Title: Time of arrival during plant disease progression and humidity additively influence

Salmonella enterica colonization of lettuce.

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Running Head: *Salmonella* Benefits from Humidity and Disease

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ABSTRACT

The interplay between plant host, phytopathogenic bacteria, and enteric human pathogens

in the phyllosphere have consequences for human health. *Salmonella enterica* has been known to

take advantage of phytobacterial infection to increase its success on plants, but there is little

knowledge of additional factors that may influence the relationship between enteric pathogen and

plant disease. In this study, we investigated the role of humidity and the extent of plant disease

progression on *S. enterica* colonization of plants. We found that high humidity was necessary for

replication of *S. enterica* on diseased lettuce, but not required for *S. enterica* ingress into the UV-

protected apoplast. Additionally, the *Xanthomonas hortorum* pv. vitians (hereafter, *X. vitians*) -

infected lettuce host was found to be a relatively hostile environment for *S. enterica* when it

arrived prior to the development of watersoaking or following necrosis onset, supporting the

existence of an ideal window during *X. vitians* infection progress that maximizes *S. enterica*

survival. *In vitro* growth studies in sucrose media suggest that *X. vitians* may allow *S. enterica* to

benefit from cross-feeding during plant infection. Overall, this study emphasizes the role of

phytobacterial disease as a driver of *S. enterica* success in the phyllosphere, demonstrates how

time of arrival during disease progress can influence *S. enterica's* fate in the apoplast, and

highlights the potential for humidity to transform an infected apoplast into a growth-promoting

environment for bacterial colonizers.

Importance: Bacterial leaf spot of lettuce caused by *X. vitians* is a common threat to leafy green

production. The global impact caused by phytopathogens, including *X. vitians*, is likely to

increase with climate change. We found that even under a scenario where increased humidity did

not enhance plant disease, high humidity had a substantial effect on facilitating *S. enterica*

growth on *Xanthomonas*-infected plants. High humidity climates may directly contribute to the

survival of human enteric pathogens in crop fields or indirectly affect bacterial survival via

changes to the phyllosphere brought on by phytopathogen disease.

INTRODUCTION

Agricultural fields serve as habitats for diverse communities of microorganisms, including bacteria. Although the surface of a leaf may seem innocuous, bacteria that colonize the phyllosphere must adapt to hostile conditions including nutrient scarcity, extreme fluctuations in moisture availability, UV irradiation, and the host immune response (1, 2). To increase survival, some bacteria abandon the leaf surface and enter the apoplast where they may evade such stresses, so long as they can evade or suppress the plant immune response. Phytobacterial pathogens overpower host defenses and destructively (3–8). For example, *Xanthomonas hortorum* pv. vitians (hereafter, *X. vitians*) causes bacterial leaf spot of lettuce(9, 10), which is characterized by symptom development of dark, water-soaked leaf lesions (9, 10)(11). Phytobacterial disease causes yield loss (7, 12–18)(11), which devastates agricultural industries worldwide and is already a major cause for concern on its own. However, growing evidence of *Salmonella enterica's* potential to benefit from host changes brought on by phytopathogen infection (7, 12–18) supports that phytobacterial disease may be linked to another issue: food-borne illness.

Salmonella enterica is an environmental microbe that effectively colonizes both mammalian and environmental hosts (19), relying on its ability to adapt and survive in diverse niches (20). Irrigation water, soils, and plant surfaces are all examples of places where *S. enterica* can persist for long periods of time, months to years (21–23). *S. enterica* is one of several enteric pathogens recognized as colonizers of plants (24), and salmonellosis outbreaks have been linked to consumption of raw produce (25). Given the prevalence of phytobacterial disease on agricultural crops, *S. enterica* is likely to interact with pathogenic phytobacteria when

S. enterica is present in a field. Considering the public health threat posed by *S. enterica*

colonization of crop plants, studying biotic and abiotic factors that influence its ability to survive

in the environment is a critical area of research.

Phytobacterial disease promotes the survival of *S. enterica* on plants pre-harvest (7, 12–

18). A recently published study from our lab showed that tomato leaves infected by *X. hortorum*

pv. gardneri enabled *S. enterica* cells that arrive on the leaf surface to become internalized within

the leaf apoplast and replicate (17). After completing this work, we questioned whether *S.*

enterica would benefit from any bacterial leaf spot disease. Lettuce has been implicated in food-

borne illness outbreaks caused by *S. enterica*, and lettuce is susceptible to the bacterial spot

disease pathogen, *X. vitians* (26–28). Because lettuce is commonly eaten raw, without food

safety intervention strategies that can lower pathogen populations below the infectious dose, we

determined that studying the romaine lettuce-*X. vitians* pathosystem would be key to expanding

our knowledge of factors that influence *S. enterica* population size on plants.

The goal of our study was to examine how *X. vitians* disease and environmental factors,

specifically high relative humidity, may impact the fate of *S. enterica* in the apoplast of lettuce

plants. By studying another pathosystem, we can discover differences that may exist for *S.*

enterica plant colonization driven by host. Additionally, we investigated how *S. enterica's*

success on *X. vitians*-infected lettuce could be influenced by how early or late during infection

that *S. enterica* arrives, effectively using *S. enterica* as a biological reporter for host changes

during phytobacterial infection and disease progress. Lastly, we measured how *S. enterica*

growth in a sucrose-rich environment is affected by *X. vitians in vitro* to determine a mechanism

by which *S. enterica* replicates in the presence of *X. vitians* infection.

METHODS

Bacterial strains, media, and culture conditions

Bacterial strains used in this study are listed in Table 1. *X. vitians* cultures were prepared by

inoculating 3 mL of nutrient broth with frozen cells and incubating at 28°C with shaking at 200

rpm for 2 days. *Salmonella enterica* cultures were prepared in a similar manner but incubated in

lysogeny broth (LB) overnight. Cultures were then diluted in sterile water and prepared to the

desired cell concentration. Nutrient agar (NA) was used for enumeration of *X. vitians,* and LB

agar amended with 20 µg/mL of nalidixic acid was used for enumerating *S. enterica*. Agar plates

were incubated for ~48 hrs at 28°C or 16-24 hr at 37°C for *X. vitians* and *S. enterica*,

respectively.

A fluorescently labeled *X. vitians* strain was produced for this study by transforming a

wild-type *X. vitians* L7 strain with high-copy plasmid pNO-mCherry (gifted from Z. Gitai lab;

modified version of plasmid described in (29)) derived from pTH18Cr (30), which carries a

chloramphenicol resistance cassette and constitutively expresses mCherry via $P_{LtetO-1}$ (31)

promoter with *tet* repressor removed. Plasmid DNA was isolated from *Escherichia coli* using a

Spin MiniPrep kit (Qiagen) and transferred to *X. vitians* via electroporation.

Bacterial inoculation of lettuce

Lactuca sativa (romaine lettuce) seedlings were cultivated in growth chambers with a 16-h

photoperiod at 24°C. Lettuce plants (4-5 weeks old) were infiltrated with *Xanthomonas vitians*

inoculum prepared to an $OD_{600} = 0.2$ (~3 x 10^8 CFU/mL) or sterile deionized H_2O as a control.

Xanthomonas infiltration was performed via needleless syringe on the abaxial side of the leaf as

described previously (32) and adapted for lettuce leaves. "Middle leaves" (the 3rd or 4th oldest

true leaves) were selected for infiltration, which were fully open and relatively flat. The

approximate volume infiltrated into each infiltration zone was 15 µL, which produced infiltration

zones 1-1.5 cm long. For each treatment group, 6-8 plants were infiltrated per experimental

replicate with 1-2 leaves infiltrated per plant. Biological replicates were considered the

individual plants.

Infiltrated lettuce plants were maintained in large plastic bins with a 16-h photoperiod at

~24°C and a moderate relative humidity (RH) of 50-70%. Lettuce plants were subsequently

inoculated with *Salmonella enterica* cell suspensions at the given time post-infiltration with H_2O

or *X. vitians* cells. *S. enterica* was diluted in sterile deionized water to a cell concentration ~10^6

CFU/mL. *S. enterica* cell suspension droplets (3 uL; ~3000 CFU/droplet) were pipetted onto the

adaxial surface of each infiltration zone to mimic arrival via irrigation or splash dispersal,

avoiding overlap between the droplet site and any microscopic damage caused by syringe

infiltration. Leaves were then destructively sampled at given time points (1 – 5) post-*S. enterica*

arrival. When experiments required sampling beyond 1-day post-*S. enterica* arrival, lids were

placed on the bins at 24 hours post-*S. enterica* arrival to raise the RH to >90%. Plants were kept

at a RH >90% unless noted; when lids were left off or removed, RH level was 55-70%.

Bacterial population sampling

Lettuce leaves were cut from the plant and when applicable, UV irradiation was utilized to

inactivate *S. enterica* cells colonizing the leaf surface and thus measure *S. enterica* colonizing the

apoplast (32). Leaf tissue was irradiated with UV-C (254 nm) by placing samples adaxial side

facing up inside a Stratalinker UV Crosslinker 1800 and dosing the tissue at an exposure level of

150,000 $\mu J/cm^2$. For the experiment described in **Figure 1,** for each plant, one of two inoculated

middle leaves was randomly selected for UV irradiation and the other leaf left non-irradiated as a

control. For all other *in planta* experiments involving UV irradiation treatment, middle leaves

that had been inoculated with *S. enterica* cells on both sides of the midrib were split in half after

sampling—one half of the leaf was randomly selected for UV irradiation and the half left non-

irradiated. Similar to what was demonstrated previously with *S. enterica*-inoculated tomato

leaves (32), UV irradiation treatment reduced the populations of *S. enterica* applied to the lettuce

leaf surface by at least 2 logs. Preliminary experiments demonstrated that *S. enterica* cells

infiltrated directly into the apoplast of lettuce leaves were not affected by UV irradiation

treatment (data not shown).

For one experiment, measurement of surface *S. enterica* populations was determined by

removing cells from sampled leaves using swabs dipped in Tween-20 as previously described

(32). The washate from the swab was then plated to quantify viable surface cells. For all sampled

leaves, bacterial colonization of leaf tissue was measured by excising 1-cm-diameter leaf disks

from infiltration zones using a tissue corer and homogenizing the tissue in 500 uL of sterile water

using a Dremel tool (33). Leaf homogenate was dilution-plated to enumerate *S. enterica* and *X.*

vitians populations. The limit of detection (LOD) for *S. enterica* colonization was 5 CFU/leaf

disk (or 10 CFU/sample for the summation of swab and leaf tissue *S. enterica* populations). The

remaining leaf homogenate was enriched with LB containing nalidixic acid (20 $\mu g/mL$) to

determine if *S. enterica* populations below the LOD were present in samples for which direct

plating did not result in the growth of *S. enterica*. For non-detects, LB-enriched samples were

plated ~24 hours after enrichment. *S. enterica* colonization datapoints plotted at zero were

confirmed to be zero based on the absence of *S. enterica* in the LB-enriched sample. Data plotted

halfway between zero and the limit of detection indicates absence of colonies via direct plating

and a positive enrichment sample.

Electrolyte leakage measurements

Lettuce plants were prepared by infiltrating two adjacent middle leaves. The relatively older leaf

was infiltrated four times, with two infiltration zones placed on each side of the leaf margin. One

infiltration zone was randomly selected for bacterial population enumeration, and the remaining

three infiltration zones were used for electrolyte leakage measurements. Electrolyte leakage was

measured as performed previously (34, 35). In brief, for each biological replicate, three 1 cm

diameter tissue disks were excised from a single leaf and pooled. Leaf tissue was placed in 12-

well plates with wells containing 4 mL of water each. An EcTestr 11 (Eutech Instruments)

conductivity tester was used to measure the leakage of electrolytes from the tissue into the water

after 6 hours of incubation. Conductivity was reported by subtracting blank measurements taken

immediately following a 45-minute wash step (time = 0 hours) from measurements taken at 6

hours.

Confocal laser scanning microscopy

Lettuce plants were infiltrated with sterile deionized H_2O or *X. vitians* L7 + pNO-mCherry cells

prepared to an $OD_{600} = 0.2$ and incubated in plastic bins under moderate RH (50-70%) as

described above. Droplets of *S. enterica* + pKT-Kan (GFP-labelled) cell suspensions containing

~10^5 CFU were applied to the surfaces of infiltrated zones at 4-days post-infiltration with H_2O

and 1- or 4-days post-infiltration with *X. vitians*. Inoculated plants were then incubated for 2

days, with high humidity (RH >90%) applied for the final 24 hours prior to sampling. Whole

leaves were excised from the plants and kept in petri plates containing a moist Kim-wipe prior to

imaging. Slides were prepared immediately before imaging by excising 0.5 cm diameter tissue

disks at the site of *S. enterica* application and wet mounting them between two glass cover slips.

Confocal laser scanning microscopy (CLSM) images were obtained using a Zeiss Elyra

LSM780 inverted confocal microscope and 40x water immersion 1.10 C-Apochromat objective.

The 488 and 561 nm lines of an argon laser were used for excitation of GFP, mCherry, and

chlorophyll A autofluorescence, which were detected at 500-550 nm (GFP), 552-624 (mCherry),

and 630-700 nm (chlorophyll A) using the Zen (Zeiss) software. GFP and chlorophyll A

autofluorescence were detected using Track 1, and mCherry detected using Track 2, with track

switching set to every line. Master gain for GFP, mCherry, and chlorophyll A was set to 700,

750, and 850, respectively. A transmitted light detector (with master gain set to 450) was used

for capturing differential interference contrast (DIC) images, which are shown overlaid with

confocal fluorescence imaging data. For each treatment, leaf samples from 2-3 plants were

imaged and 9-15 image fields were captured at both the surface level and within the apoplast at a

z-depth = 4.6-14.5 μm (mean = 8.7 μm) relative to the surface (z = 0). Observations of the

presence/absence of GFP-labelled *S. enterica* cells within the apoplast were recorded for every

field.

For representative images shown, image processing via ImageJ was applied consistently

across images, as performed previously (32). For DIC images, brightness and contrast were

linearly adjusted using the "reset" button within the "Brightness/Contrast" tool. To improve

visibility of *S. enterica* and *X. vitians* cells, the "enhance contrast" tool was applied to the GFP

and mCherry channels with level of saturated pixels set to 0.05% and "equalize histogram" box

left unchecked. Chlorophyll A channel data was omitted for representative images.

Sucrose media co-culture assay

M9 minimal media containing sucrose or glucose as the sole carbon source (hereafter, M9

sucrose and M9 glucose) was prepared fresh for every experimental replicate with the following

components diluted in de-ionized water: $MgSO_4$ (2.0 mM), D-glucose or D-sucrose (0.4% w/v),

$CaCl_2$ (0.10 mM), Na_2HPO_4 (47.8 mM), KH_2PO_4 (22.0 mM), NaCl (8.6 mM), and NH_4Cl (18.7

mM).

Stationary phase *X. vitians* cells grown in NB were washed three times in 1X phosphate-

buffered saline (PBS) and normalized to an OD = 0.2. Normalized culture was inoculated into

M9 sucrose and incubated at 28°C with shaking. Separate *X. vitians* culture flasks were

incubated for either 24 or 48 hours in advance of *X. vitians* culture or cell-free supernatant (CFS)

being introduced to *S. enterica.* CFS was prepared by successively filtering *X. vitians* culture

through 0.8 μm and 0.2 μm filters. Sterility of CFS was confirmed via nutrient broth enrichment.

S. enterica cells grown overnight in LB were prepared by washing stationary phase cells

three times in 1X PBS, normalizing to an OD = 0.1, and diluting 1000-fold in sterile water for a

final concentration of ~10^5 CFU/ml. Diluted *S. enterica* cells or sterile water (100 μL) was then

combined with 1.4 mL of *X. vitians* cell cultures or CFS per well of a 12-well plate. *S. enterica*

and *X. vitians* cell concentrations were measured for triplicate wells immediately after 12-well

plates were prepared at time = 0 hours and following 28 hours of incubation at 28°C.

Statistical analysis

Statistical analyses and plot generation were performed using R Studio version 2023.03.1 (Posit

team, RStudio: Integrated Development Environment for R. Posit Software, PBC, Boston,

MA.[http://www.posit.co/]). Data from three independent replicate experiments were aggregated,

unless otherwise noted in the figure legend. The number of biological replicates for each

replicate experiment was 6-8 lettuce plants. For the *in vitro* growth assay in sucrose media, the

number of experimental (biological) replicates was 4, with each biological replicate calculated

from the mean of three technical replicates. Biological replicates for the *in vitro* growth assay are

defined as independent sub-cultures of the frozen bacterial stocks whereas technical replicates

refer to replicate wells of a 12-well plate. Bacterial population data were plotted following a

$\log_{10}(x+1)$ transformation. Statistical analysis was performed using log-transformed bacterial

population data.

Welch's analysis of variance (ANOVA) and post-hoc Games-Howell tests, which do not

assume equal variance between treatment groups, were used for comparing *in planta* bacterial

populations among treatment groups. When comparing bacterial populations between timepoints,

a Welch two-sample T-test was used, and statistical differences displayed above boxplots using

an asterisk symbol (*). When *S. enterica in planta* populations were compared to the amount of

S. enterica applied, arrival population, a Wilcoxon one-sample test was used, and statistical

differences indicated using a dagger symbol (†). Lastly, Fisher's exact test was used for

comparing proportions of *in planta* samples with *S. enterica* colonization that exceeds the arrival

population. The significance threshold for all statistical comparisons was a *P* value of <0.05.

RESULTS

***X. vitians*-infected lettuce enables *S. enterica* growth and colonization of UV-**

protected niches. To determine whether bacterial spot of lettuce, which is caused by *X. vitians*,

can facilitate *S. enterica* growth and colonization of UV-protected niches, lettuce plants were

infiltrated with H$_2$O or *X. vitians* cells and treated with *S. enterica* cells at 4-days post-infiltration

(**Figure 1A**). The number(32) of *S. enterica* cells recovered by swab was significantly lower for

UV-irradiated leaves compared to non-irradiated leaves at 1 dpa (**Figure 1B).** Furthermore, the

number of *S. enterica* cells recoverable from the surface of the lettuce tissue by swab at 1-day

post-*S. enterica* arrival (dpa) was not significantly different between healthy and *X. vitians*-

infected plants (**Figure 1B**; *P* = 4.43 x 10^{-7}, Welch ANOVA). However, the number of *S.*

enterica cells recovered from the swab was significantly higher for *X. vitians*-infected leaves at 3

dpa compared to healthy leaves (**Figure 1B**; *P* = 9.17 x 10^{-11}, Welch ANOVA) suggesting that *S.*

enterica populations successfully colonized the leaf surface of infected leaves once disease

progressed. For *X. vitians*-infected leaves, the *S. enterica* populations measured from the swab

also increased between 1 and 3 dpa for both non-irradiated and UV-irradiated leaves, whereas

the number of *S. enterica* cells recovered from the leaf surface did not increase at 3 dpa for

healthy leaves (**Figure 1B**).

For the same leaves, *S. enterica* populations were quantified for the leaf tissue itself

following the swabbing of the surface (**Figure 1C**). The *S. enterica* populations measured from

these tissue samples represent cells that failed to be physically removed by swab—either due to

attachment to the tissue or colonization of microscopic grooves or internal spaces. For UV-

irradiated leaves in particular, the measured *S. enterica* populations represent cells colonizing

UV-protected niches. We found that at 1 dpa, the number of *S. enterica* cells measured from the

lettuce tissue was generally higher for *X. vitians*-infected lettuce than healthy lettuce, as

demonstrated by the higher *S. enterica* populations measured on both non-irradiated and UV-

irradiated leaves (**Figure 1C**; *P* = 6.79 x 10^{-13}, Welch ANOVA). This contrasts with what was

observed with the swab sampling, where *X. vitians* infection did not impact the number of *S.*

enterica cells removable from the lettuce surface at the earlier sampling time, 1 dpa (**Figure 1B**).

At 3 dpa, the number of *S. enterica* cells associated with the lettuce tissue was significantly

higher on *X. vitians*-infected leaves compared to healthy leaves, and the *S. enterica* populations

associated with *X. vitians*-infected tissue increased over time demonstrating *S. enterica*

replication (**Figure** 1C; $P = 8.36 \times 10^{-21}$, Welch ANOVA).

278   ***S. enterica* growth on *X. vitians*-infected lettuce relies on high humidity.** After

establishing that *X. vitians* infection promotes *S. enterica* growth and colonization of UV-

protected niches, we considered other factors that might influence *S. enterica's* growth, such as

humidity. We investigated whether the combination of *X. vitians* infection and high humidity

(>90% RH) could additively benefit *S. enterica*. We tested the hypothesis that high humidity

maximizes *S. enterica's* ability to grow on *X. vitians*-infected plants by measuring *S. enterica's*

colonization of healthy and *X. vitians*-infected leaves at 4 days post-arrival (**Figure 2A**). We

found that exposure to 72 hours of high humidity (Humidity Treatment III) resulted in greater *S.*

enterica populations on *X. vitians*-infected plants compared to *S. enterica* populations on *X.*

vitians-infected plants that did not experience high humidity (Humidity Treatment I, **Figure 2B**;

$P = 2.60 \times 10^{-18}$, Welch ANOVA). In addition, a full 72 hours of exposure to high humidity

resulted in greater *S. enterica* populations on *X. vitians*-infected lettuce compared to a fluctuating

humidity treatment in which 24 hours of high humidity was followed by 48 hours of drier

conditions (Humidity Treatment II). Furthermore, 72 hours of exposure to high humidity resulted

in *S. enterica* growth, based on comparison of *in planta S. enterica* populations to the amount of

S. enterica cells in the arrival population (**Figure 2B**). Meanwhile, 24 hours of exposure to high

humidity did not promote *S. enterica* growth but supported *S. enterica* survival at a population

level similar to the arriving population. For plants that were not exposed to high humidity at all

(Humidity Treatment I), *X. vitians* infection resulted in greater *S. enterica* colonization compared

to healthy leaves (**Figure 2B**), demonstrating that *X. vitians* infection influences *S. enterica*

survival even in the absence of prolonged high humidity conditions. Contrastingly, *S. enterica*

populations on healthy leaves were not significantly influenced by high humidity ($P > 0.05$), and

S. enterica populations for all healthy plants regardless of humidity treatment were below the

arrival population level at 4 days post-*S. enterica* arrival (**Figure 2B**). Additionally, fluctuating

humidity (Humidity Treatment II) resulted in a reduction in *X. vitians* populations compared to

constant moderate humidity conditions (**Supplementary Figure 1**; $P = 0.036$, Welch ANOVA).

X. vitians and *S. enterica* populations were not found to be correlated ($P > 0.05$, Pearson

correlation), demonstrating that *S. enterica's* response to increasing exposure to high humidity

on *X. vitians*-infected leaves is attributed directly to humidity and not *X. vitians* population

density. In fact, high humidity introduced during early infection at 3 dpi was found to disrupt *X.*

vitians disease progress, based on the observations that *X. vitians* populations and electrolyte

leakage measurements were lower at 4 days post-*X. vitians* infiltration for lettuce plants exposed

to 24 hours of high humidity (>90% RH) prior to sampling (**Supplementary Figures 2A-C**).

High humidity is not required for *S. enterica* colonization of the apoplast of *X.*

***vitians*-infected leaves.** Having previously shown that water-congestion within the apoplast of

tomato leaves is sufficient for *S. enterica* ingress into *Xanthomonas*-infected leaves (32), we

hypothesized that humidity could influence *S. enterica* colonization of UV-protected niches of

lettuce. To test this hypothesis, we applied *S. enterica* to lettuce plants infected with *X. vitians*

and subjected the lettuce plants to different humidity treatments (**Figure 3A**).

Similarly to the previous experiment, high humidity (Humidity Treatment ii) resulted in

higher *S. enterica* populations at 2 days post-*S. enterica* arrival on *X. vitians*-infected leaves

(**Figure 3B**; $P = 3.55 \times 10^{-5}$, Welch ANOVA). *S. enterica* populations on plants that were not

exposed to high humidity (Humidity Treatment i) were below the arrival population level at time

of sampling. Although humidity had a significant impact on *S. enterica* persistence in general,

for the viable *S. enterica* cells that were present, humidity did not significantly contribute to *S.*

enterica's ability to colonize UV-protected niches. Contrary to our hypothesis, UV irradiation

did not cause a significant reduction in *S. enterica* populations for either humidity treatment,

indicating that high humidity is not required for *S. enterica* colonization of UV-protected niches

(**Figure 3B**). Notably, the introduction of high humidity at 5 dpi was found to have no effect on

X. vitians populations and host electrolyte leakage in this experiment (**Supplementary Figures**

3A-C), demonstrating that the observed impact of humidity on *S. enterica* persistence is

attributed to the humidity environment, not plant disease or *X. vitians*.

Disease progression by *X. vitians* influences *S. enterica* ingress and survival within

infected lettuce. We observed that *X. vitians* infection alters the host over time, with visible

watersoaking onset occurring at 2 dpi (**Supplementary Figure 5**). During late infection

(approximately 5 dpi), *X. vitians*-infected tissue began to appear drier, signaling the onset of

tissue necrosis (**Supplementary Figure 5**). These observations prompted the question of

whether an ideal window during *X. vitians* infection exists that optimizes *S. enterica* growth and

apoplast colonization, which we addressed by varying the timing of *S. enterica's* arrival on *X.*

vitians-infected leaves relative to *X. vitians* infection progress (**Figure 4A**). *S. enterica* arrival on

healthy leaves or on *X. vitians*-infected leaves at 1 dpi (Treatments H and X1) generally resulted

in the lowest *S. enterica* populations after two days of *S. enterica* colonization (**Figure 4B**; non-

irradiated leaves: $P = 0.001$, Welch ANOVA; UV-irradiated leaves: $P = 1.61 \times 10^{-9}$, Welch

ANOVA). *S. enterica* populations recovered from both non-irradiated and UV-irradiated leaves

for Treatments H and X1 were significantly lower than the *S. enterica* arrival population level

(**Figure 4B**; $P < 0.001$, Wilcoxon signed rank test). *S. enterica* colonization of non-irradiated

lettuce samples revealed that arrival of *S. enterica* at 1 dpi (Treatment X1) resulted in lower *S.*

enterica populations on non-irradiated leaves than those on healthy (Treatment H) lettuce leaves,

demonstrating that *S. enterica* arrival on *X. vitians*-infected leaves can result in greater

population decline than that of healthy leaves if *S. enterica* arrival precludes the onset of *X.*

vitians-induced watersoaking (**Figure 4B**). The absence of an aqueous apoplast in Treatments H

and X1 also corresponded with the lowest *S. enterica* colonization of UV-protected niches at 2

days post-*S. enterica* arrival (**Figure 4B**).

UV irradiation had a significant impact on reducing *S. enterica* populations for

Treatments H, X1, and X5, specifically ($P = 4.76$ x 10^{-8}, $P = 3.65$ x 10^{-3}, and $P = 0.0216$,

respectively; Welch T-test) making evident that *S. enterica* colonization of the apoplast was

limited and the majority of the population remained on the leaf surface vulnerable to UV

irradiation. By contrast, UV irradiation treatment did not have a significant effect on the *S.*

enterica populations for Treatments X2-X4 ($P > 0.05$, Welch T-test), demonstrating that *S.*

enterica arrival prior to necrosis onset when the water-soaked infection zone appears to be most

translucent (**Supplementary Figure 5**) promotes *S. enterica* colonization of UV-protected

niches of a *X. vitians*-infected host. When *S. enterica* arrived between 2-4 dpi (Treatments X2-

X4), *S. enterica* populations persisted at levels similar to the arrival population level on UV-

irradiated leaves (**Figure 4B**), whereas arrival at 5 dpi resulted in UV-protected *S. enterica*

populations that were lower than the arrival population (**Figure 4B**; $P < 0.01$, Wilcoxon signed

rank test) suggesting arrival late in plant disease progress when tissue is necrotic limits *S.*

enterica to the leaf surface.

Infection progress coincided with *S. enterica's* ability to grow. We found that *X. vitians*

populations and host electrolyte leakage had reached a maximum level during late infection (5-7

dpi, **Supplementary Figures 6A**-**B**). Arrival of *S. enterica* between 2-5 dpi resulted in the

highest proportions of lettuce samples for which *S. enterica* colonization exceeded the arrival

population, indicating high incidence rates of *S. enterica* replication (**Table 2**). For Treatment

X4, arrival of *S. enterica* at 4 dpi resulted in 72% of non-irradiated samples and 61% of UV-

irradiated samples being colonized with higher *S. enterica* populations than the arrival

population (**Table 2**). Altogether, these results provide evidence that there is a window of time

during *X. vitians* infection when *S. enterica* persistence and potential to colonize UV-protected

niches is optimized—this window opens at water soaking onset and closes during necrosis onset

later in disease progression.

Confocal laser scanning microscopy (CLSM) was utilized to visualize *S. enterica*

localization *in planta* on the lettuce surface (**Figure 5A-F**) and within the apoplast (**Figure 5G-**

L). For H_2O-infiltrated leaves at 4 dpi, *S. enterica* cells were found only on the surface. *S.*

enterica cells were observed colonizing at least one stomatal opening (z-depth = 0) for 56% (*N* =

9) of images fields obtained from H_2O-infiltrated leaves (**Figure 5D**, for example), yet *S.*

enterica failed to colonize the apoplast (**Figure 5J**, for example) in all these cases. By contrast,

S. enterica colonization within substomatal areas of the apoplast was observed for *X. vitians*-

infected leaves. Congruous to *in planta S. enterica* colonization results that showed *S. enterica*

colonization of the UV-protected niches of *X. vitians*-infected leaves was higher following

arrival at 4 dpi compared to 1 dpi (**Figure 4B**), CLSM revealed greater *S. enterica* colonization

of the apoplast during late infection compared to early infection (**Figure 5H**, early infection;

Figure 5I, late infection). *S. enterica* arrival at 4 dpi resulted in relatively frequent colonization

of substomatal spaces within the apoplast, with 73% of image fields showing evidence of *S.*

enterica ingress and only 27% of image fields showing an absence of *S. enterica* ingress ($N =$

15). (**Figure 5L**). For *S. enterica* arrival at 4 dpi, 87% of image fields ($N = 15$) included *S.*

enterica colonization of at least one stomatal opening. In comparison, arrival of *S. enterica* on *X.*

vitians-infected leaves as early at 1 dpi resulted in rare apoplast colonization (15% of fields

imaged; $N = 13$; **Figure 5K**), despite 100% of fields showing *S. enterica* cells colonizing at least

one stomatal opening ($N = 13$). **Figure 5E** representatively illustrates this, with three stomatal

openings colonized by *S. enterica* cells at the surface, but only one of those same three stomata

containing *S. enterica* within its substomatal space (**Figure 5K**). Our *S. enterica* population data

(**Figure 4B**) and CLSM results altogether support that *S. enterica* arrival to leaves with

established *X. vitians* infection promotes *S. enterica* colonization of the UV-protected apoplast.

***S. enterica* grows in a sucrose-rich environment in the presence of *X. vitians*.** Sucrose

is one of the most prevalent carbohydrate sources available in plant tissues (36), yet sucrose is a

poor carbon source for *S. enterica* and not utilizable by most *S. enterica* strains (37). Having

observed that *S. enterica* successfully replicates *in planta* in the presence of an established *X.*

vitians infection (**Figures 1- 2, Table 2**), we hypothesized that *X. vitians* catabolism of plant

compounds directly aids in *S. enterica* replication via 1) *X. vitians*-associated compounds or 2)

compounds secreted by *X. vitians.* To test this hypothesis, we developed an *in vitro* experiment

in which *S. enterica* cells were introduced to turbid *X. vitians* cultures that had grown in M9

minimal media containing only sucrose as a carbon source (M9 sucrose) for 24 or 48 hours. Cell-

free supernatant (CFS) was produced from the *X. vitians* cultures and introduced to *S. enterica* to

compare the effect of intact *X. vitians* cells versus media containing secreted compounds. In

addition, *S. enterica* cells were added to M9 sucrose or M9 glucose media alone as negative and

positive controls.

We found that *S. enterica* cells incubated in co-culture with *X. vitans* cells or CFS

replicated to population levels that exceeded the initial cell concentrations after 28 hours of

incubation (**Figure 6**; $P = 1.01$ x 10^{-7}, Welch ANOVA). By contrast, *S. enterica* incubation in

M9 sucrose in monoculture (negative control; light blue bar) resulted in no growth after 28

hours. Specifically, introduction of *S. enterica* to *X. vitans* cells that had been growing in M9

sucrose for 24 hours (yellow bar) resulted in *S. enterica* cell concentrations that were greater than

the negative control and greater than either CFS treatment (emerald and dark green bars),

showing evidence for bacterial cross-feeding supporting *S. enterica* growth. Meanwhile,

introducing *S. enterica* to a 48-hour *X. vitans* culture (orange bar) resulted in higher variability

in *S. enterica* cell concentration than the 24-hour culture (yellow bar), and resulted in similar *S.*

enterica concentrations to both the negative control and CFS treatments. Notably, the 24-hour *X.*

vitans culture exhibited additional *X. vitans* growth during the 28-hour period (**Supplementary**

Figure 7), whereas the 48-hour culture did not, suggesting that replicating *X. vitans* cells confer

the greatest nutritional benefit to *S. enterica.*

DISCUSSION

Water—a habitat, vehicle for bacteria movement, and vital source of moisture needed for

growth—influences *S. enterica's* lifestyle in agricultural environments. Our study, which

involved modelling the arrival of *S. enterica* on the surface of leaves via splash dispersal

(**Figures 1-4**) and investigates the interactions between phytobacterial infection and humidity,

largely relates to water. Irrigation water is a common reservoir for *S. enterica* (21, 38, 39) and

has been previously implicated in enteric pathogen outbreaks associated with raw produce (40,

41). *S. enterica's* presence in irrigation water (40, 42) offers the potential for *S. enterica* to

migrate to leaves and fruit. Sprinkler and microsprinkler irrigation are commonly used for

agricultural fields in the United States (44, 45), including California and Arizona where most

leafy greens are cultivated (46). However, this form of irrigation has inherent risk. Splash

dispersal has been implicated as a vehicle for microbial dispersal on plant foliage (47, 48). In this

study, we investigated the relationship (49, 50) between an enteric pathogen and a plant pathogen

colonizing a lettuce host and examined how humidity may act on the enteric pathogen's ability to

benefit from plant disease. *S. enterica* was found to thrive on lettuce plants affected by bacterial

spot disease (**Figures 1B-C, 2B,** and **4B**). The potential for *S. enterica* to survive and replicate

on lettuce plants was linked to *X. vitians* infection progress (**Figure 4B**) and exposure to high

humidity **(Figure 2B**), with our results showing that the combination of water soaking caused by

disease and high humidity supported the highest *S. enterica* populations *in planta.* Lastly, by

measuring *S. enterica* growth in a sucrose-based minimal media, we identified bacterial cross-

feeding as a nutrient source for *S. enterica* in association with *X. vitians* **(Figure 6**)**.**

Humidity is recognized as a driver of plant-bacterial interactions (51). High humidity has

been shown to correlate with increases in phytobacterial disease (3, 52), including bacterial spot

caused by *X. vitians* (53), and linked to the compromise of stomatal-based defense (54). In

addition, enteric pathogen populations such as *S. enterica* have been shown to exhibit slower

population decline on healthy plants exposed to high humidity (55–58). To determine how

humidity impacts *S. enterica's* ability to benefit from *X. vitians* disease, we tested the impact of a

24-hour and 72-hour exposure to >90% RH conditions (**Figure 2A**). Our data showed that *S.*

enterica populations were higher on *X. vitians*-infected plants exposed to high humidity, yet

unaffected by humidity on healthy plants **(Figure 2B).** The latter result that high humidity did

not have a significant impact on *S. enterica* persistence on healthy plants is somewhat contrary to

published literature demonstrating that high humidity supports *S. enterica* survival on healthy

plants (55–58). However, the *S. enterica* inoculum used for this study, ~3000 CFU/droplet, is

relatively low compared to these previous studies examining humidity impacts on *S. enterica,*

and lower inoculum can result in greater variability (57). Furthermore, it is worth emphasizing

that the effect of high humidity on enhancing *S. enterica* growth in the presence of disease was

not linked directly to *X. vitians* cell density. Unexpectedly, we found that the introduction of high

humidity to *X. vitians*-infected leaves could inhibit *X. vitians* colonization (**Supplementary**

Figure 2C), though this effect was not observed when the high humidity conditions were

introduced later during infection (**Supplementary Figure 3C**). This observation about humidity

and *X. vitians* infection is contrary to the well-known association between high humidity and

phytopathogenic disease, including disease by *X. vitians* (3, 52). However, these particular

experiments only looked at the short-term impact of high humidity on *X. vitians* infection. Short-

term disruptions to *X. vitians* infection progress may not necessarily predict how high humidity

would impact infection of the course of multiple days or even weeks. Though *S. enterica* and *X.*

vitians exhibited differing responses to a 24-hour high humidity exposure, the long-term impact

of high humidity climate trends on *S. enterica* colonization of plants in association with

phytobacterial disease is unknown. Considering that precipitation and seasonality have been

shown to influence *S. enterica's* abundance in bodies of water, including irrigation ponds (43,

59, 60), the question of how humidity impacts *S. enterica* in the field is worth exploring. Plant

disease is also influenced by humidity and season, and it is plausible that *S. enterica* prevalence

on plants is influenced by humidity patterns as well.

Our previous study, which also modelled a contamination route via splash dispersal,

found that *S. enterica* applied to tomato leaves via surface droplet could become internalized into

the leaf apoplast (17). A wet apoplast, either abiotically water-logged or water-soaked from

phytobacterial disease, could enable the physical absorption of surface water and passive ingress

of *S. enterica* in a non-flagellar motility-dependent manner (17). This study expands on those

findings by examining the role of relative humidity in *S. enterica's* ability to persist on infected

leaves and colonize the apoplast. In the absence of high humidity exposure that facilitates

replication, *S. enterica* still managed to colonize the UV-protected apoplast of *X. vitians*-infected

lettuce (**Figure 3B**), demonstrating that *S. enterica's* ability to replicate under high humidity

conditions is not explained by colonization of the apoplast alone. Although moderate humidity

conditions (50-70%) were not conducive to *S. enterica* replication in the presence of *X. vitians*

infection (**Figure 3B**), *X. vitians* replicated successfully *in planta* at 50-70% RH and caused

measurable increases in electrolyte leakage (**Supplementary Figures 4A-B**) suggesting that

moderate humidity conditions can allow the liberation of apoplast nutrients during *X. vitians*

infection. Therefore, these results support the idea that the combination of extended high

humidity and a *X. vitians*-infected apoplast provides additional resources *S. enterica* can

successfully metabolize. Whether high humidity conditions must be sustained continuously or if

the accumulation of multiple high humidity events is sufficient to promote *S. enterica* growth on

Xanthomonas-infected leaves should be determined through future work.

Stomata serve as critical entry points for bacteria in the phyllosphere (61). *Xanthomonas*

infection has been previously shown to promote ingress of surface bacteria into the apoplast of

tomato leaves via stomata (17). In this study, we observed that *S. enterica* became internalized

within *X. vitians*-infected lettuce leaves, based on evidence of *S. enterica* protection from UV

irradiation (**Figures 1, 3-4**) and colonization of *S. enterica* within substomatal chambers of the

apoplast (**Figure 5**). If a bacterium can enter the apoplast via stomata and cells are found on the

leaf surface at stomata, one might assume that they would also be found in the substomatal

cavity. We found with CLSM that *S. enterica* ingress varied among stomata. *S. enterica*

colonization of stomatal openings, likely influenced by *S. enterica* chemotaxis (62), did not

always result in colonization of the lower substomatal space (**Figure 5**). Syringe infiltration of *X.*

vitians into the apoplast is assumed to create a consistent dispersal of cells within the infiltration

zone (63). However, the mottled appearance of the infected area suggests that disease onset is

not consistent throughout the inoculation zone (**Supplementary Figure 5**). Clonal *Pseudomonas*

syringae cells have been shown to exhibit heterogeneity in T3SS expression within the apoplast

(64). Our CLSM results showed a heterogeneity of *X. vitians* microcolonies on the leaf surface

and within the apoplast, and we speculate that this heterogeneity may differentially impact *S.*

enterica's interactions with stomata and colonization of the apoplast.

516   *S. enterica* was also influenced by the temporal dynamics of *X. vitians* disease progress.

Our study investigated the fate of *S. enterica* following arrival at various times during *X. vitians*

infection progress and essentially used *S. enterica* as a biological reporter for changes to a *X.*

vitians-infected apoplast. Although *X. vitians* infection was found to be generally beneficial to *S.*

enterica, (**Figures 1-2, 5**), the early infection court was a hostile environment for *S. enterica*

(**Figure 4**). Arrival of *S. enterica* during early infection at 1 dpi led to a reduction in *S. enterica*

populations, sometimes to non-detectable levels two days later (**Figure 4,** Treatment X1). We

hypothesize that *S. enterica's* population reduction and death in the host experiencing an early *X.*

vitians infection is attributed to the host defense response. Infiltration of bacteria into the

apoplast can elicit MAMP (microbe-associated molecular pattern)-triggered immune (MTI)

response (65). Recognition of phytobacterial invaders may trigger phytohormone signaling and

apoplast accumulation of reactive oxygen and nitrogen species (66, 67), which has been

demonstrated to limit *S. enterica* growth *in planta* (68). *S. enterica* flagellin is a known elicitor

of MTI (69), and *S. enterica* may benefit from suppression of MTI by phytobacteria based on its

ability to thrive in the presence of disease (17). Hence, modulation of plant defenses may

contribute to *S. enterica* success on infected leaves. However, as demonstrated in our study, the

timing of co-colonization is important. Previously, it was shown that *S. enterica* achieved greater

colonization of tomato foliage when seeds were co-treated with *Xanthomonas euvesicatoria*

(formerly known as *X. campestris* pv. vesicatoria) via inoculated soil (18). However, at the early

tomato seedling stage, *S. enterica* populations were lower in the presence of *X. euvesicatoria*.

Additionally, Potnis et al. (70) demonstrated that *S. enterica* persistence on tomato plants is

enhanced by *Xanthomonas perforans* infection but diminished by an avirulent *X. perforans* strain

that can neither cause disease, nor suppress MTI. Hence, *S. enterica* responds to both

aggravation and suppression of host defenses by phytobacteria.

Phytobacterial infection likely also supports *S. enterica* survival in the phyllosphere by

providing nutrients for growth. *S. enterica* metabolism is incredibly flexible, enabling it to utilize

many different types of carbon and nitrogen sources in an animal host, even at scant

concentrations (71). However, *S. enterica* growth is disadvantaged on plants. *S. enterica* cannot

liberate nutrients from plant cells on its own because it lacks cell-wall degrading enzymes and

the ability to manipulate the host environment via type-III effectors (72–74). Additionally, as

previously mentioned, *S. enterica* is rarely able to utilize sucrose, one of the most abundant

carbon sources on plants (75, 76). *S. enterica* can persist in the phyllosphere for months on

healthy plants (22), though its population levels steadily decline (16, 22, 77), presumably due to

stress exposure. Contrastingly, in the presence of *X. vitians* infection, *S. enterica* replicates *in*

planta (**Figures 1-2, Table 2**), indicating that infection increases nutrient availability for *S.*

enterica. However, as *X. vitians* infection leads to tissue necrosis (**Supplementary Figure 2**) and

presumably a decrease in available nutrients, *S. enterica* populations in a *X. vitians*-infected

apoplast decline, as evident by *S. enterica* populations dropping below the original arrival

population level following arrival during at 5 dpi (**Figure 4B**, Treatment X5). Late in infection,

phytobacterial pathogens migrate away from necrotic tissue, presumably to locate available

nutrients or to disperse to another host. Future studies will examine the dispersal of *S. enterica*

beyond initially infected leaf tissue to determine if the human and plant pathogens co-migrate as

they seek nutrient sources.

Nutrients metabolized by *S. enterica* in the presence of disease are likely host derived.

Xanthomonas replication in the apoplast during infection is driven by leakage of plant cell

constituents (8, 16), which *S. enterica* may be able to scavenge in the presence of *X. vitians*

infection. However, we also hypothesize that bacterial cross-feeding (78) between *S. enterica*

and *X. vitians* contributes to *S. enterica's* ability to grow *in planta.* Previously, cross-feeding has

been demonstrated to influence nutritional niches, thus affecting phytobacterial community

composition (79). Our finding that infection can promote *S. enterica* replication within the UV-

protected apoplast (**Figure 1C**) and our CLSM observations of *S. enterica* cells localized in

proximity to *X. vitians* cells *in planta* (**Figure 5**) inspired us to test whether these cells interact

directly via nutrient flow from *X. vitians* to *S. enterica.* The results of our *in vitro* experiment

demonstrated that although sucrose is a poor nutrient source for *S. enterica*, *S. enterica* could

grow in sucrose-based minimal media if replicating *X. vitians* cells were present (**Figure 6**).

Cell-free supernatant (CFS) derived from *X. vitians* cultures did not support *S. enterica* growth as

well as cultures containing *X. vitians* cells. *Xanthomonas* strains are known for producing sticky

extracellular polysaccharides, including xanthan gum (80), which may have contributed to the

exclusion of nutrients during the filtering of *X. vitians* culture supernatant. The identity of the

nutrients utilized by *S. enterica* via cross-feeding are unknown, but could include amino acids,

carbohydrates, or organic acids (75). Future studies may elucidate the carbon sources

metabolized by *S. enterica in planta* in the presence of disease.

Previous work investigating relationships between enteric pathogen persistence,

phytopathogen infection, and environment has generally studied 1-2 of these elements in

isolation. In reality, interplay between enteric pathogens, plant pathogens, and climate factors are

all likely to influence the microbial communities in the phyllosphere. In this study expanding

knowledge of *S. enterica's* fate following water droplet dispersal, we found that *S. enterica*

survival on lettuce is enhanced by bacterial spot disease caused by *X. vitians* and that *S. enterica*

proliferation was conditional on the status of infection and the environment **(Figure 7)**. Overall,

it was the combination of high humidity exposure and the timing of *S. enterica* arrival with

respect to bacterial spot disease progress that maximized *S. enterica* survival and access to

nutrients in an otherwise inhospitable host. As climate patterns continue to evolve, microbial

dynamics in the phyllosphere will evolve too, underlining the importance of studying host-

microbial interactions under various environmental conditions.

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M.H.D and J.D.B. developed the experiments. M.H.D., D.N., and S.C.Z. performed the

experiments. M.H.D. and J.D.B. wrote the manuscript, and all authors reviewed the manuscript.

M.H.D. created the original illustrations.

    TABLES

612   **TABLE 1.** Bacterial strains used in this study.

Strain name and description	Reference or source
Xanthomonas hortorum pv. vitians L7 (*X. vitians*)	J. Jones
Xanthomonas hortorum pv. vitians L7; Cm^R transformed with pNO-mCherry	This study
Escherichia coli; Cm^R; pNO-mCherry	Z. Gitai
Salmonella enterica serovar Typhimurium 14028s; Nal^R	(82)
Salmonella enterica serovar Typhimurium 14028s; Kan^R; transformed with pKT-Kan; GFP	(83)

613   ^{R} = resistance to chloramphenicol (Cm), nalidixic acid (Nal), or kanamycin (Kan)

615   **TABLE 2:** Incidence^a of *S. enterica in planta* growth depending on *X. vitians* infection progress

616   at time of *S. enterica* arrival.

UV Treatment Group^c	Infiltration Treatment Group^b					
	H	X1	X2	X3	X4	X5
Non-irradiated	7% A^d	17% AB	56% BC	56% BC	72% C	50% BC
UV-irradiated	0% a	0% a	33% ab	50% b	61% b	28% ab

^{a}Percentage of samples for which *in planta S. enterica* colonization exceeds the arrival

population.

^{b,c}Treatment groups refer directly to experiment described in **Figure 2**.

^{d}Letters indicate significance between treatment groups among non-irradiated leaves (uppercase)

and among UV-treated leaves (lowercase) based on Fisher's exact tests ($P < 0.05$).

FIGURE LEGENDS

Figure 1: *X. vitians* infection facilitates *S. enterica* replication and colonization of UV-protected

niches *in planta*. **(A)** Schematic of experimental design including color coded treatment

descriptions. *S. enterica* (*Se*) cells were applied to leaves previously infiltrated with H_2O or *X.*

vitians (*Xvit*) at 4 dpi, and plants were sampled at 1- or 3-days post-*Se* arrival (dpa). High

humidity (>90% RH) exposure is depicted as grey shading. **(B-C)** *S. enterica* (*Se*) colonization of

H_2O-infiltrated (blue boxplots) and *X. vitians*-infiltrated (orange boxplots) plants as measured

from surface swab **(B)** and homogenized lettuce tissue **(C)** at 1- and 3- days post *Se* arrival (dpa).

Darker boxplot colors for 3 dpa data signify exposure to high humidity prior to sampling. Leaves

were irradiated with UV immediately prior to sampling (unfilled triangle points) or left non-

irradiated (filled circle points). Letters above the boxplots indicate significance between

treatment groups among leaves sampled at 1 dpa (uppercase) and among leaves sampled at 3 dpa

(lowercase) based on Welch-ANOVA and *post hoc* Games-Howell means comparison tests ($P <$

0.05). Daggers (†) indicate significant increases in *Se* colonization between 1 dpa and 3 dpa

within the same infiltration treatment and UV treatment groups based on two-sample T-tests ($P <$

0.05). Solid line indicates average *Se* arrival population applied to each sampled area, and dashed

line indicates limit of detection (LOD). Values below LOD are defined in Materials and

Methods. $N = 30$ leaves/treatment group; data is pooled from five independent experimental

replicates.

Figure 2: High humidity (>90% RH) exposure and *X. vitians* infection additively enhance *S.*

enterica colonization of lettuce. **(A)** Schematic of experimental design. Lettuce plants were

divided into six treatment groups. *S. enterica* (*Se*) cells were applied to leaves previously

infiltrated with H_2O or *X. vitians* (*Xvit*) at 3 days post-infiltration. Plants were sampled following

0, 24, or 72 hours of exposure to high humidity (>90% RH) at 4 days post-*Se* arrival (Humidity

Treatments I, II, and III, respectively). **(B)** *Se* colonization of H_2O-infiltrated (blue boxplots) and

X. vitians-infiltrated (orange boxplots) plants at 2 days post-arrival (dpa) in response to varying

humidity treatments. Letters above the boxplots indicate significance between treatment groups

based on Welch-ANOVA and *post hoc* Games-Howell means comparison tests ($P < 0.05$).

Asterisks indicate that *Se in planta* colonization is significantly less than (*<) or greater than (*>)

the arrival population based on one-sample Wilcoxon tests ($P < 0.05$). Solid line indicates

average *Se* arrival population applied to each sampled area, and dashed line indicates limit of

detection (LOD). < LOD values are defined in Materials and Methods. $N = 24$ leaves/treatment

group; data is pooled from three independent experimental replicates.

Figure 3: High humidity (>90% RH) exposure is not required for *S. enterica* to colonize UV-

protected niches of *X. vitians*-infected lettuce. **(A)** Schematic of experimental design. Lettuce

plants were divided into two treatment groups. *S. enterica* (*Se*) cells were applied to leaves

previously infiltrated with *X. vitians* (*Xvit*) at 3 days post-infiltration. Plants were sampled

following 0 or 24 hours of exposure to high humidity (>90% RH) prior to sampling (Humidity

Treatments i and ii, respectively). **(B)** *S. enterica* colonization of *X. vitians*-infiltrated plants at 2

days post-arrival (dpa) in response to varying humidity treatments. Leaf halves were irradiated

with UV immediately prior to sampling (unfilled triangle points) or left non-irradiated (filled

circle points). Letters above the boxplots indicate significance between treatment groups based

on Welch-ANOVA and *post hoc* Games-Howell means comparison tests ($P < 0.05$). Asterisks

(*) indicate that *S. enterica in planta* colonization is significantly less than the arrival population

based on one-sample Wilcoxon tests ($P < 0.05$). Solid line indicates average *S. enterica* arrival

population applied to each sampled area, and dashed line indicates limit of detection (LOD). $N =$

18 leaves/treatment group; data is pooled from three independent experimental replicates.

Figure 4: The fate of *S. enterica* on lettuce leaves is influenced by *X. vitians* infection progress

at *S. enterica* arrival. **(A)** Schematic of experimental design. Lettuce plants were divided into six

treatment groups. *S. enterica* (*Se*) cells were applied to leaves previously infiltrated with H_2O or

X. vitians (*Xvit*) at various days post-infiltration (dpi). Plants were sampled following 24 hours of

exposure to high humidity (>90% RH). **(B)** *Se* colonization of H_2O-infiltrated (blue boxplots,

Treatment H) and *X. vitians*-infiltrated (orange boxplots, Treatments X#) plants at 2 days *post-Se*

arrival (dpa). Leaf halves were irradiated with UV immediately prior to sampling (unfilled

triangle points) or left non-irradiated (filled circle points). Letters above the boxplots indicate

significance between treatment groups (H-X5) for non-irradiated leaves (uppercase) or UV-

treated leaves (lowercase) based on Welch-ANOVA and *post hoc* Games-Howell means

comparison tests ($P < 0.05$). Asterisks (*) indicate that *Se in planta* colonization is significantly

less than the arrival population based on one-sample Wilcoxon tests ($P < 0.05$). Solid line

indicates average *Se* arrival population applied to each sampled area, and dashed line indicates

limit of detection (LOD). $N = 15$-18 leaves/treatment group; data is pooled from three

independent experimental replicates.

Figure 5: *S. enterica* colonizes the apoplast of *X.* vitians-infected lettuce leaves. CLSM images

depict GFP-labelled *S. enterica* colonization of the lettuce surface **(A-F)** and apoplast (**G-L**) for

three sites **(columns A-C)** representative of three treatments and imaged at the given z-depths

(μm). *S. enterica* cells were applied to the surface of leaves previously infiltrated with H_2O

(column A) or mCherry-labelled *X. vitians* cells **(columns B-C)**. Horizontal labels describe

infiltration treatment and days-post infiltration (dpi) at time of *S. enterica* arrival. **A-C, G-I**: GFP

channel only. **D-F, J-L**: merged channels (GFP, green; mCherry, magenta; DIC, bright-field).

Stomata (S) and substomatal *S. enterica* cells (sS) are highlighted with white arrows and white

triangles. Scale bar = 20 μm.

Figure 6: *X. vitians* metabolism of sucrose produces nutrients *S. enterica* can utilize for growth.

S. enterica cells were added to fresh M9 sucrose (M9 suc, light blue points) or M9 glucose (M9

glc, dark blue points), mixed with *X. vitians* (*Xvit*) cell cultures grown for 24 (yellow points) or

48 hours (orange points) in M9 sucrose, or mixed with *Xvit* cell-free supernatant (CFS, emerald

green & dark green points) at time (t) = 0 hr. Dotted line represents the initial *S. enterica* cell

concentration at t = 0 hr. Each horizontal colored bar represents the average *S. enterica* cell

concentrations of four independent experiments at t = 28 hr. Letters above the boxplots indicate

significance between treatment groups based on Welch-ANOVA and *post hoc* Games-Howell

means comparison tests ($P < 0.05$). Daggers (†) indicate a significant increase in *S. enterica* cell

concentration compared to t = 0 hr based on two-sample T-tests ($P < 0.05$).

Figure 7: The fate of *Salmonella enterica* in the phyllosphere is influenced by *Xanthomonas*

infection progress and humidity. **(A)** Early *Xanthomonas* infection. *X. vitians* (magenta bacteria)

begin to modify the host environment, but the infection court is not yet habitable for *S. enterica.*

(B) Established *Xanthomonas* infection. *S. enterica* (green bacteria) successfully colonize the

apoplast of *Xanthomonas*-infected leaves via ingress through stomata. **(C)** *Xanthomonas*

infection plus high humidity. High humidity (>90% RH) promotes replication of *S. enterica*

within a *Xanthomonas*-infected apoplast, though is not required for *S. enterica* ingress.

REFERENCES

1. Schlechter RO, Miebach M, Remus-Emsermann MNP. 2019. Driving factors of epiphytic bacterial communities: A review. J Adv Res 19:57–65.
2. Vorholt JA. 2012. Microbial life in the phyllosphere. Nat Rev Microbiol 10:828–840.
3. Xin XF, Nomura K, Aung K, Velásquez AC, Yao J, Boutrot F, Chang JH, Zipfel C, He SY. 2016. Bacteria establish an aqueous living space in plants crucial for virulence. Nature 539:524–529.
4. Hu Y, Ding Y, Cai B, Qin X, Wu J, Yuan M, Wan S, Zhao Y, Xin X-F. 2022. Bacterial effectors manipulate plant abscisic acid signaling for creation of an aqueous apoplast. Cell Host Microbe 1–12.
5. Roussin-Léveillée C, Lajeunesse G, St-Amand M, Veerapen VP, Silva-Martins G, Nomura K, Brassard S, Bolaji A, He SY, Moffett P. 2022. Evolutionarily conserved bacterial effectors hijack abscisic acid signaling to induce an aqueous environment in the apoplast. Cell Host Microbe 1–13.
6. Schornack S, Minsavage G V, Stall RE, Jones JB, Lahaye T, Jones JB. 2006. Characterization of AvrHah1 , a novel AvrBs3-like effector from Xanthomonas gardneri with virulence and avirulence activity. New Phytologist 179:546–556.
7. Cowles KN, Block AK, Barak JD. 2022. Xanthomonas hortorum pv. gardneri TAL effector AvrHah1 is necessary and sufficient for increased persistence of Salmonella enterica on tomato leaves. Sci Rep 12:1–13.
8. Schwartz AR, Morbitzer R, Lahaye T, Staskawicz BJ. 2017. TALE-induced bHLH transcription factors that activate a pectate lyase contribute to water soaking in bacterial spot of tomato. Proceedings of the National Academy of Sciences 114:E897–E903.
9. Dia NC, Morinière L, Cottyn B, Bernal E, Jacobs JM, Koebnik R, Osdaghi E, Potnis N, Pothier JF. 2022. *Xanthomonas hortorum* – beyond gardens: Current taxonomy, genomics, and virulence repertoires. Mol Plant Pathol 23:597–621.
10. Robinson PE, Jones JB, Pernezny K. 2006. Bacterial leaf spot of lettuce: Relationship of temperature to infection and potential host range of Xanthomonas campestris pv. vitians. Plant Dis 90:465–470.
11. Savary S, Willocquet L, Pethybridge SJ, Esker P, McRoberts N, Nelson A. 2019. The global burden of pathogens and pests on major food crops. Nat Ecol Evol 3:430–439.
12. Goudeau DM, Parker CT, Zhou Y, Sela S, Kroupitski Y, Brandl MT. 2013. The Salmonella transcriptome in lettuce and cilantro soft rot reveals a niche overlap with the animal host intestine. Appl Environ Microbiol 79:250–262.
13. Kwan G, Charkowski AO, Barak JD. 2013. Salmonella enterica Suppresses Pectobacterium carotovorum subsp. carotovorum Population and Soft Rot Progression by Acidifying the Microaerophilic Environment. mBio 4:1–9.
14. Meng F, Altier C, Martin GB. 2013. Salmonella colonization activates the plant immune system and benefits from association with plant pathogenic bacteria. Environ Microbiol 15:2418–2430.
15. Potnis N, Soto-Arias JP, Cowles KN, van Bruggen AHC, Jones JB, Barak JD. 2014. Xanthomonas perforans Colonization Influences Salmonella enterica in the Tomato Phyllosphere. Appl Environ Microbiol 80:3173–3180.

765   16.   Potnis N, Colee J, Jones JB, Barak JD. 2015. Plant Pathogen-Induced Water-Soaking
766   Promotes Salmonella enterica Growth on Tomato Leaves. Appl Environ Microbiol
767   81:8126–8134.
768   17.   Dixon MH, Cowles KN, Zaacks SC, Marciniak IN. 2022. Xanthomonas Infection
769   Transforms the Apoplast into an Accessible and Habitable Niche for Salmonella enterica.
770   Appl Environ Microbiol.
771   18.   Barak JD, Liang AS. 2008. Role of soil, crop debris, and a plant pathogen in Salmonella
772   enterica contamination of tomato plants. PLoS One 3.
773   19.   Teplitski M, Moraes M De. 2018. Of Mice and Men .... and Plants : Comparative
774   Genomics of the Dual Lifestyles of Enteric Pathogens. Trends Microbiol 26:748–754.
775   20.   Spector MP, Kenyon WJ. 2012. Resistance and survival strategies of Salmonella enterica
776   to environmental stresses. Food Research International 45:455–481.
777   21.   Liu H, Whitehouse CA, Li B. 2018. Presence and Persistence of Salmonella in Water: The
778   Impact on Microbial Quality of Water and Food Safety. Front Public Health 6.
779   22.   Islam M, Morgan J, Doyle MP, Phatak SC, Millner P, Jiang X. 2004. Persistence of
780   *Salmonella enterica* Serovar Typhimurium on Lettuce and Parsley and in Soils on Which
781   They Were Grown in Fields Treated with Contaminated Manure Composts or Irrigation
782   Water. Foodborne Pathog Dis 1:27–35.
783   23.   Islam M, Morgan J, Doyle MP, Phatak SC, Millner P, Jiang X. 2004. Fate of Salmonella
784   enterica Serovar Typhimurium on Carrots and Radishes Grown in Fields Treated with
785   Contaminated Manure Composts or Irrigation Water. Appl Environ Microbiol 70:2497–
786   2502.
787   24.   Brandl MT. 2006. Fitness of Human Enteric Pathogens on Plants and Implications for
788   Food Safety. Annual Reviews of Phytopathology 44.
789   25.   Carstens CK, Salazar JK, Darkoh C. 2019. Multistate Outbreaks of Foodborne Illness in
790   the United States Associated With Fresh Produce From 2010 to 2017. Front Microbiol.
791   Frontiers Media S.A. https://doi.org/10.3389/fmicb.2019.02667.
792   26.   Horby PW, O'Brien SJ, Adak GK, Graham C, Hawker JI, Hunter P, Lane C, Lawson AJ,
793   Mitchell RT, Reacher MH, Threlfall EJ, Ward LR. 2003. A national outbreak of multi-
794   resistant *Salmonella enterica* serovar Typhimurium definitive phage type (DT) 104
795   associated with consumption of lettuce. Epidemiol Infect 130:169–178.
796   27.   Lienemann T, Niskanen T, Guedes S, Siitonen A, Kuusi M, Rimhanen-Finne R. 2011.
797   Iceberg Lettuce as Suggested Source of a Nationwide Outbreak Caused by Two
798   Salmonella Serotypes, Newport and Reading, in Finland in 2008. J Food Prot 74:1035–
799   1040.
800   28.   McClure M, Whitney B, Gardenhire I, Crosby A, Wellman A, Patel K, McCormic ZD,
801   Gieraltowski L, Gollarza L, Low MSF, Adams J, Pightling A, Bell RL, Nolte K, Tijerina
802   M, Frost JT, Beix JA, Boegler KA, Dow J, Altman S, Wise ME, Bazaco MC, Viazis S.
803   2023. An Outbreak Investigation of Salmonella Typhimurium Illnesses in the United
804   States Linked to Packaged Leafy Greens Produced at a Controlled Environment
805   Agriculture Indoor Hydroponic Operation – 2021. J Food Prot 86:100079.
806   29.   Ouzounov N. 2015. Establishment and maintenance of rod shape by the bacterial actin
807   homologue MreB. Princeton University, Princeton, NJ.
808   30.   Hashimoto-Gotoh T, Yamaguchi M, Yasojima K, Tsujimura A, Wakabayashi Y,
809   Watanabe Y. 2000. A set of temperature sensitive-replication/-segregation and

temperature resistant plasmid vectors with different copy numbers and in an isogenic
background (chloramphenicol, kanamycin, lacZ, repA, par, polA). Gene 241:185–191.

31. Lutz R, Bujard H. 1997. Independent and tight regulation of transcriptional units in
escherichia coli via the LacR/O, the TetR/O and AraC/I1-I2 regulatory elements. Nucleic
Acids Res 25:1203–1210.

32. Dixon MH, Cowles KN, Zaacks SC, Marciniak IN. 2022. Xanthomonas Infection
Transforms the Apoplast into an Accessible and Habitable Niche for Salmonella enterica.
Appl Environ Microbiol.

33. Cowles KN, Groves RL, Barak JD. 2018. Leafhopper-Induced Activation of the Jasmonic
Acid Response Benefits Salmonella enterica in a Flagellum-Dependent Manner. Front
Microbiol 9:1–15.

34. Harrod VL, Groves RL, Guillemette EG, Barak JD. 2022. Salmonella enterica changes
Macrosteles quadrilineatus feeding behaviors resulting in altered S. enterica distribution
on leaves and increased populations. Sci Rep 12:1–13.

35. Kessens R, Sorensen N, Kabbage M. 2018. An inhibitor of apoptosis (SfIAP) interacts
with SQUAMOSA promoter-binding protein (SBP) transcription factors that exhibit pro-
cell death characteristics. Plant Direct 2:1–17.

36. Fatima U, Senthil-Kumar M. 2015. Plant and pathogen nutrient acquisition strategies.
Front Plant Sci 6:1–12.

37. Reid SJ, Abratt VR. 2005. Sucrose utilisation in bacteria: Genetic organisation and
regulation. Appl Microbiol Biotechnol 67:312–321.

38. Steele M, Odumeru J. 2004. Irrigation Water as Source of Foodborne Pathogens on Fruit
and Vegetables. J Food Prot 67:2839–2849.

39. Jacobsen CS, Bech TB. 2012. Soil survival of Salmonella and transfer to freshwater and
fresh produce. Food Research International 45:557–566.

40. Centers for Disease Control and Prevention (CDC). 2008. Outbreak of Salmonella
Serotype Saintpaul Infections Associated with Multiple Raw Produce Items --- United
States, 2008. Morbidity and Mortality Weekly Report 57:929–934.

41. Centers for Disease Control and Prevention (CDC). 2018. Surveillance for Foodborne
Disease Outbreaks United States, 2016, Annual Report. Atlanta, Georgia.

42. Centers for Disease Control and Prevention (CDC). 2018. Multistate Outbreak of E. coli
O157:H7 Infections Linked to Romaine Lettuce (Final Update).
https://www.cdc.gov/ecoli/2018/o157h7-04-18/index.html. Retrieved 11 January 2022.

43. Haley BJ, Cole DJ, Lipp EK. 2009. Distribution, Diversity, and Seasonality of Waterborne
Salmonellae in a Rural Watershed. Appl Environ Microbiol 75:1248–1255.

44. Johnson R, Cody BA. 2015. California Agricultural Production and Irrigated Water Use.

45. Mpanga IK, Idowu OJ. 2021. A Decade of Irrigation Water use trends in Southwestern
USA: The Role of Irrigation Technology, Best Management Practices, and Outreach
Education Programs. Agric Water Manag 243:106438.

46. Davis W, Weber C, Wechsler S, Lucier G, Soria Rodriguez M, Yeh A, Fan X. 2023.
Vegetable and Pulses Outlook: April 2023.

47. Hirano SS, Baker LS, Upper CD. 1996. Raindrop Momentum Triggers Growth of Leaf-
Associated Populations of Pseudomonas syringae on Field-Grown Snap Bean Plants. Appl
Environ Microbiol 62:2560–2566.

48.   Kim S, Park H, Gruszewski HA, Schmale DG, Jung S. 2019. Vortex-induced dispersal of
a plant pathogen by raindrop impact. Proceedings of the National Academy of Sciences
116:4917–4922.
49.   Pérez-Lavalle L, Carrasco E, Vallesquino-Laguna P, Cejudo-Gómez M, Posada-Izquierdo
GD, Valero A. 2021. Internalization capacity of Salmonella enterica sv Thompson in
strawberry plants via root. Food Control 126:108080.
50.   Reyes Esteves RG, Gerba CP, Slack DC. 2022. Control of Viral and Bacterial
Contamination of Lettuce by Subsurface Drip Irrigation. Journal of Irrigation and
Drainage Engineering 148.
51.   Beattie GA. 2011. Water Relations in the Interaction of Foliar Bacterial Pathogens with
Plants. Annu Rev Phytopathol 49:533–555.
52.   Yunis H, Bashan Y, Okon Y, Henis Y. 1980. Weather Dependence, Yield Losses, and
Control of Bacterial Speck of Tomato Caused by Pseudomonas tomato. Plant Dis 64:937–
939.
53.   Toussaint V. 2001. Ecology of Xanthomonas campestris pv. vitians in relation to
development of bacterial leaf spot of lettuce. McGill University, Montreal.
54.   Panchal S, Chitrakar R, Thompson BK, Obulareddy N, Roy D, Hambright WS, Melotto
M. 2016. Regulation of stomatal defense by air relative humidity. Plant Physiol 172:2021–
2032.
55.   Stine SW, Song I, Choi CY, Gerba CP. 2005. Effect of relative humidity on preharvest
survival of bacterial and viral pathogens on the surface of cantaloupe, lettuce, and bell
peppers. J Food Prot 68:1352–1358.
56.   Roy D, Panchal S, Rosa BA, Melotto M. 2013. Escherichia coli O157:H7 Induces
Stronger Plant Immunity than Salmonella enterica Typhimurium SL1344. Phytopathology
103:326–332.
57.   López-Gálvez F, Gil MI, Allende A. 2018. Impact of relative humidity, inoculum carrier
and size, and native microbiota on Salmonella ser. Typhimurium survival in baby lettuce.
Food Microbiol 70:155–161.
58.   Deblais L, Helmy YA, Testen A, Vrisman C, Madrid MJ, Kathayat D. 2019. Specific
Environmental Temperature and Relative Humidity Conditions and Grafting Affect the
Persistence and Dissemination of Salmonella enterica subsp. enterica Serotype
Typhimurium in Tomato Plant Tissues. Appl Environ Microbiol 85:1–17.
59.   Walters SP, Thebo AL, Boehm AB. 2011. Impact of urbanization and agriculture on the
occurrence of bacterial pathogens and stx genes in coastal waterbodies of central
California. Water Res 45:1752–1762.
60.   Harris CS, Tertuliano M, Rajeev S, Vellidis G, Levy K. 2018. Impact of storm runoff on
Salmonella and *Escherichia coli* prevalence in irrigation ponds of fresh produce farms in
southern Georgia. J Appl Microbiol 124:910–921.
61.   Melotto M, Underwood W, He SY. 2008. Role of Stomata in Plant Innate Immunity and
Foliar Bacterial Diseases. Annu Rev Phytopathol 46:101–122.
62.   Kroupitski Y, Golberg D, Belausov E, Pinto R, Swartzberg D, Granot D, Sela S. 2009.
Internalization of Salmonella enterica in Leaves Is Induced by Light and Involves
Chemotaxis and Penetration through Open Stomata. Appl Environ Microbiol 75:6076–
6086.
63.   Chincinska IA. 2021. Leaf infiltration in plant science: old method, new possibilities.
Plant Methods 17:83.

64.   Rufian J, Sanchez-Romero M, Lopez-Marquez D, Macho A, Mansfield J, Arnold D, Ruiz-
Albert J, Casadesus J, Beuzon C. 2016. Pseudomonas syringae differentiates into
phenotypically distinct subpopulations during colonization of a plant host. Environ
Microbiol 18:3593–3605.
65.   Newman M-A, Sundelin T, Nielsen JT, Erbs G. 2013. MAMP (microbe-associated
molecular pattern) triggered immunity in plants. Front Plant Sci 4.
66.   Qi J, Wang J, Gong Z, Zhou J-M. 2017. Apoplastic ROS signaling in plant immunity.
Curr Opin Plant Biol 38:92–100.
67.   Khan M, Ali S, Al Azzawi TNI, Saqib S, Ullah F, Ayaz A, Zaman W. 2023. The Key
Roles of ROS and RNS as a Signaling Molecule in Plant–Microbe Interactions.
Antioxidants 12:268.
68.   Ferelli AMC, Bolten S, Szczesny B, Micallef SA. 2020. Salmonella enterica Elicits and Is
Restricted by Nitric Oxide and Reactive Oxygen Species on Tomato. Front Microbiol
11:1–15.
69.   García A V., Hirt H. 2014. Salmonella enterica induces and subverts the plant immune
system. Front Microbiol 5:1–6.
70.   Potnis N, Soto-Arias JP, Cowles KN, van Bruggen AHC, Jones JB, Barak JD. 2014.
Xanthomonas perforans Colonization Influences Salmonella enterica in the Tomato
Phyllosphere. Appl Environ Microbiol 80:3173–3180.
71.   Steeb B, Claudi B, Burton NA, Tienz P, Schmidt A, Farhan H, Mazé A, Bumann D. 2013.
Parallel Exploitation of Diverse Host Nutrients Enhances Salmonella Virulence. PLoS
Pathog 9.
72.   Teplitski M, Barak JD, Schneider KR. 2009. Human enteric pathogens in produce : un-
answered ecological questions with direct implications for food safety. Curr Opin
Biotechnol 20:166–171.
73.   Abbott DW, Boraston AB. 2008. Structural Biology of Pectin Degradation by
Enterobacteriaceae. Microbiology and Molecular Biology Reviews 72:301–316.
74.   Chalupowicz L, Nissan G, Brandl MT, McClelland M, Sessa G, Popov G, Barash I,
Manulis-Sasson S. 2018. Assessing the Ability of *Salmonella enterica* to Translocate
Type III Effectors Into Plant Cells. Molecular Plant-Microbe Interactions® 31:233–239.
75.   Fatima U, Senthil-Kumar M. 2015. Plant and pathogen nutrient acquisition strategies.
Front Plant Sci 6:1–12.
76.   Reid SJ, Abratt VR. 2005. Sucrose utilisation in bacteria: Genetic organisation and
regulation. Appl Microbiol Biotechnol 67:312–321.
77.   Zheng J, Allard S, Reynolds S, Millner P, Arce G, Blodgett RJ, Brown EW. 2013.
Colonization and Internalization of Salmonella enterica in Tomato Plants. Appl Environ
Microbiol 79:2494–2502.
78.   Smith NW, Shorten PR, Altermann E, Roy NC, McNabb WC. 2019. The Classification
and Evolution of Bacterial Cross-Feeding. Front Ecol Evol 7.
79.   Murillo-Roos M, Abdullah HSM, Debbar M, Ueberschaar N, Agler MT. 2022. Cross-
feeding niches among commensal leaf bacteria are shaped by the interaction of strain-level
diversity and resource availability. ISME J 16:2280–2289.
80.   Palaniraj A, Jayaraman V. 2011. Production, recovery and applications of xanthan gum by
Xanthomonas campestris. J Food Eng 106:1–12.
81.   Lovelace AH, Ma W. 2022. How do bacteria transform plants into their oasis? Cell Host
Microbe 30:412–414.

82.   Cowles KN, Willis DK, Engel TN, Jones JB, Barak JD. 2016. Diguanylate cyclases AdrA
947   and STM1987 regulate salmonella enterica exopolysaccharide production during plant
948   colonization in an environment-dependent manner. Appl Environ Microbiol 82:1237–
949   1248.
950   83.   Barak J, Whitehand L, Charkowski A. 2002. Differences in Attachment of Salmonella
951   enterica Serovars and Escherichia coli O157:H7 to Alfalfa Sprouts. Appl Environ
952   Microbiol 68:4758 LP – 4763.
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A

Se arrival day 0

Sampling day 2 Humidity Treatment

Xvit infil day -4 ··········· ◯ ··········· ◯ i

Xvit infil day -4 ··········· ◯ ··········· High RH ◯ ii

A

Se arrival day 0   Sampling day 2   Treatment Group

High RH

H₂O infil day -4   H

Xvit infil day -1   X1

Xvit infil day -2   X2

Xvit infil day -3   X3

Xvit infil day -4   X4

Xvit infil day -5   X5

B

non-irradiated

UV-irradiated

Log CFU/leaf disk

Treatment Group

H   X1   X2   X3   X4   X5