## Supporting information for

## High levels of primary biogenic organic aerosols in the atmosphere in summer are driven by only a few microbial taxa from the leaves of surrounding plants

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![](_page_1_Figure_0.jpeg)

Figure S1: Atmospheric concentrations of carbonaceous components in PM<sub>10</sub>. Temporal variations of primary sugar compounds in composite PM<sub>10</sub> and calcium concentrations along with daily agricultural activities performed around the study site.

 Table S1: Identification of PM<sub>10</sub> composite sample. Some daily filter samples were pooled together to from the composite samples used in MiSeq sequencing analysis.

Sampling date		Sample identifier	
12/06/2017	14/06/2017	Al	
15/06/2017		A2	
16/06/2017	17/06/2017	A3	
18/06/2017	19/06/2017	A4	
22/06/2017	23/06/2017	A5	
24/06/2017	25/06/2017	A6	
26/06/2017		A7	
27/06/2017	28/06/2017	A8	
29/06/2017	30/06/2017	A9	
01/07/2017		A10	
02/07/2017	03/07/2017	A11	
04/07/2017	06/07/2017	A12	
07/07/2017		A13	
08/07	/2017	A14	
09/07	/2017	A15	
10/07	/2017	A16	
11/07/2017	12/07/2017	A17	
14/07/2017	15/07/2017	A18	
17/07/2017	18/07/2017	A19	
22/07/2017	23/07/2017	A20	
24/07	/2017	A21	
25/07/2017	26/07/2017	A22	
27/07	/2017	A23	
28/07/2017	29/07/2017	A24	
30/07/2017	31/07/2017	A25	
01/08	/2017	A26	
02/08/2017	03/08/2017	A27	
06/08/2017	07/08/2017	A28	
08/08	/2017	A29	
09/08/2017	10/08/2017	A30	
13/08/2017	15/08/2017	A31	
16/08/2017		A32	
17/08/2017		A33	
18/08/2017		A34	
19/08	/2017	A35	
20/08/2017	21/08/2017	A36	

Table S2: Minimum number of MOTUs reads per sample types. Unless specified otherwise, samples are randomly normalized to the smallest number of reads for within and between sample comparisons.

	Aerosols (PM <sub>10</sub> )	Leaves	Surface soils
Fungi	7 223	6 628	4 287
Bacteria	2 865	16 502	5 043

![](_page_3_Figure_0.jpeg)

Figure S2: Rarefaction curves of MOTUs abundance grouped by types of samples. (A) Fungal and (B) Bacterial MOTUs. Solid curves represent the observations while the dashed ones show the interpollation.

![](_page_4_Figure_0.jpeg)

Figure S3: Statistical comparisons of MOTUs richness and diversity across different types of samples. (A) Fungal and (B) bacterial MOTUs abundance. Data sets are rarefied at the same sequencing depth for each library.

![](_page_5_Figure_0.jpeg)

Figure S4: Temporal dynamics of microbial relative abundance (normalized to sum 1). Only the most pronounced top 21 of respectively (A) fungal (B) and bacterial genera are labelled.

![](_page_6_Figure_0.jpeg)

Figure 5 : Heatmap of Spearman's rank correlation between SCs and abundance of airborne communities at the study site. (A) Fungal class-level (B) bacterial phylum-level, respectively. Only genera with relative abundance ≥ 1 are shown.

![](_page_7_Figure_0.jpeg)

![](_page_7_Figure_1.jpeg)

Figure 6 : Unsupervised hierarchical clustering of all samples (Aerosols, Leaves and Soils) based on Horn distance matrix. Dissimilarity matrixes have been calculated on the rarefied MOTUs tables.

![](_page_7_Figure_3.jpeg)

Figure 7 : Temporal covariation cycles of daily particulate levoglucosan and primary sugar compounds during the sampling campaign period.