Biogeochemical cycles and health implications potentially mediated by active dust-borne bacteria

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Abstract

Understanding microbial migration and survival mechanisms in dust events can elucidate genetic and metabolic exchange between environments and help predict the atmospheric pathways of ecological and health-related microbial stressors. Dust-borne microbial communities have been previously characterized, but the impact of active bacteria within transported communities remains limited. Here, we analyzed samples collected during dust events in Israel, using amplicon sequencing of the 16S rRNA genes and transcripts. Different air trajectories and wind speeds were associated not only with microbial community composition variations but also with those of active bacteria. Active dust-borne bacteria exhibited positive interactions, including highly active carbon and nitrogen cycling bacteria, potential degraders of heavy metals and organic compounds, biofilm-forming, and pathogenic bacteria. This study provides insights into the potential interactive relationships and survival of active microorganisms within the extreme dust environment.

Introduction

Airborne microorganisms disperse across continents and oceans, facilitating genomic and metabolic exchanges across different ecosystems. Moreover, they can significantly impact not only aquatic, atmospheric and terrestrial ecosystems, but also human health (Risely*et al.* 2018; Lang-Yona *et al.* 2020; Gat *et al.*2021). Extensive research has focused on dust-borne microbial diversity including bacteria, eukaryotes, archaea, and viruses (Aalismail *et al.* 2019), with the majority of bacterial group, with predominance of Actinobacteriota, Bacteroidota, Firmicutes and Proteobacteria (Aalismail*et al.* 2019; Elmassry *et al.* 2020; Gat *et al.* 2021; Erkorkmaz *et al.* 2023). *Bacillus* species were detected in Asian dust events and in several East Asian countries (An *et al.*2013; Maki *et al.* 2014), and are known for spore-forming, which provide protection and enabling long-distance atmospheric transport (Wainwright *et al.* 2003a; Griffin 2004; An *et al.* 2013).

Dust storms facilitate extensive transport of microbiota across vast distances, subjecting them to harsh conditions (Goudie *et al.*2006). Therefore, both viable and non-viable microorganisms are present within the dust-transported microbiota. Distinguishing between active and inactive microbes offers meaningful ecological insights into microbial survival strategies and their interactions with the dust environment (Schuerger *et al.* 2006). A few studies have utilized ribosomal RNA (rRNA) sequencing to characterize the active airborne bacterial community (Blazewicz *et al.* 2013; Šantl-Temkiv *et al.* 2018; Erkorkmaz *et al.* 2023), focusing primarily on the active microbial community structure in relation to environmental factors such as air mass origination, atmospheric particulate matter (<10 μm; PM10), and particle-size (Erkorkmaz *et al.*2023). However, the potential influence of geochemical elemental cycles (e.g., carbon, nitrogen and sulfur) and the possible interaction mechanism within microbial communities remained elusive. Exploring these aspects could provide valuable insights into the survival and transportation of active microorganisms within the challenging dust macro-environment. Furthermore, it may provide deeper understanding of the impact of the dust microbiome on global biogeochemical cycles.

In this study we investigate dust-borne bacterial communities by utilizing high-throughput amplicon sequencing of the rRNA gene and transcript to characterize these communities and construct a preliminary understanding of elemental cycles and microbial interactions among the active dust-borne microorganisms. This research shed light on their survival strategies and transportation in dust events.

Materials and Methods

Sampling. Dust event (DE) samples were collected during March and April of 2022. Before sampling, 30-seconds blank sample was taken to ensure proper sampling and check for any contaminations. Air samples were collected on a sterile single-packed filter (S-Pac, Millipore, Massachusetts, US) at 14 L/min for ˜6-6.5 hours, during both day and night (Table 1). The samples were stored at -80 for nucleic acid extraction.

Meteorological conditions and backward trajectory analyses. Data on wind speed, direction, temperature, and relative humidity were obtained from a nearby station (https://ims.gov.il/en). The origin of sampled dust was determined by calculating back trajectories using the hybrid single-particle Lagrangian integrated trajectory model (HYSPLIT; https://www.ready.noaa.gov/HYSPLIT_traj.php). Each back trajectory was computed for 48 hours at three different altitudes (50, 100, and 500 meters above ground level).

DNA/RNA extraction, amplification, and sequencing. The DNA/RNA extraction was performed using the ZymoBIOMICS DNA/RNA Kit (Zymo research, California, US), utilized with high-yield improvements according manufacturer protocols. The DNA extracts were stored at -80 °C, while RNA were promptly utilized for complementary DNA (cDNA) synthesis. The remaining RNA was kept at -80 °C. For cDNA synthesis, the Qiagen's QuantiTect Reverse Transcription Kit (Cat #: 205313, Hilden, Germany) was employed. The total cDNA reaction of 20 µL consisted of 1x reverse transcription (RT) enzyme, 4 µL of RT mix, 1 µL of random primer mix, and 5 µL of RNA extract. Thermocycling was performed using the MiniAmp Plus Thermocycler (Applied Biosystems, Thermo Fisher Scientific, Massachusetts, US). The thermocycling program included 25.0°C for 3 min, 45°C for 10 min, 85°C for 5 min, and 10°C until the process was terminated. The cDNA samples were stored at -20°C for subsequent analysis.

The bacterial 16S rRNA gene and 16S rRNA were amplified using the primers CS1 515F - CS2 926R targeting the biodiversity and active community compositions (Walters *et al.* 2016). The amplification was performed in a 25 µL reaction volume containing a polymerase mix of 12.5 µL, 400 nM of each primer, 5 µL of DNA/cDNA template, and water. The cycling program consisted of an initial denaturation step at 95.0ºC for 1 min, 30 cycles of 95ºC for 15 sec, 55ºC for 15 sec, 72ºC for 10 sec, and a final extension at 72ºC for 10 min. PCR products were verified on 1% agarose gel, and the triplicates were pooled. Gel visualization was performed using a ChemiDOC^{TM} MP Imaging System (BioRad, California, US).

High-throughput sequencing and taxonomic analysis. High-throughput sequencing was conducted at the at the Technion - Israel Institute of Technology, Haifa, using the Illumina Miniseq platform, with a sequencing depth of 100 kbp per sample. Sequences analysis was performed using QIIME2. Raw data from each sample were introduced into QIIME2 for quality control following the standard procedure (Bolyen*et al.* 2019). Specifically, raw sequences were denoised and filtered for invalid reads, mitochondrial sequences, and chloroplast sequences contamination using the software packages DADA2 (Callahan*et al.* 2016) and Deblur (Hanshew *et al.* 2013; Rowan-Nash*et al.* 2019). After quality control, taxonomic assignment of the amplicon sequence variants (ASVs) was performed using dada2 against the SILVA 138.1 reference database (Quast*et al.* 2012). Biodiversity was assessed using Chao1, Abundance-based Coverage Estimator (ACE), Shannon, and Simpson indices, as well as principal component analysis (PCoA) were calculated using the Vegan package after normalizing the sequence number of the 16S rRNA gene. Statistical significance between groups was calculated using Permutational multivariate analysis of variance (PERMANOVA). Venn diagram was contracted using the ggvenn package. The sequence data has been deposited in the NCBI GenBank Database under the accession number: PRJNA982604.

Network construction of active microorganisms. The interactions within the core dust microbial communities were investigated using a network of the active microorganisms by calculating Spearman correlation coefficients between genera (Barberán *et al.* 2012; Varsadiya*et al.* 2021). Microorganisms from the top five

phyla were merged at the genus level, as pre-determined from 16S rRNA result. A two-by-two correlation matrix (Table S3) was generated using the "Hmisc" package in R (Varsadiya *et al.* 2021). The false discovery rate (FDR) controlling procedure was used to calculate p -values, and the Benjamini-Hochberg method was applied for correction (Benjamini & Hochberg 2018). Correlation coefficients with an absolute value of 0.6 or greater, or -0.6 or less was defined as the cut-off for a meaningful co-occurrence network, with p -values < 0.01. Network visualizations were generated using the "igraph" package in R (Csárdi & Nepusz 2006). In the undirected network, nodes represent genera and edges represent correlations between nodes.

Results

The microbial communities from three different dust storms (during both day and nighttime) were analyzed for co-existence, and biogeochemical contributions of active dust-borne microorganisms.

Environmental Variables.

Substantial day-night fluctuations in relative humidity (RH) and temperature were observed during the dust events (Table 1). These factors are known to influence the viability of microbial communities (Aarnink *et al.* 2015; Dannemiller *et al.* 2017; Haines*et al.* 2020). Daytime events exhibited lower RH levels than nighttime. It has been shown that bacteria can endure and travel within 40-80% RH range (Aarnink *et al.* 2015), indicating conducive environmental conditions during the sampled dust-events for their survival and migration (Table 1).

Table 1 also shows the favorable temperature range (within 10-30) for long-distance microorganism survival (Aarnink *et al.* 2015), supporting microbial translocation with the dust events. Notably, DE-II displayed significant daytime-nighttime wind speed difference (7.78 m/s*vs.* 3.38 m/s, respectively). Wind speed has been linked with dust generation and bacteria transportation (Fujiyoshi *et al.* 2017; Ulrich 2021; Sorkheh *et al.* 2022; Erkorkmaz *et al.* 2023), possibly explaining the observed microbial composition variation during this event.

The distinct origins of the three dust events were revealed by air-mass backward trajectories (Fig. S1). On March 29, 2022, the air mass mainly originated from the mainland (DE-I_D & N). On April 6, 2022, it crossed the Mediterranean Sea from west to south and reached Haifa (DE-II_D & N). On April 25, 2022, the air mass primarily originated from the northwest (DE-III_D & N). Interestingly, DE-III_D had a mixed origin, with inland source at 500 meters above ground (Fig. S1).

Dust-borne microbial community characterization. Each dust sample yielded at least 1893 high-quality ASVs in 16S rRNA gene and 1667 in 16S rRNA. In DE-I and III, daytime samples displayed lower biodiversity compared to the nighttime, whereas in DE-II, daytime samples presented higher biodiversity (Table 1). However, based on PCoA and PERMANOVA analysis showed no significant differences in beta-diversity among events (Fig. 1A). The Venn diagram revealed three core ASVs shared among the six groups (Fig. 1B). However, the shared microorganisms were closely associated with the dust origin. For example, DE-II and III daytime samples shared 44 core ASVs (Table S1), accounting for 20.21% and 10.23% of the microbial communities, respectively. This aligns with air mass back trajectories of these events (Fig. S1), indicating a significant exposure of the air-mass to Mediterranean Sea environment, likely leading to shared microorganisms, including those associated with the marine environment (e.g.,*Prochlorococcus* sp.). The remaining microbial composition differences may stem from the additional east origins of DE-III air-mass.

The relative abundance was calculated by averaging the ASVs of two sequenced sample replicates. The airborne bacterial populations analyzed from the 16S rRNA gene were composed of several bacterial types (Table S1 and Fig. 1). The predominant ASVs identified in the dust samples belonged to the phyla Proteobacteria, Bacteroidota, and Actinobacteriota. Cyanobacteria and Firmicutes, common in marine and terrestrial environments, were also detected in the dust samples with some variation. Specifically, Proteobacteria accounted for 90% and 80% in DE-II and III daytime samples, reducing to 79 and 63% during daytime, respectively. In contrast, the trend was opposite in DE-I. (Fig. 1C). Predominant taxonomic groups within Proteobacteria included Comamonadaceae (13.10% in DE-I_D, 28.55% in DE-II_N),*Pseudoalteromonas* (22.66 % in DE-II_-

D), *Alteromonas*(9.07 % in DE-I_N, 31.93% in DE-II_D, 15.50 % in DE-III_D) and*Sphingomonas* (7.97% in DE-II_D, 14.12% in DE-II_N, 20.18% in DE-III_D, 3.54 % in DE-III_N). These genera are common in marine environments, aligning with back trajectory analysis indicating Mediterranean Sea influence (Fig. S1). Bacteroidota emerged as the second dominant phylum in all three night sampling events, (11.65% in DE-I_N, 16.84% in DE-II_N, 11.71 % in DE-III_N), in contrast to the lower values in daytime samples (3% in DE-II_D, 6% in DE-III_D) compared to nighttime samples (16.84% and 11.71% in DE-II_N and III_N). Actinobacteriota constituted 21.13% of the microbial composition in DE-I_D samples, but less than 10% in other samples, except DE-III_N (12%).

Table S4 shows that the dominant family in DE-I_D was Comamonadaceae (13.10%), while in DE-I_N it was only 1.69%. In DE-II and III daytime samples, *Alteromonas* (31.93% in DE-II) and *Sphingomonas*(20.18% in DE-III), were the dominant microorganisms, which are common marine microorganisms (Yoon *et al.* 2003; Romanenko *et al.*2007). Conversely, nighttime samples were primarily dominated by Comamonadaceae (28.55% in DE-II) and Frankiales (6.48% in DE-III).

Bioactive dust-borne microbial community. To investigate the core active microbial community within dust events, we further analyzed the 16S rRNA (Table S2). In general, Proteobacteria dominated the 16S rRNA libraries, which reflects its likely abundance as an active phylum in the dust samples (Fig.2A). The abundance of other active microbial groups was less consistent compared to the 16S rRNA gene library. For example, DE-I_D samples had a higher abundance of active Firmicutes, Cyanobacteria and Actinobacteriota than Bacteroidota. In DE-I_N night sample, active Actinobacteriota and Firmicutes also exceeds Bacteroidota, but there was an abrupt increase in the abundance of active Cyanobacteria. This may be attributed to the nighttime short air path through the Mediterranean Sea (Fig. S1). In DE-II, active microorganisms were consistent with 16S rRNA gene results, but active Bacteroidota was less abundant in night samples of this dust event, despite its higher abundance in the 16S rRNA gene results. In DE-III daytime samples the active microorganisms were primarily clustered within Bacteroidota, Actinobacteriota and Firmicutes, with a relatively lower abundance of Proteobacteria. Specifically, Actinobacteriota and Firmicutes displayed relatively high activity, compared to a relatively low abundance of Actinobacteriota and Firmicutes in DE-III_D 16S rRNA gene results (Fig. 2A). In contrast, night samples showed no significant variation.

Genus-level analysis shows diverse abundances of microorganisms within and between dust events (Fig. 2B). In DE-I daytime,*Staphylococcus, Chroococcidiopsis* and *Cutibacterium*exhibited relative abundances > 5%, followed by*Actinetobacter* , *Corynebacterium* and*Methylobacterium* with > 2% relative abundance. DE-I nighttime had highly active *Oleibacter* , *Hymenobacter* ,*Chroococcidiopsis* , *Bergeyella* , *Staphylococcus* (2 – 5% relative abundance). Interestingly, in DE-II active*Oleibacter* also displayed high abundance during daytime (24.13%), however this dynamic shifted during nighttime, where*Alteromonas* became the prevailing active microorganism (13.33%). In DE-III, *Bacillus* emerges as the predominant active microorganism (6.02%), with night samples dominated again by*Alteromonas* (14.26%). These findings collectively suggest varying active microbial compositions in different dust events.

Potential survival strategies of active dust-borne microorganisms. Adaptation strategies of microorganisms for surviving harsh conditions include mutual feeding and the formation of protective measures against environmental stressors (Haruta & Kanno 2015; Yin*et al.* 2019; Thakur *et al.* 2022). Notably, such interactions appear to be prevalent within the core active microorganism communities of the sampled dust events (Fig. 2C). The cycling of essential elements, such as carbon and nitrogen, play a crucial role in the survival of microorganisms in unfavorable environments (Yan *et al.* 2008; Bollmann *et al.* 2013; Aasfar *et al.* 2021; Jawaharraj *et al.* 2021; Sahoo *et al.* 2021; Aronson*et al.* 2023). Our analysis revealed the presence of highly active microorganisms engaged in carbon and nitrogen metabolism, suggesting a positive element cycle within the community. *Methylobacterium* ,*Geodermatophilus* , *Bacillus* and *Dietzia* contribute to carbon availability through organic compound biodegradation (Zhang*et al.* 2013; Yoshikawa *et al.* 2017; Venil *et al.*2021; Kong *et al.* 2022; Sandhu *et al.* 2022; Yao *et al.* 2022). *Pseudomonas* exhibited metabolic activity across all samples, suggesting active heterotrophic nitrification and aerobic denitrification processes over the

dust particulates (Zhang *et al.* 2022). Additionally, the highly active *Corynebacterium* ,*Mucilaginibacter* and *Acinetobacter* convert inorganic nitrogen compounds into ammonia and nitrate (Madhaiyan *et al.*2010; Lee *et al.* 2016; Shelly *et al.* 2021; Amrutha & Nampoothiri 2022), providing a stable nitrogen source for the microbial community.

Biodegradation potential of microorganisms carried over dust particles. High levels of dust particles can lead to adverse health effects associated with the presence of heavy metals, organic pollutant particles and harmful minerals carried in the wind during dust events (Liu *et al.* 2004; Tian *et al.* 2019; Aili *et al.*2022). Microorganisms possessing the ability to transform and utilize these pollutants might have the advantages of thriving in polluted dust events. Our 16S rRNA analysis revealed pollutant-degrading genera, including *Comamonas* (Lu *et al.* 2022), *Sphingomonas*(Zhou *et al.* 2022), *Comamonadaceae* (Fahy *et al.*2006) and *Acinetobacter* (Tesso *et al.* 2019) in Proteobacteria, as well as *Hymenobacter* (Guo *et al.* 2020) and *Frankiales* (Wang *et al.* 2021) in Bacteroidota, and*Bacillus* (Ikram *et al.* 2022) in Firmicutes. These microorganisms have the potential to degrade a wide range of organic pollutants.

The genus *Staphylococcus* demonstrated consistent activity across all samples (Fig. 2B) and its close interactions with other genera (Fig. 2C) suggests its key role in dust-borne community. Different*Staphylococcus* species are known for their tolerance to high salt concentrations and arid conditions, enabling their survival and long-distance traveling during dust events (Tsai *et al.* 2011; Kozajda *et al.* 2019; Feng *et al.* 2022). Additionally, certain *Staphylococcus* species can induce quorum sensing (Lyon & Novick 2004; Otto 2009), promoting inter-bacterial communication and collaboration through signaling molecules, supporting coexisting bacterial adaptation in unstable environments (Gobbetti *et al.*2007; Novick & Geisinger 2008). Moreover, *Staphylococcus* species (Hou *et al.* 2018), along with *Cutibacterium* ,*Bacillus* , and *Paenibacillus* (Timmusk *et al.* 2019; Arnaouteli *et al.* 2021; Coenye *et al.* 2022), have been found to release extracellular polymeric substances, supporting biofilm formation, nutrient supply, and attachment in the community.

Discussion

In this study we aimed to explore the active microbial communities within dust events, to better understand their traits in the environment and to human and the ecology.

Our result illustrates that distinct trajectories and wind speeds induce significant variations in microbial composition of active microbiota. This is in correspondence with previous studies exploring these effects on the metagenomic community composition (Gat *et al.* 2017).

Diurnal shifts in biodiversity patterns were observed and are likely due to air-mass exposure to the Mediterranean Sea environment. There is relatively little research on diurnal shifts in bioaerosols, with Saari et al (2015) utilizing fluorescent technology to monitor their concentration variations between day and night (Saari *et al.*2015), Hu et al (2020) exploring diurnal pathogens diversity in the urban environment (Hu *et al.* 2020), and Gusareva et al (2019) exploring variations in airborne community composition showing a robust diurnal repetitive dynamics in the tropical air ecosystem (Gusareva*et al.* 2019). To the best of our knowledge, diurnal variations in microbial composition have not been explored in dust events to date and may allow a better understanding of the dynamics of the microbial migration along the dust transport.

Investigating active microorganisms allows exploring interactions between different active communities. These interactions encompass collaborative metabolic processes such as carbon and nitrogen metabolism, the degradation of organic compounds and heavy metals, and the promotion of microbial biofilm formation through quorum sensing. Other studies have explored dust contribution to nutrient cycles such as N_2 fixation through diazotrophs in dust (Rahav *et al.* 2016; Rahav *et al.* 2018). Our findings not only shed light on the potential survival strategies of active microorganisms during dust events but also uncover their inherent ability for active genetic and metabolic exchanges across various ecosystems.

Prolonged exposure to airborne dust particles can result in various health issues, including conjunctivitis, meningitis, and coccidioidomycosis (Aghababaeian *et al.* 2021). Nevertheless, the causing factors are not fully understood. While a range of potential pathogenic microorganisms have been identified during dust

events, their viability remains unknown.

Of particular note is *Staphylococcus* , consistently detected in nearly all samples, suggesting its widespread presence during dust events. This species reported to be abundant (Kakikawa *et al.*2008) and active (White *et al.* 2020) in other dust events. Beyond its activity in the microenvironment, certain *Staphylococcus*species are associated with human pathogens (Balasubramanian *et al.* 2017; Vestergaard *et al.* 2019), that could induce dust-associated health effects.

Another key genus in our dust samples was the spore-forming*Bacillus* , which includes potential traits such as biomineralization (Keren-Paz *et al.* 2022), biofilm formation (Ma*et al.* 2017), and toxicity (Azarkar & Zare Bidaki 2016). Other studies have managed to detect and isolate *Bacillus* species in dust and other high-altitude samples, and it is hypothesized that their survival is due to sporulation abilities (Wainwright *et al.*2003b; Griffin 2004; Yoo *et al.* 2019).

In conclusion, our findings demonstrate positive interactions among active dust-borne microorganisms, facilitating element cycling, pollutant degradation, and biofilms formation. These interactions likely play a vital role in microorganism survival and adaptation in the challenging dust environment, while also potentially influencing broader phenomena like biogeochemical cycling and implications for human health. Further exploration could shed light on microbial resilience and adaptation in extreme environments and may pave the way for novel insights into the broader implications of these versatile microorganisms.

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Figure captions

Figure 1. Abundance of Bacterial Phyla in Dust Samples. (A) Principal coordinate analysis of dust samples collected during three dust events using Weighted UniFrac metrics. **(B)** Venn diagram illustrating the shared microbes Amongst the sampled dust events. Both day (_D) and night (_N) samples are analyzed. **(C)** The top 13 abundant phyla, ranked by average abundance, as represented in percentages for each dust sample.

Figure 2. Abundance and interactions of active dust-borne bacteria. (**A**) Comparison of abundances of the top five phyla in dust events based on 16S rRNA gene (DNA) and 16S rRNA (cDNA) libraries. (**B**) Heatmap presenting the predominant active genera within the top five phyla. (**C**) Visualization of the interactions between different genera of the microbial community.

Figure 1.

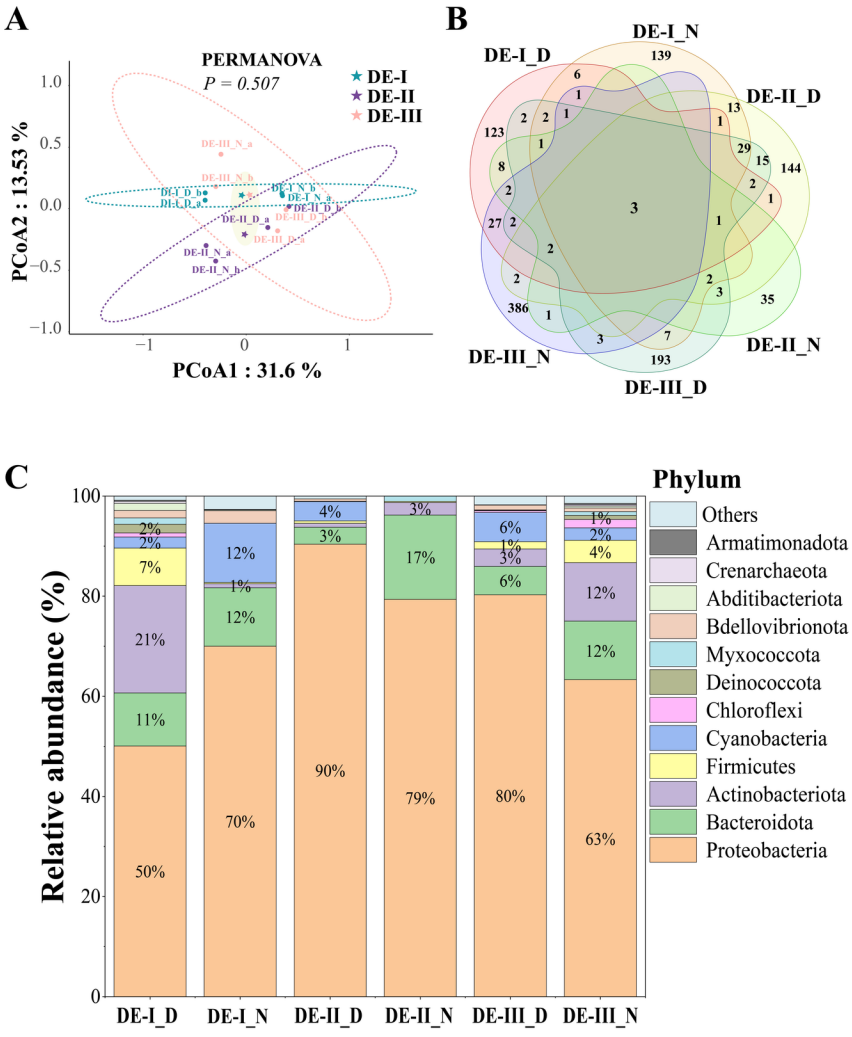
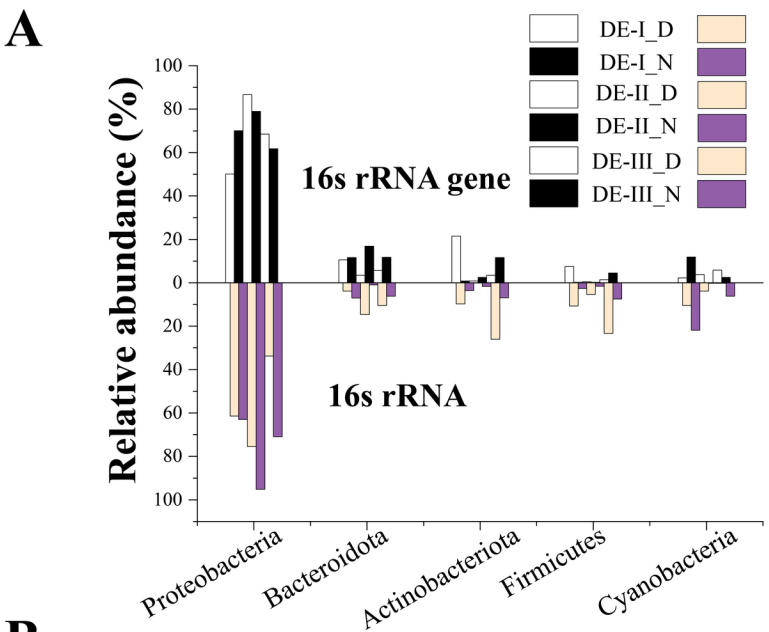
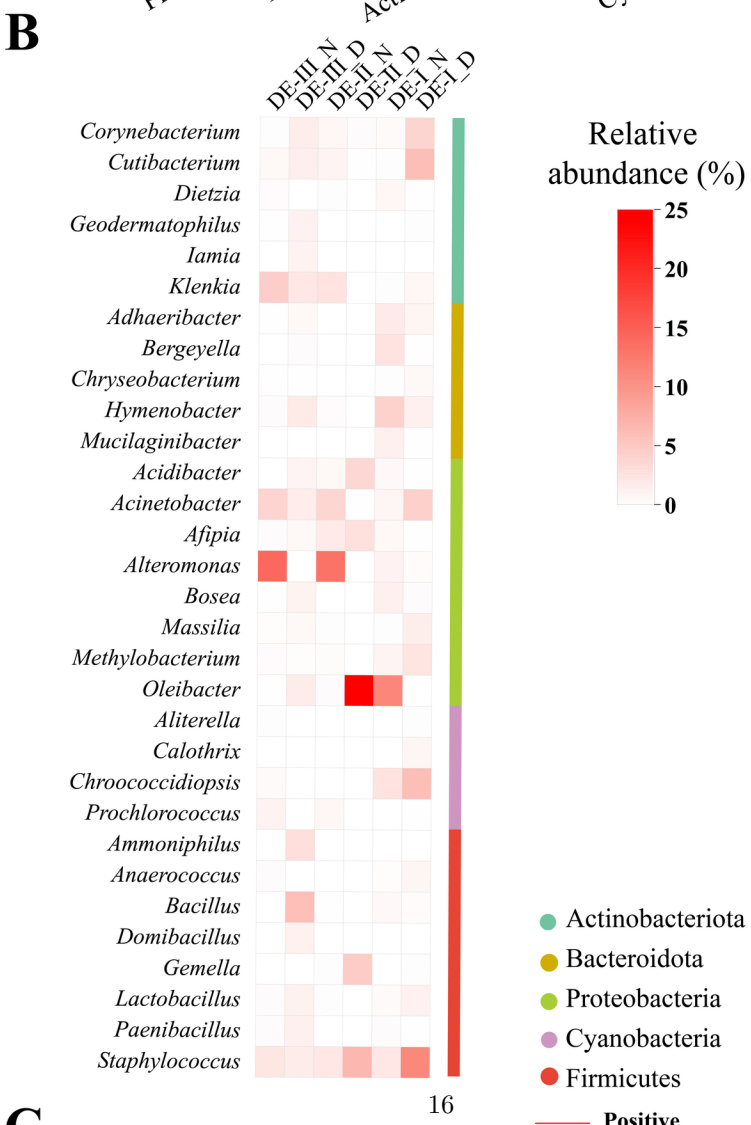


Figure 2.





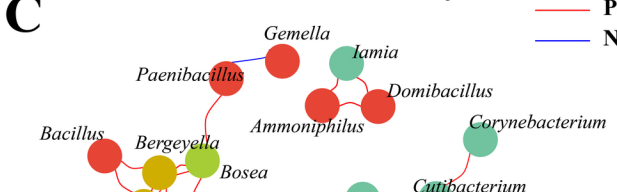


Table 1. Sampling parameters, meteorological conditions, and dust microbiome diversity parameters during sampled dust events. The relative humidity (RH), temperature, wind speed and directions, as well as air sampling time, duration and rate are denoted. The different ∝-diversity values (Observe ASVs, Chao1, Abundance-based Coverage Estimator; ACE, Shannon, Simpson) are listed per the different samples.

Sample ID	Sampling date	Sampling times (UTC+2)	Sampling duration (h)	Flow rates (L min^{-1})	Air volume (m^3)	RH (%)	Temperature (°C)	Wind speed (ms^{-1})	Wind direction(°)	Observe ASVs	Chao1	ACE	Sha
Blank I	29-Mar-2022	11:40	0.008	14.00	0.007	26.15	22.22	4.63	122.87	-	-	-	-
DE-I_D_a	29-Mar-2022	11:45 - 18:00	6.25	14.00	5.25	26.15	22.22	4.63	122.87	82	89.80	89.53	3.83
DE-I_D_b										88	91.06	93.75	3.79
DE-I_N_a	30-Mar-2022	0:00 - 6:00	6.00	14.00	5.04	55.05	16.75	5.08	166.57	111	126.40	124.28	4.11
DE-I_N_b										116	134.00	136.21	4.04
Blank II	06-Apr-2022	10:55	0.008	14.00	0.007	61.41	20.63	7.78	244.08	-	-	-	-
DE-II_D_a	06-Apr-2022	11:00 - 17:00	6.00	14.00	5.04	61.41	20.63	7.78	244.08	79	100.43	103.95	3.06
DE-II_D_b										132	142.34	148.81	3.83
DE-II_N_a	07-Apr-2022	0:00 - 06:00	6.00	14.00	5.04	88.62	15.06	3.38	213.16	22	22.00	22.00	2.46
DE-II_N_b										43	43.25	43.69	2.86
Blank III	25-Apr-2022	10:55	0.008	14.00	0.007	50.51	25.57	2.05	127.22	-	-	-	-
DE-III_-D_a	25-Apr-2022	11:00 - 17:00	6.00	14.00	5.04	50.51	25.57	2.05	127.22	125	136.81	145.21	3.18
DE-III_-D_b										168	201.44	197.15	4.02

Sample ID	Sampling date	Sampling times (UTC+2)	Sampling duration (h)	Flow rates (L min^{-1})	Air volume (m^3)	RH (%)	Temperature (°C)	Wind speed (ms^{-1})	Wind direction(°)	Observe ASVs	Chao1	ACE	Sha
DE-III_-N_a	26-Apr-2022	0:00 - 06:00	6.00	14.00	5.04	45.92	18.42	1.26	231.81	98	98	98.28	4.22
DE-III_-N_b										294	337.33	329.75	5.35