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Article

Short-Term Microbial Community Responses to an Intense Simulated Precipitation Pulse in the Hyperarid Atacama Desert Soil

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Abstract

Understanding how microbial communities from hyperarid environments respond to sporadic water availability is crucial for predicting ecosystem responses to unpredictable precipitation related to climate change. Here, we experimentally simulated a short-term precipitation pulse (50 mm) in soils from the hyperarid Atacama Desert to evaluate shifts in microbial community composition, diversity, and functional potential, as well as changes in soil physicochemical properties. Using a microcosm experiment with time-structured sampling and high-throughput amplicon sequencing, we found that changes in soil properties after precipitation do not significantly influence microbial community composition. However, carbon dynamics exhibit significant variation. Actinobacteria and Proteobacteria dominated bacterial communities, exhibiting functional stability over time, which suggests high resilience. In contrast, fungal communities, primarily composed of Ascomycota, displayed greater temporal variation in both taxonomic and functional profiles, particularly during intermediate hydration stages. Notably, fungal functional richness increased despite a limited taxonomic change, indicating lower redundancy and, thus, potentially higher community fragility. Our findings highlight distinct microbial strategies for coping with hydration pulses in extreme drylands, underscoring the role of fungi in nutrient cycling, decomposition, and soil structure, while also revealing their increased vulnerability to environmental fluctuations. Our results reinforce the importance of microbial dynamics in maintaining ecosystem functioning in pulse-reserve systems under ongoing climatic changes.

Keywords: atacama desert; microbial communities; pulse precipitation; functional resilience

1. Introduction

Drylands cover over 45% of Earth's terrestrial surface [4], which harbors a third of the global human population [5]. Although previous studies have focused on the impact of current climate change trends, which are globally increasing the total dryland surface [6], the vulnerability of these habitats to unpredictable rainfall events remains understudied [7].

The pulse-reserve paradigm (PRP) explains how dryland ecosystems respond to infrequent rainfall, with episodic water pulses triggering bursts of biological activity [8–10]. Microbial growth in arid environments is driven by reserves—mainly carbon—stored during previous periods of moisture. During rainfall pulses, microorganisms use these reserves to grow, reproduce, and acquire new resources, replenishing what is needed to survive dry phases [10,11]. As moisture declines, microbes transition into dormancy, relying on accumulated reserves for survival [12]. The duration and intensity of these pulses strongly influence microbial dynamics: shorter pulses reduce growth

efficiency and alter community composition, while longer pulses support net growth and effective reserve replenishment [11–13].

The short-term effects of a hydration pulse on desert soil microbial communities are significant and multifaceted, influencing microbial diversity, community composition, and metabolic activity. Following a hydration pulse, there is often a decrease in microbial diversity [8,11,12]. These patterns are attributed to the rapid growth of specific taxa that thrive in wet conditions, which can outcompete others during these brief periods of moisture availability. For instance, specialist phylotypes may become more prominent in response to specific pulse durations [12]. The composition of microbial communities undergoes significant shifts after hydration events [12,14]. Studies have shown that distinct microbial communities emerge under varying moisture conditions—one during high hydration, another during gradual desiccation, and a third in arid conditions [12]. These shifts reflect the community's adaptation to fluctuating moisture levels. Hydration pulses trigger a surge in microbial metabolic activity, leading to increased respiration rates and CO₂ release. This metabolic activation is crucial for nutrient cycling and can enhance overall soil fertility temporarily [14]. However, this activity can rapidly deplete resources if not replenished [12,13]. Microbial diversity often returns to pre-pulse levels as soils dry, a recovery essential for maintaining ecosystem resilience [11,15].

The Atacama Desert in northern Chile is the most arid desert on the planet and one of the oldest [16]. Here, the mean annual precipitation is only a few millimeters (< 2 mm), with rainfall events occurring approximately every 10–20 years [17,18]. In the core of the Atacama Desert, biological activity is triggered by rare precipitation events following prolonged drought, as exemplified by the “blooming desert” phenomenon [11,19]. During rainy periods, years that generally involve the El Niño phenomenon [20–22], increased water availability can trigger flowering desert events caused by a rapid biological response by microorganisms and dormant vegetation in the soil [20,21]. These increases in above and belowground productivity trigger new trophic cascades, altering the structure and functioning of this ecosystem [18,20,21].

In this study, we experimentally evaluated the short-term effects of an intense precipitation pulse on the composition, taxonomic, and functional diversity of soil microbial communities in one of the world's driest ecosystems. Specifically, we aimed to assess how a single hydration event - simulating the magnitude of the extraordinary 2015 rainfall in the Atacama Desert - alters microbial diversity, taxonomic structure, and the relative dominance of major microbial groups. Focusing on community responses across bacteria and fungi, we aimed to identify taxon-specific changes and patterns of resilience that reflect ecological strategies for coping with extreme moisture fluctuations in hyper-arid soils and infer how these changes in taxonomic diversity are related to functions.

2. Materials and Methods

2.1. Study Site

The Atacama UC Oasis Niebla Alto Patache Station (20° 49' S - 70° 09' W) is located in the Atacama Desert, Iquique, Tarapacá Region (Figure 1). The topographical characteristics of this area allow limited entry of coastal fog or “camanchaca” inland, maintaining a relative humidity of 30% with a mean annual precipitation of <1 mm [23]. The mean annual temperature during the day is 25°C and 10°C at night. The vertical soil profile consists of alternating layers of sand and clay, which prevent water from diffusing into deeper layers, which in turn makes the soil virtually devoid of vegetation cover [24].

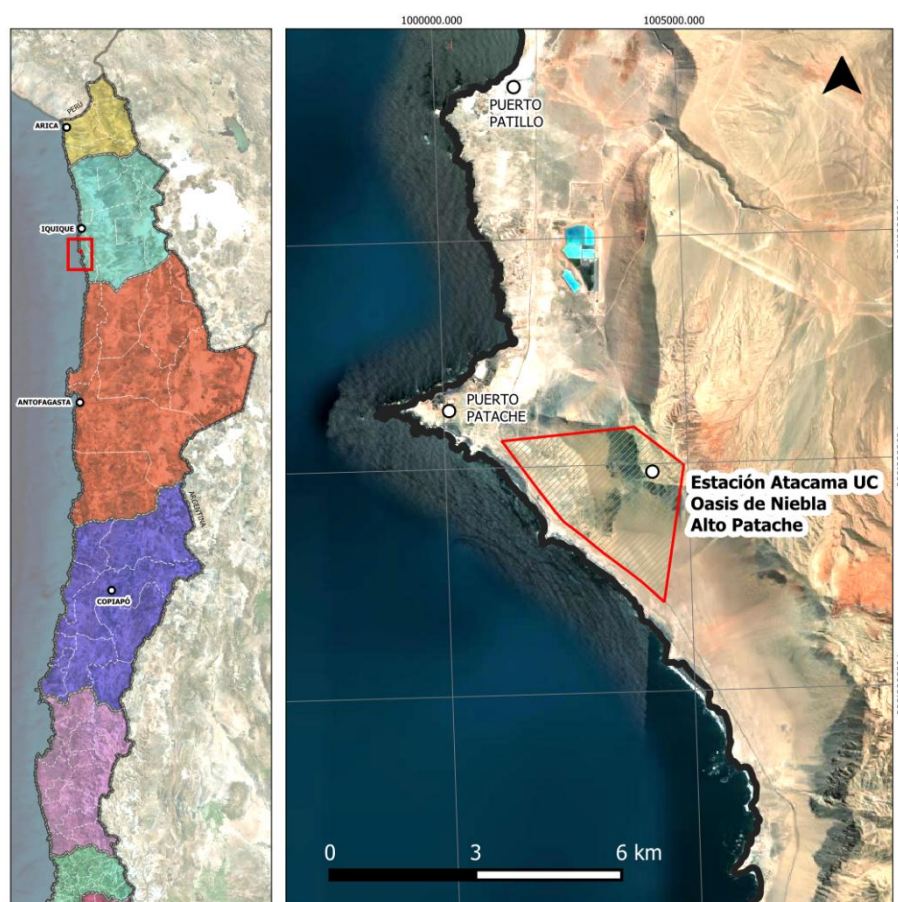


Figure 1. Map showing the location of the study site and sampling area, in the Atacama UC Oasis Niebla Alto Patache Station. Coordinates are in UTM.

2.2. Soil Sampling

We collected composite soil samples (five subsamples) of topsoil (~5cm depth) using sterilized spatulas. Larger gravel and organic materials were removed from the samples by sieving them through a 2 mm mesh and then stored in plastic bags at room temperature. During the microcosm experiment, we divided the samples into two fractions. The first fraction was immediately frozen (-20°C) for molecular analyses, and the second was air-dried for physicochemical analyses. We measured abiotic properties for each sample. Soil pH was determined using a pH sensor in a CaCl_2 solution [25]. Soil organic matter (SOM) content was assessed by ignition [26]. Soil water holding capacity (WHC) was measured using gravimetric methods, employing 5 g of soil, a filter, and 10 ml of water, and calculating the percentage of water retained relative to the soil weight [27]. Gravimetric methods also determined moisture content in soil (SM) [25].

2.3. Microcosm Experiment

To evaluate the short-term effects of flooding pulses on soil properties and the structure of soil microbial communities, thirty pots containing 50 g of soil samples were flooded to simulate a 50mm-rainfall event, based on the last major flooding event in the Atacama Desert (2015), then incubated for 7 days in two culture chambers (111L CLIMACELL® Incubator, MMM Group) simulating the summer conditions of the Atacama Desert, with a mean temperature of 18°C , relative humidity of 30% and a photoperiod of 14 hours of light and 10 hours of darkness. Six microcosms were sacrificed just before the start of the experiment (time 0), and then at 12, 24, 96, and 168 hours after incubation.

2.4. DNA Extraction and Amplicon Sequencing

DNA extraction was performed using the DNeasy® PowerSoil® Pro Kit (Qiagen), following the manufacturer's protocol, and DNA concentration was determined using a Qubit™ 4.0 fluorimeter (ThermoFisher Scientific). The 16S ribosomal RNA gene, targeting the V3-V4 region, and the ITS ribosomal RNA were sequenced at Zymo Research. Primers for sequencing were provided by the same company, and sequencing was performed using the Illumina® MiSeq™ platform. Zymo Research conducted the taxonomic assignment of fungi and bacteria using UCLUST in QIIME v.1.9.1, referencing their proprietary database. The absolute abundance of Amplicon Sequence Variants (ASVs) was determined by Zymo Research using qPCR, with a standard curve for both the 16S and ITS genes. We standardized sampling effort by applying rarefaction without replacement in both domains. Bacterial libraries ranged from 145 to 2545 reads per sample; all samples were rarefied to 145 reads (the minimum). Fungal libraries ranged from 159 to 60641 reads per sample; all samples were rarefied to 159 reads. Thresholds were selected to maximize sample retention across time points. After rarefaction, the bacterial dataset retained six replicates at all time points, except at 12 h, which retained five. In the fungal dataset, rarefaction reduced replication: the first three timepoints retained five replicates each, whereas the last two time points retained three replicates each.

2.5. Data Analysis

Microbial community analyses and biodiversity indices were assessed using the 'microeco' package [28] in R. To evaluate microbial community composition at the phylum level, we determined the relative abundance of major soil phyla at each time point and generated bar plots. For genus-level analyses, we used heatmaps, grouping genera by phyla. To assess the relationship between diversity indices and physicochemical factors over time, we performed a series of linear models (LM) where diversity metrics (i.e., Shannon, Chao1, Simpson) and soil physicochemical variables were treated as response variables and sampling time (0, 12, 24, 96, and 168 h) as a fixed factor. To determine the relationship between environmental factors and microbial communities, we performed a Canonical Correspondence Analysis (CCA) with a Hellinger transformation using the R package *vegan* [29]. Additionally, microbial functional composition was assessed by classifying genera using FUNGuild [30] for fungal functional groups and Tax4Fun2 [31] for bacterial functions. To compare microbial biodiversity and functional composition, we performed regression analyses between taxonomic richness and functional diversity, calculating the adjusted R^2 and corresponding p-values. Statistical analyses were conducted using the R statistical software [32].

3. Results

3.1. Biogeochemical Changes During Short Pulse Precipitation

Soil physicochemical properties exhibited significant changes in response to increased water availability. Specifically, a significant increase was observed in the proportion of the $\delta^{13}\text{C}$ isotope, soil carbon content (%C), and soil organic matter (SOM) throughout the experiment. Concurrently, soil pH progressively decreased, indicating a shift toward more neutral conditions compared to the initial measurements. In contrast, neither soil nitrogen content (%N) nor the proportion of the $\delta^{15}\text{N}$ isotope showed significant changes over time (Figure 2).

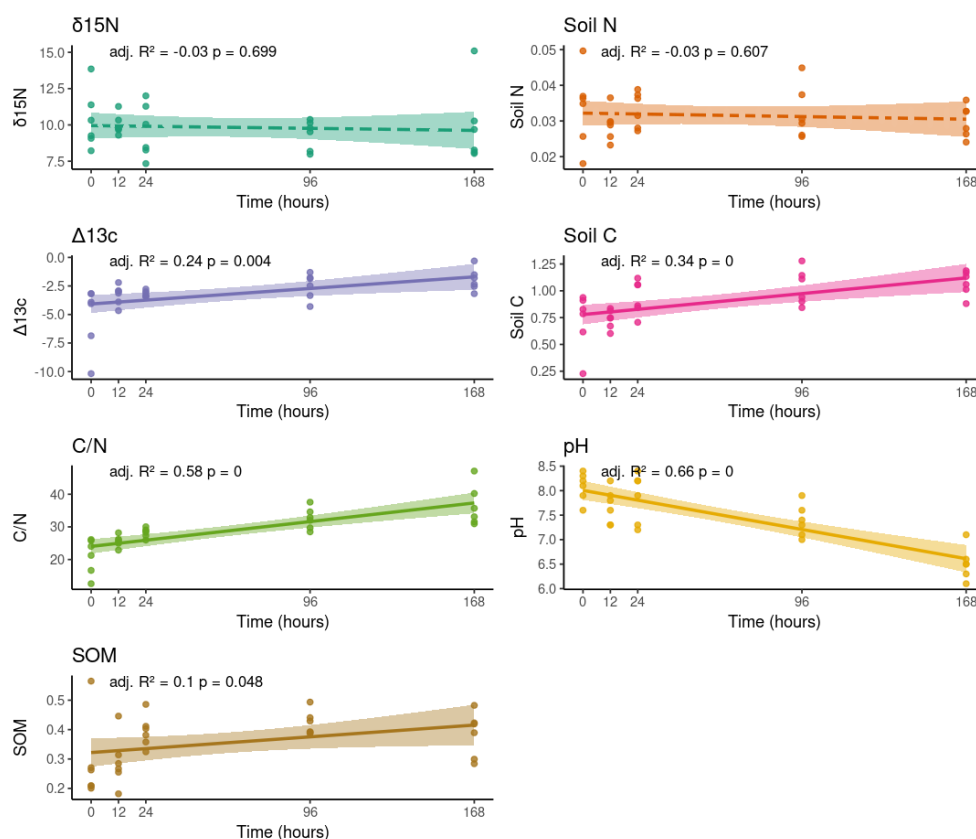


Figure 2. Changes in soil physicochemical properties in response to increased water availability. Ordinary Least Squares regressions illustrates the distribution of values and linear trends for $\delta^{15}\text{N}$, $\delta^{13}\text{C}$, nitrogen content, carbon content, pH, and soil organic matter across five time points (0, 12, 24, 96, and 168 hours). The diversity panel includes the adjusted R^2 and P values from linear model tests for temporal differences. Statistical significance was considered at $P < 0.05$, indicated with a continuous line.

We then evaluated whether these changes in soil properties influence soil bacterial and fungal community composition over time. In the case of bacteria, the first two dimensions (CCA1 and CCA2) account for 20% and 16.3% of the variance, respectively (Figure S1a). For fungi, the first and second axes of CCA account for 24.4% and 17.2% of the variance, respectively (Figure S1b). The analyses showed that, together, the environmental variables did not significantly explain the changes in microbial community composition for either group (global ANOVA CCA for bacteria: $p = 0.495$; for fungi: $p = 0.300$) (Table S1). Furthermore, none of the measured physicochemical variables individually showed a significant effect on bacterial or fungal composition, except for Soil C, which was significant for fungi ($p = 0.015$), but not for bacteria ($p = 0.088$) (Table S1). On the other hand, the PERMANOVA analysis based on Bray-Curtis's dissimilarity index revealed that time had a clear and significant effect on both bacterial ($R^2 = 22.98\%$, $p = 0.001$) and fungal ($R^2 = 33.45\%$, $p = 0.001$) (Table S1) community structures.

3.2. The Impact of Pulse Precipitation on Soil Microbial Abundances and Diversity

The most dominant bacterial phyla were Actinobacteria (61.42%), Chloroflexi (10.77%), Proteobacteria (10.36%) and Firmicutes (6.82%) (Figure 3a), and their abundances varied over time after the water event. For example, Actinobacteria abundances decreased with time, while Proteobacteria showed an opposite trend (Figure 3a). At a more detailed taxonomic level, the most abundant bacterial genera across treatments were *Rubrobacter*, *Gaiella*, and *Pseudonocardia*, from the Actinobacteriota phylum. Additionally, some genera, such as *Ammoniphilus* (Firmicutes) and *Gemmatimonas* (Gemmatimonadota), increase in abundance during the later stages of this immediate

response (Figure 3b). Bacterial alpha-diversity remains relatively high and stable, with no significant differences over time (Figure 3c).



Figure 3. (a) Bar plot showing the relative abundance of the five most dominant bacterial phyla at each sampling time. Phyla with significant differences ($P < 0.05$) are marked with an asterisk. (b) Heatmap of the relative abundance of bacterial genera, grouped by phylum on the y-axis and by sampling time on the x-axis, with each sample detailed. (c) Diversity indices (Shannon, Simpson, and Chao1) linear trends for bacterial communities across sampling times (p -values < 0.05 are considered significant, indicated with a continuous line).

The fungal communities were highly dominated by members of the Ascomycota (82.03%) phylum, followed by Basidiomycota (14.16%), Mortierellomycota (1.16%), Rozellomycota (1.13%), and Chytridiomycota (0.14%). However, no fungal phyla displayed any temporal trends (Figure 4a). At the genus level (Figure 4b), *Alternaria* (Ascomycota) stands out as one of the most abundant genera (representing 20.73% of the communities); particularly at 12 h (54%) and 24 h (44%) after the water pulse. In contrast, *Fusarium* and *Oidiodendrum* (Ascomycota) were more abundant at the beginning (31% and 33% at 0 h, respectively), and *Fusarium* and *Colletotrichum* were more abundant at the end of the experiment (33% and 21% at 168 h, respectively). Across the full experiment, *Fusarium* accounted for 13.0%, *Colletotrichum* for 4.5%, and *Oidiodendrum* for 6.1% of the total fungal community. Fungal diversity remains stable, though increasing toward the later stages, showing a significant positive trend in the Chao1 index (Figure 4c), suggesting this domain has a higher sensitivity to environmental changes.

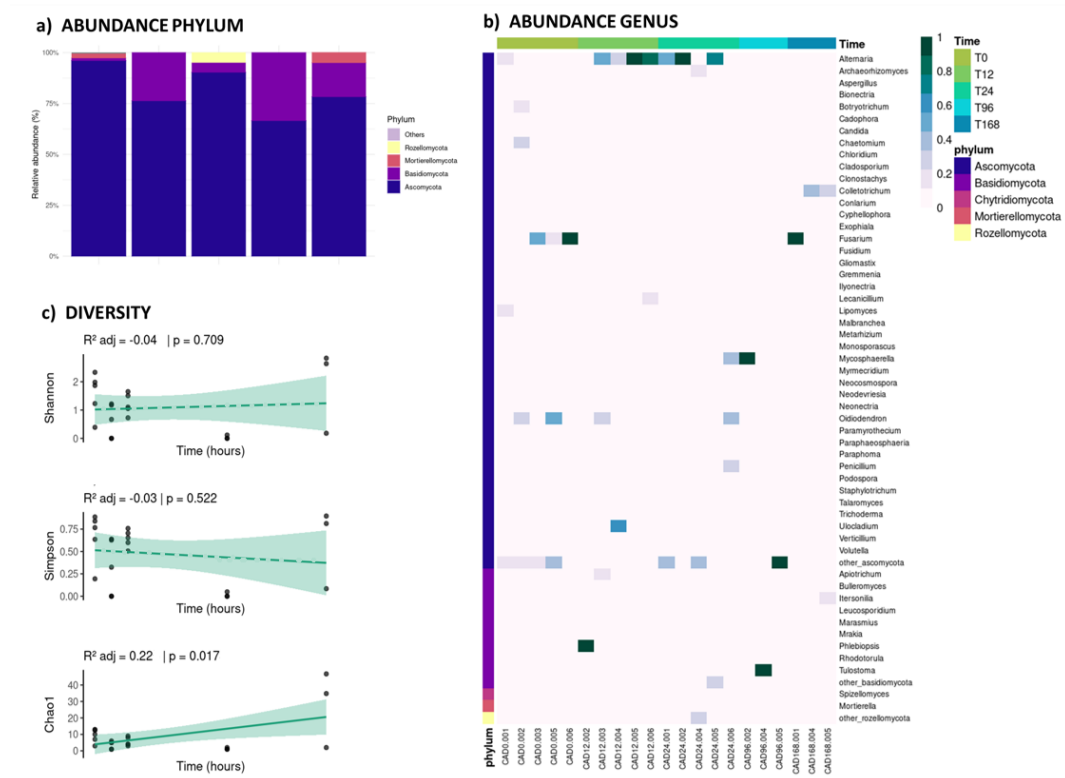


Figure 4. (a) Bar plot showing the relative abundance of the five most dominant fungal phyla at each sampling time. (b) Heatmap of the relative abundance of fungal genera, grouped by phylum on the y-axis and by sampling time on the x-axis, with each sample detailed. (c) Diversity indices (Shannon, Simpson, and Chao1) linear trends for fungal communities across sampling times (p-values < 0.05 are considered significant, indicated with a continuous line).

3.3. The Impact of Pulse Precipitation on Soil Microbial Composition and Function

The ecological functions associated with bacteria remained stable over time, with aerobic chemoheterotrophy being the most frequently observed function (Figure 5a). Additionally, a less frequent but also stable function is nitrate reduction. In the case of fungi, a greater number of ecological functions were observed, the most frequent including roles as plant pathogens and saprotrophs (Figure 5b), particularly related to the presence of *Alternaria* in the intermediate stages (12 and 24 hours) and *Fusarium*, though less dominant, in the early and late stages (0 and 168 hours) (Figure S2). The main fungal lifestyles are as soil and aquatic fungi, which abundances change with water availability (Figure 5b).

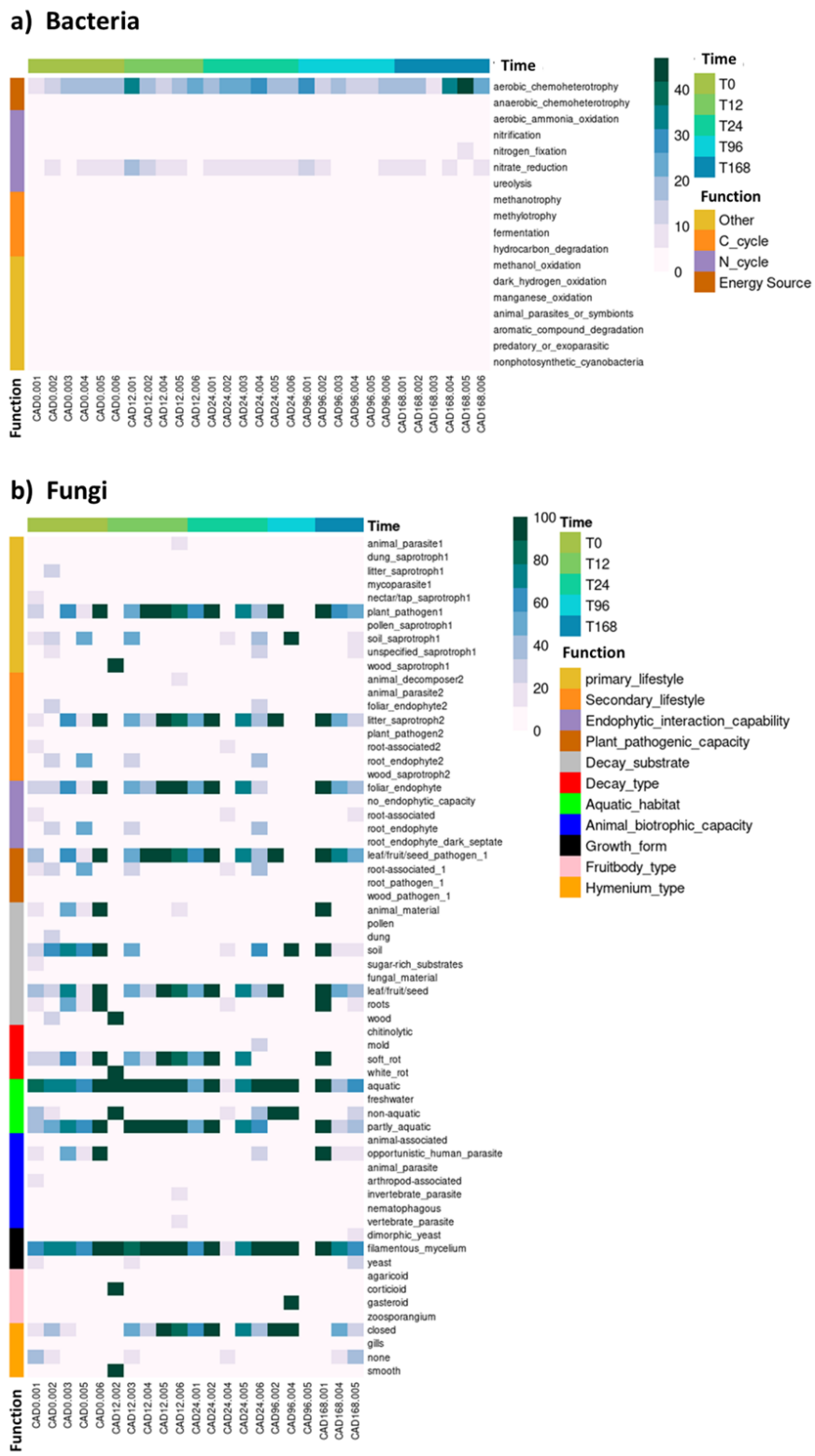


Figure 5. Heatmaps of functions associated with taxonomy, grouped by functional categories and sampling time for bacteria (a) and fungi (b).

The bacterial community composition over time revealed that early-stage communities harbored fewer unique species, while species tend to become more specific in the later stages (Figure 6a). In contrast, fungal community composition exhibited the opposite trend, with more specific fungal species found in the initial stages and less specificity observed as time progressed (Figure 6b), except at 168 hours, which shows the most unique composition among timepoints.

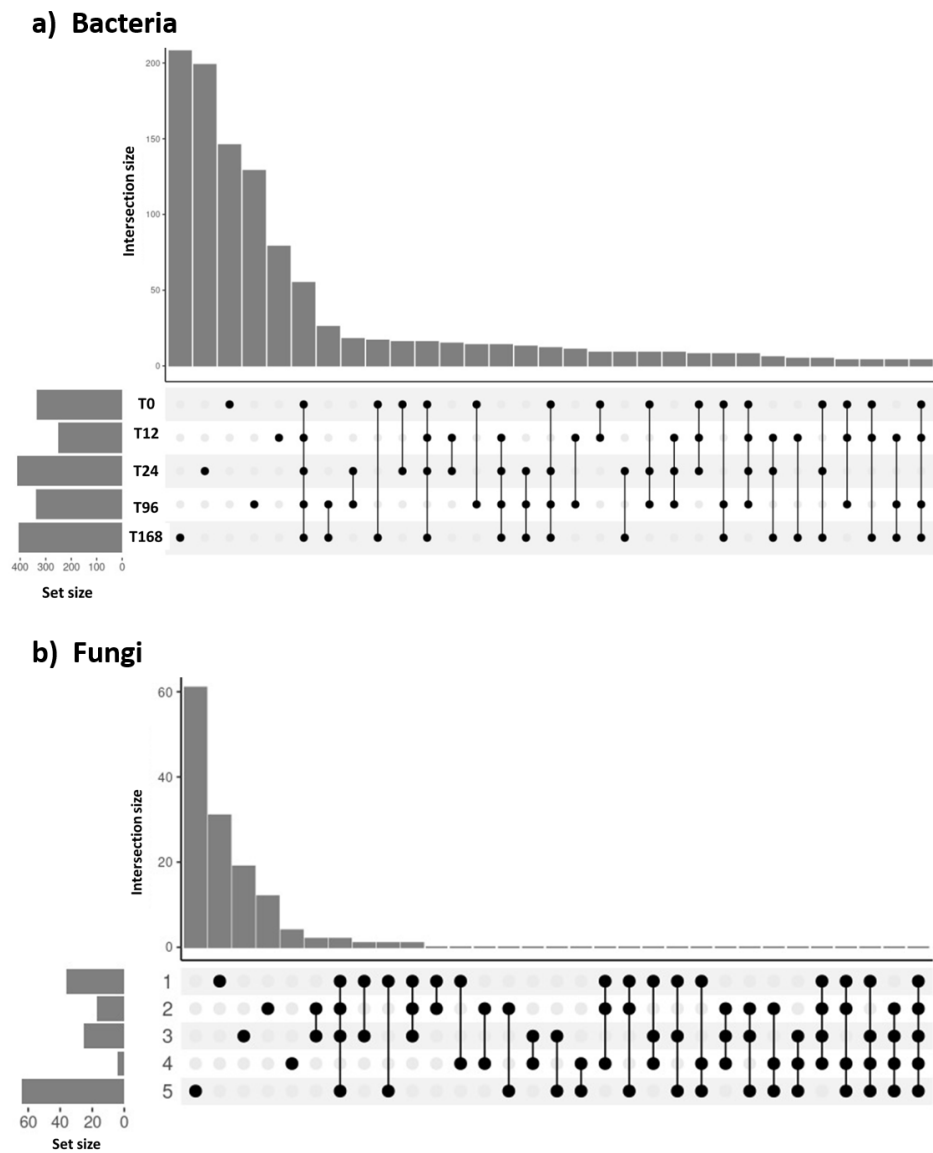


Figure 6. Upset plots illustrating the number of ASVs shared among bacterial (a) and fungal (b) communities at different sampling times. The matrix layout displays the intersections among the five sampling times, sorted by size. Dark circles in the matrix indicate the sets included in each intersection.

To assess a relative functional stability in these microbial groups, we evaluated the relationship between functional and taxonomic richness. Functional richness in bacterial communities does not correlate with taxonomic richness, as both metrics remained stable over time (Figure S3a). However, we observed a sharp increase in fungal community functional richness while taxonomic richness remained much lower in comparison (Figure S3b).

4. Discussion

Short-term precipitation pulses in hyperarid soils can generate rapid and multidimensional responses in both abiotic and biotic components, despite the extreme water limitations that typically constrain microbial activity [33]. In this study, we demonstrate that even a brief hydration event can trigger shifts in soil chemical properties, particularly in carbon dynamics, alongside changes in microbial composition and functional potential. These changes were not immediate or linear but rather reflected a mosaic of transient responses driven by microbial physiological traits and ecological

interactions. Our results support the notion that microbial communities in pulse-reserve systems exhibit differential strategies for coping with water pulses, with bacteria maintaining stable functions through metabolic versatility and a possible functional asynchrony, while fungi respond with greater compositional specificity and functional shifts.

The fungi-bacteria ratio in desert soils can shift markedly during hydration pulses, driven by microbial community interactions and resource availability [15]. Initially, bacterial activity increases due to sudden water and nutrient inputs, often outpacing fungal growth in the immediate response [12,13]. Moreover, mycelium-forming fungi can facilitate bacterial growth by redistributing water and nutrients within the soil, creating microhabitats that enhance bacterial survival and proliferation [34], therefore favoring bacterial dominance over fungi immediately after a pulse. Subsequently, as moisture levels stabilize or decrease, fungi may regain prominence due to their ability to form resilient structures, such as spores and hyphae, that can withstand dry conditions [15]. Both groups, bacteria and fungi, display physiological flexibility to alternate between active and passive phases, a key survival pattern in extreme arid environments. These findings suggest that short water pulses can reset soil microbial trajectories and influence key ecosystem functions in desert environments.

An increase in the $\delta^{13}\text{C}$ isotope, soil carbon content (%C), and soil organic matter (SOM) (Figure 2) could be due to the Birch effect, where the decomposition of previously protected or newly available labile organic carbon is accelerated with the rapid flush of microbial activity after a water pulse [35,36]. Microbes often preferentially metabolize organic compounds containing the lighter ^{12}C isotope due to lower energy requirements for breaking those bonds. This leaves behind a residual SOM pool that is relatively enriched in the heavier ^{13}C isotope, thus increasing the overall $\delta^{13}\text{C}$ value [37]. The decomposition processes activated by the precipitation pulse cause the release of various organic acids. Microbial respiration from increased metabolic activity during a precipitation pulse also produces carbon dioxide (CO_2). When this CO_2 dissolves in soil water, it forms carbonic acid (H_2CO_3), a weak acid that directly contributes hydrogen ions (H^+) to the soil solution, thus lowering the pH [38]. However, the increased water flow can lead to the leaching of basic cations, especially calcium in the calcium carbonate-rich (CaCO_3) Atacama Desert soils, from the upper soil layers [39]. The rate of pH decrease might be slowed due to the CaCO_3 buffering capacity (Figure 2). Together with the production of CO_2 , it can influence the carbonate equilibrium, affecting soil pH in nuanced and complex ways, and possibly temporarily and/or locally lowering the pH [40,41].

In this context, bacteria tend to have greater adaptability than fungi to changes in environmental conditions [36,42]. They are therefore able to form specialized communities as soil conditions change during the pulse [12,33]. Fungi form highly specialized ecological networks but with less immediate plasticity and probably struggle to adapt to the abrupt input of water [43–45]. In this sense, the interactions between fungal genera and between fungi and bacteria become essential to produce balanced ecosystems [43]. For instance, fungi like *Alternaria* [46] and *Oidiodendrum* [47] can influence bacterial populations through their different decomposition activities. This could also help modulate carbon dynamics in the soil, as seen in Figure 2.

Ascomycetes are versatile fungi capable of decomposing a variety of organic materials, including dead microbial biomass and organic matter derived from other sources [47]. Their ability to break down complex compounds and their saprophytic activity are crucial for nutrient cycling in nutrient-poor soils [48,49]. At the genus level, *Alternaria* stands out as one of the most abundant genera, particularly in the intermediate stages (12 and 24 hours), while *Fusarium*, *Colletotrichum* and *Oidiodendrum* are more abundant at both earlier and later stages (Figure 4b). *Alternaria* species likely thrive on decomposing organic matter from microbial sources or other detritus, helping to recycle nutrients back into the soil [46]. In fact, *Alternaria* contributed the most to saprotrophic functions (Figure S2). Genera like *Fusarium* and *Oidiodendrum* can also have these ecological functions by decomposing recalcitrant materials, enhancing soil fertility over time [47,50]. *Fusarium* and *Alternaria* dominate as endophytes, saprotrophs and plant pathogens. However, they seem to outcompete each other at different stages of the pulse, with the first strongly present in drier soil (0

and 168 hours), and the latter present in wetter stages (12 and 24 hours), hinting at a possible functional asynchrony (Figure S1).

In the case of bacteria, the Actinobacteria phylum is recognized for its ability to break down complex organic matter. The decrease in abundance could be due to increased competition from other groups and changes in nutrient availability [51] (Figure 3a). On the other hand, Proteobacteria is a highly diverse phylum that includes many metabolically versatile bacteria. Its increase in abundance could be due to their ability to rapidly colonize new niches, utilize a wide range of substrates, or form beneficial associations with other organisms [51,52] (Figure 2A). These patterns were also observed in other studies of desert soil microbiome stimulation by hydration events [19,53,54]. The most abundant bacterial genera, such as *Rubrobacter*, *Gaiella* and *Pseudonocardia* (Figure 3b), are often associated with dry environments, and are known for their role in carbon cycling and nutrient mobilization in harsh conditions [55]. Additionally, some genera, such as *Ammoniphilus* and *Gemmatimonas*, increase in abundance during the later stages of this immediate response, suggesting a shift towards bacteria that can utilize nitrogen sources or thrive under specific nutrient conditions that arise after initial hydration events [56]. This shift could reflect changes in soil chemistry or microbial interactions as communities mature.

Aerobic chemoheterotrophy and nitrate reduction are the most prominent bacterial functions, with the former being much more abundant than the latter, but both being stable over time (Figure 5a). The stability in bacterial functions suggests that these communities are well-adapted to their environment and consistently rely on organic carbon sources for energy and growth, primarily through the decomposition of available organic matter, which is critical in ecosystems with low to no vegetation. Versatility in nutrient uptake is crucial in extreme environments, especially in pulse-reserve systems, where conditions can abruptly change in an instant [10].

Although no plants are present in the studied soils, the presence of fungal functions as plant pathogens (Figure 5b) suggests that these fungi may still play a role in breaking down organic matter [57]. The presence of filamentous mycelium suggests that fungi are likely forming extensive networks, which enhance nutrient absorption and decomposition processes within the soil. Fungal mycelium can create microhabitats that support bacterial growth by providing moisture and nutrients, while bacteria can help decompose organic matter more efficiently when associated with fungal partners [34,43]. In this sense, the interactions between bacterial and fungal communities can enhance overall ecosystem functioning [58].

Certain functional groups in fungi exhibited changes over time. For example, the increase in the variety of decay substrates and the presence of aquatic fungi during the intermediate stages highlight a shift in fungal community dynamics as conditions evolve (Figure 4b). This indicates a response to changing moisture levels or organic matter availability. This, along with the simultaneous rise of fungi with filamentous mycelium, suggests that as microbial communities mature, they may begin to explore and exploit new niches or resources that become available due to changes in environmental conditions or interactions with other microorganisms [15].

The presence of these functions in this analysis, however, only indicates their potential, not actual functional activity, as these data are annotations associated with a specific taxonomic group. Nonetheless, the relationship between functional potential and microbial taxonomic composition can inform us about functional stability, which is particularly important in light of current climatic trends [59,60]. Altogether, the results suggest that fungal communities at each timepoint may be more specialized, less functionally stable, and possibly more fragile and sensitive to environmental conditions than bacterial communities (Figures 6b and S3). This pattern has been observed in recent studies [61–63], where fungi resulted to have less taxonomic richness than bacterial communities, allowing them to form unique communities and highly specialized ecological networks for each niche, but consequently causing them to have less adaptability to changing environments.

The fact that we are learning how fragile fungal communities in arid and hyperarid soils are to these infrequent pulse precipitation events is of the highest importance in the face of climate change [64]. Fungi can produce a wide variety of extracellular enzymes that enable them to decompose

various types of organic matter, regulating carbon and nutrient balance in the soil, an especially vital process in environments where organic matter is scarce [65]. Fungi also contribute to soil structure formation by creating networks of mycelium that bind soil particles together. This process enhances soil stability and improves water retention capabilities, which is critical in hyperarid regions where moisture is limited. Additionally, it creates habitats for other microorganisms, promoting biodiversity within the soil ecosystem [34,43,65]. Moreover, deserts are among the largest carbon sinks on the planet [66,67], making carbon management a crucial aspect of soil conservation. These results reinforce the crucial role of soil microbial communities in arid and hyperarid ecosystems, particularly in carbon and nitrogen cycling, as well as overall soil health.

In conclusion, soil microbial communities of the Atacama Desert exhibit dynamic responses to precipitation pulses. Bacterial communities, dominated by Actinobacteria and Proteobacteria, show temporal shifts in relative abundance patterns, with Proteobacteria increasing over time. Fungal communities, primarily composed of Ascomycota, exhibit greater variation, with shifts in many functional groups occurring in response to changes in water and nutrient availability during the pulse. Both bacteria and fungi play crucial roles in nutrient cycling, decomposition, and the formation of soil structure. However, fungal communities may be more sensitive to environmental changes. Understanding the intricate interactions between these microbial groups is crucial to comprehend the resilience and functioning of arid ecosystems, particularly in the face of climate change.

Supplementary Materials: The following supporting information can be downloaded at the website of this paper posted on Preprints.org. Figure S1: CCA to assess the effect of environmental factors on community composition; Figure S2: Relative contribution of fungal genera to the main functional guilds; Figure S3: Relationship between functional richness and taxonomic richness; Table S1: Summary of Canonical Correspondence Analysis (CCA) and PERMANOVA results.

Author Contributions: Conceptualization, Marlene Manzano and Fernando Alfaro; Data curation, María del Pilar Fernandez-Murillo; Formal analysis, Antonia Beggs and María del Pilar Fernandez-Murillo; Funding acquisition, Fernando Alfaro; Investigation, Antonia Beggs, María del Pilar Fernandez-Murillo and Marlene Manzano; Methodology, Marlene Manzano and Fernando Alfaro; Project administration, Fernando Alfaro; Resources, Fernando Alfaro; Software, María del Pilar Fernandez-Murillo; Supervision, Fernando Alfaro; Validation, Antonia Beggs and María del Pilar Fernandez-Murillo; Visualization, Antonia Beggs and María del Pilar Fernandez-Murillo; Writing – original draft, Antonia Beggs; Writing – review & editing, Cameron Wagg and Jean-Baptiste Ramond. All authors have read and agreed to the published version of the manuscript.

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