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Diversity and seasonal dynamics of airborne archaea

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Supplement Text

Aerosol sampling at additional sites

China

Samples of total suspended particles (TSP) were collected on quartz fiber filters with a high-volume filter sampler (Anderson Instruments, Smyrna, GA; 1.5 m above the ground, sample air flow 1 m^3 min^{-1}; sampling time ~24 h) during the Program of Regional Integrated Experiments of the Pearl River Delta Region (PRIDE-PRD) Campaign in July 2006 in Backgarden (21 m elevation, 23°54'80.56'' N, 113°06'63.89'' E, South China). Prior to sampling the 14 filters were decontaminated at 500 °C for at least 12 h. The samples were stored in a freezer at −80 °C until DNA extraction. The sampling site was situated in a rural farming environment ˜60 km northwest of the megacity Guangzhou on the edge of the highly populated PRD region. Due to the prevailing monsoon circulation at the time of sampling, the marine air masses came mainly from the south to southeast, making this site a rural receptor site for the regional pollution resulting from the outflow of the urban cluster around Guangzhou (Garland et al., 2008; Rose et al., 2010).

North America

The sampling site was located in a part of the Manitou Experimental Forest in a semi-arid, montane ponderosa pine zone in the Central Rocky Mountains 35 km northwest of Colorado Springs, CO and 15 km north of Woodland Park, CO (2370 m elevation, latitude 39°6'0" N, longitude 105°5'30" W). Total aerosol samples for DNA analysis were collected during the BEACHON-RoMBAS campaign in July 2011 onto 150 mm diameter glass fiber filters (Machery-Nagel, Type MN 85/90, 406015) using a free-standing high-volume sampler (Digitel DHA-80) operated at 1 m^3 min^{-1}, 1 m above the ground and located approximately 50 m from the sampling trailer. Filters were baked at 500 °C for 12 h prior to sampling. After sampling, filters were stored in decontaminated aluminum bags at -80 °C until DNA extraction. Twenty samples were tested for Archaea presence. The sampled air represents rural continental boundary layer air (Huffman et al., 2013).

United Kingdom

Samples on glass fiber filters (Graseby Andersen Hi-Vol six-stage impactor, sample air flow 1.120 m^3 min^{-1}, sampling time 21–35 h) were provided by the School of Earth, Atmospheric, and Environmental Sciences, University of Manchester, United Kingdom (UK). The 12 sam-

ples were collected as part of the Tropospheric ORganic CHemistry (TORCH) field campaign during spring 2004. Prior to use, the glass fiber filters were decontaminated by baking, and the loaded filters were transported frozen and stored in a freezer at −20 °C until DNA extraction. The TORCH2 campaign took place at the Weybourne Atmospheric Observatory (WAO, 52°57'02'' N, 1°07'19'' E), which is located on the North Norfolk coastline near Weybourne, UK. Norfolk is a sparsely populated rural region without large population centers or industrial areas. As detailed by Gysel et al. (2007) the air masses encountered at this station represent aged polluted outflow from London, the West Midlands or the European continent, or relatively clean air masses transported across the North Sea region by northerly winds.

Quantitative analysis of airborne Archaea

In contrast to other airborne microorganisms (e.g., Fungi, Fröhlich-Nowoisky et al., 2009 and Bacteria (data not shown)), which were studied from the identical air filter samples, the amplification of airborne Archaea 16S rRNA gene sequences was more challenging and PCR products were often only produced in a nested PCR or not at all. This was also true for air filter samples from China, the United Kingdom, and North America which were analyzed successfully for Fungi (Fröhlich-Nowoisky et al., 2012; Huffman et al., 2013) while Archaea could only be amplified for some of the samples (this study).

One explanation might concern the primer choice. Primers that are supposed to cover Archaea or subgroups might not have 100% identity across all Archaea lineages (Klindworth et al., 2013; Nicol and Prosser, 2011). In addition, Archaea taxonomy is continuously increasing due to the discovery of new species. However, the primers used for amplification in this study have been used successfully for soil samples (Angel et al., 2012; Grosskopf et al., 1998). To increase amplification success we also used a combination of 3 primer pairs as well as nested PCR as described in section 2.2. The primer pairs used amplify Archaea sequences from several taxonomic lineages, thus it can be assumed that they would equally amplify at least these lineages in air filter samples. Therefore, it is more likely that the Archaea lineages were either not present in the air or only in very limited amounts. To judge and compare Archaea to Bacteria abundance on the air filter samples we quantified Archaea and Bacteria by performing qPCR assays including a standard with a correlation coefficient of 0.98 in Bacteria and 0.99 in Archaea and PCR efficiencies of 102.6% in Bacteria and 91.5% in Archaea.

We compared the abundance of airborne Archaea and Bacteria with those in environments that are potential bioaerosol sources (see material and methods, Table S4). Although

only very rough estimates can be made as concentrations vary between regions, depth, temperatures, seasons etc., in general Archaea represent about ~10% of the total prokaryotes quantities in ocean surface water as well as in normal soil (Bates et al., 2011, Cao et al., 2012; DeLong, 1992; Karner et al., 2001; Kemnitz et al., 2007; Yin et al., 2013,).

In one kg of soil the copy numbers of Archaea 16S rRNA genes range, very roughly, between ~10^9 to 10^{11} while Bacteria have between ~10^{11} to 10^{12} copies (Table S4). *Thaumarchaeota AOA* often even prevail over *AOB* (Leininger et al., 2006, Pereira e Silva et al., 2012). For air, our results show that Bacteria were easily quantifiable and varied between 10^5 and 10^6 16S rRNA gene copies per m^3 of air, which is close to abundances measured for ocean surface water and in agreement with other studies (Bauer et al., 2002, Burrows et al., 2009, Harrison et al., 2005, DeLeon-Rodriguez et al., 2013). In contrast, Archaea 16S rRNA gene copies were often below the detection limit (< 10 copies), and varied approximately between 1 and 10 copies per m^3 air. Although the quantification is based on six filter samples only, Archaea are likely orders of magnitude lower than the Bacteria in the same air masses.

Supposing that soil is the primary source of airborne Archaea and Bacteria, the questions remains why Archaea are so difficult to amplify in air, or are not present in amplifiable quantities, while Bacteria are. It might be that Bacteria have important sources other than soils (e.g., plant surfaces), which Archaea might not have. Another possibility might be that Archaea are more susceptible to UV damage or other damaging compounds associated with fine particulate matter than Bacteria, or decompose faster after sampling. Thirdly, in contrast to Bacteria, Archaea might occur in larger particles and thus deposit faster from the air. However, the explanations can currently only be speculative and future studies are needed. The observation that airborne Archaea are low in number has also been made by Woo and colleagues (2013), and our observation that airborne Archaea are difficult to amplify in general is also consistent with the experience other researchers have made (Bowers et al., 2009, 2013; Fierer et al., 2008; Woo et al., 2013; Woo, 2012).

The difficulty to obtain DNA extracts that yielded enough archaeal DNA to be amplified, also limited the number of samples that could successfully be analyzed. We calculated rarefaction curves for the air filter samples from Mainz and Cape Verde which agree with our assumptions that although we exhausted laboratory possibilities the gained data can currently only serve as a first rough estimate of the actual species richness of Archaea in air.

Statistical analysis of airborne Archaea diversity with meteorological parameters

Meteorological conditions are also known to influence airborne communities and bioaerosol composition (Despres et al., 2012 and references therein), e.g., temperature and relative humidity have been found to correlate with airborne fungal composition (Fröhlich-Nowoisky et al., 2009). We thus compared the diversity of airborne Archaea (the normalized (S_n) and relative species richness ($S_{R,i,}$, see material and methods)) with meteorological parameters, such as averaged wind speed, temperature, relative humidity and the sum of precipitation for the individual sampling periods. To discriminate between short and long term influences, we performed linear correlation analyses on a sample to sample basis and also on a monthly basis.

In an initial step, the influence of single meteorological factors was assessed. The Pearson coefficients were calculated between the diversity parameters, $S_{R,j,}$ S_n and $S_{R,k}$, and the meteorological factors to preselect possible dependencies for further testing. The results of the averaged meteorological parameters can be seen in Table S6. Due to the nature of environmental samples and the limitations of the applied methods a high variance was expected within the diversity parameters. To account for this, relatively low Pearson coefficient boundaries, of +/- 0.3 for the sample to sample diversity parameter ($S_{R,i}$) and +/- 0.5 for the a monthly diversity parameters (S_n and $S_{R,k}$), were set as a threshold for further testing. The higher boundary for the monthly parameters was chosen as these are based on more data, thus reducing the expected intrinsic error.

Detailed single factor linear regression analyses were then performed on promising candidates. The results can be seen in Table S7 and Figures S2a, S3.

In a second step to assess the dependency of the diversity parameters on combined meteorological factors, multiple factor linear regression analyses were performed. To preselect the best combinations of factors, the best factor subsets were selected using the AIC method. Detailed linear regression analyses were then performed, the results of which can be seen in Table S7 and Figures S2b and 4 of the main text.

On a sample to sample basis, $S_{R,i}$ showed a significant negative correlation to average wind speed (p-value=0.012; Figure S2a). The incorporation of additional variables also revealed a negative correlation to wind speed with a positive correlation to relative humidity (p-value=0.015; Figure S2b).

While on the short term the influence of wind speed seems to play an important role for the observed diversity, on a monthly basis the Pearson's coefficients showed that relative humidity correlated best with diversity. The best single factor for both, S_n and $S_{R,k}$, was found to be relative humidity which in both cases was positively correlated (p-values=0.05 and 0.005; see Figure S3a and b). A negative correlation to temperature was also shown by $S_{R,k}$ (p-value=0.049; See Figure S3c). The multiple linear correlation analysis revealed that S_n negatively correlated with both average temperature and wind speed, while $S_{R,k}$ showed a significant positive correlation with average relative humidity and wind speed, though wind speed in both variable sets played a secondary role (p-value (S_n)=0.02, p-value ($S_{R,k}$)=0.01; Figure 4, main text).

The sampling site is situated in an area which has a seasonal cycle with lower temperatures and high relative humidity in the fall/winter period. Also, on average the wind speed increases due to the Westerlies prevailing at this time of the year. Thus, the observed positive correlation with relative humidity, as well as the negative correlation with temperature on a long term basis, coincides with our finding that the Archaea diversity increases in the fall/winter period. However, it is not possible at this point to determine whether the meteorological parameters influence the diversity of Archaea directly. For the soil environment it has been found that Archaea diversity reacts to changes in soil temperature and soil moisture (Rasche et al., 2011) thus meteorological parameters could indirectly due to their effect on soil conditions, influence the Archaea diversity. On the other hand the diversity could just be influenced by the changing accessibility of aerosolization sources, e.g., availability of bare, harvested fields. In this case the meteorological parameters would not cause changes in diversity, but only be characteristic for the season when the number of bare fields increases.

Supplement Figures S1-S3

Figure S1a

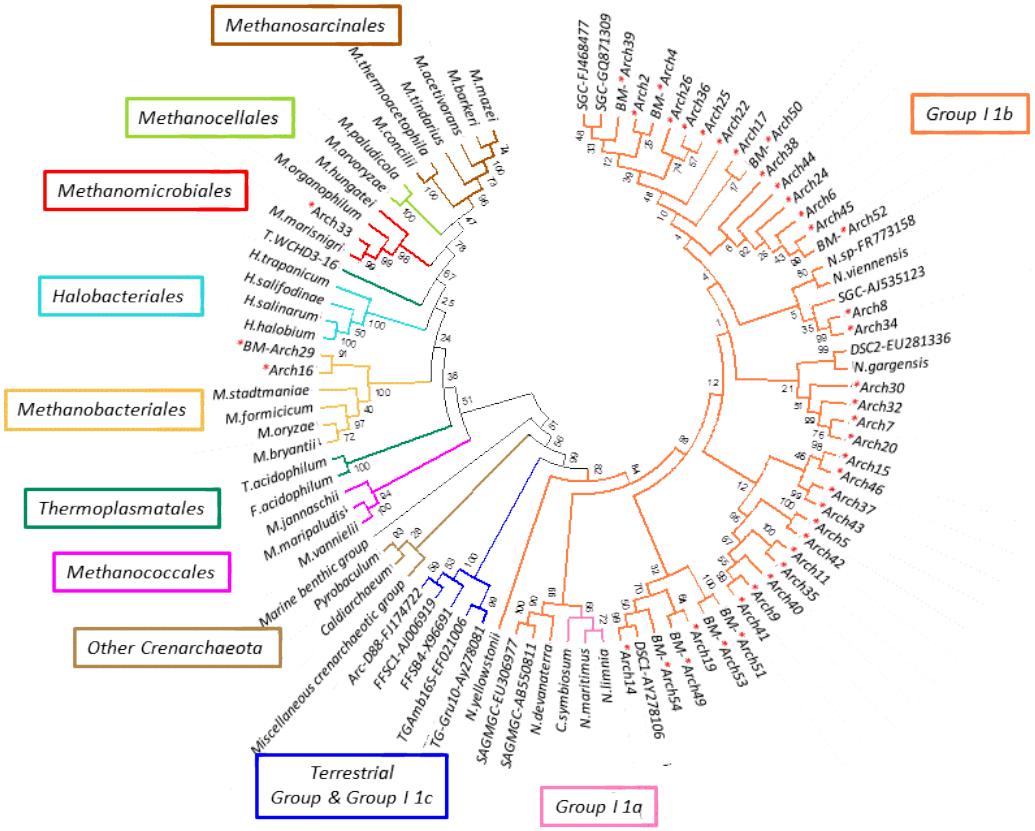

Figure S1b

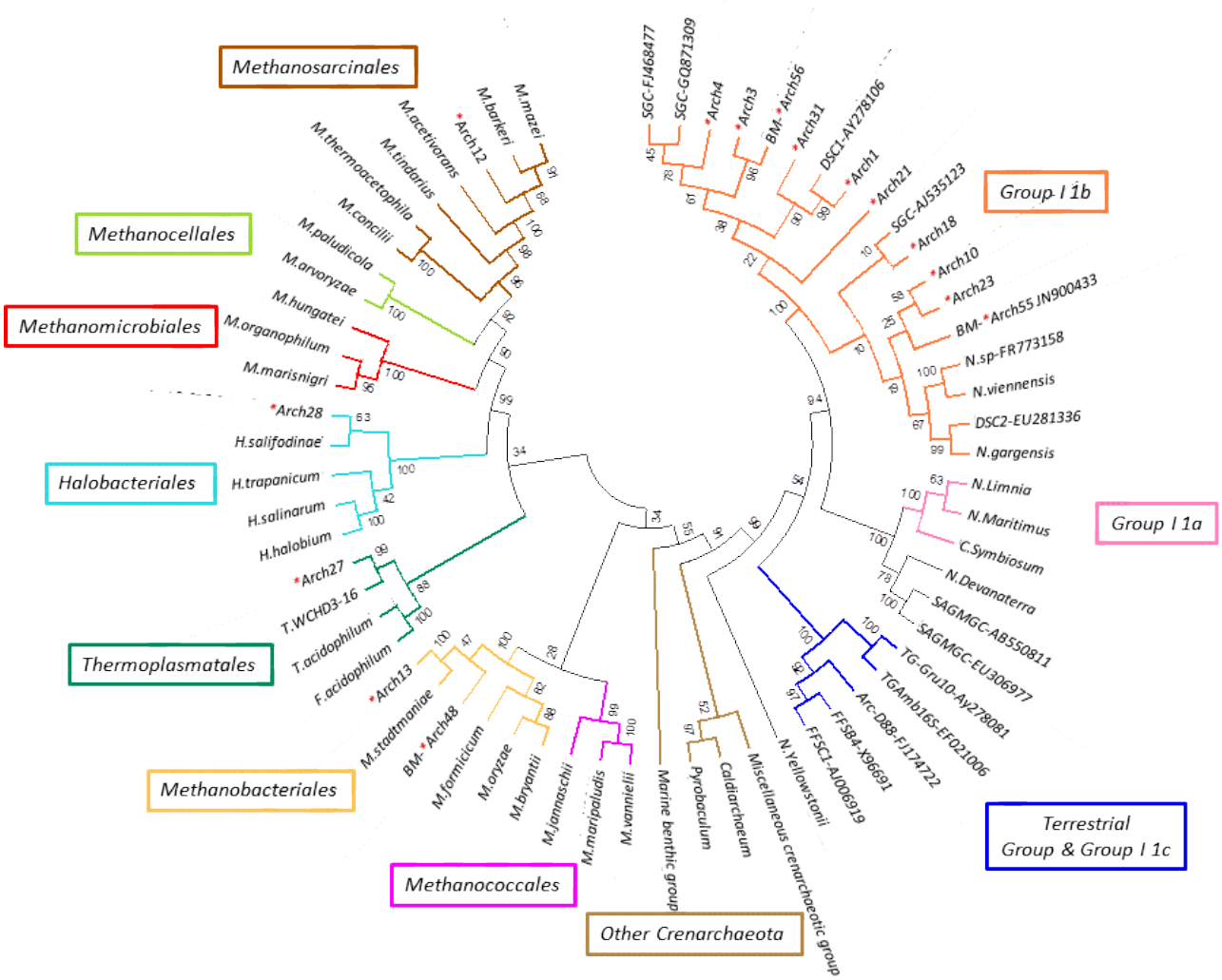
Methanosarcinales
Methanocellales
Methanomicrobiales
Halobacteriales
Thermoplasmatales
Methanobacteriales
Methanococcales
Other Crenarchaeota
Terrestrial Group & Group I 1c
Group I 1a
Group I 1b
M.mazei
M.barkeri
*Arch12
M.acetivorans
M.tindarius
M.thermoacetophilo
M.concilii
M.paludicola
M.arvoryzae
M.hungatei
M.organophilum
M.marisnigri
*Arch28
H.salifodinae
H.trapanicum
H.salinarum
H.halobium
*Arch27
T.WCHD3-16
T.acidophilum
F.acidophilum
*Arch13
M.stadtmaniae
BM-*Arch48
M.formicicum
M.oryzae
M.bryantii
M.jannaschii
M.maripaludis
M.vannielii
Marine benthic group
Pyrobaculum
Caldiarchaeum
Miscellaneous crenarchaeotic group
N.Yellowstonii
FFSC1-AJ006919
FFSB4-X96691
Arc-D88-FJ174722
TGAmb16S-EF021006
TG-Gru10-Ay278081
SAGMGC-EU306977
SAGMGC-AB550811
N.Devanaterra
C.Symbiosum
N.Maritimus
N.Limnia
N.gargensis
DSC2-EU281336
N.viennensis
N.sp-FR773158
BM-*Arch55 JN900433
*Arch23
*Arch10
*Arch18
SGC-AJ535123
*Arch21
*Arch1
DSC1-AY278106
BM-*Arch56
*Arch31
*Arch3
*Arch4
SGC-GQ871309
SGC-FJ468477

Figure S1: Phylogenetic Tree of airborne Archaea in Germany. A Maximum Likelihood Tree was calculated for the published and obtained sequences of this study representing known phylogenetic lineages (given here species names). They are also summarized in Table S2. Two different sequence parts of the 16S region were used, depending on the coverage by the OTUs of the airborne Archaea (a, b). Different orders are given in different colors. Red stars mark the presence of airborne Archaea of Mainz.

Figure S2a

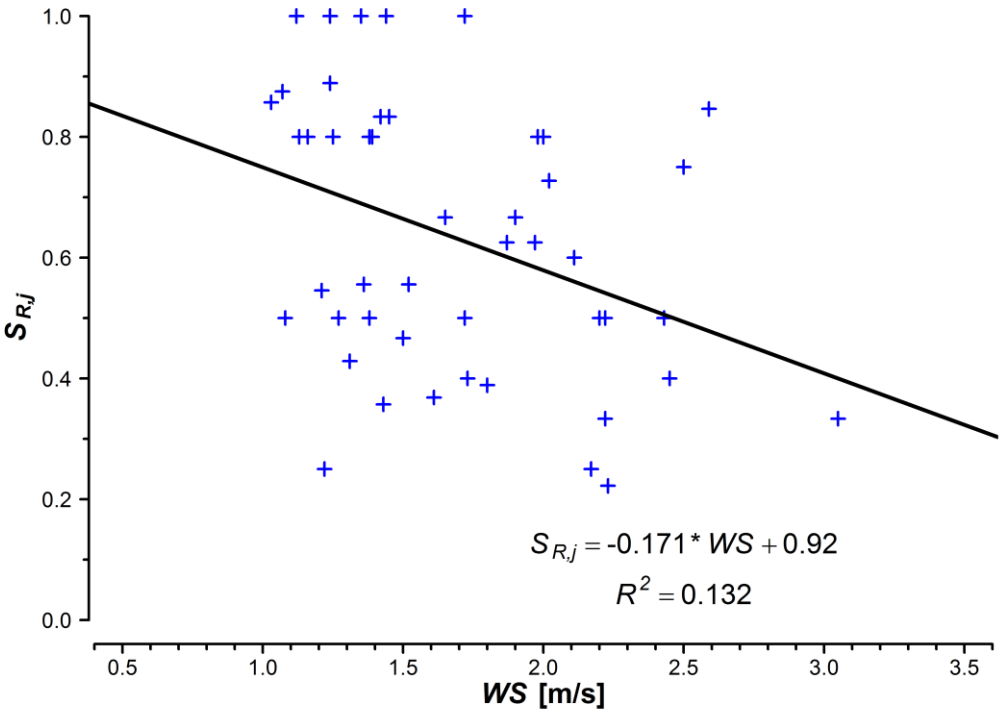

Figure S2b

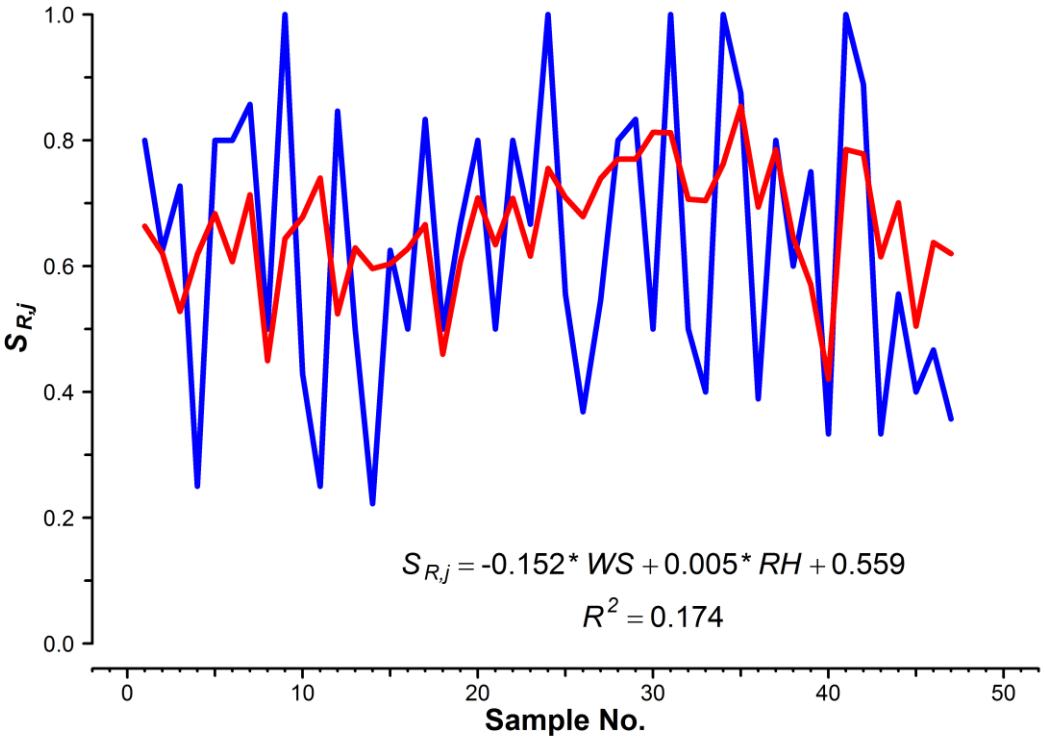

Figure S2: The most significant results of the linear regression analysis between the relative species diversity per sample ($S_{R,j}$) and meteorological factors. (a) Best single factor: $S_{R,j}$ as a function of wind speed (p-value = 0.012). (b) Best variable subset (*WS* and *RH*): The sample IDs given on the x-axis correspond to the sampling time given in Table S1. The values for the observed $S_{R,j}$ curve (blue) were calculated using the equation given in Table S3. The modeled $S_{R,j}$ curve (red) was estimated using the depicted equation that was obtained by regression analysis (p-value = 0.015) including the *RH* and *WS* values measured during each individual sampling period. *WS*: average wind Speed [m/s]; *RH*: average relative humidity [%].

Figure S3a

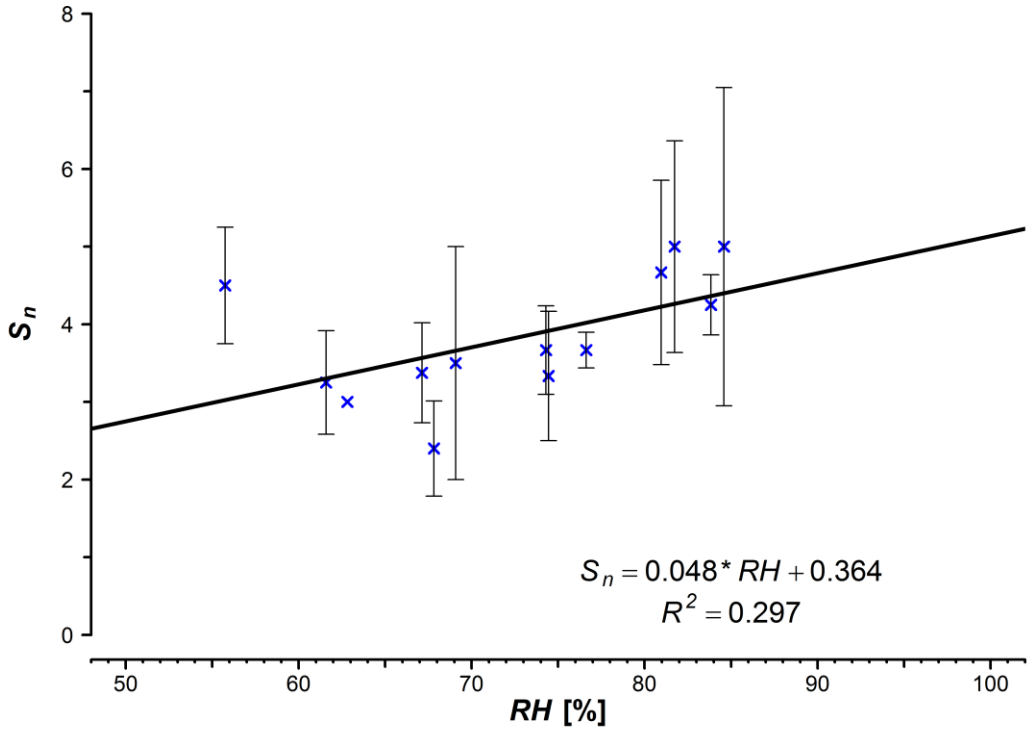

Figure S3b

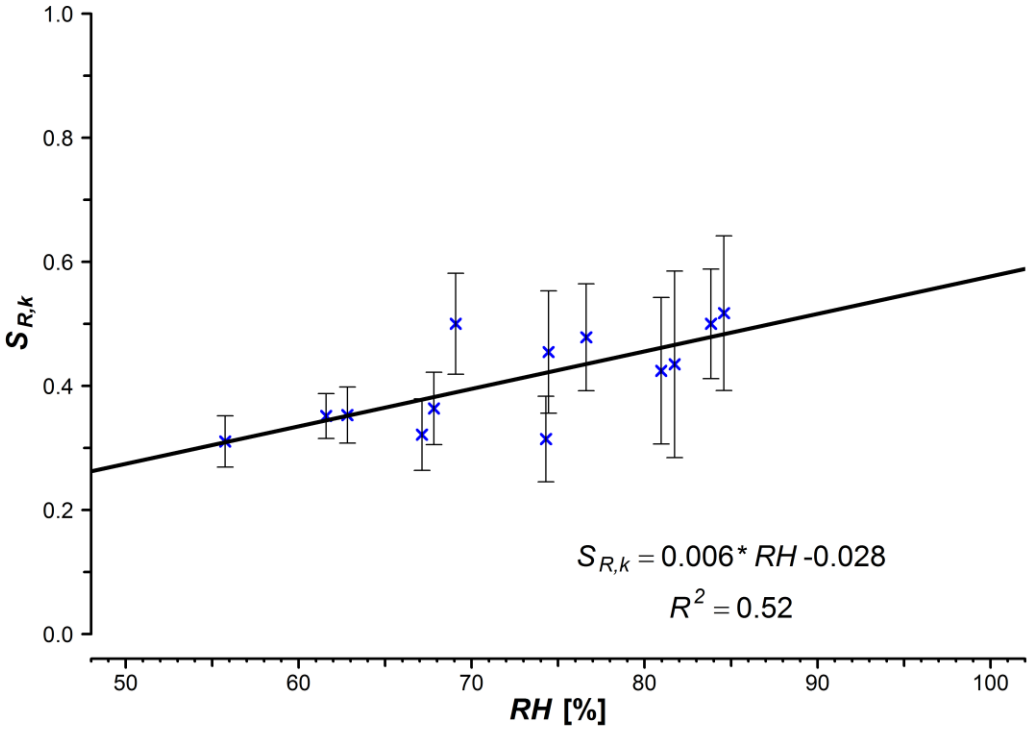

Figure S3c

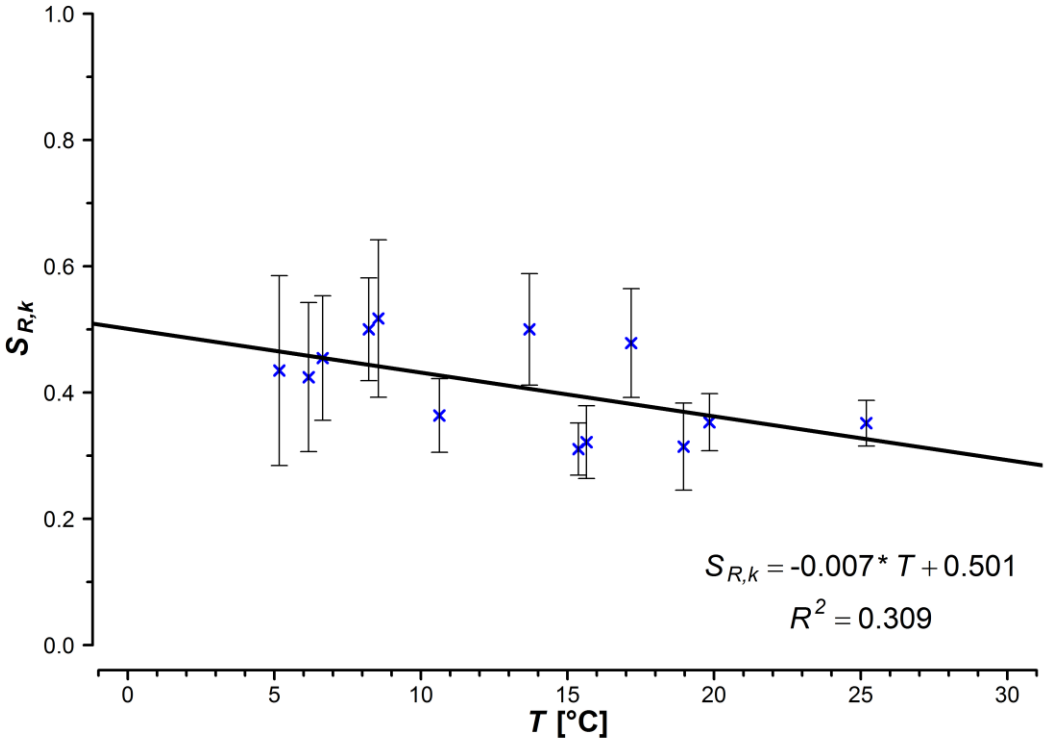

Figure S3: The most significant results of a single variable linear regression analysis between the two dependent variables, normalized species richness per month (S_n) and relative species diversity per month ($S_{R,k}$), and meteorological factors. The values for S_n and $S_{R,k}$ were calculated with the equations given in Table S3 (a) S_n as a function of *RH* (p-value = 0.055). Error bars: $SE_n(S_n)$ (b) The relative species diversity per month ($S_{R,k}$) as a function of *RH* (p-value = 0.005). Error bars: $SE_n(S_{R,k})$ (c) The relative Species per month ($S_{R,k}$) as a function of T (p-value = 0.048). Error bars: $SE_n(S_{R,k})$. *RH*: average relative humidity [%], *T*: average temperature [°C].

Supplement Tables S1-S7

Table S1. Overview of air samples (aerosol filters) positive for DNA analysis. Sample ID (location and running number), sampling period, sequence region (16S rRNA gene, *amoA*), number of sequences obtained. Abbreviation of sampling location: Cape Verde (CV), China (CH), Germany (MZ), North America (NA), United Kingdom (UK).

Sample ID	**Sampling period**	**Sequence region**	**Number of sequences (16S, *amoA*)**
MZ 1	24.03.2006 - 31.03.2006	16S	5
MZ 2	31.03.2006 - 07.04.2006	16S	8
MZ 4	07.04.2006 - 12.04.2006	16S, *amoA*	11, 12
MZ 6	15.04.2006 - 18.04.2006	16S	4
MZ 9	20.04.2006 - 27.04.2006	16S	5
MZ 10	27.04.2006 - 02.05.2006	16S	5
MZ 11	02.05.2006 - 03.05.2006	16S	7
MZ 15	04.05.2006 - 09.05.2006	16S, *amoA*	16, 12
MZ 18	12.05.2006 - 15.05.2006	16S	7
MZ 19	15.05.2006 - 16.05.2006	16S	7
MZ 21	17.05.2006 - 18.05.2006	16S	4
MZ 24	18.05.2006 - 22.05.2006	16S	13
MZ 25	22.05.2006 - 23.05.2006	16S	12
MZ 26	23.05.2006 - 30.05.2006	16S, *amoA*	18, 12
MZ 31	01.06.2006 - 06.06.2006	16S	8
MZ 33	08.06.2006 - 13.06.2006	16S	10
MZ 35	14.06.2006 - 21.06.2006	16S	6
MZ 36	21.06.2006 - 22.06.2006	16S, *amoA*	10, 4
MZ 40	27.06.2006 - 04.07.2006	16S, *amoA*	9, 12
MZ 41	04.07.2006 - 11.07.2006	16S	5
MZ 45	19.07.2006 - 21.07.2006	16S	18
MZ 47	26.07.2006 - 02.08.2006	16S	5
MZ 50	02.08.2006 - 09.08.2006	16S, *amoA*	9, 12
MZ 51	09.08.2006 - 16.08.2006	16S	5
MZ 52	16.08.2006 - 23.08.2006	16S, *amoA*	9, 3
MZ 54	30.08.2006 - 06.09.2006	16S, *amoA*	19, 12
MZ 59	11.09.2006 - 18.09.2006	16S	11

MZ 60	18.09.2006 - 25.09.2006	16S, *amoA*	5, 12
MZ 62	02.10.2006 - 09.10.2006	16S, *amoA*	6, 9
MZ 63	09.10.2006 - 16.10.2006	16S, *amoA*	12, 9
MZ 66	16.10.2006 - 23.10.2006	16S	4
MZ 67	23.10.2006 - 30.10.2006	16S, *amoA*	12, 12
MZ 69	02.11.2006 - 09.11.2006	16S	20
MZ 71	16.11.2006 - 23.11.2006	16S	1
MZ 74	23.11.2006 - 30.11.2006	16S	8
MZ 75	30.11.2006 - 07.12.2006	16S	18
MZ 77	14.12.2006 - 21.12.2006	16S	5
MZ 81	28.12.2006 - 04.01.2007	16S	5
MZ 82	04.01.2007 - 11.01.2007	16S	8
MZ 84	18.01.2007 - 25.01.2007	16S	9
MZ 88	01.02.2007 - 08.02.2007	16S, *amoA*	3, 7
MZ 90	15.02.2007 - 22.02.2007	16S, *amoA*	9, 9
MZ 93	22.02.2007 - 01.03.2007	16S, *amoA*	21, 11
MZ 95	08.03.2007 - 15.03.2007	16S, *amoA*	9, 4
MZ 97	22.03.2007 - 29.03.2007	16S	5
MZ 101	05.04.2007 - 12.04.2007	16S, *amoA*	15, 12
MZ 103	19.04.2007 – 26.04.2007	16S, *amoA*	14, 12
CV 1*	03.02.2011 - 04.02.2011	16S	10
CV 2	04.02.2011 - 05.02.2011	16S	9
CV 4	05.02.2011 – 06.02.2011	16S	10
CV 5	06.02.2011 - 07.02.2011	16S	11
CV 6	07.02.2011 - 08.02.2011	16S	4
CV 17	17.02.2011 - 19.02.2011	16S	6
CV 19	21.02.2011 - 23.02.2011	16S	5
CV 20	23.02.2011 - 24.02.2011	16S	9
CV 21	24.02.2011 - 27.02.2011	16S	4
CV 27	08.03.2011 - 11.03.2011	16S	4
NA 1*	24.07.2011 - 25.07.2011	16S	20
CH 4*	10.07.2006 - 11.07.2006	16S	7
UK 1*	06.05.2004 - 13.05.2004	16S	11

*For CV 26, NA 20, CH 14 and UK 12 air filter samples were tested in total (Table 1)

Table S2. Information on the sequences (16S rRNA gene) used for constructing phylogenetic trees. Accession numbers are given as well as the name of the species if available. Phylogenetic trees where these sequences have been used can be found in Figures 2 and S1.

	Acc Nr	Taxonomy
Euryarchaeota	**Methanosarcinales**	
	M59144	*Methanosarcina barkeri*
	AF028691	*Methanosarcina mazei*
	M59137	*Methanosarcina acetivorans*
	M59135	*Methanolobus concilii*
	M59141	*Methanosaeta thermoacetophila*
	Methanomicrobiales	
	M60880	*Methanospirillum hungatei*
	M59134	*Methanoculleus marisnigri*
	M59131	*Methanogenium organophilum*
	Methanobacteriales	
	M59124	*Methanobacterium bryantii*
	AF028690	*Methanobacterium oryzae*
	M36508	*Methanobacterium formicicum*
	AY196684	*Methanosphaera stadtmaniae*
	NR074235	*Methanobrevibacter smithii*
	NR044801	*Methanobrevibacter filiformis*
	Methanocellales	
	AB196288	*Methanocella paludicola*
	AM114193	*Methanocella arvoryzae*
	Thermoplasmatales	
	M38637	*Thermoplasma acidophilum*
	AJ224936	*Ferroplasma acidophilum*
	AF050618	*WCHD3-16, Thermoplasmatales*
	Methanococcales	
	M36507	*Methanococcus vannielii*
	M59126	*Methanocaldococcus jannaschii*
	U38484	*Methanococcus maripaludis*
Euryarchaeota	**Halobacteriales**	
	DQ256409	*Haladaptatus jilantaiense*
	EU887285	*Haladaptatus litoreus*
	DQ344973	*Haladaptatus paucihalophilus*
	DQ344974	*Haladaptatus paucihalophilus*
	GQ282623	*Halgranum amylolyticum*
	GQ282624	*Halgranum gelatinilyticum*
	EF645681	*Haloarcula argentinensis*
	EF645693	*Haloarcula marismortui*
	EF645688	*Haloarcula vallismortis*
	GQ282625	*Halobacteriaceae archaeon*
	AJ002949	*Halobacterium halobium*
	M38280	*Halobacterium halobium*
	U17364	*Halobacterium saccharovorum*
	AJ002947	*Halobacterium salinarium*
	AJ496185	*Halobacterium salinarum*
	U68538	*Halobacterium salinarum*
	AJ548827	*Halobacterium sp*
	D11106	*Halococcus morrhuae*
	AB004877	*Halococcus salifodinae*

Euryarchaeota	Z28387	*Halococcus salifodinae*
	AB037474	*Haloferax alexandrines*
	D14128	*Haloferax denitrificans*
	AJ420376	*Haloferax dombrowskii*
	AY458601	*Haloferax sulfurifontis*
	AY425724	*Haloferax volcanii*
	AF002984	*Halogeometricum borinquenss*
	EU887286	*Halogeometricum rufum*
	EU887283	*Halogranum rubrum*
	DQ417339	*Haloplanus natans*
	EU931578	*Haloplanus sp.*
	DQ987877	*Halorubrum luteum*
	AY149598	*Halorubrum tibetense*
	D14125	*Halorubrum trapanicum*
	EU931577	*Halosarcina limi*
	AB454051	*Salarchaeum japonicum*
	JN196516	*Salarchaeum sp.*
Thaumarchaeota	**Group I.1a**	
	U51469	*Cenarchaeum symbiosum*
	DQ085097	*Nitrosopumilus maritimus*
	AEGP01000029	*Cnitrosoarchaeum limnia*
	Group I.1b	
	EU281334	*Nitrososphaera gargensis*
	FR773157	*Nitrososphaera viennensis*
	FR773158	*Nitrososphaera sp.*
	Group I.1c	
	AJ006919	*FFSC1, Thaumarchaeota, I.1c*
	X96691	*FFSB4, Thaumarchaeota, I.1c*
	Group III	
	EU239960	*Nitrosocaldus yello*wstonii
	Soil Crenarchaeotic Group (SGC)	
	GQ871309	*W5P1-DO1, Thaumarchaeota, SGC*
	FJ468477	*F5, Thaumarchaeota, SCG*
	AJ535123	*Gitt-GR, Thaumarchaeota, SCG*
Thaumarchaeota	**Terrestrial Group (TG)**	
	EF021006	*Amb_16S, Thaumarchaeota, TG*
	AY278081	*GRU10, Thaumarchaeota, TG*
	FJ174722	*Arc-D88, Thaumarchaeota, TG*
	South African Gold Mine Group (SAGMGC)	
	AB550811	*NG-W-081028-3-5. Thaumarchaeota, SAGMGC*
	EU306977	*ArcB-cD06, Thaumarchaeota, SAGMGC*
	Dominant Soil Crenarchaeotic Group (DSC)	
	AY278106	*Thaumarchaeota, DSC1*
	EU281336	*Thaumarchaeota, DSSC2*
Crenarchaeota	**Crenarchaeota**	
	JN881579	*Caldiarchaeum*
	HQ214608	*Miscellaneous Crenarchaeotic Group*
	GQ267189	*Marine Benthic Group*
	JN227488	*Nitrosotalea devanaterra*
	Thermoproteales	
	NR040935	*Pyrobaculum*
	HF546082	*Sulfolobales*
	KC139249	*Desulfurcoccales*
	NR041774	*Acidilobales*
	EF552404	*Fervivicoccales*

Table S3. Definitions.

Symbol	Quantity/ Definition
D	Simpson's index (Hill et al., 2003), $\mathrm{D} = \sum_{i=1}^{S} \frac{n_i(n_i-1)}{N(N-1)}$
E	Shannon evenness, $E=H'/\ln S$
H'	Shannon index, $H' = -\sum_{i=1}^{S}(P_i \ln P_i)$
m_j	Number of sequences analyzed for air sample j
m_k	Number of sequences analyzed for air samples in a month k
n_i	Frequency of occurrence of an individual species i (number of samples in which species i was detected)
N	Cumulative frequency of occurrence of investigated sample, $N = \sum_{i=1}^{S} n_i$
n	Number of investigated air samples
P_i	Relative proportion of an individual species i, $P_i = n_i/N$
S	Species richness measured (number of detected individual species)
S_j	Number of detected individual species in air sample j
S_k	Number of detected individual species in air samples of a month k
S^*	Species richness estimated with the Chao-1 approach (Chao, 1984; Hill et al., 2003), $S^*=S + a^2/(2b)$, a = number of species detected only once (singletons) b = number of species detected twice (doubletons)
S_n	Normalized species richness, $S_n = S/n$
$S_{R,j}$	Relative species diversity per sample, $S_{R,j} = S_j/m_j$
$S_{R,k}$	Relative species diversity per month, $S_{R,k} = S_k/m_k$
$SE_n(S_n)$	Normalized standard error of S_n: $= \frac{SE_{\bar{S}}}{\bar{S}} S_n$ $\bar{S}$ = average number of species per sample $SE_{\bar{S}}$ = standard error of $\bar{S}$
$SE_n(S_{R,k})$	Normalized standard error of $S_{R,k}$: $= \frac{SE_{\overline{S_{R,J}}}}{\overline{S_{R,J}}} S_{R,k}$ $\overline{S_{R,J}}$ = average relative species diversity per sample $SE_{\overline{S_{R,J}}}$ = standard error of $\overline{S_{R,J}}$

Table S4: Estimates of the abundance of Bacteria and Archaea in different environments. The number of copies (cp) of the 16S rRNA gene was quantified using qPCR.

Source	Archaea	Bacteria	Ratio A/B	Reference
Soil [cp kg^{-1}]	~10^{9} – 10^{11}	~10^{11} – 10^{12}	~10^{-2} – 10^{-1}	Cao et al., 2012; Kemnitz et al., 2007
Ocean surface water [cp L^{-1}]	~10^{6} – 10^{7}	~10^{8} – 10^{9}	~10^{-2}	Yin et al. 2013
Air [cp m^{-3}]	~1 – ~10^{1}	~10^{4} – 10^{6}	~10^{-4} – 10^{-6}	This study

Table S5. Operational taxonomic units (OTUs) attributed to Archaea 16S rRNA genes. Operational ID; frequency of occurrence (number of air samples and coarse or fine particle filters in which the OTU was detected (n.a.= not available); taxonomic family and genus name according to phylogenetic analysis based on the Maximum likelihood approach. Information is given for Germany, Cape Verde, United Kingdom, China, and North America.

OTU	**Frequency of occurrence**			**Family, genus**
Germany	**total**	**coarse**	**fine**	
Arch1	33	32	2	*Thaumarchaeota, former Group I 1b*
Arch2	26	26	0	*Thaumarchaeota, former Group I 1b*
Arch3	20	20	4	*Thaumarchaeota, former Group I 1b*
Arch4	17	16	2	*Thaumarchaeota, former Group I 1b*
Arch5	15	15	0	*Thaumarchaeota, former Group I 1b*
Arch6	13	13	1	*Thaumarchaeota, former Group I 1b*
Arch7	11	11	0	*Thaumarchaeota, former Group I 1b*
Arch8	9	9	0	*Thaumarchaeota, former Group I 1b*
Arch9	8	7	1	*Thaumarchaeota, former Group I 1b*
Arch10	8	7	1	*Thaumarchaeota, former Group I 1b*
Arch11	7	7	0	*Thaumarchaeota, former Group I 1b*
Arch12	5	4	1	*Methanosarcinaceae, Methanosarcina*
Arch13	5	4	1	*Methanobacteriaceae; Methanosphaera*
Arch14	5	5	0	*Thaumarchaeota, former Group I 1b*
Arch15	4	4	0	*Thaumarchaeota, former Group I 1b*
Arch16	3	2	1	*Methanobacteriaceae*
Arch17	3	3	0	*Thaumarchaeota, former Group I 1b*

Arch18	3	3	0	*Thaumarchaeota, former Group I 1b*
Arch19	3	3	0	*Thaumarchaeota, former Group I 1b*
Arch20	3	3	0	*Thaumarchaeota, former Group I 1b*
Arch21	2	2	0	*Thaumarchaeota, former Group I 1b*
Arch22	2	2	0	*Thaumarchaeota, former Group I 1b*
Arch23	2	2	0	*Thaumarchaeota, former Group I 1b*
Arch24	2	2	0	*Thaumarchaeota, former Group I 1b*
Arch25	2	2	0	*Thaumarchaeota, former Group I 1b*
Arch26	2	2	0	*Thaumarchaeota, former Group I 1b*
Arch27	1	1	0	*Thermoplasmatales*
Arch28	1	0	1	*Halobacteriaceae, Halococcus*
Arch29	1	1	0	*Methanobacteriaceae, Methanobrevibacter*
Arch30	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch31	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch32	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch33	1	1	0	*Methanomicrobiaceae; Methanoculleus*
Arch34	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch35	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch36	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch37	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch38	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch39	1	0	1	*Thaumarchaeota, former Group I 1b*

Arch40	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch41	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch42	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch43	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch44	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch45	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch46	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch47	1	0	1	*Thaumarchaeota, former Group I 1b*
Arch48	1	1	0	*Methanobacteriaceae, Methanobrevibacter*
Arch49	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch50	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch51	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch52	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch53	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch54	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch55	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch56	1	1	0	*Thaumarchaeota, former Group I 1b*
Arch57	1	1	0	*Thaumarchaeota, former Group I 1b*

OTU	**Frequency of occurrence**			**Family, genus**
Cape Verde				
	total	**coarse**	**fine**	
CV1	1	n.a.	n.a.	*Halobacteriaceae*

CV2	1	n.a.	n.a.	*Thaumarchaeota, former Group I 1b*
CV3	1	n.a.	n.a.	*Halobacteriaceae, Halococcus*
CV4	1	n.a.	n.a.	*Thaumarchaeota, former Group I 1b*
CV5	1	n.a.	n.a.	*Thaumarchaeota, former Group I 1b*
CV6	1	n.a.	n.a.	*Thaumarchaeota, former Group I 1b*
CV7	1	n.a.	n.a.	*Thermoplasmatales*
CV8	1	n.a.	n.a.	*Thaumarchaeota, former Group I 1b*
CV9	1	n.a.	n.a.	*Halobacteriaceae*
CV10	1	n.a.	n.a.	*Thaumarchaeota, former Group I 1b*
CV11	1	n.a.	n.a.	*Thaumarchaeota, former Group I 1b*
CV12	1	n.a.	n.a.	*Thermoplasmatales*
CV13	1	n.a.	n.a.	*Thermoplasmatales*
CV14	1	n.a.	n.a.	*Thaumarchaeota, former Group I 1b*
CV15	1	n.a.	n.a.	*Halobacteriaceae*
CV16	1	n.a.	n.a.	*Halobacteriaceae*
CV17	1	n.a.	n.a.	*Halobacteriaceae*
CV18	1	n.a.	n.a.	*Thaumarchaeota, former Group I 1b*
CV19	1	n.a.	n.a.	*Thaumarchaeota, former Group I 1b*
CV20	1	n.a.	n.a.	*Thaumarchaeota, former Group I 1b*
CV21	1	n.a.	n.a.	*Thaumarchaeota, former Group I 1b*
CV22	1	n.a.	n.a.	*Thermoplasmatales*
CV23	1	n.a.	n.a.	*Thaumarchaeota, former Group I 1b*

CV24	1	n.a.	n.a.	*Thaumarchaeota, former Group I 1b*
CV25	1	n.a.	n.a.	*Thaumarchaeota, former Group I 1b*
OTU	**Frequency of occurrence**			**Family, genus**
UK	**total**	**coarse**	**fine**	
UK1	1	n.a.	n.a.	*Thermoplasmatales*
UK2	1	n.a.	n.a.	*Thermoplasmatales*
UK3	1	n.a.	n.a.	*Thermoplasmatales*
UK4	1	n.a.	n.a.	*Thermoplasmatales*
OTU	**Frequency of occurrence**			**Family, genus**
China	**total**	**coarse**	**fine**	
Ch1	1	n.a.	n.a.	*Methanobacteriaceae*
OTU	**Frequency of occurrence**			**Family, genus**
North America	**total**	**coarse**	**fine**	
Col1	1	n.a.	n.a.	*Thaumarchaeota, former Group I 1b*

Table S6: Pearson coefficients results. Pearson coefficients between the diversity indices $S_{R,j}$, S_n and $S_{R,k}$, and the meteorological factors, average temperature (Temp), average relative humidity (RH), average wind speed (WS) and sum of precipitation (Precip). The asterix mark the cases selected for further testing (See Table S7 and Figures S2a, S3).

	Temp	**RH**	**WS**	**Precip**
$S_{R,j}$	-0.051	0.238	-0.357 *	0.087
S_n	-0.431	0.545 *	-0.302	-0.265
$S_{R,k}$	-0.556*	0.721 *	0.170	0.236

Table S7: Overview the most significant results of the linear regression analysis between the Archaea 16S rRNA gene sequence diversity and meteorological parameters. The "+" and "–" specify whether the diversity parameter has a positive or negative correlation to the meteorological factor (Temp = temperature, RH = relative humidity, WS = wind speed, Precip = precipitation, Sign = significance).

		Temp	RH	WS	Precip	R^2	p-value	Sign.
per sample	Best single variable							
	$S_{R,j}$ (Fig. S2a)			-		0.132	0.012	<0.05
	Best variable subset							
	$S_{R,j}$ (Fig. S2b)		+	-		0.174	0.015	<0.05
per month	Best single variable							
	S_n (Fig. S3a)		+			0.297	0.054	~0.05
	$S_{R,k}$ (Fig. S3b)		+			0.520	0.005	<0.01
	$S_{R,k}$ (Fig. S3c)	-				0.309	0.049	<0.05
	Best variable subset							
	S_n (Fig. 4a)	-		-		0.533	0.022	<0.05
	$S_{R,k}$ (Fig. 4b)		+	+		0.598	0.011	~ 0.01

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