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High levels of primary biogenic organic aerosols are driven by only a few plant-associated microbial taxa

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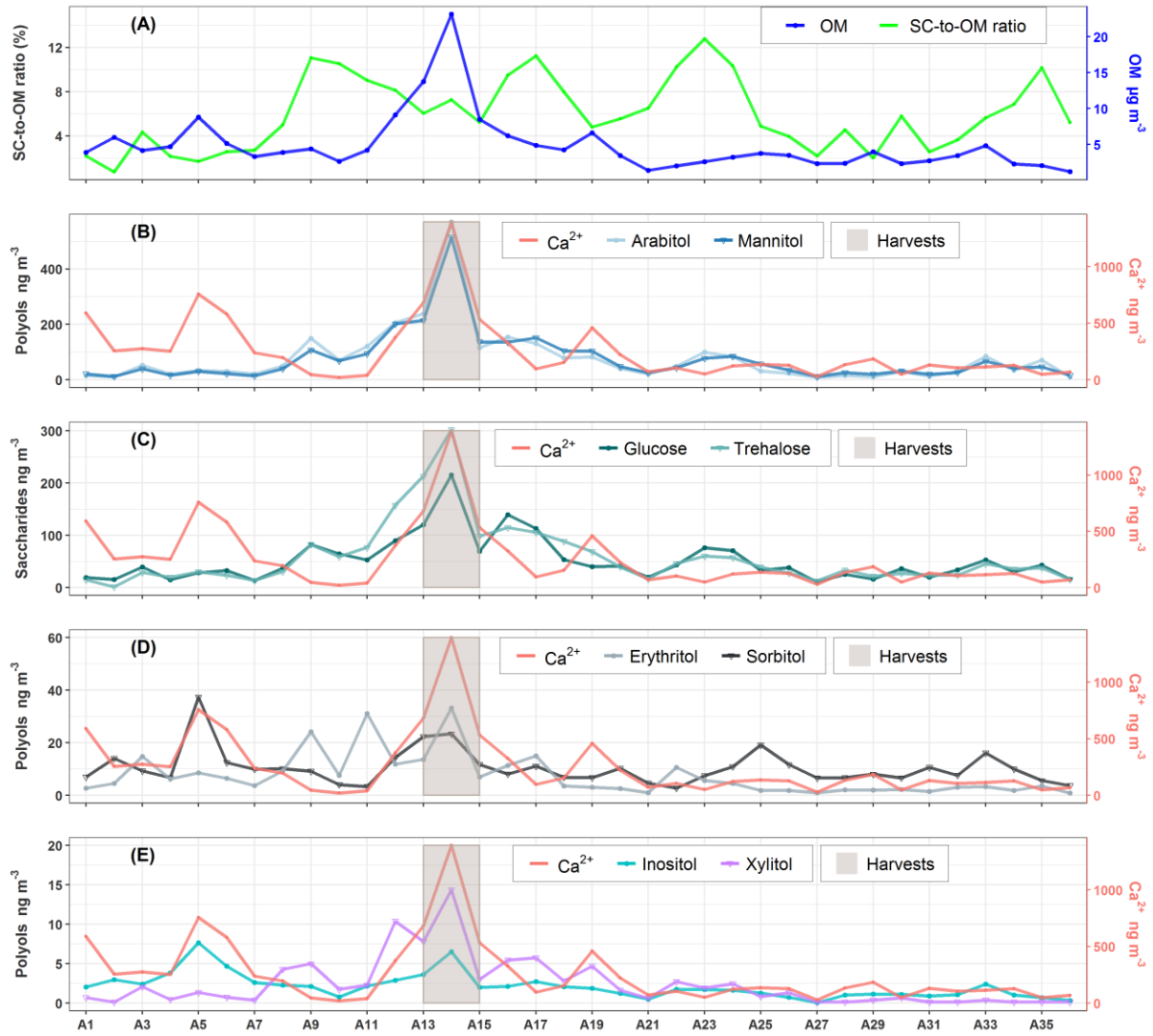

Figure S1: Atmospheric concentrations of carbonaceous components in PM_{10}. Temporal variations of primary sugar compounds in composite PM_{10} and calcium concentrations along with daily agricultural activities performed around the study site.

Table S1: Identification of PM_{10} 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	*A1*
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_{10})	Leaves	Surface soils
Fungi	7 223	6 628	4 287
Bacteria	2 865	16 502	5 043

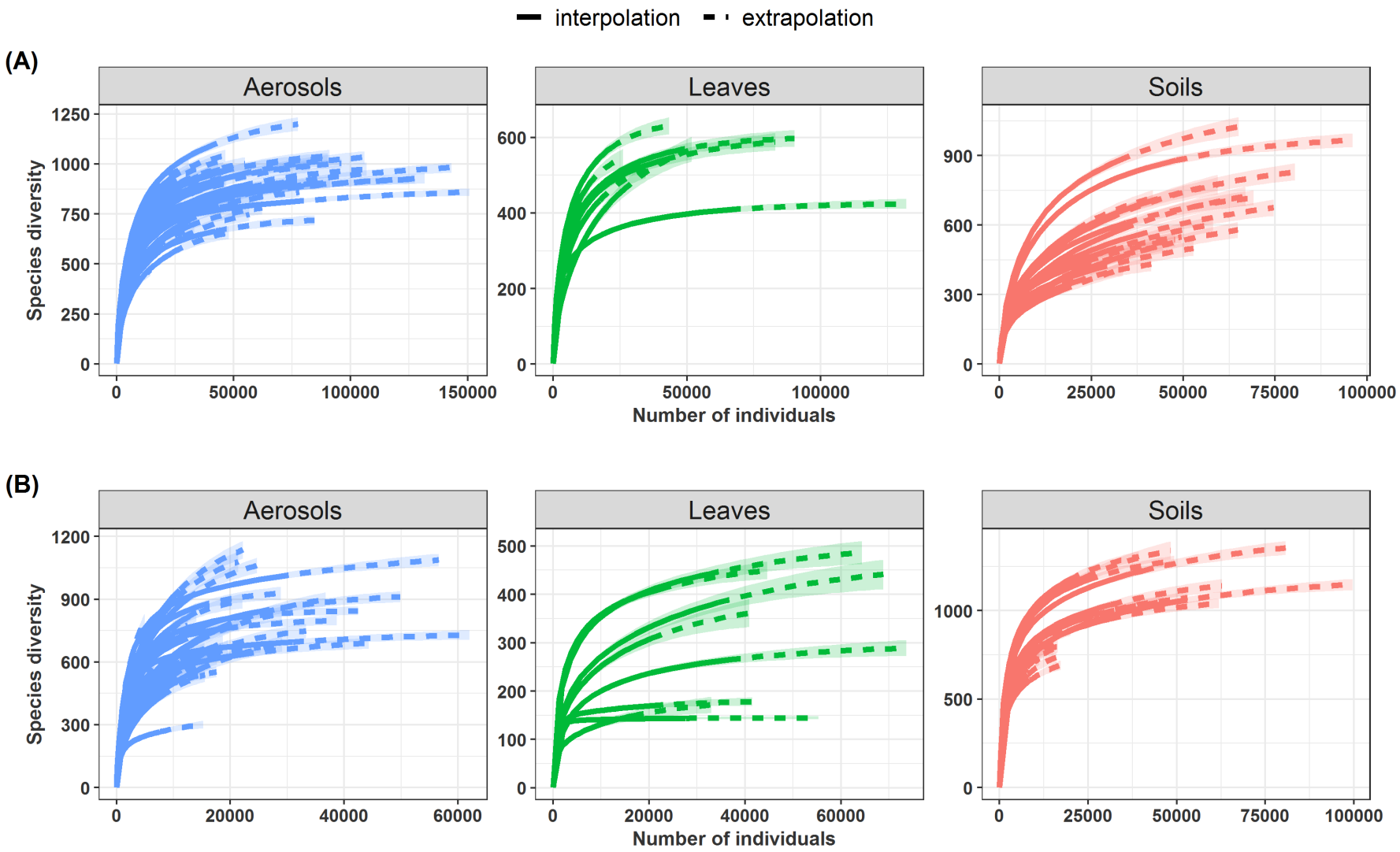

Figure S2: Rarefaction curves of MOTUs abundance grouped by types of samples. (A) Fungal and (B) bacterial MOTUs. Solid curves represent the observations while the dashed ones show the interpolation.

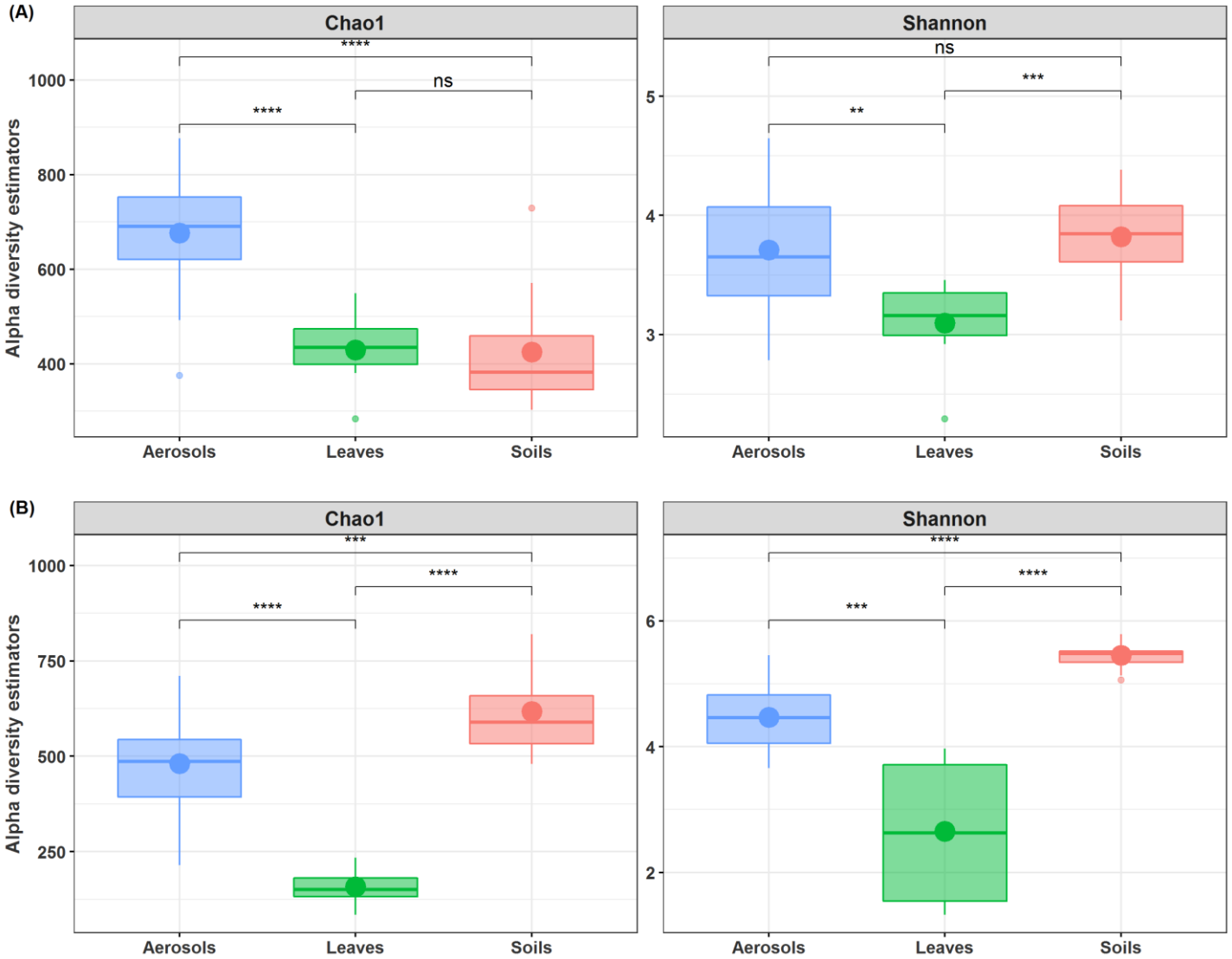

Figure S3: Statistical comparisons of MOTUs richness and diversity across different types of samples. (A) Fungal and (B) bacterial MOTUs abundance. Data sets are rarefied at the same sequencing depth for each library.

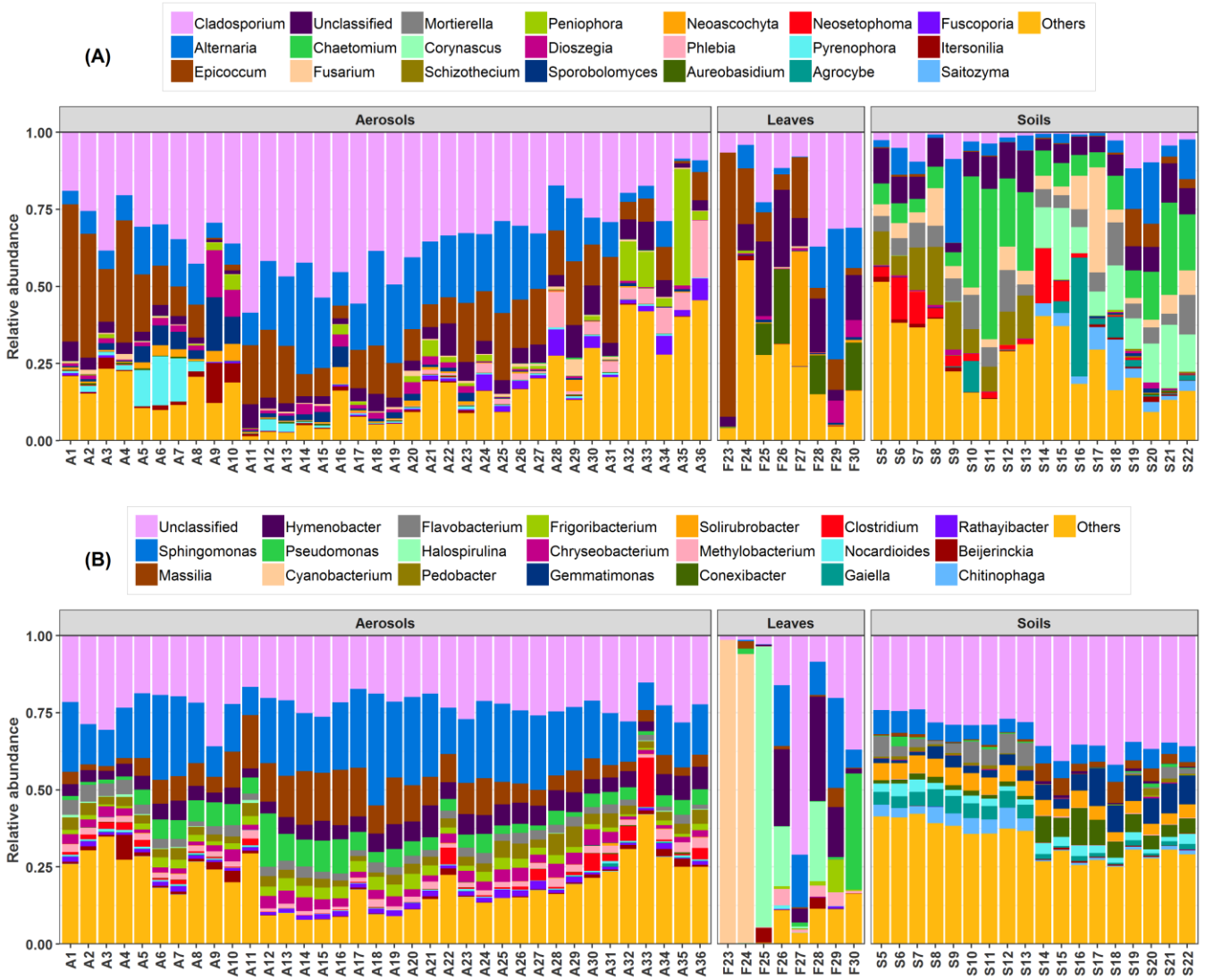

Figure S4: Temporal dynamics of microbial relative abundance (normalized to sum 1). Only the most pronounced top 21 of respectively (A) fungal (B) and bacterial genera are labelled.

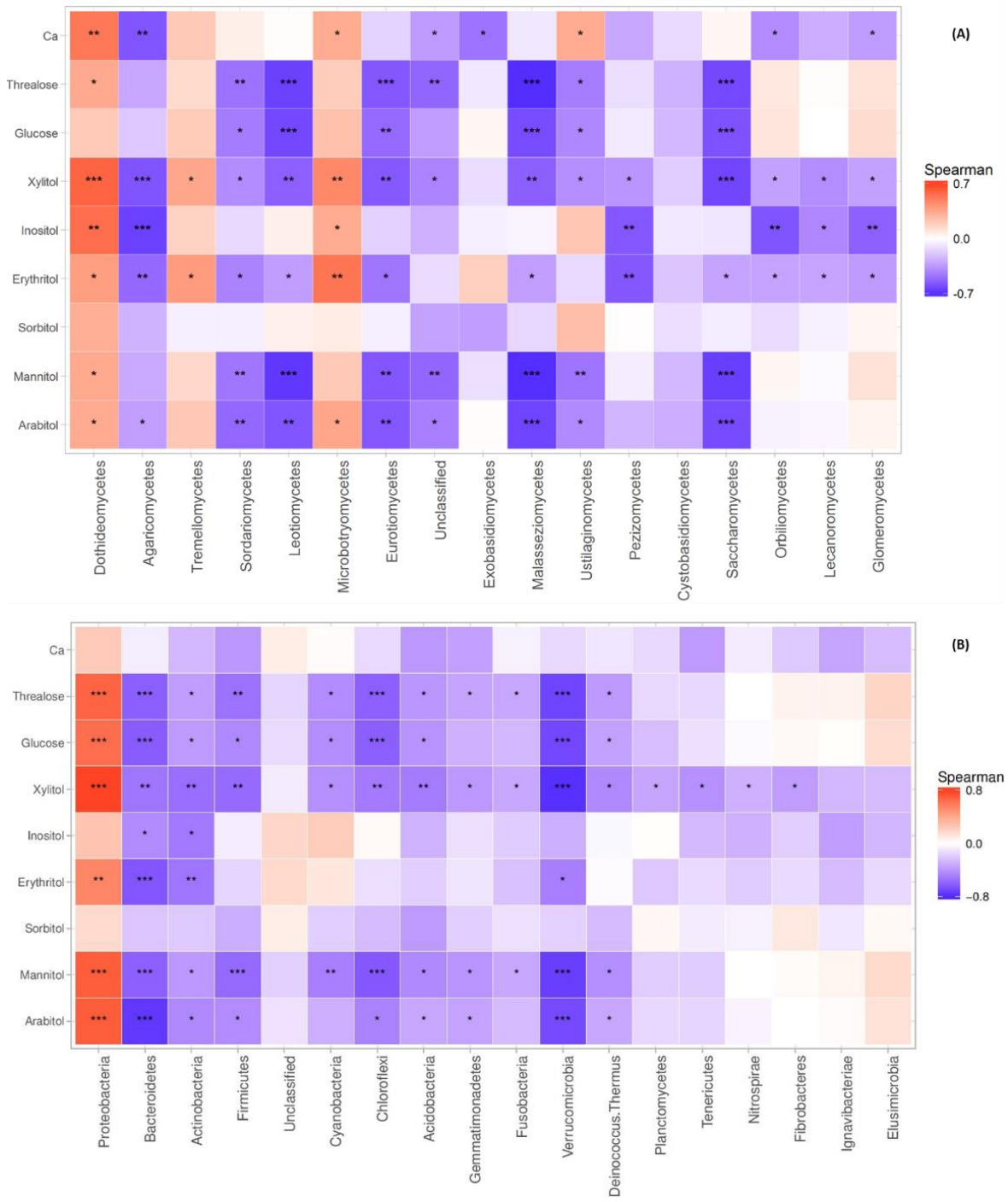

Figure 5 : Heatmap of Spearman's rank correlation between SCs and abundance of airborne communities at the study site. (A) Fungal class-level and and (B) bacterial phylum-level, respectively. Only genera with relative abundance ≥ 1 are shown.

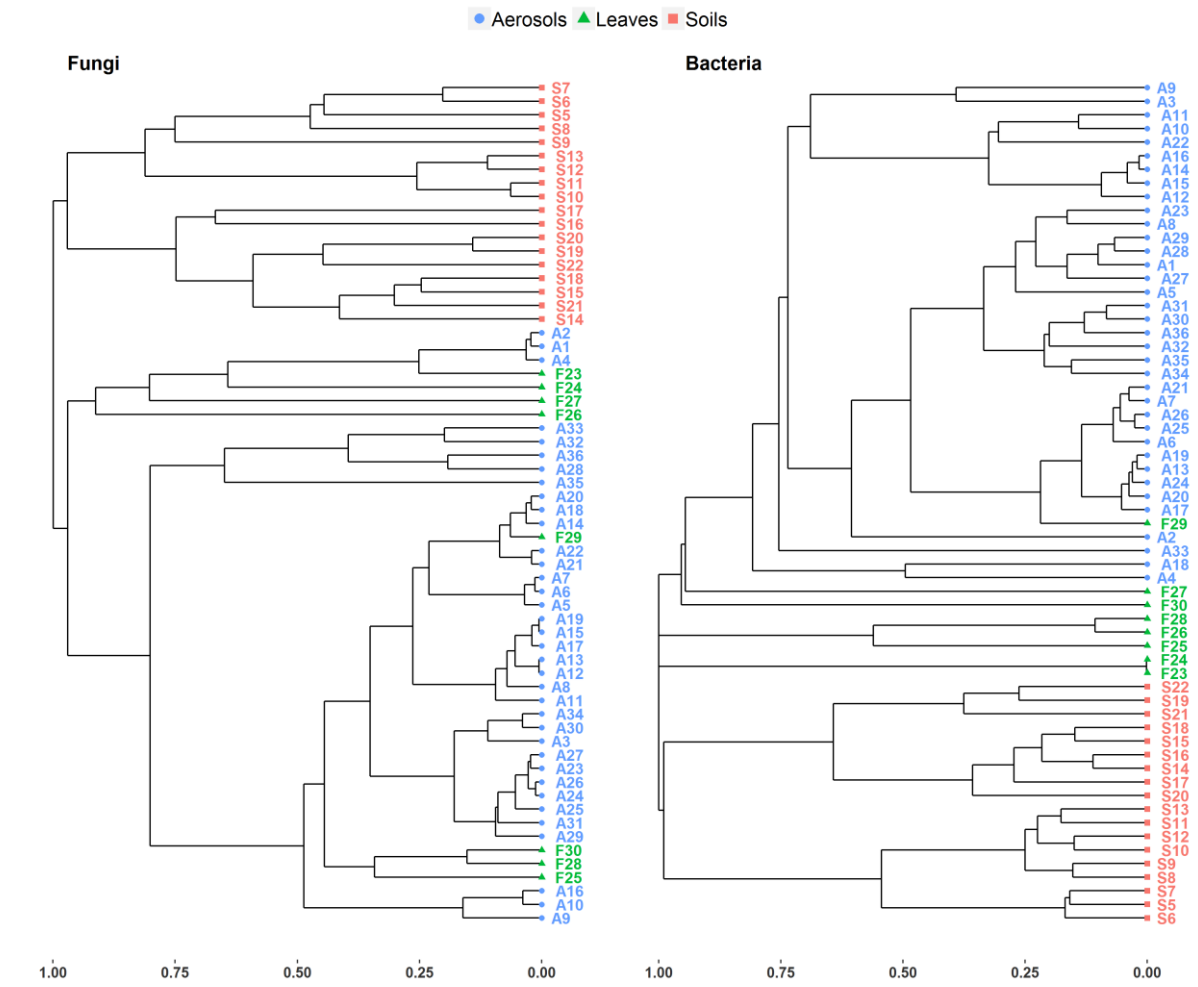

Figure 6 : Unsupervised hierarchical clustering of all samples (Aerosols, Leaves and Soils) based on Horn distance matrix. Dissimilarity matrixes have been calculated on the rarefied MOTUs tables.

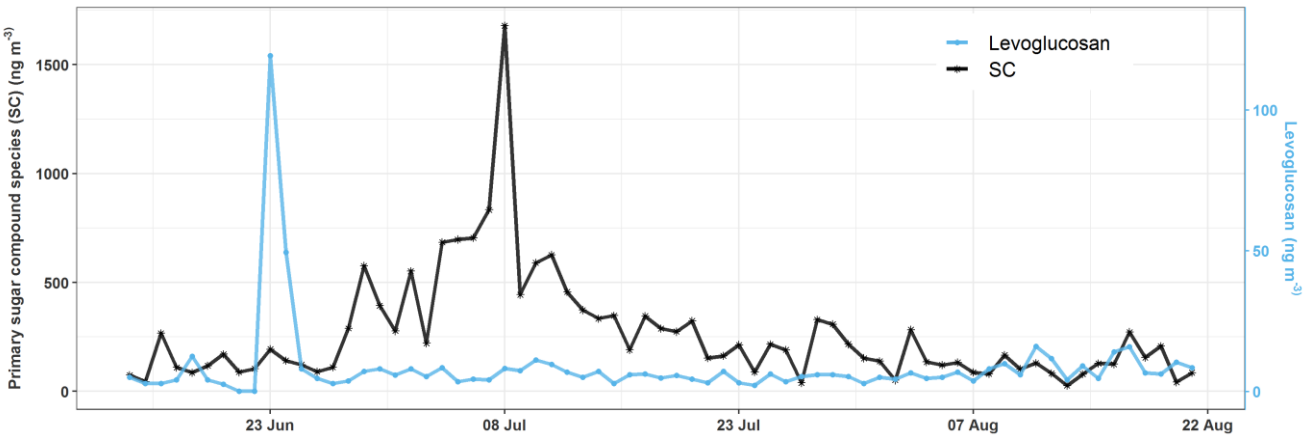

Figure 7 : Temporal covariation cycles of daily particulate levoglucosan and primary sugar compounds during the sampling campaign period.