

Hydration conditions as a critical factor in antibiotic-mediated bacterial competition outcomes

Yana Beizman-Magen,¹ Tomer Orevi,¹ Nadav Kashtan¹

AUTHOR AFFILIATION See affiliation list on p. 16.

ABSTRACT Antibiotic secretion plays a pivotal role in bacterial interference competition; yet, the impact of environmental hydration conditions on such competition is not well understood. Here, we investigate how hydration conditions affect interference competition among bacteria, studying the interactions between the antibiotic-producing *Bacillus velezensis* FZB42 and two bacterial strains susceptible to its antibiotics: *Xanthomonas euvesicatoria* 85-10 and *Pseudomonas syringae* DC3000. Our results show that wet-dry cycles significantly modify the response of the susceptible bacteria to both the supernatant and cells of the antibiotic-producing bacteria, compared to constantly wet conditions. Notably, *X. euvesicatoria* shows increased protection against both the cells and supernatants of *B. velezensis* under wet-dry cycles, while *P. syringae* cells become more susceptible under wet-dry cycles. In addition, we observed a reciprocal interaction between *P. syringae* and *B. velezensis*, where *P. syringae* inhibits *B. velezensis* under wet conditions. Our findings highlight the important role of hydration conditions in shaping bacterial interference competition, providing valuable insights into the microbial ecology of water-unsaturated surfaces, with implications for applications such as biological control of plant pathogens and mitigating antibiotic resistance.

IMPORTANCE Our study reveals that hydration conditions, particularly wet-dry cycles, significantly influence antibiotic-mediated competition between bacterial species. We revealed that the effectiveness of antibiotics produced by *Bacillus velezensis* against two susceptible bacterial species: *Xanthomonas* and *Pseudomonas* varies based on these hydration conditions. Unlike traditional laboratory environments, many real-world habitats, such as soil, plant surfaces, and even animal skin, undergo frequent wet-dry cycles. These conditions affect bacterial competition dynamics and outcomes, with wet-dry cycles providing increased protection for some bacteria while making others more susceptible. Our findings highlight the importance of considering environmental hydration when studying microbial interactions and developing biological control strategies. This research has important implications for improving agricultural practices and understanding natural microbial ecosystems.

KEYWORDS bacterial interactions, interspecies competition, hydration conditions, microbial ecology, antibiotic-mediated competition, microscopic surface wetness, environmental microbiology, biological control

Bacteria, ubiquitous members of every ecosystem on our planet, play important roles in the maintenance and functioning of ecological processes (1–3). These microorganisms do not live in isolation, but within complex communities, where interactions among different species are common (4, 5). The intricate interactions among bacterial species play a large role in shaping community composition and dynamics (4, 6–10). Such interactions underlie important features of microbial communities such as diversity and stability (9, 10). Deciphering the nature and outcomes of these interactions is crucial

Editor Isaac Cann, University of Illinois Urbana-Champaign, Urbana, Illinois, USA

Address correspondence to Nadav Kashtan, nadav.kashtan@mail.huji.ac.il.

The authors declare no conflict of interest.

See the funding table on p. 16.

Received 10 October 2024

Accepted 27 November 2024

Published 23 December 2024

Copyright © 2024 Beizman-Magen et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

for understanding the complexities of microbial ecology and its impact on ecological systems and processes (4, 9).

Bacterial interspecies competition is a common interaction that can take on active or passive forms (11–13). The passive form involves competition for resources such as nutrients or space, whereas active competition involves one species secreting compounds that actively inhibit the growth or kill other species. This type of competition is called interference competition (11, 13, 14). While interference competition commonly occurs naturally, it can also be artificially induced, as in the application of bacterial biological control against plant pathogens (12, 15), or in bioremediation practices (16).

The outcome and dynamics of most interspecific interactions among bacteria can be influenced by the chemical, physical, and biological characteristics of the environment. Factors such as nutrient availability, temperature, pH, and surface type significantly affect these interactions (17–22). Among these factors, hydration conditions—which refer to the availability of water or moisture, ranging from extremely dry to fully saturated environments—play a pivotal role in many terrestrial microbial habitats. Hydration conditions are governed by the complex interplay of the presence of water or vapor, relative humidity, temperature, and the chemical and physical characteristics of surfaces (23–29). Typically, in environments that are not constantly saturated with water, hydration conditions are not static, but rather fluctuate dynamically, often characterized by recurring wet-dry cycles (30, 31).

During the “dry” phases of wet-dry cycles, surfaces can retain microscopic surface wetness (MSW [25, 30, 31]). MSW can take the form of microscopic droplets or thin liquid films, often invisible to the naked eye. A primary factor driving MSW formation and retention on surfaces is the presence of deliquescent substances, such as highly hygroscopic salts. For example, on leaf surfaces, a major source of salts comes from atmospheric aerosols present ubiquitously across plant foliage globally (25, 30). These salts can form, or retain, microscopic wetness when the relative humidity is above the deliquescence, or efflorescence, points (25, 30). MSW is prevalent on both biotic and abiotic surfaces (25, 31–34) and has been shown to often form around bacterial aggregates and other microorganisms (25, 31). Moreover, MSW has been found to protect bacteria and other microorganisms from desiccation and affect their survival rates (25, 31, 35). Microscopic wetness has been shown to significantly impact bacterial life and ecology, affecting mobility, communication, horizontal gene transfer (36), and spatial organization during colonization of surfaces (25, 37).

In a recent study, we have revealed that wet-dry cycles with MSW can protect bacteria from major antibiotic classes (38). We found that under wet-dry cycles, bacterial response to major antibiotic classes, markedly differs from their reaction under constantly wet conditions. Under wet-dry cycles with a period of MSW conditions (at the “dry” period), bacteria showed increased protection from diverse antibiotic classes, mostly antibiotic classes that are effective against actively growing cells. Through a combination of experiments and computational modeling, we suggested four mechanisms, operating at different phases of wet-dry cycles, that lead to increased protection from antibiotics under wet-dry cycles: (i) cross-protection due to high salt concentrations, (ii) “tolerance by slow growth,” (iii) deactivation of antibiotics by the physicochemical conditions associated with drying and MSW, and (iv) “tolerance by lag” during rewetting (38). Given that hydration conditions and the presence of MSW notably affect bacterial responses to antibiotics, we hypothesize that these factors may also exert an impact on antibiotic-mediated bacterial interference competition outcomes. Throughout this study, we adhere to the definition of antibiotics or antimicrobials as compounds produced by one microorganism that inhibit or kill another microorganism (39, 40).

To explore how wet-dry cycles with MSW affect interference competition among bacteria, we selected the biological control agent *Bacillus velezensis* FZB42 (BvFZB42) (41), renowned for its ability to produce a broad spectrum of antimicrobial compounds (41) (Table S1). These antimicrobial compounds produced by BvFZB42 include a variety of secondary metabolites that can affect bacterial and fungal pathogens. Key

metabolites include lipopeptides (surfactin, bacillomycin D, and fengycin) and polyketides (bacillaene, diffidin, and macrolactin) (41–43). Surfactin plays a role in inducing systemic resistance in plants, while bacillomycin D and fengycin are highly effective against fungi, causing morphological changes and cell death (44, 45), and also exhibit activity against bacteria by cell membrane disruption (46). Polyketides like bacillaene and diffidin possess potent antibacterial properties (42, 44, 47). In addition, *BvFZB42* produces bacilysin, which has antimicrobial effects on both Gram-positive and Gram-negative bacteria (43).

As competition partners for *BvFZB42*, we chose two well-studied plant foliar pathogens: *Xanthomonas euvesicatoria* pv. *vesicatoria* 85-10 (*Xee85-10*) (48, 49), and *Pseudomonas syringae* DC3000 (*PstDC3000*) (50). Secondary metabolites produced by *BvFZB42* can affect these or similar species. Notably, three of these antibiotic compounds—diffidin, bacillaene, and bacilysin—are effective against *Xanthomonas* strains (47, 51, 52). Diffidin, a macrolide, inhibits protein synthesis by binding to ribosomal subunits (53), and may also compromise cell membranes (54). Similarly, bacillaene also inhibits protein synthesis through diverse mechanisms (55) and was found to play a major role in the inhibition of *Pseudomonas chlororaphis* by interacting with the protein elongation factor FusA (56). Bacilysin, on the other hand, disrupts peptidoglycan biosynthesis through anticapsin, impacting bacterial growth in a similar way to beta-lactam antibiotics (57, 58).

We designed an experimental setup that enables the incubation of bacterial cultures within droplets of various sizes, maintained either wet (at 100% relative humidity) or subjected to wet-dry cycles (at 85% relative humidity) featuring MSW periods. We hypothesize that the response of antibiotic-sensitive bacteria, to antibiotic-producing bacteria, under a wet-dry cycle with MSW, can be significantly different from their response under constantly wet conditions. We incubated cells of *Xee85-10* or *PstDC3000* in droplets of various sizes, either alone or in the presence of *BvFZB42* supernatants, cells, or both. Experiments were conducted under wet-dry cycle conditions or constantly wet conditions. At the end of the experiment, cells were extracted from the drops and plated on agar plates and CFUs were counted to determine the competition outcomes.

RESULTS

Inhibition of *Xee85-10* and *PstDC3000* by *BvFZB42* supernatants and cells under standard laboratory assays

Initially, we sought to determine the inhibitory capabilities of *BvFZB42* cells and/or their supernatants (see Materials and Methods) against *Xee85-10* and *PstDC3000*. Through two established assays—an inhibition zone assay and a MIC assay (specifically for supernatants)—we observed that both the cells and the supernatants of *BvFZB42* exerted a significant antagonistic effect against both *Xee85-10* and *PstDC3000*. This effect was evident in the results of inhibition zone assays (Fig. 1A), as well as MIC assays (as depicted in Fig. 1B).

Notably, *PstDC3000* was inhibited in 50% vol/vol concentration of *BvFZB42* supernatants (meaning when the volume consisted of 50% *BvFZB42* supernatants), while *Xee85-10* required a lower concentration of 12.5% vol/vol for inhibition.

Design of an experimental setup for bacterial culturing under constant wetness or wet-dry cycle conditions

To explore the effects of hydration conditions on bacterial interference competition, our experimental setup involved culturing bacteria within drying droplets, as detailed in Materials and Methods. A key variable influencing the drying dynamics of these droplets is their initial size. To comprehensively investigate a range of drying dynamics and corresponding “drying times,” we utilized droplets varying in volume from 1 μ L to 100 μ L. This range was selected to represent a spectrum of drying durations under controlled conditions (under moderate relative humidity). Our observations confirmed that droplet

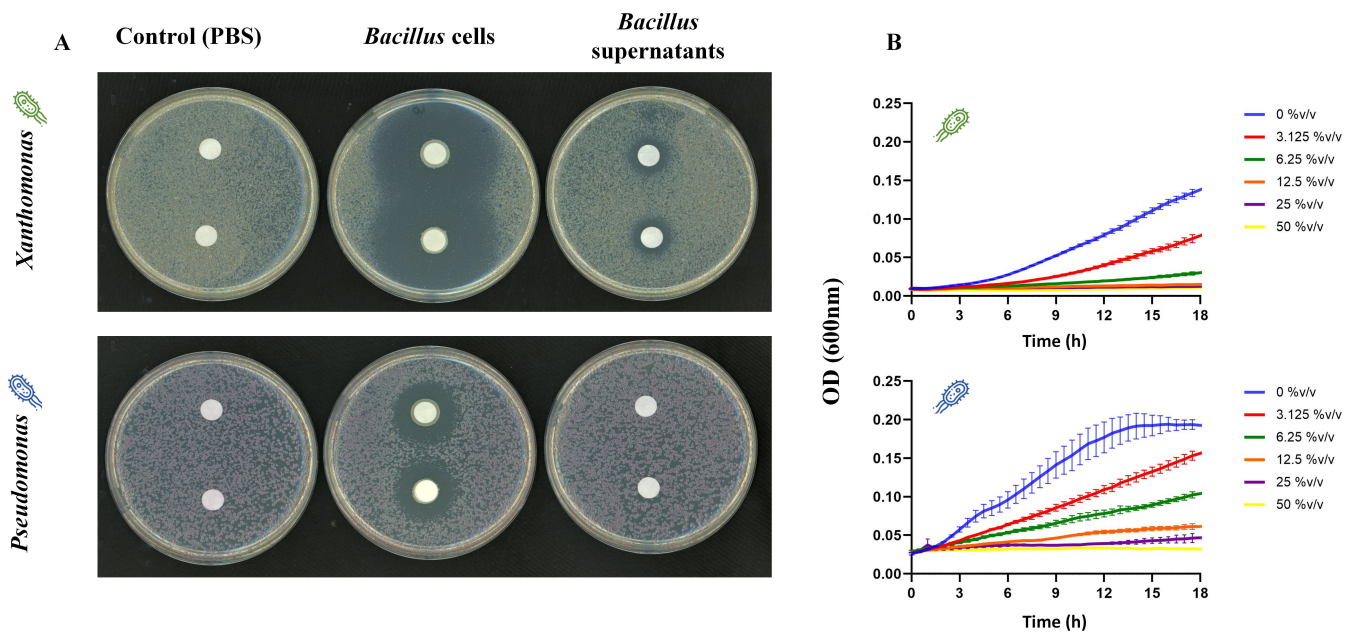


FIG 1 *Bacillus velezensis* FZB42 cells or supernatants inhibit *Xanthomonas euvesicatoria* 85-10 and *Pseudomonas syringae* DC3000. (A) Inhibition zone assay of *Xee*85-10 (top) and *Pst*DC3000 (bottom) by *Bv*FZB42 supernatants (pure 100% supernatants solution, right), cells ($OD_{600} = 0.1$, center) and control (PBS, left). Inhibition is more effective as the halo zone around the discs is larger. (B) Determination of MIC of *Xee*85-10 (top) and *Pst*DC3000 (bottom) by *Bv*FZB42 supernatants. Each line and error bars represent the mean \pm SE of three repeats (see Materials and Methods).

volume dictates the time required to reach MSW conditions, with a short drying duration of ~ 1 h in the smallest droplets and longer drying times of ~ 8 h in the largest droplets (Fig. S1).

To assess and compare the influence of continuous wet conditions versus a 24 h wet-dry cycle, we maintained a subset of droplets at a constant humidity of 100% RH, ensuring they remained static (i.e., minimizing droplets' evaporation) throughout the experiment. In parallel, a second subset of droplets was subjected to a cycle of drying (under moderate relative humidity, RH = 85%) until stable MSW formed and followed by rewetting. This design allowed us to closely monitor and analyze the effects of hydration dynamics on the competition outcome (by CFU plating at the beginning and end of the experiments) under these distinct environmental conditions.

*Xee*85-10 is less affected by *Bv*FZB42 supernatants under a wet-dry cycle compared to constantly wet conditions

First, we established a baseline by evaluating *Xee*85-10's growth over 24 h without the presence of *Bv*FZB42's supernatants. Under constantly wet conditions, *Xee*85-10 exhibited up to a 100-fold increase in CFU in the larger droplet volumes, indicating robust growth capacity in an environment free from desiccation stress (one-way ANOVA, $P < 0.05$, Fig. 2A; Fig. S2). By contrast, under a wet-dry cycle, a different pattern emerged. In all droplet volumes except for the largest (100 μ L), we observed a reduction in *Xee*85-10 CFUs, which suggests that the bacterium's survival was adversely affected by the cyclic drying and rewetting process. This impact was more pronounced in smaller droplets indicating that the faster drying dynamics of the smaller droplets reduced cell viability (one-way ANOVA, $P < 0.05$, Fig. 2; Fig. S2 and S3).

Upon the addition of *Bv*FZB42 supernatants at a concentration of 30% vol/vol (Materials and Methods), a notable reduction in CFU, of ~ 3 – 5 orders of magnitude, was observed under constantly wet conditions, aligning with expectations set by previous inhibition assays (Fig. 1) and given that the supernatant concentration exceeded the MIC of 12.5% vol/vol (one-way ANOVA, $P < 0.0005$, Fig. 2A; Fig. S2). Under the wet-dry cycle,

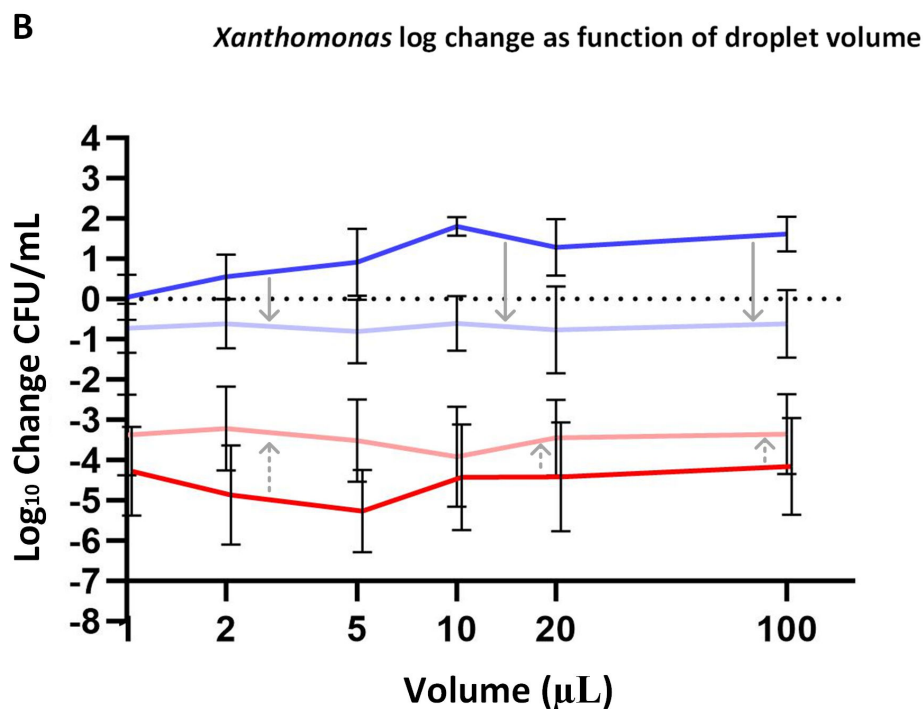
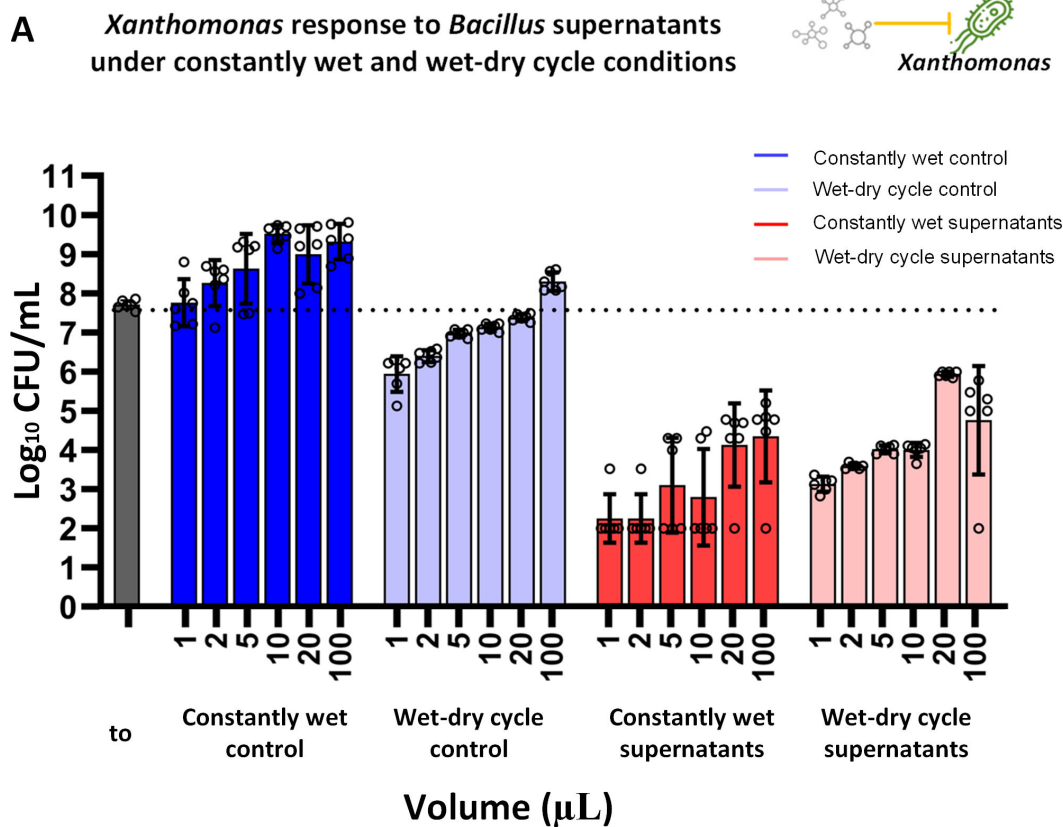


FIG 2 *Xanthomonas euvesicatoria* response to *Bacillus velezensis* supernatants under wet-dry cycle and constantly wet conditions. (A) Log_{10} CFU/mL of Xee85-10 exposed to BvFZB42 supernatants under constantly wet and wet-dry cycle conditions, at $t = 24$ h, at five different droplet volumes. The most left gray bar represents log_{10} CFU/mL at $t = 0$ h. Bars and error bars represent mean \pm SE log_{10} CFU/mL. Black circles represent technical replicates. CFU measurements were (Continued on next page)

Fig 2 (Continued)

conducted as described in Materials and Methods. One-way ANOVA was performed to compare the means of all conditions with each other (Fig. S2). (B) Log change in CFU/mL (\log_{10} CFU/mL at $t = 24$ h minus \log_{10} CFU/mL at $t = 0$ h), as a function of droplet size (X-axis in log scale), in the presence and absence of supernatants. Lines and error bars represent mean \pm SD. Linear regression and Spearman correlation were performed for statistical assessment (Fig. S3). Gray arrows represent the changes between the wet-dry cycle and constantly wet conditions in control (solid arrows) and with the addition of supernatants (dashed arrows).

cells in all drop volumes demonstrated a significant CFU reduction from the baseline ($t = 0$ h) (ANOVA, $P < 0.05$, Fig. 2A; Fig. S2).

Notably, the CFU reduction was less pronounced under wet-dry cycles when supernatants were introduced, compared to the scenario without supernatant (ANOVA, $P < 0.05$, Fig. 2A and B; Fig. S2). These results show that *Xee85-10* is more protected from *BvFZB42* supernatants under wet-dry conditions relative to constant wetness.

The effectiveness of *BvFZB42* supernatants against *PstDC3000* was markedly more pronounced under a wet-dry cycle as opposed to constantly wet conditions

Without supernatants, *PstDC3000* CFU counts increased under constantly wet conditions and decreased under wet-dry cycles, with a larger decrease in smaller droplets (Fig. 3; Fig. S4 and S5), similar to the response pattern of *Xee85-10*. This pattern suggests a general decline in bacterial viability under the stress of wet-dry cycles, although larger droplets show an improved survival rate (one-way ANOVA, $P < 0.05$, Fig. 3; Fig. S4).

Introducing *BvFZB42* supernatants at a 30% vol/vol concentration (an equal concentration to the treatment for *Xee85-10*) elicited a distinct response in *PstDC3000*. Under constant wetness, *PstDC3000*'s CFU levels still increased from the baseline, as could be anticipated, given the supernatant concentration was below the MIC for *PstDC3000* (30% vol/vol versus a MIC of 50% vol/vol) (Fig. 3A; Fig. S4). Intriguingly, the wet-dry cycle conditions triggered a dramatic CFU reduction across all droplet volumes, much more than under constant wet conditions (one-way ANOVA, $P < 0.0001$, Fig. 3A; Fig. S4), as well as in comparison to wet-dry cycle without supernatants (one-way ANOVA, $P < 0.0001$, Fig. 3A; Fig. S4). Thus, *PstDC3000* cells were much more affected by *BvFZB42* supernatants under a wet-dry cycle compared to constantly wet conditions.

Co-culture experiments representing two ecological scenarios

Next, we introduced an additional layer of complexity by performing co-culture experiments of the sensitive bacteria together with cells of the antibiotic-producing bacteria, *BvFZB42*, with or without its supernatants. We employed two types of co-culture experiments; each represents a different ecological scenario. In both scenarios, there were similar concentrations of both *BvFZB42* and the sensitive bacteria at $t = 0$ h ($\sim 10^7$ CFU/mL). In the first, cells from *BvFZB42* and the pathogen (*Xee85-10* or *PstDC3000*) were co-cultured at an initial 1:1 cell ratio, simulating their concurrent arrival in a habitat (we term this scenario 1:1). The second scenario included both *BvFZB42* cells and its supernatants, resembling a situation where *BvFZB42* was already established and producing antibiotics before the pathogen's arrival (we term this scenario 1:1 plus supernatants; 1:1 cell ratio of both species plus supernatants at $t = 0$). This setup also resembles biological control practices, such as foliar spraying, where both live microbial agents and their products are applied together (59–62).

Xee85-10 is less affected by *BvFZB42* cells under a wet-dry cycle, with and without supernatants

Under constantly wet conditions, there was a decrease in *Xee85-10* CFUs when *BvFZB42* cells were added with, or without, their supernatants (Fig. 4A). Co-culturing *Xee85-10* with *BvFZB42* cells without supernatants showed a modest decrease in *Xee85-10* CFUs under wet conditions, and a more significant reduction under wet-dry conditions.

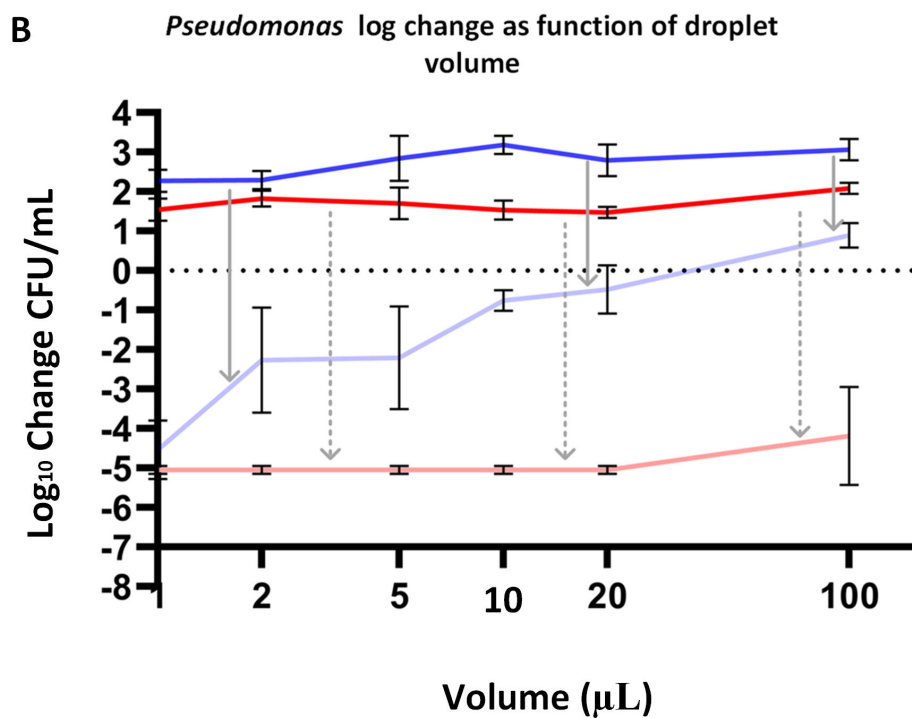
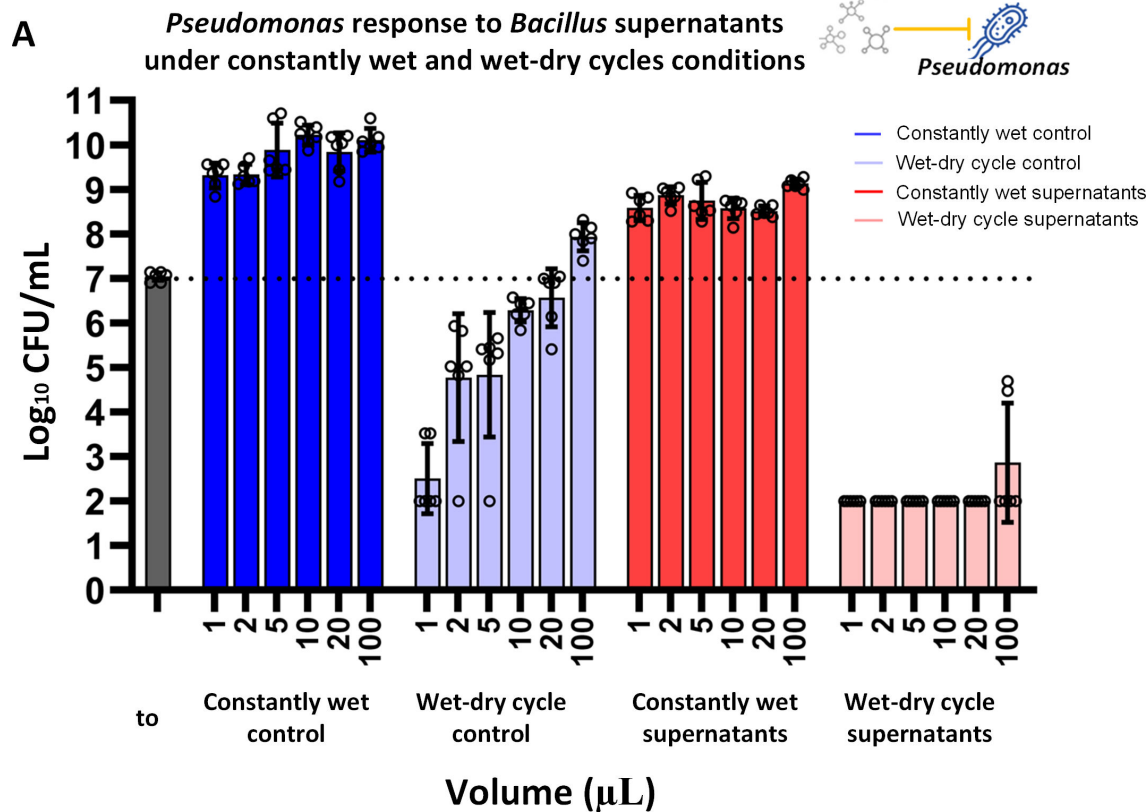


FIG 3 *Pseudomonas syringae* response to *Bacillus velezensis* supernatants under wet-dry cycle and constantly wet conditions. (A) Log₁₀ CFU/mL of *PstDC3000* exposed to *BvFZB42* supernatants under constantly wet and wet-dry cycle conditions, at t = 24 h, at five different droplet volumes. The most left gray bar represents log₁₀ CFU/mL at t = 0 h. Bars and error bars represent mean ± SE log₁₀ CFU/mL. Black circles represent technical replicates. CFU measurements were (Continued on next page)

Fig 3 (Continued)

conducted as described in Materials and Methods. One-way ANOVA was performed to compare the means of all conditions with each other (Fig. S4). (B) Log change in CFU/mL (\log_{10} CFU/mL at $t = 24$ h minus \log_{10} CFU/mL at $t = 0$ h), as a function of droplet size (X-axis in log scale), in the presence and absence of supernatants. Lines and error bars represent mean \pm SD. Linear regression and Spearman correlation were performed for statistical assessment (Fig. S5). Gray arrows represent the changes between the wet-dry cycle and constantly wet conditions in control (solid arrows) and with the addition of supernatants (dashed arrows).

Adding supernatants to the mix increased the CFU reduction further, under both conditions. Interestingly, when comparing the effects of constant wetness to a wet-dry cycle with supernatants, CFU numbers were similar or slightly higher in the wet-dry cycle with supernatants only (Fig. 4A; Fig. S6). This observation reinforces the finding that *Xee85-10* is less impacted by *BvFZB42* under wet-dry cycles.

The pronounced sensitivity of *Xee85-10* to cells and supernatants of *BvFZB42* under constantly wet conditions is in agreement with suspended liquid co-cultures in microwells (quantified *via* plate reader, see Materials and Methods). In such microwell co-cultures, *Xee85-10* growth was completely inhibited by *BvFZB42* cells, supernatants, or both (Fig. S7).

BvFZB42, however, appeared to be unaffected by the presence of *Xee85-10*. Under both constantly wet and wet-dry cycle conditions, CFU counts were comparable in the monoculture and co-culture setups (control, 1:1, and 1:1 plus supernatants). Under constantly wet conditions, there was a significant increase in *BvFZB42* CFU counts (one-way ANOVA, $P < 0.0001$, Fig. 4B; Fig. S8). During a wet-dry cycle, a slight reduction in *BvFZB42* CFU counts was observed, which was more pronounced when supernatants were added (1:1 plus supernatants) (Fig. 4B). These results indicate that *BvFZB42*'s growth, or survival, is not significantly affected by the presence of *Xee85-10* in most conditions.

To enhance our understanding of the interactions between these two bacterial species, we have supplemented our previous data with area plots (Fig. S9). These plots offer a visual representation of changes in the abundance of each species within a competitive context. Under constantly wet conditions, *Xee85-10* was generally outcompeted by *BvFZB42*, particularly in the presence of supernatants with a clear decrease in *Xee85-10*'s abundance. During wet-dry cycles, the growth of both bacteria was inhibited regardless of supernatant presence (Fig. S9). In most scenarios, *BvFZB42* was the dominant competitor after 24 h. However, in the 1:1 scenario within small 2 μ L droplets, *Xee85-10* managed to outcompete *BvFZB42* (Fig. S9).

In summary, our findings suggest that *BvFZB42* inhibits *Xee85-10* primarily due to the antibiotic compounds it secretes (present in its supernatants), yet this inhibitory effect is reduced under wet-dry cycles.

The response of *PstDC3000* to *BvFZB42* cells and supernatants under the wet-dry cycle differed from that of *Xee85-10*

Under constantly wet conditions, *PstDC3000* exhibited a variable response when co-cultured with *BvFZB42*. A moderate reduction in *PstDC3000* CFUs was observed in 1:1 co-culture with *BvFZB42* cells alone, which became more pronounced when both *BvFZB42* cells and their supernatant were present (Fig. 5A; Fig. S10). Remarkably, consistent with experiments using only supernatants (Fig. 3), under wet-dry cycles, there was a complete reduction of *PstDC3000* (resulting in zero observed CFU) in co-culture with *BvFZB42*, regardless of the presence of supernatants. The response of *BvFZB42* to interaction with *PstDC3000* in co-culture differed significantly from that with *Xee85-10*. Under both constantly wet and wet-dry conditions, *BvFZB42* experienced significant inhibition, with the exception being under constantly wet conditions with supernatants in 10 and 100 μ L droplets (one-way ANOVA, $P < 0.005$, Fig. 5B; Fig. S11).

These findings, revealing a complete reduction of *PstDC3000* under wet-dry cycles, were also very different from the results from co-cultures in suspended liquid cultures in microwells, where *PstDC3000* remained viable in the presence of both *BvFZB42* cells and

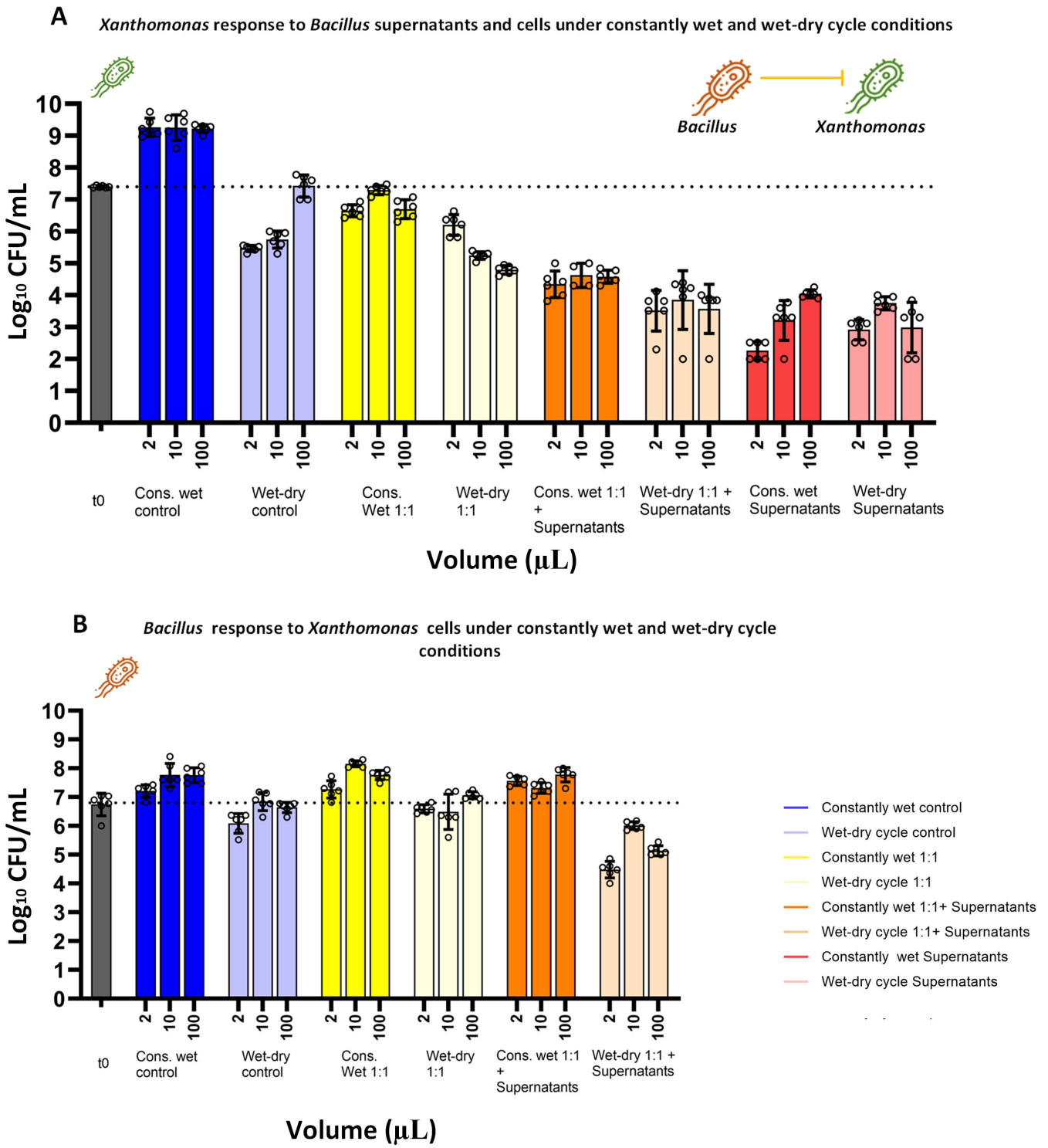


FIG 4 Co-culture experiments of *Xanthomonas euvesicatoria* and *Bacillus velezensis* under constantly wet and wet-dry cycle conditions. (A) Log₁₀ CFU/mL of Xee85-10 at t = 24 h under both constantly wet and wet-dry cycle conditions across different co-culture scenarios: equal ratio of both bacteria (1:1); equal ratio of both bacteria with BvFZB42 supernatants (1:1 + supernatants) and controls (Xee85-10 monoculture, BvFZB42 monoculture, and Xee85-10 with BvFZB42 supernatant) at three different droplet volumes. The left gray bar represents log₁₀ CFU/mL at t = 0 h. Bars and error bars represent mean ± SE CFU/mL. Black circles represent technical replicates. One-way ANOVA was performed to compare the means between conditions and droplet volumes with each other (Fig. S6 and S8). (B) Same as in panel A but the bars represent BvFZB42 CFU/mL (at t = 24 h).

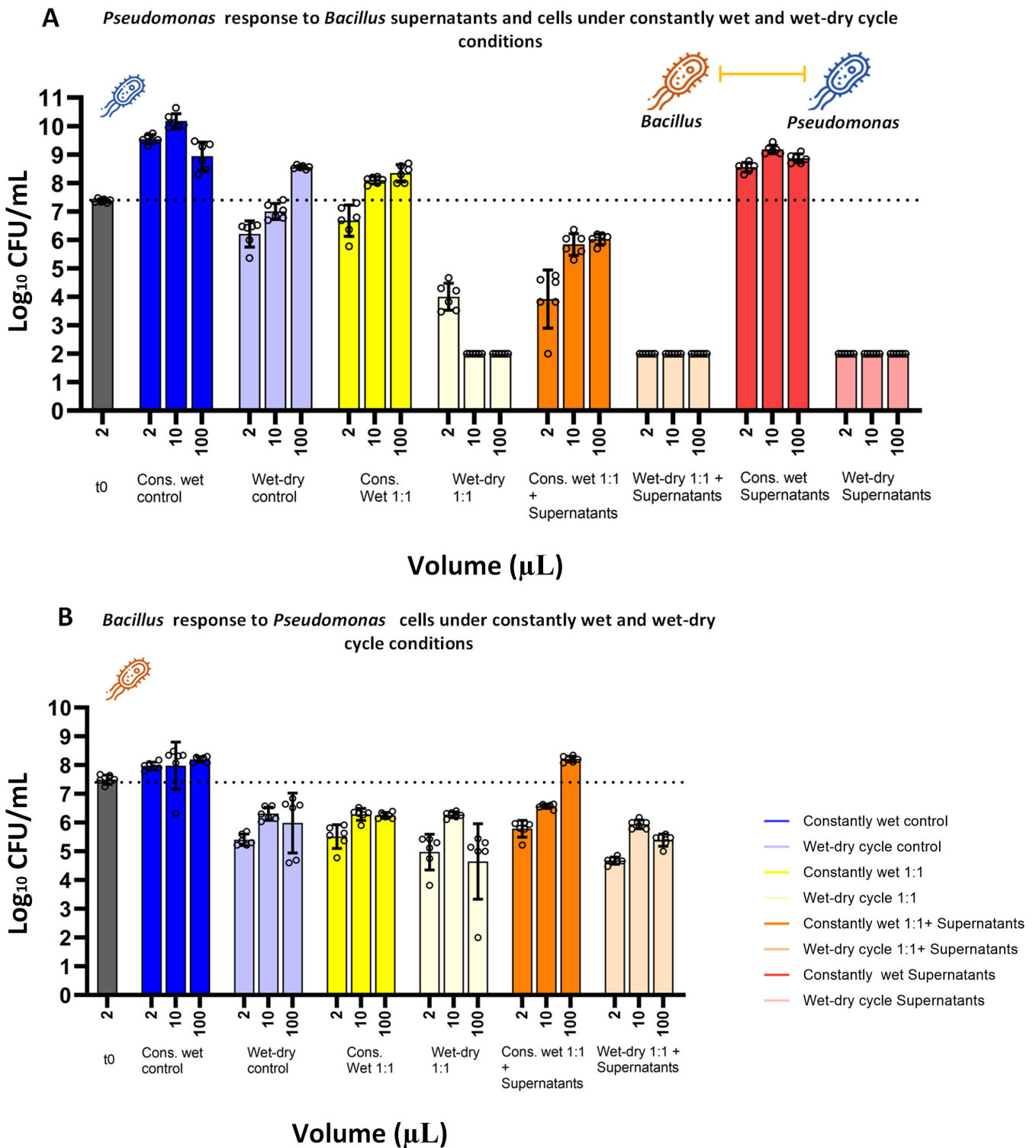


FIG 5 Co-culture experiments of *Pseudomonas syringae* and *Bacillus velezensis* under constantly wet and wet-dry cycle conditions. (A) Log_{10} CFU/mL of *PstDC3000* at $t = 24$ h under both constantly wet and wet-dry cycle conditions across different co-culture scenarios (equal ratio of both bacteria 1:1; equal ratio of both bacteria with *BvFZB42* supernatants 1:1 + supernatants) and controls (*PstDC3000* monoculture, *BvFZB42* monoculture, and *PstDC3000* with *BvFZB42* supernatant) at three different droplet volumes. The left gray bar represents log_{10} CFU/ml at $t = 0$ h. Bars and error bars represent mean \pm SE CFU/mL. Black circles represent technical replicates. One-way ANOVA was performed to compare the means between conditions and droplet volumes with each other (Fig. S10 and S11). (B) Same as in panel A but the bars represent *BvFZB42* CFU/mL (at $t = 24$ h).

supernatants (1:1 ratio) (Fig. S12), mirroring the outcomes observed under constantly wet conditions in droplet experiments. Under suspended liquid conditions, consistent with the droplet experiment, *BvFZB42* was inhibited. These observations further suggest that *PstDC3000* exerts an inhibitory effect on *BvFZB42*, indicating a mutual inhibition between these two bacterial species (Fig. S12C and S13B).

The dynamics of competition between *BvFZB42* and *PstDC3000* in co-culture experiments reveal varied outcomes, as illustrated by the area plots (Fig. S14). Consistent with the above results, under constantly wet conditions in co-culture without supernatant, *PstDC3000* took over the population. This outcome was reversed in the large drops (100 μ L) when supernatants were added, where *BvFZB42* outcompeted *PstDC3000*. In scenarios involving wet-dry cycles, regardless of the supernatant presence, both *PstDC3000* and *BvFZB42* experienced a decline in CFUs. However, despite this reduction, the relative fraction of *BvFZB42* was larger (Fig. S14). These results highlight the significant impact of wet-dry cycles on the competition dynamics between these two bacterial species.

DISCUSSION

In this study, we explored the interactions between the antibiotic-producing bacteria *BvFZB42* and two susceptible bacterial strains—*Xee85-10* and *PstDC3000*, under different hydration conditions, including constant wetness and wet-dry cycles. Our findings reveal that hydration conditions play a crucial role in determining the outcome of bacterial interference competition and the effectiveness of antibiotic-mediated interference. The differential responses of *Xee85-10* and *PstDC3000* to *BvFZB42* cells and supernatants containing antibiotic compounds, highlight the potential for environmental factors, such as hydration conditions studied here, to modulate these interactions.

Our results demonstrate how hydration conditions critically influence the dynamics of antibiotic-mediated interference competition among bacteria, with the potential to either diminish or enhance the inhibitory effect. Notably, under constant wet conditions, *Xee85-10* experienced inhibition by *BvFZB42*, yet it showed increased protection from *BvFZB42*'s supernatants during wet-dry cycles. By contrast, *PstDC3000* showed relative insensitivity to *BvFZB42*'s supernatants under constantly wet environments but complete reduction under wet-dry cycles. This variation in competitive outcomes across different hydration scenarios highlights the importance of considering environmental conditions when predicting competition results, rather than relying only on standard laboratory assays in suspended liquid or on agar plates.

A deeper understanding of how hydration conditions modulate bacterial interactions can be achieved by characterizing the chemical components, such as antimicrobial molecules, involved in these interactions (47, 63–66). Further testing of the response of *Xee85-10* and *PstDC3000* to the supernatants of two *BvFZB42* mutants that are deficient in the production of the antibiotics bacillaene and bacillomycin D demonstrated their involvement in these interspecies interactions. Specifically, we observed that supernatants of bacillaene-deficient mutant were less effective against both *Xee85-10* and *PstDC3000* compared to the wild-type supernatants (at intermediate supernatant concentrations; Fig. S15). In addition, bacillomycin D-deficient mutants were less effective against *PstDC3000* than the wild-type supernatants (at the higher concentrations of supernatants, Fig. S15). However, at least one other antibiotic is likely involved in the interaction between *BvFZB42* and *Xee85-10* or *PstDC3000*, as the inhibition increased with higher supernatant concentrations. Comparable inhibition to the wild type was observed with both mutants' supernatants at concentrations of 12.5% vol/vol and 75% vol/vol for *Xee85-10* and *PstDC3000*, respectively (Fig. S15).

Thus, bacillaene is involved in the inhibition of both *Xee85-10* and *PstDC3000*, while bacillomycin D is involved solely in the inhibition of *PstDC3000*. The participation of these two types of antibiotics in the studied interference interactions may explain the different effects that wet-dry cycles impose on the interactions between *Bacillus* and *Xee85-10* or *PstDC3000* (Fig. 2 and 3). Bacillaene's mode of action involves the inhibition

of protein synthesis, and it is therefore mostly potent on metabolically active target cells (55, 67, 68). The increased protection of *Xee85-10* from bacillaene and other antibiotic compounds produced by the *Bacillus* (Fig. 2) could stem from decreased susceptibility due to the slow or halted growth induced by drying, coupled with the low metabolic state associated with MSW conditions (38). This aligns with previous findings on the enhanced protection from beta-lactams under wet-dry cycles (38).

By contrast, both bacillaene and bacillomycin D produced by *BvFZB42* are involved in the inhibition of *PstDC3000*. Given that bacillomycin D is a lipopeptide that damages bacterial membranes (44, 46), it is likely effective even against cells that are not actively growing, enabling it to kill cells during drying or under MSW conditions. In addition, another mechanism at play during drying is the dramatic increase of solute concentrations, including antibiotics, due to water evaporation. This process can potentially concentrate the active compounds beyond their MIC, thereby amplifying their lethal effects (25, 38). Bacillomycin D and possibly other antibiotic compound(s) from *BvFZB42*, aside from bacillaene, that target *PstDC3000*, might retain stability and activity, similar to certain antibiotics previously shown to maintain or even increase the effectiveness in such variable hydration environments (38). Thus, the specific mode of action of bacillomycin D, coupled with the elevated concentrations associated with drying, may explain the transition from insensitivity to eradication of *PstDC3000* under constant wetness and drying environments, respectively.

The involvement of antibiotics produced by *BvFZB42* in the inhibition of *PstDC3000* and *Xee85-10* is further supported by the observation that commercially available antibiotics with similar modes of action to those produced by *BvFZB42* displayed comparable effects in wet-dry cycle experiments. Specifically, chloramphenicol (10 µg/mL) and norfloxacin (10 µg/mL) showed similar trends to *BvFZB42* supernatants in the case of *Xee85-10* (protection under wet-dry cycles), while chloramphenicol (5 µg/mL) and erythromycin (5 µg/mL) had similar effects on *PstDC3000* (increased susceptibility under wet-dry cycle) (Fig. S16 and S17).

The mutual antagonism between *BvFZB42* and *PstDC3000*, as observed in our study, has not been reported before to the best of our knowledge. Notably, our experiments demonstrated that *PstDC3000* is capable of inhibiting *BvFZB42* under both constant wetness and wet-dry cycles (Fig. 5; Fig. S13). The mechanism underlying the inhibition of *BvFZB42* by *PstDC3000* is unknown, though many works describe the antagonistic interactions between other *Bacillus* and *Pseudomonas* species (69, 70). These antagonistic interactions may include diverse mechanisms ranging from contact-dependent interactions such as T6SS to contact-independent interactions that are mediated by the production of different antimicrobial compounds (69, 70). One study also hints at a potential mechanism involving competitive behaviors linked to siderophore production (71).

Our study provides important insights into microbial ecology in water-unsaturated environments, but it has certain limitations. Our experiments, designed to simulate bacterial life on surfaces undergoing changes in wetness, were conducted using a medium that, while capturing some aspects of these conditions, lacks the complexity found on surfaces in natural microbial habitats (72, 73). Furthermore, while our findings suggest that mechanisms acting at the microscale, and populations with small census sizes within MSW droplets (74), may offer a potential explanation for some of the observed phenomena, we did not investigate these mechanisms at the single-cell, single-droplet level. Identifying and examining these microscale interactions represents an important direction for future research, which could provide valuable insights into the underlying processes.

This study highlights the profound influence of hydration conditions on interspecies bacterial interactions, in particular antibiotic-mediated interference competition. We observed that competition outcomes under wet-dry cycles can significantly differ from those in constantly wet environments. These variations are likely influenced by the unique properties of microscopic surface wetness—prevalent in terrestrial microbial

habitats—and by its effect on bacterial physiology. Furthermore, the outcome of interactions in droplets may also diverge from those observed in standard laboratory experiments, whether in liquid suspension or on agar plates. Our research has potential implications for biocontrol applications of plant pathogens, suggesting that the dynamics observed could influence the effectiveness of biological control strategies. It shows that hydration conditions are important and that optimal hydration conditions can vary depending on the exact agent-pathogen pair. In conclusion, hydration conditions and their dynamics, in particular wet-dry cycles, play a pivotal role in shaping the outcomes of antibiotic-mediated competition among bacteria.

MATERIALS AND METHODS

Bacterial strains and growth conditions

The following bacterial strains were used in this study: *Xanthomonas euvesicatoria* pv. *euvesicatoria* 85-10, *Pseudomonas syringae* DC3000 (both strains obtained from the late Guido Sessa), both were transformed with the mCherry fluorescent plasmid pmp7605 (75) (transformation details below). *Bacillus velezensis* FZB42_FB01 expressing *gfp*, BvFZB42 Δ bmyA::EmR (defective in Bacillomycin D production), and BvFZB42 Δ pks1KS1::cat (defective in bacillaene production) were obtained from Rainer Borriss, AmyloWiki (76).

At the beginning of each experiment, a small portion of the thawed glycerol stock was streaked on fresh LB agar + antibiotics plate (1 μ g/mL Erythromycin for *B. velezensis*, 50 μ g/mL Gentamicin sulfate for *Xee*85-10, and *Pst*DC3000). A single colony of each strain was inoculated into 5 mL of a fresh LB broth + appropriate antibiotic medium. Bacterial cultures were grown for 24 h under agitation set at 220 rpm, at 28°C. Then, each culture was centrifuged (2,935 rcf for 5 min) washed and resuspended in MTG medium (M9 \times 1, glucose 4%, tryptone 1%) to reach an OD₆₀₀ = 0.1 in 5 mL volume. Next, the cultures were grown for another 24 h under agitation set at 220 rpm, at 28°C.

The preparation of supernatants of BvFB42 was done in a similar method to the one mentioned above. However, after centrifugation, the pellet was resuspended in 20 mL of MTG medium to reach OD₆₀₀ = 0.1 and grown for 24 h in similar conditions. Then, the culture was centrifuged and filtered using a 0.22 μ m filter to separate between the bacteria cells and their secreted products. Centrifugation and filtration were done twice. Supernatants were kept at 4°C for up to 4 days.

Each experiment was initiated with a bacterial inoculum of $\approx 5 \times 10^7$ to 10^8 CFU/mL.

Electroporation

To transform both *Xee*85-10 and *Pst*DC3000 with pmp7605 plasmid (mCherry+), electrocompetent cells were prepared as described previously (77). The transformation was performed by electroporation (micropulser, BIO-RADUSA, program 1).

Minimal inhibitory concentration and inhibition zone assays

To evaluate the antibacterial effect of BvFZB42 cells and supernatants on *Xee*85-10 and *Pst*DC3000, MIC and inhibition zone assays were performed. To perform the MIC assay, cells were diluted into 96 microtiter plates (final OD₆₀₀ = 0.06 for *Xee*85-10 and 0.2 for *Pst*DC3000) set with a twofold serial dilution of supernatants whereas the highest concentration of supernatants was 50% vol/vol. OD₆₀₀ reads were taken every 30 min for 24 h using a plate reader (Synergy H1 Microplate Reader, BioTek Instruments, USA). MIC values were determined by the minimal concentration in which there was no significant bacterial growth. MIC assay was conducted before each experiment to validate that different supernatant batches had the same effect. The MIC chosen for all subsequent experiments, which will be described below, corresponds to 2.4 times the MIC determined for *Xee*85-10 (30% vol/vol).

For the inhibition zone assay, 1 mL of *Xee85-10* and *PstDC3000* cells with an $OD_{600} = 0.5$ or 1, respectively, were serially diluted to 10^{-4} , and evenly spread onto LB-agar plates (130 mm). After a 1 h incubation, discs containing deionized water (D_1H_2O), *BvFZB42* supernatants or live bacterial cells ($OD_{600} = 0.5$) were carefully placed on the inoculated plates. Subsequently, the plates were incubated at 28°C for 3 days, and the effectiveness of inhibition was qualitatively assessed by the presence of a clear area around the discs.

Monoculture experiment with *BvFZB42* supernatants: wet-dry cycles and constantly wet conditions experimental setup

Monoculture experiments were performed to evaluate the effect of a wet-dry cycle on *Xee85-10* and *PstDC3000* response to the supernatants of *BvFZB42*. Two conditions were investigated in these experiments, the first condition was bacteria without supernatants, as a control, and the second was bacteria (*Xee85-10* or *PstDC3000*) with 30% vol/vol supernatants (30% of the total volume was *BvFZB42* supernatants, prepared as described above). In these experiments, droplets of the following volumes: 1 μ L, 2 μ L, 5 μ L, 10 μ L, 20 μ L, and 100 μ L were deposited on the center of a well of a glass-bottom 24-well plate (24-well glass-bottom plate #1.5—Cellvis, USA). A total of six repeats (i.e., drops) was used for each tested drop volume. The 24-well plates were incubated in a growth chamber (Aralab, FITOCLIMA 600-PLH) for 24 h at 25°C and 85% relative humidity. To induce drying the wet-dry cycles plates were kept without their plastic lid. For constantly wet conditions, the empty cavities between the wells in these plates were filled with 300 μ L of H_2O , and the lid was sealed with tape, to maintain close to 100% relative humidity. The graphical representation of the monoculture experiment is presented in Fig. 6.

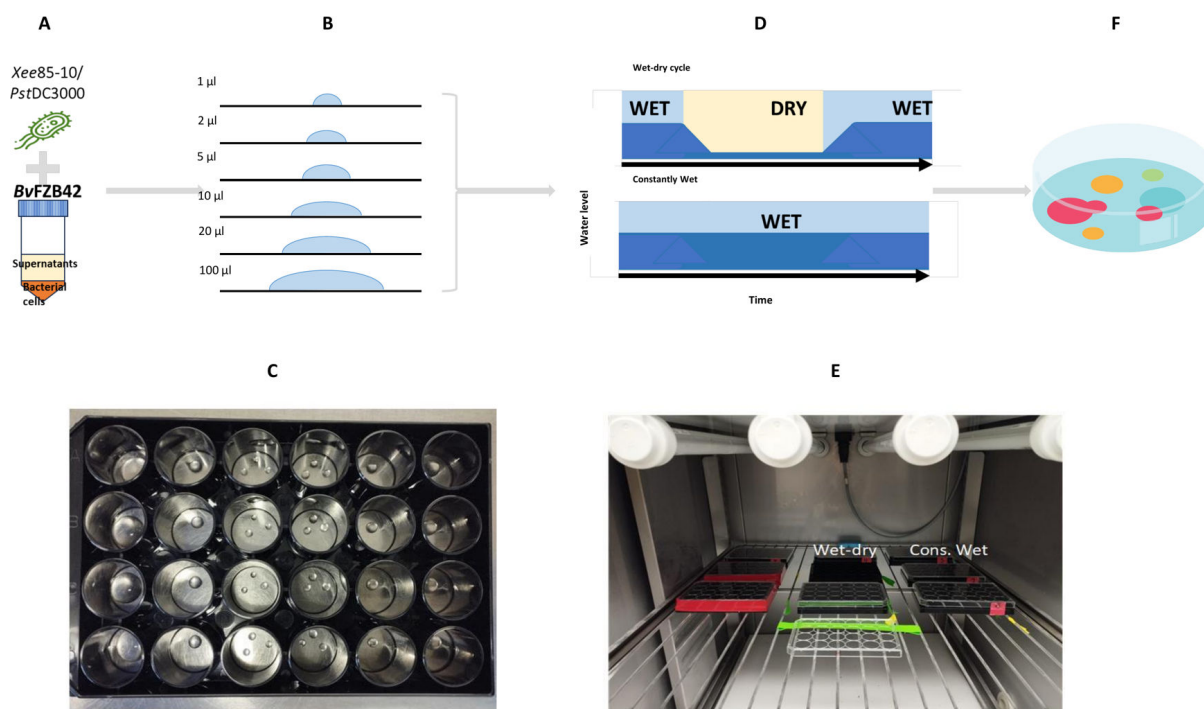


FIG 6 Experimental setup for droplet experiments under wet-dry cycle and constantly wet conditions. (A) In a monoculture experiment, one of the antibiotic-susceptible bacteria, either *Xee85-10* or *PstDC3000* was mixed with 30% vol/vol of *BvFZB42* supernatants. (B) Then, droplets ranging from 1 to 100 μ L volume were deposited into a 24-well plate (C). (D) Well plates were incubated in an environmental chamber with controlled temperature and relative humidity (E). (F) At the end of the experiment, droplets were re-suspended and plated on selective agar plates and CFU were counted.

Drying dynamics experiments

To characterize the drying dynamics of droplets of various volumes (1–100 μL), a microscopy method was employed by capturing time-lapse images of droplets' area dynamics. The individual droplet was deposited onto the center of a well in a glass-bottom 24-well plate (#1.5 high-performance cover glass, Cellvis, USA). Three droplets (repeats) were used for each tested drop volume. The plate, without the lid, was then placed within a stage-top environmental control chamber (H301-K-FRAME, Okolab, Italy), pre-equilibrated to a temperature of 28°C, and a relative humidity of 75%. Images of the droplets were systematically captured every hour over a total duration of 22 h. The determination of droplet areas was performed using NIS elements software 5.03.

Co-culture experiments: wet-dry cycle and constantly wet condition experimental setup

Co-culture experiments were performed to evaluate the effect of the wet-dry cycle on interference competition between *BvFZB42* and *Xee85-10* or *PstDC3000*. In this set of experiments, five conditions were investigated, two controls (monocultures of each strain of the pair), 1:1 ratio (*Xee85-10* or *PstDC3000* cells in a similar concentration to *BvFZB42* cells), 1:1 ratio with 30% vol/vol supernatants and monoculture with 30% vol/vol supernatants. These experiments were conducted with three droplet volumes (2 μL , 10 μL , and 100 μL). Droplets were deposited on the center of a well of a glass-bottom 24-well. A total of six repeats (i.e., drops) were used for each volume. Incubation conditions for both wet-dry cycles and constantly wet treatments were identical to the monoculture experiments.

All five conditions were investigated, in parallel, also in well-mixed suspended liquid cultures. The experimental setting mirrored that of the MIC experiments, with similar treatments. For co-cultures, plate-reader experiments fluorescence was measured in addition to optical density (OD). For *Xee85-10* and *PstDC3000*, changes in fluorescence signal were measured (mCherry, Em579/Ex616). Similarly, for *BvFZB423* change in fluorescence signal was measured (GFP, Ex479/Em520).

Gradual rewetting protocol

For the rewetting phase of the wet-dry cycle experiments, at time $t = 24$ h, the empty cavities between the wells were filled with 300 μL of H_2O , and the lid was placed on the plate and sealed with tape. The sealed plate was incubated for 30 min at 28°C (leading to RH >95% inside the plate). By the end of this step, the "dried" droplets (in MSW form) adsorbed moisture from the humidified air by condensation and deliquescence. At this point, 30 μL of medium was added to each well, then the plates were sealed again and incubated for an additional 30 min. Finally, medium was added to get a dilution of 10^{-1} , 30 μL was taken for serial dilutions and drop assay and the rest was plated on plates with LB agar with appropriate antibiotics. CFUs were counted 24 h or 48 h after plating for *BvFZB42* and *PstDC3000*, respectively, because each requires a different amount of time to form visible colonies on agar plates.

Results from entire repetitions of these experiments are shown in Fig. S18 to 20.

Statistical analysis

Comparisons of cell viability (based on CFU counts) among all conditions in wet-dry cycles and constantly wet conditions were conducted using one-way ANOVA, followed by Tukey's test. The determination of correlations and relationships between droplet size and changes in cell viability (the difference between the number of CFUs at $t = 24$ h and the number of CFUs at $t = 0$ h) was performed using linear regression and Spearman correlation. Six technical replicates were performed for each condition in each experiment. All statistical analyses were performed using GraphPad Prism version 10.2.3 for Windows (GraphPad Software, USA).

ACKNOWLEDGMENTS

This work was supported by research grants to N.K. from the James S. McDonnell Foundation (Studying Complex Systems Scholar Award, Grant #220020475) and the Ministry of Agriculture & Rural Development, Israel (#12-02-0046).

Y.B.-M., T.O., and N.K. conceived the study. Y.B.-M. and T.O. designed the experiments. Y.B.-M. performed the experiments and performed data and statistical analyses. All authors discussed the results and contributed to the final manuscript. N.K. supervised the project. Y.B.-M., T.O., and N.K. wrote the manuscript.

ChatGPT was used for assistance in enhancing the readability and language clarity of the manuscript.

AUTHOR AFFILIATION

¹Institute of Environmental Sciences, Department of Plant Pathology and Microbiology, Robert H. Smith Faculty of Agriculture, Food, and Environment, Hebrew University, Rehovot, Israel

AUTHOR ORCID*s*

Yana Beizman-Magen  <http://orcid.org/0009-0005-3610-9790>

Nadav Kashtan  <http://orcid.org/0000-0002-7475-1363>

FUNDING

Funder	Grant(s)	Author(s)
James S. McDonnell Foundation (JSMF)	220020475	Nadav Kashtan
The ministry of Agriculture and rural development, Israel	12-02-0046	Nadav Kashtan

AUTHOR CONTRIBUTIONS

Yana Beizman-Magen, Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Writing – original draft, Writing – review and editing | Tomer Orevi, Conceptualization, Methodology, Writing – original draft, Writing – review and editing | Nadav Kashtan, Conceptualization, Funding acquisition, Investigation, Supervision, Writing – original draft, Writing – review and editing

DATA AVAILABILITY

Data and code are available at [10.6084/m9.figshare.25998925](https://doi.org/10.6084/m9.figshare.25998925). All data needed to evaluate the conclusions in the paper are present in the paper and/or the supplemental material.

ADDITIONAL FILES

The following material is available [online](#).

Supplemental Material

Supplemental Material (AEM02004-24-s0001.pdf). Table S1; Figures S1 to S20.

REFERENCES

1. Finlay BJ, Maberly SC, Cooper JI. 1997. Microbial diversity and ecosystem function. *Oikos* 80:209. <https://doi.org/10.2307/3546587>
2. Schulz S, Dümig A, Kögel-Knabner I, Schloter M, Zeyer J. 2013. The role of microorganisms at different stages of ecosystem development for soil formation. *Biogeosciences* 10:3983–3996. <https://doi.org/10.5194/bg-10-3983-2013>
3. Laforest-Lapointe I, Paquette A, Messier C, Kembel SW. 2017. Leaf bacterial diversity mediates plant diversity and ecosystem function relationships. *Nature New Biol* 546:145–147. <https://doi.org/10.1038/nature22399>
4. Cordero OX, Datta MS. 2016. Microbial interactions and community assembly at microscales. *Curr Opin Microbiol* 31:227–234. <https://doi.org/10.1016/j.mib.2016.03.015>

5. Stubbendieck RM, Vargas-Bautista C, Straight PD. 2016. Bacterial communities: interactions to scale. *Front Microbiol* 7:1234. <https://doi.org/10.3389/fmicb.2016.01234>
6. Klitgord N, Segrè D. 2011. Ecosystems biology of microbial metabolism. *Curr Opin Biotechnol* 22:541–546. <https://doi.org/10.1016/j.copbio.2011.04.018>
7. Zengler K, Palsson BO. 2012. A road map for the development of community systems (CoSy) biology. *Nat Rev Microbiol* 10:366–372. <https://doi.org/10.1038/nrmicro2763>
8. Ponomarova O, Patil KR. 2015. Metabolic interactions in microbial communities: untangling the Gordian knot. *Curr Opin Microbiol* 27:37–44. <https://doi.org/10.1016/j.mib.2015.06.014>
9. Friedman J, Higgins LM, Gore J. 2017. Community structure follows simple assembly rules in microbial microcosms. *Nat Ecol Evol* 1:109. <https://doi.org/10.1038/s41559-017-0109>
10. Gralka M, Szabo R, Stocker R, Cordero OX. 2020. Trophic interactions and the drivers of microbial community assembly. *Curr Biol* 30:R1176–R1188. <https://doi.org/10.1016/j.cub.2020.08.007>
11. Palmer JD, Foster KR. 2022. Bacterial species rarely work together. *Science* 376:581–582. <https://doi.org/10.1126/science.abn5093>
12. Hibbing ME, Fuqua C, Parsek MR, Peterson SB. 2010. Bacterial competition: surviving and thriving in the microbial jungle. *Nat Rev Microbiol* 8:15–25. <https://doi.org/10.1038/nrmicro2259>
13. Ghoul M, Mitri S. 2016. The ecology and evolution of microbial competition. *Trends Microbiol* 24:833–845. <https://doi.org/10.1016/j.tim.2016.06.011>
14. Bauer MA, Kainz K, Carmona-Gutierrez D, Madeo F. 2018. Microbial wars: competition in ecological niches and within the microbiome. *Microb Cell* 5:215–219. <https://doi.org/10.15698/mic2018.05.628>
15. Chowdhury SP, Hartmann A, Gao XW, Borriss R. 2015. Biocontrol mechanism by root-associated *Bacillus amyloliquefaciens* FZB42 - a review. *Front Microbiol* 6:780. <https://doi.org/10.3389/fmicb.2015.00780>
16. Phyto AK, Jia Y, Tan Q, Sun H, Liu Y, Dong B, Ruan R. 2020. Competitive growth of sulfate-reducing bacteria with bioleaching acidophiles for bioremediation of heap bioleaching residue. *Int J Environ Res Public Health* 17:2715. <https://doi.org/10.3390/ijerph17082715>
17. Dharanishanthi V, Orgad A, Rotem N, Hagai E, Kerstnus-Banchik J, Ben-Ari J, Harig T, Ravella SR, Schulz S, Helman Y. 2021. Bacterial-induced pH shifts link individual cell physiology to macroscale collective behavior. *Proc Natl Acad Sci USA* 118:e2014346118. <https://doi.org/10.1073/pnas.2014346118>
18. Islam W, Noman A, Naveed H, Huang Z, Chen HYH. 2020. Role of environmental factors in shaping the soil microbiome. *Environ Sci Pollut Res Int* 27:41225–41247. <https://doi.org/10.1007/s11356-020-10471-2>
19. Schlechter RO, Miebach M, Remus-Emsermann MNP. 2019. Driving factors of epiphytic bacterial communities: a review. *J Adv Res* 19:57–65. <https://doi.org/10.1016/j.jare.2019.03.003>
20. Toyofuku M, Inaba T, Kiyokawa T, Obana N, Yawata Y, Nomura N. 2016. Environmental factors that shape biofilm formation. *Biosci Biotechnol Biochem* 80:7–12. <https://doi.org/10.1080/09168451.2015.1058701>
21. Vasse M, Fiegna F, Kriesel B, Velicer GJ. 2024. Killer prey: ecology reverses bacterial predation. *PLoS Biol* 22:e3002454. <https://doi.org/10.1371/journal.pbio.3002454>
22. Daniels M, van Vliet S, Ackermann M. 2023. Changes in interactions over ecological time scales influence single-cell growth dynamics in a metabolically coupled marine microbial community. *ISME J* 17:406–416. <https://doi.org/10.1038/s41396-022-01312-w>
23. Beattie GA. 2011. Water relations in the interaction of foliar bacterial pathogens with plants. *Annu Rev Phytopathol* 49:533–555. <https://doi.org/10.1146/annurev-phyto-073009-114436>
24. Brewer CA, Smith WK. 1997. Patterns of leaf surface wetness for montane and subalpine plants. *Plant Cell Environment* 20:1–11. <https://doi.org/10.1046/j.1365-3040.1997.d01-15.x>
25. Grinberg M, Orevi T, Steinberg S, Kashtan N. 2019. Bacterial survival in microscopic surface wetness. *Elife* 8:e48508. <https://doi.org/10.7554/eLife.48508>
26. Lindow SE, Leveau JHJ. 2002. Phyllosphere microbiology. *Curr Opin Biotechnol* 13:238–243. [https://doi.org/10.1016/s0958-1669\(02\)00313-0](https://doi.org/10.1016/s0958-1669(02)00313-0)
27. Magarey RD, Weiss A, Gillespie T, Huber L. 2005. Estimating surface wetness on plants estimating surface wetness on plants new york state agricultural experiment station. *Micrometeorol Agric Syst* 47:199–226. <https://doi.org/10.2134/agronmonogr47.c10>
28. Klemm O, Milford C, Sutton MA, Spindler G, van Putten E. 2002. A climatology of leaf surface wetness. *Theor Appl Climatol* 71:107–117. <https://doi.org/10.1007/s704-002-8211-5>
29. Tian Y, Jin N, Jin X. 2018. Coupling effect of temperature and relative humidity diffusion in concrete under ambient conditions. *Constr Build Mater* 159:673–689. <https://doi.org/10.1016/j.conbuildmat.2017.10.128>
30. Burkhardt J, Hunsche M. 2013. “Breath figures” on leaf surfaces: formation and effects of microscopic leaf wetness. *Front Plant Sci* 4:422. <https://doi.org/10.3389/fpls.2013.00422>
31. Orevi T, Kashtan N. 2021. Life in a droplet: microbial ecology in microscopic surface wetness. *Front Microbiol* 12:655459. <https://doi.org/10.3389/fmicb.2021.655459>
32. Campbell TD, Febrian R, McCarthy JT, Kleinschmidt HE, Forsythe JG, Bracher PJ. 2019. Prebiotic condensation through wet-dry cycling regulated by deliquescence. *Nat Commun* 10:4508. <https://doi.org/10.1038/s41467-019-11834-1>
33. Rubasinghe G, Grassian VH. 2013. Role(s) of adsorbed water in the surface chemistry of environmental interfaces. *Chem Commun* 49:3071. <https://doi.org/10.1039/c3cc38872g>
34. Vejerano EP, Marr LC. 2018. Physico-chemical characteristics of evaporating respiratory fluid droplets. *J R Soc Interface* 15:20170939. <https://doi.org/10.1098/rsif.2017.0939>
35. Fedorenko A, Grinberg M, Orevi T, Kashtan N. 2020. Survival of the enveloped bacteriophage Phi6 (a surrogate for SARS-CoV-2) in evaporated saliva microdroplets deposited on glass surfaces. *Sci Rep* 10:22419. <https://doi.org/10.1038/s41598-020-79625-z>
36. Orevi T, Sørensen SJ, Kashtan N. 2022. Droplet size and surface hydrophobicity enhance bacterial plasmid transfer rates in microscopic surface wetness. *ISME Commun* 2:72. <https://doi.org/10.1038/s43705-022-00159-8>
37. Steinberg S, Grinberg M, Beitelman M, Peixoto J, Orevi T, Kashtan N. 2021. Two-way microscale interactions between immigrant bacteria and plant leaf microbiota as revealed by live imaging. *ISME J* 15:409–420. <https://doi.org/10.1038/s41396-020-00767-z>
38. Beizman-Magen Y, Grinberg M, Orevi T, Kashtan N. 2022. Wet-dry cycles protect surface-colonizing bacteria from major antibiotic classes. *ISME J* 16:91–100. <https://doi.org/10.1038/s41396-021-01051-4>
39. Hutchings MI, Truman AW, Wilkinson B. 2019. Antibiotics: past, present and future. *Curr Opin Microbiol* 51:72–80. <https://doi.org/10.1016/j.mib.2019.10.008>
40. Waksman SA, Schatz A, Reynolds DM. 2010. Production of antibiotic substances by actinomycetes. *Ann N Y Acad Sci* 1213:112–124. <https://doi.org/10.1111/j.1749-6632.2010.05861.x>
41. Fan B, Wang C, Song X, Ding X, Wu L, Wu H, Gao X, Borriss R. 2018. *Bacillus velezensis* FZB42 in 2018: the gram-positive model strain for plant growth promotion and biocontrol. *Front Microbiol* 9:2491. <https://doi.org/10.3389/fmicb.2018.02491>
42. Fazle Rabbee M, Baek KH. 2020. Antimicrobial activities of lipopeptides and polyketides of *Bacillus velezensis* for agricultural applications. *Molecules* 25:4973. <https://doi.org/10.3390/molecules25214973>
43. Chen XH, Koumoutsis A, Scholz R, Eisenreich A, Schneider K, Heinemeyer I, Morgenstern B, Voss B, Hess WR, Reva O, Junge H, Voigt B, Jungblut PR, Vater J, Süßmuth R, Liesegang H, Strittmatter A, Gottschalk G, Borriss R. 2007. Comparative analysis of the complete genome sequence of the plant growth-promoting bacterium *Bacillus amyloliquefaciens* FZB42. *Nat Biotechnol* 25:1007–1014. <https://doi.org/10.1038/nbt1325>
44. Jin P, Wang H, Tan Z, Xuan Z, Dahar GY, Li QX, Miao W, Liu W. 2020. Antifungal mechanism of bacillomycin D from *Bacillus velezensis* HN-2 against colletotrichum gloeosporioides Penz. *Pestic Biochem Physiol* 163:102–107. <https://doi.org/10.1016/j.pestbp.2019.11.004>
45. Ramarathnam R, Bo S, Chen Y, Fernando WGD, Xuwen G, de Kievit T. 2007. Molecular and biochemical detection of fengycin- and bacillomycin D-producing *Bacillus* spp., antagonistic to fungal pathogens of canola and wheat. *Can J Microbiol* 53:901–911. <https://doi.org/10.1139/W07-049>
46. Rajaofera MN, Kang X, Jin P-F, Chen X, Li C-C, Yin L, Liu L, Sun Q-H, Zhang N, Chen C-Z, He N, Xia Q-F, Miao W-G. 2020. Antibacterial activity of bacillomycin D-like compounds isolated from *Bacillus amyloliquefaciens*

- HAB-2 against *Burkholderia pseudomallei*. Asian Pac J Trop Biomed 10:183. <https://doi.org/10.4103/2221-1691.280295>
47. Wu L, Wu H, Chen L, Yu X, Borriss R, Gao X. 2015. Difficidin and bacilysin from *Bacillus amyloliquefaciens* FZB42 have antibacterial activity against *Xanthomonas oryzae* rice pathogens. Sci Rep 5:1–9. <https://doi.org/10.1038/srep12975>
 48. Dhakal U, Dobhal S, Alvarez AM, Arif M. 2019. Phylogenetic analyses of xanthomonads causing bacterial leaf spot of tomato and pepper: *Xanthomonas euvesicatoria* revealed homologous populations despite distant geographical distribution. Microorganisms 7:462. <https://doi.org/10.3390/microorganisms7100462>
 49. Moretti C, Amatulli MT, Buonauro R. 2009. PCR-based assay for the detection of *Xanthomonas euvesicatoria* causing pepper and tomato bacterial spot. Lett Appl Microbiol 49:466–471. <https://doi.org/10.1111/j.1472-765X.2009.02690.x>
 50. Xin XF, He SY. 2013. *Pseudomonas syringae* pv. tomato DC3000: a model pathogen for probing disease susceptibility and hormone signaling in plants. Annu Rev Phytopathol 51:473–498. <https://doi.org/10.1146/annurev-phyto-082712-102321>
 51. Oliševska S, Nickzad A, Restieri C, Dagher F, Luo Y, Zheng J, Déziel E. 2023. *Bacillus velezensis* and *Paenibacillus peoriae* strains effective as biocontrol agents against *Xanthomonas* bacterial spot. Appl Microbiol 3:1101–1119. <https://doi.org/10.3390/applmicrobiol3030076>
 52. Rabbee MF, Islam N, Baek KH. 2022. Biocontrol of citrus bacterial canker caused by *Xanthomonas citri* subsp. *citri* by *Bacillus velezensis*. Saudi J Biol Sci 29:2363–2371. <https://doi.org/10.1016/j.sjbs.2021.12.005>
 53. Canu A, Malbruny B, Coquemont M, Davies TA, Appelbaum PC, Leclercq R. 2002. Diversity of ribosomal mutations conferring resistance to macrolides, clindamycin, streptogramin, and telithromycin in *Streptococcus pneumoniae*. Antimicrob Agents Chemother 46:125–131. <https://doi.org/10.1128/AAC.46.1.125-131.2002>
 54. Zweerink MM, Edison A. 1987. Difficidin and oxydifficidin: novel broad spectrum antibacterial antibiotics produced by *Bacillus subtilis*. III. Mode of action of difficidin. J Antibiot (Tokyo) 40:1692–1697. <https://doi.org/10.7164/antibiotics.40.1692>
 55. Butcher RA, Schroeder FC, Fischbach MA, Straight PD, Kolter R, Walsh CT, Clardy J. 2007. The identification of bacillaen, the product of the PksX megacomplex in *Bacillus subtilis*. Proc Natl Acad Sci U S A 104:1506–1509. <https://doi.org/10.1073/pnas.0610503104>
 56. Molina-Santiago C, Vela-Corcia D, Petras D, Díaz-Martínez L, Pérez-Lorente AI, Sopena-Torres S, Pearson J, Caraballo-Rodríguez AM, Dorresteijn PC, de Vicente A, Romero D. 2021. Chemical interplay and complementary adaptative strategies toggle bacterial antagonism and co-existence. Cell Rep 36:109449. <https://doi.org/10.1016/j.celrep.2021.109449>
 57. Cho H, Uehara T, Bernhardt TG. 2014. Beta-lactam antibiotics induce a lethal malfunctioning of the bacterial cell wall synthesis machinery. Cell 159:1300–1311. <https://doi.org/10.1016/j.cell.2014.11.017>
 58. Wu L, Wu H, Chen L, Xie S, Zang H, Borriss R, Gao X. 2014. Bacilysin from *Bacillus amyloliquefaciens* FZB42 has specific bactericidal activity against harmful algal bloom species. Appl Environ Microbiol 80:7512–7520. <https://doi.org/10.1128/AEM.02605-14>
 59. Preston GM. 2000. *Pseudomonas syringae* pv. tomato: the right pathogen, of the right plant, at the right time. Mol Plant Pathol 1:263–275. <https://doi.org/10.1046/j.1364-3703.2000.00036.x>
 60. Lee J, Kim S, Jung H, Koo B-K, Han JA, Lee H-S. 2023. Exploiting bacterial genera as biocontrol agents: mechanisms, interactions and applications in sustainable agriculture. J Plant Biol 66:485–498. <https://doi.org/10.1007/s12374-023-09404-6>
 61. Morales-Cedeño LR, Orozco-Mosqueda Ma del C, Loeza-Lara PD, Parra-Cota FI, de los Santos-Villalobos S, Santoyo G. 2021. Plant growth-promoting bacterial endophytes as biocontrol agents of pre- and post-harvest diseases: fundamentals, methods of application and future perspectives. Microbiol Res 242:126612. <https://doi.org/10.1016/j.micres.2020.126612>
 62. Preininger C, Sauer U, Bejarano A, Berninger T. 2018. Concepts and applications of foliar spray for microbial inoculants. Appl Microbiol Biotechnol 102:7265–7282. <https://doi.org/10.1007/s00253-018-9173-4>
 63. Amaning Danquah C, Minkah PAB, Osei Duah Junior I, Amankwah KB, Somuah SO. 2022. Antimicrobial compounds from microorganisms. Antibiotics (Basel) 11:285. <https://doi.org/10.3390/antibiotics11030285>
 64. Tran C, Cock IE, Chen X, Feng Y. 2022. Antimicrobial *Bacillus*: metabolites and their mode of action. Antibiotics (Basel) 11:88. <https://doi.org/10.3390/antibiotics11010088>
 65. Abdalla MA, Sulieman S, McGaw LJ. 2017. Microbial communication: a significant approach for new leads. S Afr J Bot 113:461–470. <https://doi.org/10.1016/j.sajb.2017.10.001>
 66. Wu T, Chen M, Zhou L, Lu F, Bie X, Lu Z. 2020. Bacillomycin D effectively controls growth of *Malassezia globosa* by disrupting the cell membrane. Appl Microbiol Biotechnol 104:3529–3540. <https://doi.org/10.1007/s00253-020-10462-w>
 67. Li H, Han X, Dong Y, Xu S, Chen C, Feng Y, Cui Q, Li W. 2021. Bacillaenes: decomposition trigger point and biofilm enhancement in *Bacillus*. ACS Omega 6:1093–1098. <https://doi.org/10.1021/acsomega.0c03389>
 68. Patel PS, Huang S, Fisher S, Pirnik D, Aklonis C, Dean L, Meyers E, Fernandes P, Mayerl F. 1995. Bacillaene, a novel inhibitor of prokaryotic protein synthesis produced by *Bacillus subtilis*: production, taxonomy, isolation, physico-chemical characterization and biological activity. J Antibiot 48:997–1003. <https://doi.org/10.7164/antibiotics.48.997>
 69. Lyng M, Kovács ÁT. 2023. Frenemies of the soil: *Bacillus* and *Pseudomonas* interspecies interactions. Trends Microbiol 31:845–857. <https://doi.org/10.1016/j.tim.2023.02.003>
 70. Lyng M, Þórisdóttir B, Sveinsdóttir SH, Hansen ML, Jelsbak L, MarótiG, Kovács AT. 2024. Taxonomy of *Pseudomonas* spp. determines interactions with *Bacillus subtilis*. mSystems 9:e0021224. <https://doi.org/10.1128/mSystems.00212-24>
 71. Gram L. 1993. Inhibitory effect against pathogenic and spoilage bacteria of *Pseudomonas* strains isolated from spoiled and fresh fish. Appl Environ Microbiol 59:2197–2203. <https://doi.org/10.1128/aem.59.7.2197-2203.1993>
 72. Fisher RA, Koven CD. 2020. Perspectives on the future of land surface models and the challenges of representing complex terrestrial systems. J Adv Model Earth Syst 12. <https://doi.org/10.1029/2018MS001453>
 73. Koch K, Bhushan B, Barthlott W. 2008. Diversity of structure, morphology and wetting of plant surfaces. Soft Matter 4:1943. <https://doi.org/10.1039/b804854a>
 74. Batsch M, Guex I, Todorov H, Heiman CM, Vacheron J, Vorholt JA, Keel C, van der Meer JR. 2024. Fragmented micro-growth habitats present opportunities for alternative competitive outcomes. Nat Commun 15:7591. <https://doi.org/10.1038/s41467-024-51944-z>
 75. Lagendijk EL, Validov S, Lamers GEM, de Weert S, Bloemberg GV. 2010. Genetic tools for tagging Gram-negative bacteria with mCherry for visualization in vitro and in natural habitats, biofilm and pathogenicity studies. FEMS Microbiol Lett 305:81–90. <https://doi.org/10.1111/j.1574-6968.2010.01916.x>
 76. Fan B, Chen XH, Budiharjo A, Bleiss W, Vater J, Borriss R. 2011. Efficient colonization of plant roots by the plant growth promoting bacterium *Bacillus amyloliquefaciens* FZB42, engineered to express green fluorescent protein. J Biotechnol 151:303–311. <https://doi.org/10.1016/j.jbiotec.2010.12.022>
 77. Wang X, Zheng D, Liang R. 2016. An efficient electro-competent cells generation method of *Xanthomonas campestris* pv. *campestris*: its application for plasmid transformation and gene replacement. Adv Microbiol 06:79–87. <https://doi.org/10.4236/aim.2016.62008>