Supplementary Materials

Fig. S1 Airborne bacteria in the northern, central, and southern areas of Mexico City during 2017

Fig. S2 Bacterial in the atmosphere of Mexico City during the dry and rainy season of 2017

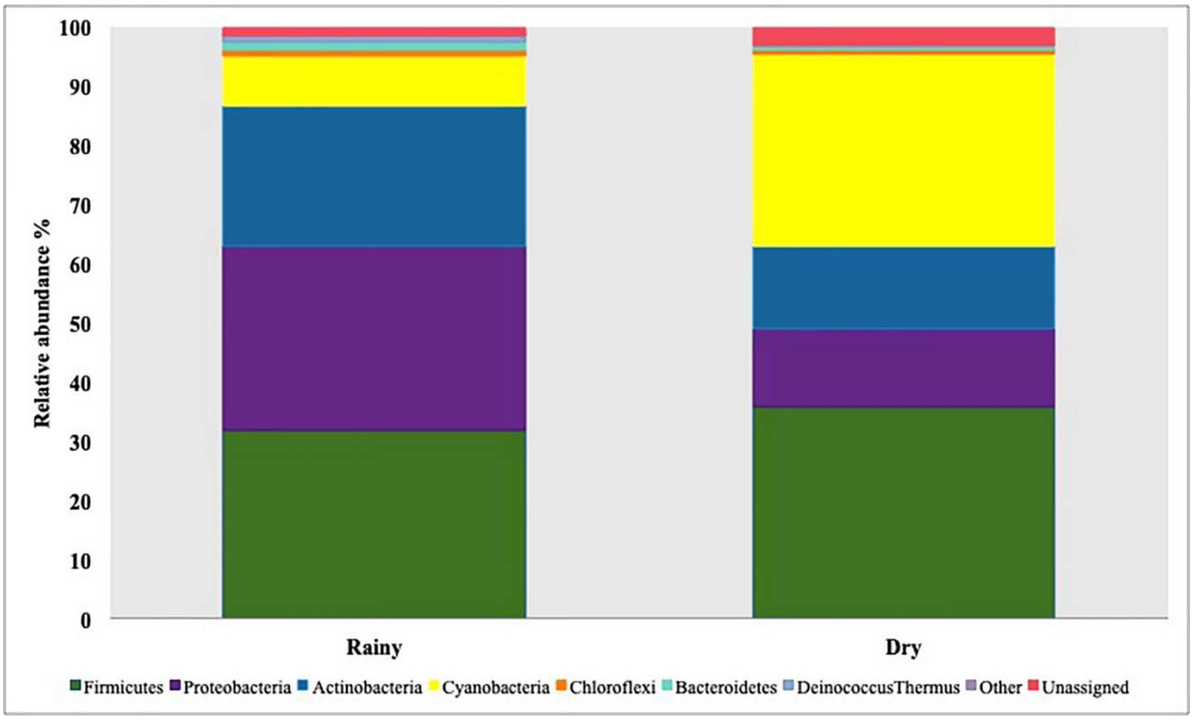


Fig. S3 Relative abundance of the main airborne bacterial phyla during the dry season and the rainy season in Mexico City

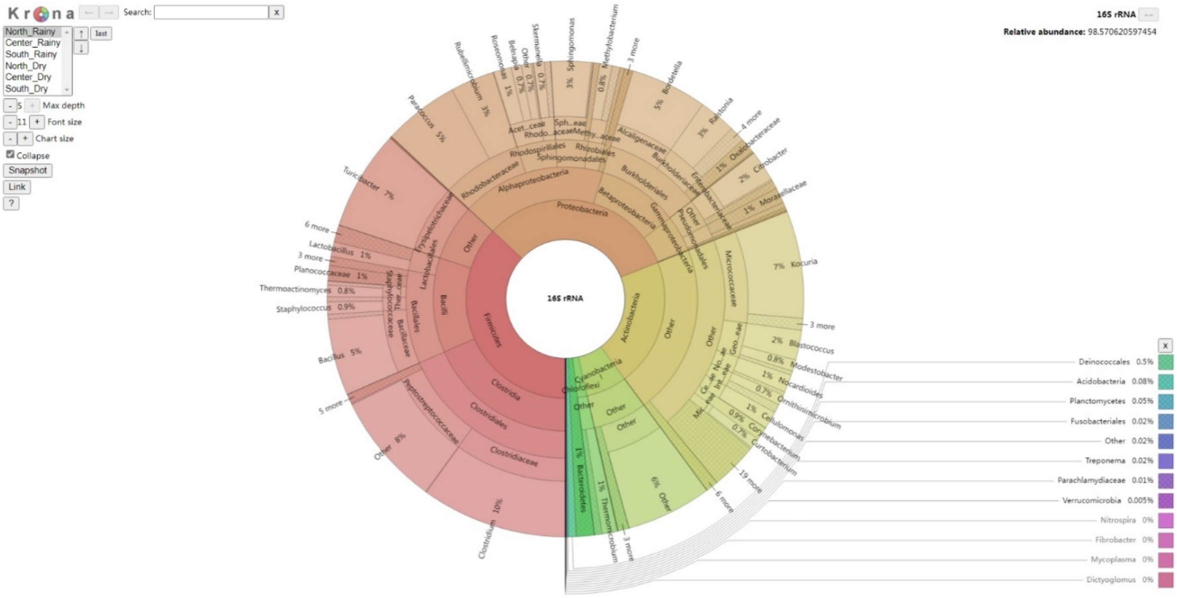


Fig. S4 Airborne bacteria by zone and season of the year in the atmosphere of Mexico City during 2017

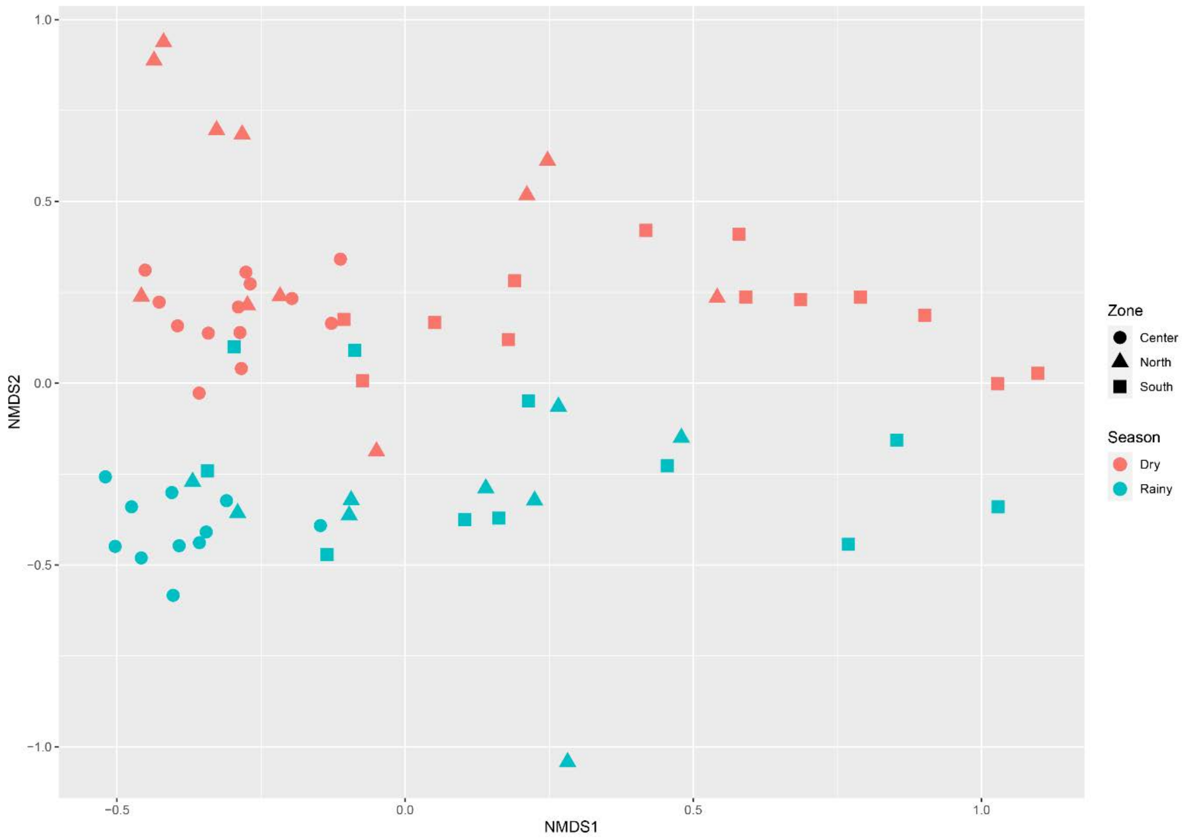
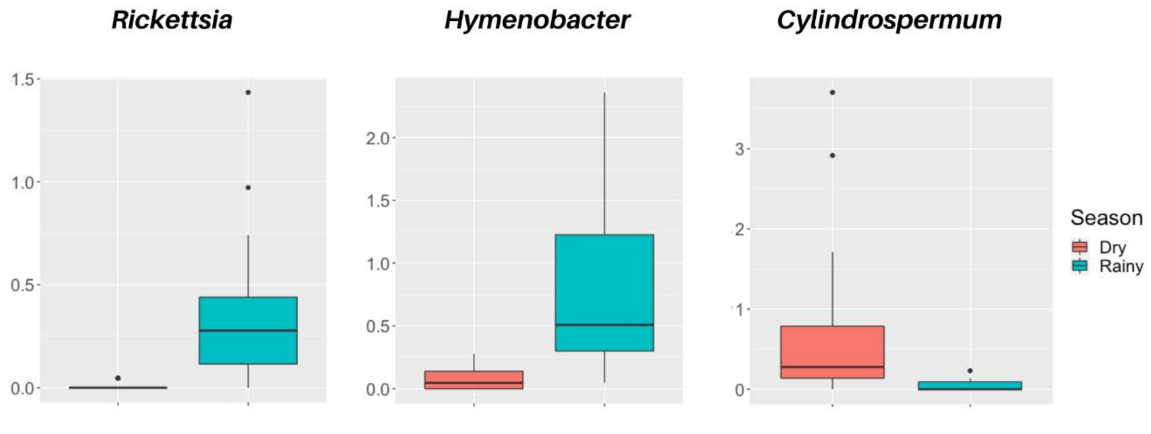


Fig. S5 Non-metric dimensional analysis (NMDS) at the class level of the Bray-Curtis distances



Rickettsia

Hymenobacter

Cylindrospermum

Fig. S6 Relative abundance of indicator taxa from bioaerosols collected in Mexico City. *Rickettsia* and *Hymenobacter* were found in the rainy season. *Cylindrospermun* (Cyanobacteria) was present in the dry season

Table S1 Taxa with more than 1% relative abundance and significative differences ($p<0.001$) in bioaerosols from different zones in Mexico City, determined with the Kruskal-Wallis test

	Relative abundance (%)						Post hoc Dunn test		
	Centre		North		South		p value		
Taxa	Rainy	Dry	Rainy	Dry	Rainy	Dry	CD vs CR	ND vs NR	SD vs SR
Kocuria❖1)	18.49	8.16	7.74	4.30	5.20	1.18	0.010^{**}	1.000	0.021^{*}
Paracoccus❖2)	8.20	3.69	4.88	2.31	3.16	1.15	0.002^{**}	0.018^{*}	0.004^{**}
*Blastococcus*1)	2.39	1.57	1.94	0.92	1.48	0.53	0.020^{*}	0.017^{*}	0.014^{*}
*Acetobacteraceae*2)	1.40	1.20	0.68	0.56	0.84	0.39	0.333	0.502	0.084
Roseomonas❖2)	1.88	0.76	1.12	0.43	0.96	0.34	0.0004^{**}	0.014^{*}	0.007^{**}
*Arthrobacter*1)	1.10	0.58	0.53	0.29	0.52	0.16	0.023^{*}	0.109	0.032^{*}
Nocardioides❖1)	1.12	1.26	1.17	0.64	0.70	0.40	0.656	0.048^{*}	0.203
Staphylococcus❖3)	0.68	0.63	0.81	0.40	0.53	0.12	0.804	0.013^{*}	0.029^{*}
Acinetobacter❖4)	0.79	0.59	0.50	0.43	0.31	0.14	0.298	0.410	0.108
Corynebacterium❖1)	0.83	1.10	0.88	0.52	0.50	0.15	0.503	0.069	0.040^{*}
*Lactobacillus*3)	0.66	0.61	0.91	0.45	0.58	0.15	0.479	0.031^{*}	0.032^{*}
*Skermanella*2)	1.01	0.98	0.73	0.64	0.38	0.42	0.797	0.530	0.796
*Belnapia*2)	0.81	0.30	0.64	0.33	0.30	0.18	0.002^{**}	0.020^{*}	0.200
Dietzia❖1)	0.79	0.50	0.48	0.29	0.23	0.04	0.173	0.182	0.037^{*}
*Massilia*5)	0.85	0.38	0.56	0.38	0.37	0.09	0.007^{**}	0.152	0.034^{*}
*Phycicoccus*1)	0.69	0.69	0.39	0.35	0.35	0.15	0.977	0.865	0.064
*Thermomicrobium*6)	0.66	0.56	0.96	0.45	0.30	0.21	0.708	0.043^{*}	0.557
Citrobacter❖4)	0.03	0.02	1.88	0.01	0.64	0.00	0.657	0.001^{**}	0.004^{**}

Notes: Post hoc Dunn test * $p < 0.05$ and ** $p < 0.01$; Centre dry (CD), centre rainy (CR), north dry (ND), north rainy (NR), south dry (SD), south rainy (SR). 1) Actinobacteria, 2) Alphaproteobacteria, 3) Bacilli, 4) Gammaproteobacteria, 5) Betaproteobacteria, 6) Chloroflexi. ❖ Bacteria genera with potential anthropopathogenic species. Many of these species act as opportunistic pathogens that mainly affect immunocompromised individuals

Table S2 Relative abundance of taxa (frequently found in faecal microbiome reported in the literature) by zone and season (King et al., 2019)

Taxonomic group		Rainy			Dry		
Family	Genus	North	Centre	South	North	Centre	South
Enterobacteriaceae	*Citrobacter*❖	2.09	0.03	0.64	0.01	0.02	0.00
	Escherichia❖	0.11	0.02	0.01	0.02	0.02	0.01
	Klebsiella❖	0.02	0.01	0.00	0.00	0.00	0.00
	Salmonella❖	0.00	0.00	0.00	0.01	0.00	0.00
Lactobacillaceae	*Lactobacillus*	0.98	0.66	0.58	0.45	0.58	0.15
Streptococcaceae	*Streptococcus*❖	0.27	0.28	0.18	0.24	0.31	0.08
	Lactococcus	0.07	0.09	0.01	0.01	0.04	0.01
Leuconostocaceae	*Leuconostoc*❖	0.02	0.19	0.07	0.03	0.12	0.01
Enterococcaceae	*Enterococcus*❖	0.06	0.03	0.04	0.01	0.04	0.00
Lachnospiraceae	*Blautia*	0.05	0.06	0.05	0.02	0.04	0.01
	Dorea	0.00	0.00	0.00	0.00	0.01	0.00
Bifidobacteriaceae	*Bifidobacterium*	0.05	0.03	0.03	0.03	0.05	0.01
	Gardnerella❖	0.01	0.00	0.00	0.00	0.00	0.00
Ruminococcaceae	*Faecalibacterium*	0.03	0.04	0.04	0.02	0.01	0.00
	Ruminococcus	0.02	0.01	0.01	0.00	0.02	0.01
	Ethanoligenens	0.00	0.00	0.00	0.00	0.01	0.00
Prevotellaceae	*Prevotella*❖	0.01	0.01	0.00	0.03	0.00	0.01
Selenomonadaceae	*Megamonas*	0.02	0.00	0.00	0.01	0.01	0.00
Veillonellaceae	*Megasphaera*	0.01	0.00	0.00	0.00	0.00	0.00
Oscillospiraceae	*Oscillibacter*❖	0.01	0.00	0.00	0.00	0.00	0.01
Bacteroidaceae	*Bacteroides*❖	0.01	0.01	0.01	0.01	0.01	0.00
Coriobacteriaceae	*Collinsella*	0.01	0.00	0.00	0.00	0.00	0.00
Eubacteriaceae	*Eubacterium*	0.00	0.00	0.00	0.00	0.01	0.00
Clostridiaceae	*Butyricicoccus*	0.00	0.00	0.00	0.01	0.00	0.00

Notes: ❖ Bacteria genera with potential anthropopathogenic species. Many of these species act as opportunistic pathogens that mainly affect immunocompromised individuals

Table S3 Relative abundance of taxa with significant differences (p<0.001), according to the Kruskal-Wallis test, in bioaerosols from different zones in Mexico City during the rainy and dry seasons

Annual Season	Taxa	Relative abundance (%)		
		North	Centre	South
Rainy	Cytophagia	0.51A	1.71A	0.55A
	Actinobacteria	20.57A	36.05A	14.64A
	Deinococci	0.51A	1.73A	0.58A4
	Kocuria❖	7.74A	**18.49A**	5.20A
	*Paracoccus**	5.05B	**8.20AB**	3.16A
	Deinococcus	0.46A	**1.67A**	0.53A
	Micrococcus❖	0.25A	**1.08A**	0.15A
	Hymenobacter	0.37A	**1.50A**	0.42A
	Skermanella	0.74B	**1.01A**	0.38AB
	Moraxellaceae	0.13A	**0.74A**	0.16A
	Dietzia❖	0.43B	**0.79AB**	0.23A
	Thermoactinomyces	0.77B	0.19AB	1.02A
Dry	Actinobacteria	12.74B	22.66AB	6.70A
	Cyanobacteria	44.41A	33.77B	19.14AB
	Bacilli	10.59A	11.39A	27.52A
	Clostridia	11.27B	7.01A	20.09AB
	Betaproteobacteria	1.65A	1.30A	8.17A
	Gammaproteobacteria	1.37B	1.88A	0.37AB
	Kocuria❖	4.30B	**8.16AB**	1.18A
	Paracoccus❖	2.31B	**3.69AB**	1.15A
	Oscillatoriales	43.44A	31.87B	18.14AB
	Bacillus❖	5.30A	4.02A	19.30A
	Ralstonia	0.93A	0.46A	7.15A
	Acetobacteraceae	0.56B	1.20AB	0.39A
	Deinococcus	0.12A	0.38A	0.07A
	Micrococcus❖	0.14B	**0.39AB**	0.02A
	Arthrobacter	0.29B	**0.58AB**	0.16A
	Hymenobacter	0.05B	**0.14AB**	0.02A
	Nocardioides❖	0.64B	**1.26AB**	0.40A
	Staphylococcus❖	0.40B	**0.63A**	0.12AB
	Corynebacterium❖	0.52B	**1.10AB**	0.15A
	Lactobacillus	0.45B	**0.61A**	0.15AB
	Moraxellaceae	0.02A	0.10A	0.01A
	Dietzia❖	0.29B	**0.50A**	0.04AB
	Phycicoccus	0.35B	**0.69AB**	0.15A
	Ornithinimicrobium	0.48B	**0.56A**	0.15AB
	Thermoactinomyces❖	0.32B	0.20A	1.50AB

Burkholderiaceae	0.10A	0.12A	0.79A
Sporosarcina	0.47A	0.41A	1.85A

Notes: Post hoc Dunn test; A = $p<0.001$; B = $p<0.05$. ❖ Bacteria genera with potential anthropopathogenic species. Many of these species act as opportunistic pathogens that mainly affect immunocompromised individuals

References

King C H, Desai H, Sylvetsky A C, LoTempio J, Ayanyan S, Carrie J, Crandall K A, Fochtman B C, Gasparyan L, Gulzar N, Howell P, Issa N, Krampis K, Mishra L, Morizono H, Pisegna J R, Rao S, Ren Y, Simonyan V, Smith K, VedBrat S, Yao M D, Mazumder R, Mazumder R (**2019**). Baseline human gut microbiota profile in healthy people and standard reporting template. PloS one, 14(9): e0206484