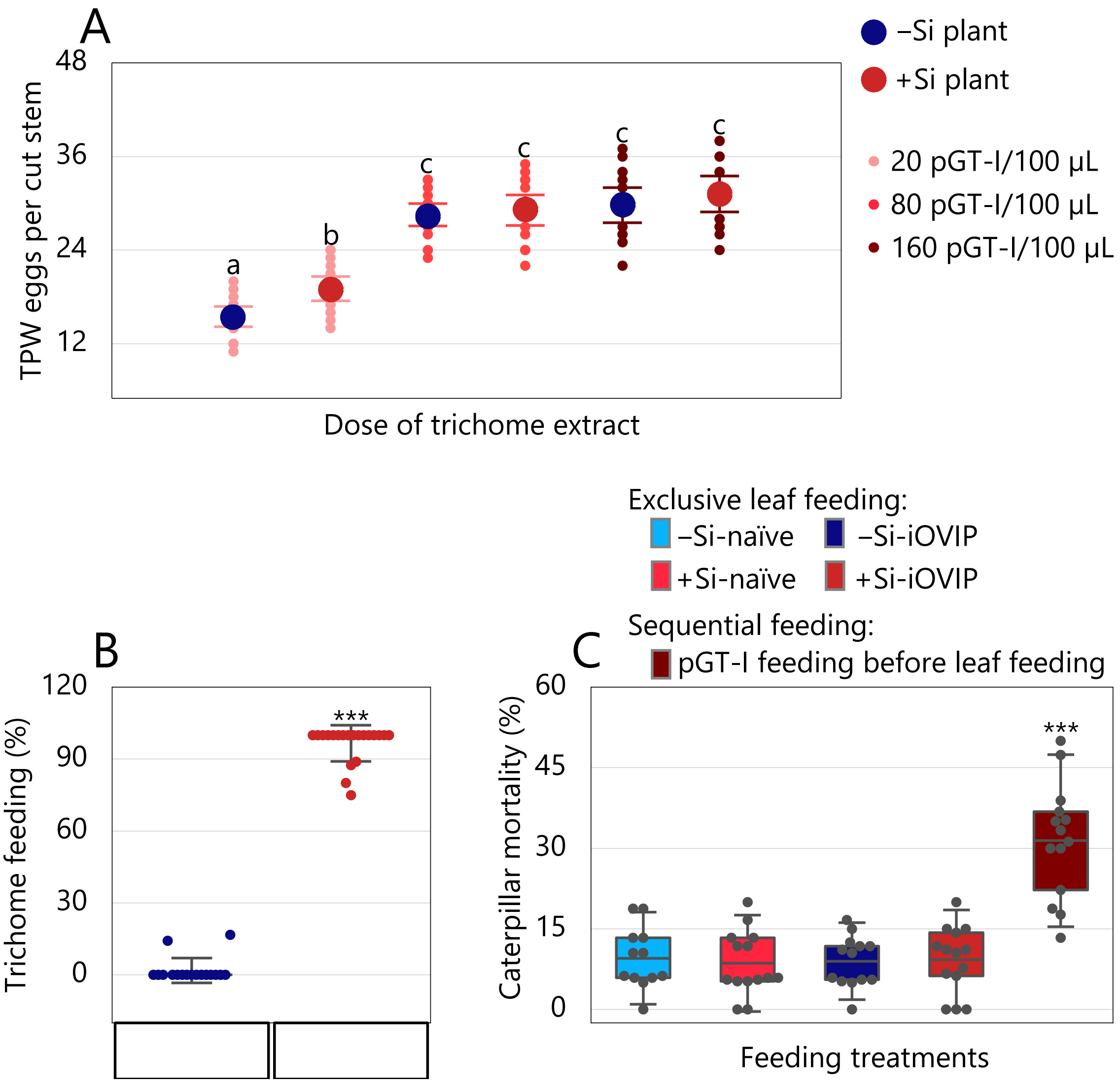

Fig S4. Dose-Response Pilot Experiment Assessing the Effect of GT-I Extracts on TPW Oviposition. (A) The number of TPW eggs per stem was quantified after applying GT-I extracts derived from +Si-iOVIP (pGT-I) and –Si-iOVIP (npGT-I) plants at three trichome densities (20, 80, and 160 trichomes per 100 µL). Significant differences were observed across treatments (χ^2 = 151.88, $p < 0.0001$). The 80 pGT-I/100 µL treatment elicited a similar oviposition response as the 160 pGT-I/100 µL treatment, suggesting a saturation point. Lower oviposition was observed with the 20 pGT-I/100 µL dose compared to higher doses. Based on these results, 80 pGT-I/100 µL was selected for subsequent experiments. Different letters above bars indicate statistically significant differences between treatments (GLM with LR, $p < 0.05$). (B) Proportion of neonate TPW caterpillars that fed on trichomes. 96.6% of TPW neonates that hatched on +Si stems fed on pGT-I trichomes, whereas only 1.8% fed on trichomes on −Si stems (χ^2 = 2106.2, $p < 0.0001$). No caterpillars exhibited stem-mining behavior during this period. (C) Neonate TPW caterpillar mortality in response to trichome ingestion before leaf feeding versus exclusive leaf feeding. No significant differences in mortality were observed among neonates that fed exclusively on leaves from naïve and iOVIP plants, regardless of Si supplementation (χ^2 = 0.71, p = 0.871). However, caterpillars that ingested pGT-I trichomes before transitioning to leaf feeding exhibited significantly higher mortality compared to those that fed exclusively on leaves (χ^2 = 328.39, $p < 0.0001$). Different letters above bars indicate statistically significant differences between treatments (GLM with LR, $p < 0.05$). Boxes represent the median and interquartile range, while whiskers indicate the data range. Dots represent individual data points. Statistical significance is denoted as *** ($p < 0.001$). These findings highlight the dose-dependent response of TPW oviposition to GT-I extracts and the lethal effect of trichome ingestion prior to leaf feeding on TPW caterpillars.

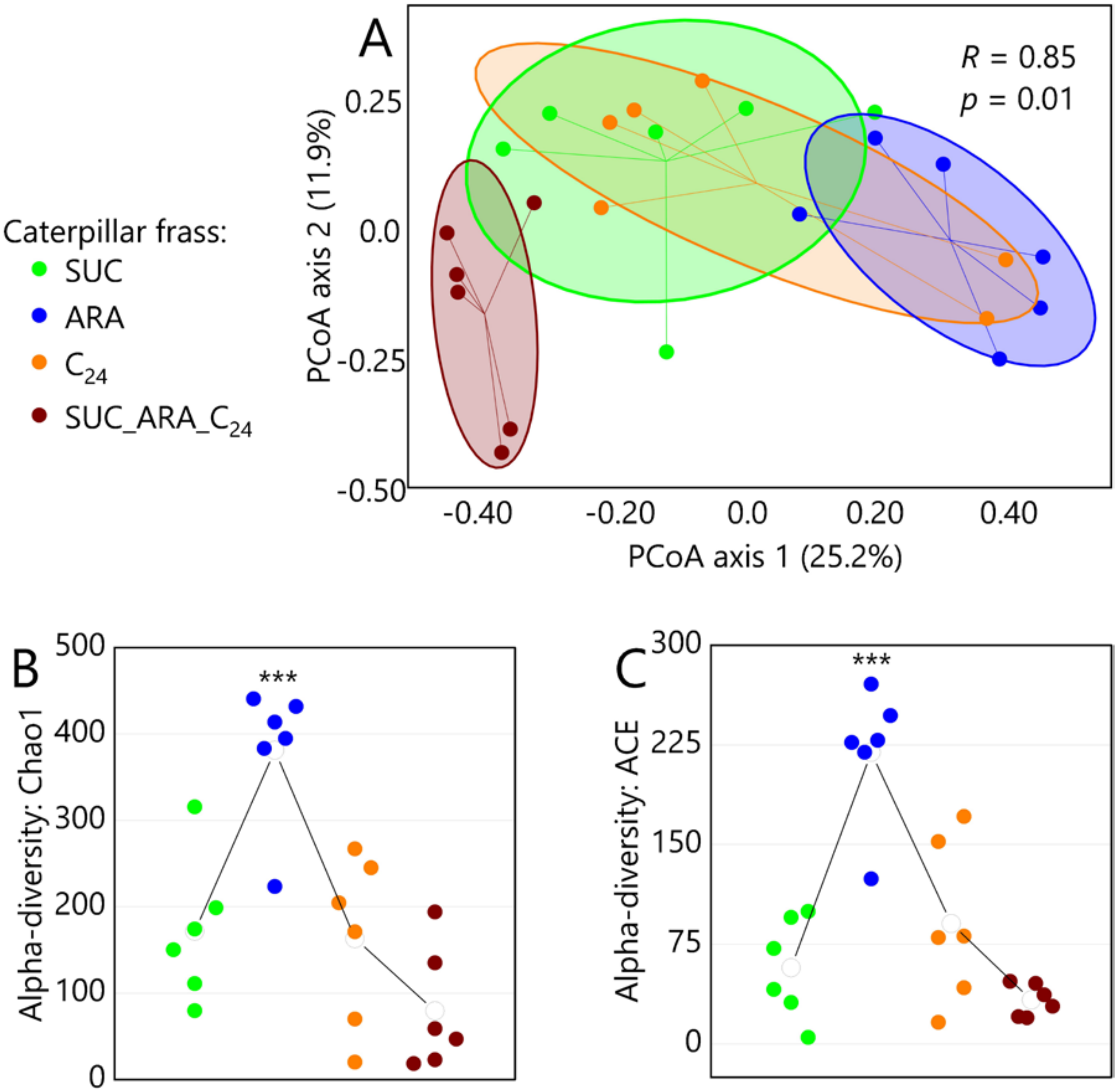

Fig S5. Distinct Clustering of Bacterial Communities in TPW Caterpillar Frass Following Tomato Leaf Feeding. (A) Principal Coordinates Analysis (PCoA) showing distinct clustering of bacterial communities in TPW caterpillar frass following tomato leaf feeding. The treatments include sucrose (SUC), L-arabinose (ARA), tetracosane (C_{24}), and their three-component blend (SUC_ARA_C_{24}) (*n* = 6). The clustering patterns indicate distinct microbial community structures associated with each treatment. Statistical analysis revealed a significant difference ($R = 0.85$, $p = 0.01$), highlighting the influence of plant treatments on TPW frass microbial composition. (B) Alpha-diversity of the TPW gut microbiome based on the Chao1 index. Significant differences were observed between treatments ($\chi^2 = 1417.07$, $p < 0.0001$). Higher alpha diversity is evident in the SUC-treated plants, with lower diversity in the SUC_ARA_C_{24}-treated plants. Different letters above points indicate statistically significant differences (GLM with LR, $p < 0.05$). (C) Alpha-diversity of the TPW gut microbiome based on the ACE index. Similar to Chao1, significant differences were observed between treatments ($\chi^2 = 1134.74$, $p < 0.0001$). The SUC-treated plants exhibited higher alpha diversity, while the SUC_ARA_C_{24}-treated plants showed reduced diversity. Statistical significance is denoted as *** ($p < 0.001$). Dots show individual data points.

These findings demonstrate that different tomato leaf treatments significantly influence both the composition (PCoA) and alpha diversity (Chao1, ACE) of the TPW gut microbiome.

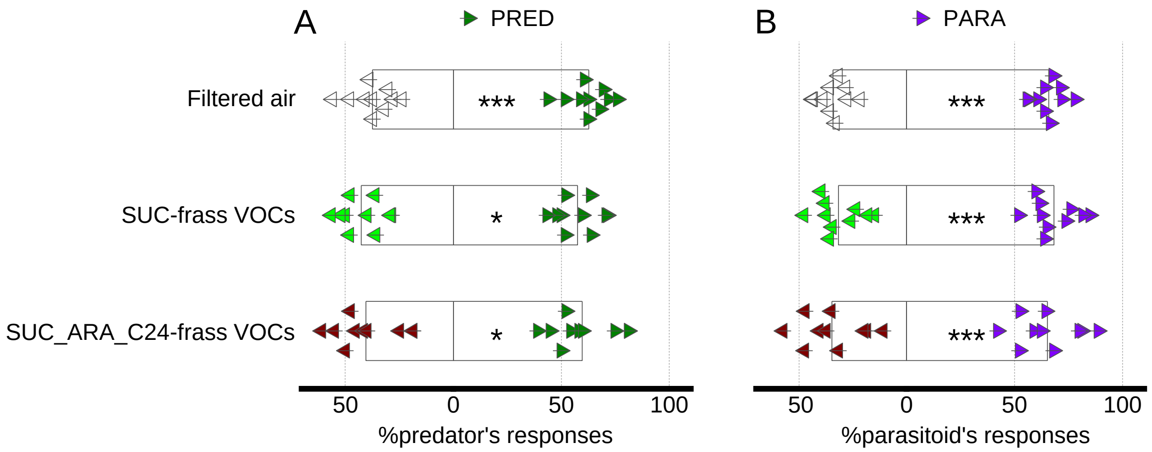

Fig. S6. Olfactory Responses of Predator (*Nesidiocoris tenuis*) and Parasitoid (*Neochrysocharis formosa*) to VOC blends Compared to SUC-frass and SUC_ARA_C_{24}-frass VOCs, and Filtered Air. (A) Predator (*N. tenuis*) exhibited a significant attraction to the PRED VOC blend (*β*-phellandrene, *δ*-3-carene, 3-octanol, and *α*-humulene) compared to filtered air ($p < 0.001$). When exposed to SUC-frass VOCs, predator attraction remained significant but comparatively weaker ($p = 0.03$). Similarly, predator responses to SUC_ARA_C_{24}-frass VOCs showed significant attraction ($p = 0.02$), and (B) Parasitoid (*N. formosa*) displayed a highly significant preference for the PARA VOC blend (3-octanol and *n*-hexanol) compared to filtered air ($p < 0.0001$). Attraction to SUC-frass VOCs was highly significant ($p < 0.0001$) and responses to SUC_ARA_C_{24}-frass VOCs were also highly significant ($p < 0.001$). These findings highlight distinct chemical communication mediated by VOCs derived from TPW frass- the predator responds to the complex VOC blend (PRED), while the parasitoid preferentially responds to the less complex blend (PARA). Statistical significance (two-tailed test) is denoted as $p < 0.05$ (*), and $p < 0.0001$ (***).

Table S1. Sugar Composition of GT-I Trichomes from Tomato Stems.

RT	**RI$_{cal}$**	**Compound Name$^{\#}$**	**GT-I on naïve plant stem**		**GT-I on iOVIP plant stem**		***p***
			–Si plant	**+Si plant**	**–Si plant**	**+Si plant**	
20.00	1573	Myo-Inositol	69.6±15.80^{a}	69.7±16.56^{a}	80.7±17.33^{a}	67.7±14.70^{a}	0.674
23.50	1936	D-Ribopyranose	10.5±1.10^{a}	11.6±1.40^{a}	10.9±1.2^{a}	12.4±1.51^{a}	0.323
23.61	1914	Glyceryl-glycoside	9.9±2.68^{a}	10.6±1.24^{a}	8.1±3.43^{a}	11.7±2.99^{a}	0.509
23.78	1925	L-Mannopyranose	9.7±0.96^{ab}	9.6±2.4^{b}	11.6±1.49^{ab}	13.1±1.14^{a}	0.021
23.82	1947	L-Arabinose	9.1±2.73^{b}	7.4±1.15^{b}	5.7±1.05^{b}	46.2±5.53^{a}	< 0.001
24.25	1990	α-L-Galactofuranose	8.1±0.74^{b}	7.5±2.08^{b}	9.5±1.59^{ab}	12.6±2.49^{a}	0.041
24.33	2001	β-Gentiobiose	9.0±1.02^{b}	11.5±1.22^{ab}	7.6±1.95^{b}	16.0±2.02^{a}	< 0.001
24.73	2044	Sucrose	15.4±4.08^{b}	17.1±5.28^{b}	10.1±4.16^{b}	90.8±14.48^{a}	0.004
25.25	2108	L-(-)-Fucose	23.1±4.51^{ab}	19.5±4.23^{ab}	13.7±4.32^{b}	25.7±5.63^{a}	0.034
25.68	2140	D-(+)-Trehalose	3.8±0.86^{b}	4.4±0.60^{b}	5.7±0.42^{ab}	12.9±4.70^{a}	0.001
25.71	2151	D-(+)-Turanose	5.1±0.42^{a}	5.7±1.06^{a}	6.1±0.80^{a}	6.5±0.86^{a}	0.064
27.73	2384	L-Mannose	10.0±1.07^{a}	10.9±1.26^{a}	10.2±1.24^{a}	11.6±1.37^{a}	0.395
28.88	2536	Galactinol	3.8±1.00^{a}	4.4±1.49^{a}	4.1±1.13^{a}	4.2±1.76^{a}	0.854
29.01	2549	D-(+)-Cellobiose	3.1±0.98^{a}	2.7±0.76^{a}	3.2±0.49^{a}	2.6±0.87^{a}	0.598

Mean ± SD concentrations of sugars (ng g^{-1} FW) detected in glandular trichome type I (GT-I) extracted from tomato stems ($n = 5$). Data are presented for +Si and –Si plants, comparing naïve stems and iOVIP (oviposited plant) stems. Listed compounds include their retention time (RT) and calculated retention index (RI$_{cal}$). The RI$_{cal}$ values were determined using a homologous series of *n*-alkanes and a linear GC ramp program. Different letters indicate statistically significant differences between treatments ($p < 0.05$, Kruskal-Wallis test), determined through multiple pairwise comparisons using Dunn's post hoc test.

Table S2. Hydrocarbon Composition of Type I Glandular Trichomes from Tomato Stems.

RT	**RI$_{cal}$**	**RI$_{Lit}$**	**Compound Name**	**GT-I on naïve plant stem**		**GT-I on iOVIP plant stem**		***p***
				–Si plant	**+Si plant**	**–Si plant**	**+Si plant**	
25.79	2000	2000	Eicosane (C_{20})	1.69±0.53^{a}	1.73±0.61^{a}	1.7±1.03^{a}	1.55±0.21a	0.995
26.67	2100	2100	Heneicosane (C_{21})	2.89±1.59^{a}	2.99±1.86^{a}	2.76±1.11^{a}	4.7±1.65^{a}	0.233
27.51	2200	2200	Docosane (C_{22})	4.24±1.31^{a}	4.89±1.24^{a}	5.13±1.68^{a}	4.45±1.44^{a}	0.643
28.32	2300	2300	Tricosane (C_{23})	12.4±3.44^{a}	12.76±3.37^{a}	11.3±3.78^{a}	14.03±4.62^{a}	0.835
29.10	2400	2400	Tetracosane (C_{24})	25.71±5.88^{a}	38.98±7.81^{ab}	49.43±12.61^{b}	56.56±13.44^{b}	0.002
29.84	2500	2500	Pentacosane (C_{25})	12.46±1.56^{a}	27.7±2.09^{ab}	11.61±2.36^{a}	49.66±5.48^{b}	< 0.001
30.68	2600	2600	Hexacosane (C_{26})	7.55±2.48^{a}	11.79±1.67^{ab}	16.55±2.62^{b}	15.46±4.59^{b}	0.002
31.63	2800	2800	Octacosane (C_{28})	3.67±0.22^{a}	4.37±1.35^{ab}	4.72±1.53^{ab}	6.21±1.88^{b}	0.033

Mean ± SD concentrations of hydrocarbons (ng g^{-1} FW) detected in glandular trichome type I (GT-I) extracted from tomato stems ($n = 6$). Data are presented for +Si and –Si plants, comparing naïve stems and iOVIP (oviposited plant) stems. Listed compounds include their retention time (RT), calculated retention index (RI$_{cal}$) and literature retention index (RI$_{Lit}$). The RI$_{cal}$ values were determined using a homologous series of *n*-alkanes and a linear GC ramp program. The RI$_{Lit}$ values were obtained from references (3, 4). Different letters indicate statistically significant differences between treatments ($p < 0.05$, Kruskal-Wallis test), determined through multiple pairwise comparisons using Dunn's post hoc test.

Table S3. Headspace Volatile Compounds in TPW Neonate Frass Across Different Treatments.

RT	$\mathrm{RI}_{\mathrm{cal}}$	$\mathrm{RI}_{\mathrm{Lit}}$	Compound Name	Treatments				*p*
				SUC	ARA	C_{24}	SUC_ARA_C_{24}	
6.30	787	790	4-methyl-2-Pentanol	2.70±0.81 ^{a}	6.56±0.21 ^{ab}	7.14±0.18 ^{b}	7.4±0.61 ^{b}	< 0.001
6.43	796	790	3-methyl-2-Butenal	3.46±0.17 ^{b}	2.47±0.14 ^{ab}	2.32±0.19 ^{a}	2.15±0.18 ^{a}	< 0.001
6.87	804	800	Octane	N.D.	6.09±0.86 ^{b}	4.69±1.32 ^{ab}	4.21±0.93 ^{a}	0.031
7.84	841	846	(*E*)-3-Hexenol	1.06±0.14 ^{a}	17.84±4.26 ^{c}	2.61±0.16 ^{ab}	13.46±1.59 ^{bc}	< 0.001
8.03	849	851	(*Z*)-3-Hexenol	19.55±1.55 ^{a}	20.55±3.70 ^{a}	19.32±6.91 ^{a}	17.33±3.55 ^{a}	0.546
8.20	855	855	*n*-Hexanol$^{\#}$	7.36±0.64 ^{ab}	28.63±5.19 ^{c}	6.72±0.60 ^{a}	8.89±0.29 ^{bc}	< 0.001
8.62	872		Unidentified_1	46.95±3.08 ^{a}	67.37±2.53 ^{a}	78.62±6.08 ^{a}	72.66±1.57 ^{a}	0.271
9.30	898		Unidentified_2	18.64±0.82 ^{a}	19.36±0.79 ^{a}	19.19±0.34 ^{a}	18.86±0.46 ^{a}	0.957
9.35	900	903	2-Heptanol	13.62±1.60 ^{ab}	13.71±2.00 ^{b}	11.92±5.27 ^{a}	13.48±2.76 ^{a}	< 0.001
9.53	908	911	*α*-Thujene	16.01±3.08 ^{ab}	18.66±3.94 ^{b}	8.28±0.38 ^{a}	4.4±0.59 ^{a}	0.002
9.65	914	914	Tricyclene	81.03±9.64 ^{a}	96.28±11.08 ^{ab}	99.64±6.46 ^{b}	100.3±4.62 ^{b}	< 0.001
9.98	928	928	*α*-Pinene$^{\#}$	253.15±55.96 ^{b}	213.49±29.02 ^{ab}	169.55±26.26 ^{a}	180.99±7.74 ^{a}	0.002
10.34	945	944	Sabinene	165.52±66.68 ^{a}	261.71±50.55 ^{c}	251.37±43.65 ^{bc}	174.47±3.78 ^{ab}	0.001
10.45	950	950	Myrcene$^{\#}$	7.90±0.14 ^{a}	214.20±18.59 ^{c}	19.52±0.53 ^{ab}	70.79±2.91 ^{bc}	< 0.001
10.49	951	954	1-Octen-3-ol	5.45±2.18 ^{a}	44.65±5.09 ^{b}	5.54±0.45 ^{a}	6.45±0.47 ^{ab}	< 0.001
10.57	955	955	3-Octanone	N.D.	4.69±0.19 ^{ab}	5.55±0.77 ^{b}	2.82±0.12 ^{a}	< 0.001
10.66	959		Unidentified_3	26.43±3.13 ^{c}	26.43±2.39 ^{bc}	11.14±1.90 ^{a}	11.25±0.62 ^{ab}	< 0.001
10.78	980	982	3-Octanol$^{\#}$	12.35±3.24 ^{a}	69.69±10.84 ^{c}	21.79±3.10 ^{ab}	38.04±2.75 ^{bc}	< 0.001
10.89	985	986	*δ*-2-Carene	195.22±18.54 ^{a}	172.55±15.13 ^{a}	182.23±12.57 ^{a}	187.54±11.38 ^{a}	0.213
10.98	989	995	*α*-Phellandrene	148.07±13.54 ^{b}	108.42±1.20 ^{b}	49.64±10.22 ^{a}	89.99±3.98 ^{ab}	< 0.001
11.13	996	997	*δ*-3-Carene	137.67±13.32 ^{a}	177.13±14.36 ^{a}	195.03±39.18 ^{ab}	270.91±28.25 ^{b}	< 0.001
11.48	1015	1016	*p*-Cymene	18.50±2.76 ^{ab}	24.79±0.91 ^{bc}	10.76±0.19 ^{a}	29.76±1.94 ^{c}	< 0.001
11.54	1018		Unidentified_4	N.D.	6.66±2.19	N.D.	N.D.	-
11.63	1023	1024	*α*-Terpinene	136.82±8.95 ^{bc}	145.68±10.81 ^{c}	73.57±11.32 ^{a}	73.76±11.87 ^{ab}	< 0.001
11.78	1032	1029	*o*-Cymene	68.61±3.57 ^{a}	124.69±6.44 ^{b}	130.02±26.73 ^{b}	81.51±8.34 ^{ab}	< 0.001
11.87	1037	1136	*β*-Phellandrene	140.88±13.51 ^{a}	431.69±36.61 ^{b}	253.01±23.44 ^{ab}	236.19±24.38 ^{ab}	< 0.001
11.97	1042	1042	(*Z*)-β-Ocimene	N.D.	37.97±1.21 ^{ab}	29.28±1.34 ^{a}	43.19±1.85 ^{b}	< 0.001
12.13	1051	1051	(*E*)-β-Ocimene	58.03±1.07 ^{bc}	60.37±2.26 ^{c}	32.22±7.04 ^{ab}	32.71±1.2 ^{a}	< 0.001
12.17	1053	1062	*γ*-Terpinene	81.03±9.64 ^{a}	96.28±11.08 ^{ab}	99.64±6.46 ^{b}	100.3±4.62 ^{b}	< 0.001
12.58	1076	1076	Terpinolene	45.40±8.21 ^{b}	30.26±1.71 ^{a}	38.77±1.81 ^{ab}	40.01±2.17 ^{b}	0.001
12.69	1082	1085	Linalool	47.15±4.01 ^{bc}	36.41±6.36 ^{a}	41.79±3.79 ^{ab}	108.19±1.67 ^{c}	< 0.001
13.21	1113	1113	neo-allo-Ocimene	9.64±3.33 ^{a}	133.74±23.50 ^{b}	159.40±29.09 ^{b}	51.61±6.16 ^{ab}	< 0.001
14.28	1180	1180	Myrcenol	N.D.	37.02±1.68 ^{b}	0.85±0.10 ^{a}	8.96±1.59 ^{ab}	< 0.001
16.54	1337	1337	*δ*-Elemene	14.72±1.71 ^{a}	46.37±4.15 ^{ab}	60.25±3.01 ^{b}	62.42±2.18 ^{b}	< 0.001
16.76	1353	1354	*α*-Cubebene	51.72±14.58 ^{b}	7.04±1.38 ^{a}	30.76±31.15 ^{ab}	13.92±8.35 ^{ab}	0.004
17.09	1378	1383	*α*-Cedrene	288.01±15.36 ^{c}	48.38±1.99 ^{a}	95.54±4.55 ^{ab}	145.49±9.18 ^{bc}	< 0.001
17.40	1400	1400	6,9-Guaiadiene	88.77±4.44 ^{ab}	103.57±13.31 ^{b}	99.66±5.93 ^{b}	32.86±1.77 ^{a}	< 0.001
17.69	1423	1423	(*E*)-Caryophyllene	288.01±15.36 ^{c}	48.38±1.99 ^{a}	95.54±4.55 ^{ab}	145.49±9.18 ^{bc}	< 0.001
17.97	1445	1444	*α*-Himachalene	N.D.	N.D.	N.D.	34.49±3.95	-
18.00	1448	1452	α-Humulene	147.39±25.20	133.87±17.41	340.23±22.16	162.39±15.87	0.001
18.13	1458	1459	*β*-Copaene	81.51±4.76 ^{bc}	50.24±4.57 ^{a}	154.62±11.95 ^{c}	58.63±1.47 ^{ab}	< 0.001
18.48	1486	1490	Dauca-4(11),8-diene	0.97±0.12 ^{a}	15.08±2.17 ^{b}	13.35±1.22 ^{ab}	17.17±1.37 ^{b}	< 0.001
18.78	1510	1516	Germacrene B	29.69±3.79 ^{b}	22.39±3.55 ^{ab}	13.72±1.80 ^{a}	12.95±2.23 ^{a}	< 0.001
19.00	1528	1540	*α*-Bisabolene	N.D.	34.13±5.73 ^{b}	N.D.	6.19±2.28 ^{a}	0.004
19.44	1565	1558	9,10-dehydro-Isolongifolene	N.D.	8.63±1.27^{b}	5.85±0.77^{a}	8.19±2.63^{ab}	0.032
19.76	1571	1572	(-)-Spathulenol	N.D.	N.D.	5.70±0.79	N.D.	-
22.07	1751	1750	TMTT	0.47±0.11 ^{a}	0.53±0.10 ^{a}	0.92±0.15 ^{b}	0.62±0.02 ^{ab}	< 0.001

Mean ± SD concentrations of headspace volatile compounds (ng g^{-1} FW) detected in TPW neonate frass from caterpillars fed on sucrose (SUC), L-arabinose (ARA), tetracosane (C_{24}), and their three-component blend (SUC_ARA_C_{24})-treated tomato leaves ($n = 7$). Listed compounds include their retention time (RT), calculated retention index ($\mathrm{RI}_{\mathrm{cal}}$) and literature retention index ($\mathrm{RI}_{\mathrm{Lit}}$). The $\mathrm{RI}_{\mathrm{cal}}$ values were determined using a homologous series of *n*-alkanes and a linear GC ramp program. The $\mathrm{RI}_{\mathrm{Lit}}$ values were obtained from references (3, 4). Different letters indicate statistically significant differences between treatments ($p < 0.05$, Kruskal-Wallis test with Dunn’s post hoc comparisons). TMTT (*E,E*-4,8,12-Trimethyltridecatetraene); N.D. (Not Detected).

Movie S1. *Phthorimaea absoluta* (TPW) neonate caterpillar feeding on glandular trichome type I (GT-I) on the stem of a tomato plant grown in a mesoporous nanosilica-supplemented substrate.

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