

**Comparison of Airborne Bacterial Populations Determined by Passive and Active Air  
Sampling at puy de Dôme, France**

Kevin P. Dillon, Romie Tignat-Perrier, Muriel Joly, Sydonia Manibusan, Catherine Larose,  
Pierre Amato, Gediminas Mainelis

SUPPLEMENTARY MATERIAL

Table S1: Biomass load and total sequences from REPS and filter samples. <sup>a</sup> not applicable; <sup>b</sup> not detected. Cultivation and cell counts were not conducted for the filter samples.

Week	Colony-forming units (CFU) Average $\pm$ Std Dev	Total Cells Average $\pm$ Std Dev	Total Sequences		Filtered Sequences	
Sampler	REPS	REPS	REPS	Filter	REPS	Filter
1	900 $\pm$ 0	208,710 $\pm$ 18,090	162586	67953	1803	77
2	n/a <sup>a</sup>	1,256,730 $\pm$ 260,760	52913	44945	1705	5184
3	n/a	142,320 $\pm$ 22,740	70625	47867	5206	8930
4	1200 $\pm$ 174	173,130 $\pm$ 5,880	72621	44109	1319	437
5	n/a	90,720 $\pm$ 16,620	42344	56504	12144	4964
6	2400 $\pm$ 600	207,630 $\pm$ 13,980	121543	64908	3570	622
REPS Blank 1	n.d. <sup>b</sup>	6,120 $\pm$ 6,960	1381	n/a	799	n/a
REPS Blank 2	n.d.	19,440 $\pm$ 8,310	5412	n/a	735	n/a
REPS Blank 3	n/a	n/a	11358	n/a	7891	n/a

Table S2: Relative abundance of all detected genera across all weeks and samplers.

Genera Sampler	Week 1 (%)		Week 2 (%)		Week 3 (%)		Week 4 (%)		Week 5 (%)		Week 6 (%)	
	Filter	REPS	Filter	REPS	Filter	REPS	Filter	REPS	Filter	REPS	Filter	REPS
<i>Blautia</i>	0	0.554	0.0578	0	0.414	0	0	0	0	0	0	0
uncultured	0	0	0	0	0	0	0	0	0	0.0576	0	0
<i>Bacillus</i>	0	3.77	5.30	3.93	5.54	6.781	1.60	4.17	3.83	2.81	3.22	1.32
<i>Turicibacter</i>	7.79	1.28	5.54	0.469	7.38	0.826	2.06	0	2.12	0.132	9.65	0.532
<i>Desulfonema</i>	0	0	0	0	0	0	0	0	0	0.206	0	0
<i>Streptococcus</i>	0	0	0	0	0	0	0	0	0.342	0	0	0
<i>Cellulosimicrobium</i>	0	3.27	0	0	0	0	1.37	2.20	1.35	0.807	0	0.448
<i>Sphingomonas</i>	20.8	24.8	8.82	30.9	6.45	23.2	34.8	25.5	33.2	32.8	12.7	40.4
<i>Leuconostoc</i>	0	0	0	0	0	0.346	0	0	0	0	0	0
<i>Bergeyella</i>	0	1.44	0	0.235	0	1.71	0.458	1.36	0.584	0.716	0	0.0840
<i>Escherichia-Shigella</i>	0	3.55	0.251	3.22	0	1.77	0	2.73	0.725	1.11	0	1.06
<i>Rummeliibacillus</i>	0	0.333	0.965	0.352	0.873	0	1.14	0	0.705	0.0741	0	0.504
MBA03	0	0	0.347	0.587	0.773	0.154	0	0	0.141	0.601	0	0.112
uncultured	0	0	0	0	0	0	0	0	0.665	0.749	0	0.952
UCG-002	0	0.554	0	0	0	0	0	0	0	0	0	0.112
<i>Paenarthrobacter</i>	0	0	0	0	0	0.557	0	1.14	0.141	0	0	0
<i>Aquibacter</i>	2.60	0.943	0.617	0.704	0	0.672	0	0	0.504	1.79	0	0.308
<i>Enterococcus</i>	0	1.94	0	0.293	0.0223	0	0	0.834	0.665	0.420	0	0
NK4A214_group	0	0	0	0	0.0560	0	0	0	0.0806	0	0.322	0
<i>Streptomyces</i>	0	5.55	0.231	8.21	0.347	4.07	0	5.23	1.45	3.48	1.45	1.20
uncultured	0	0	0	0.293	0	0	0	0	0	0	0	0
NKB15	0	0.499	0	0.235	1.14	3.73	0	0.682	1.91	7.10	0	5.55
<i>Jatrophihabitans</i>	0	5.05	2.97	13.3	4.01	12.9	0	3.26	14.4	17.0	3.54	12.4
<i>Acinetobacter</i>	0	0.555	0	0	0	1.19	0	0.227	0.806	0.0576	0	0
<i>Comamonas</i>	0	0	0	0	0	0.173	0	0	0	0.560	0	0
<i>Tyzzerella</i>	0	0.610	0	0	0	0	0	0	0	0.132	0	0
[Eubacterium]_coprostanoligenes_group	0	0.333	0	0	0	0.346	0	0	0.121	0	0	0

Genera	Week 1		Week 2		Week 3		Week 4		Week 5		Week 6	
	(%)		(%)		(%)		(%)		(%)		(%)	
Sampler	Filter	REPS	Filter	REPS	Filter	REPS	Filter	REPS	Filter	REPS	Filter	REPS
<i>Staphylococcus</i>	0	0	0	0	0.0112	0.327	1.60	0	0.544	0.115	0	0
<i>Calditerrivibrio</i>	0	1.16	0.154	0.235	0.246	0	0	0	0.121	0.140	0.482	0
Lachnospiraceae_NK4A136_group	0	0	0	0	0.157	0	0	0	0	0.0329	0	0
<i>Holdemanella</i>	0	0	0	0.293	0	0	0	0	0	0	0	0
<i>Epulopiscium</i>	0	0.444	0.193	0.117	0.638	0	0	0	0	0	0	0
<i>Paenibacillus</i>	0	0.666	2.30	1.23	2.46	0.807	0	2.58	0.363	0	1.45	0.644
<i>Pandoraea</i>	0	1.16	0	4.63	0.302	3.50	10.8	7.96	3.06	1.66	1.93	12.7
<i>Pseudomonas</i>	0	0.499	0.154	0.117	0.0895	2.15	2.75	0	0.806	0.856	0	0.840
uncultured	0	0	0	0.235	0	0	0	0	0	0.0576	0	0
<i>Marmoricola</i>	0	2.94	0	1.17	0.101	4.71	0	0	0.302	0.873	0	1.04
<i>Ruminococcus</i>	0	0	0	0.704	0	0	0	0	0	0	0.482	0
<i>Halarcobacter</i>	0	0.222	0	0	0	0	0	0	0	0	0	0
<i>Microbacterium</i>	0	2.83	0.675	3.40	0	3.09	9.38	2.05	2.92	2.23	0	1.34
<i>Tepidimonas</i>	0	0	0	0	0	0.423	0	0	0	0.0494	0	0
C39	0	0	0.386	0.762	0.302	3.21	0	0	0.302	0	0	0
uncultured	0	0.166	0.0771	0	0	0.403	0	0.531	0	0.0823	0	0.0840
uncultured	0	0.111	0	0	0	0	0	0	0	0.0330	0	0
<i>Clostridioides</i>	0	4.38	6.46	0	8.70	0.884	3.43	0	2.32	0.535	11.7	1.23
<i>Lysinibacillus</i>	68.8	23.2	56.3	10.9	51.9	4.80	15.3	21.6	10.9	5.23	48.9	7.28
<i>Ignavibacterium</i>	0	0	0	0	0	0	0	0	0.0402	0	0	0
<i>Mycobacterium</i>	0	4.49	0.617	2.229	1.06	4.94	0	5.38	1.23	1.85	0	1.18
<i>Corynebacterium</i>	0	1.39	0.887	1.88	0.0112	1.63	4.12	1.21	2.60	1.56	0	0.364
<i>Sedimentibacter</i>	0	0	0.0386	0	0.0896	0	0	0	0	0.0659	0	0
<i>Thiovirga</i>	0	0	0.579	1.35	0.179	1.17	1.14	0	0.101	1.00	0.643	0.756
<i>Listeria</i>	0	0	0.193	0	0.235	0	0	1.29	0	0	0	0
Candidatus_Nitrososphaera	0	0	0	0.469	0	0	0	0	0	0	0	0
<i>Latescibacterota</i>	0	0	0	0	0	0.595	0	0	0	0.321	0	0
<i>Prevotella</i>	0	0	0	0.176	0	0.595	2.52	0	0.201	0.0659	1.13	0
<i>Gracilibacteria</i>	0	0.166	0.0579	0	0	0.0576	0	7.13	0.141	0.420	0.482	0.896



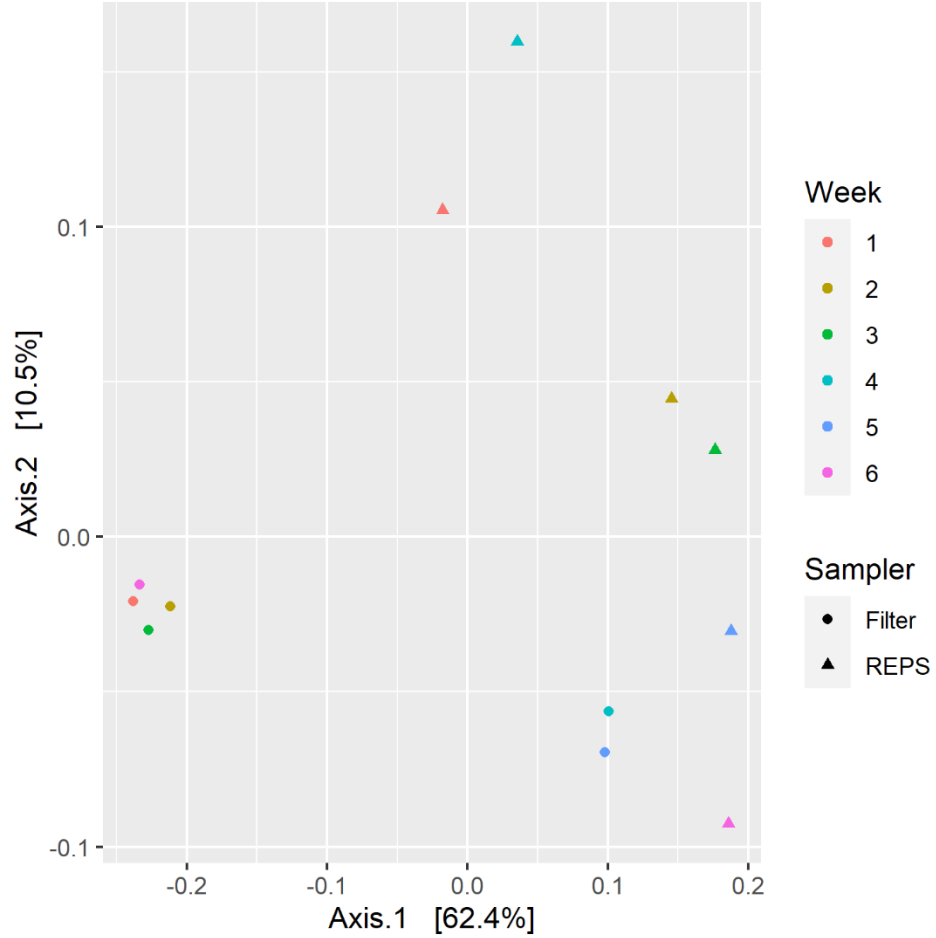


Figure S1: Weighted UniFrac Distance PCoA of samples. The samples are separated based upon the collection week and the sampler (Table 1).