Supporting Information

The Microbiome of Size-Fractionated Airborne Particles from the Sahara Region

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Table S1. Average meteorological conditions on sampling days at the collection site in Bamako, Mali (Latitude 12.332 N, Longitude -7.578 W, 389 m above sea level).

Date	Sampling Day	Wind speed (m/s)	Relative humidity (%)	Majority wind direction[a]	Air temperature (°C)	Barometric pressure (mm Hg)
Feb. 11, 2018	1	1.51	6.1	NNE	30.3	29.87
Feb. 13, 2018	2	1.23	6.5	NNE	33.5	29.86
Feb. 14, 2018	3	0.99	4.8	NE	35.1	29.84
Feb. 15, 2018	4	1.41	2.6	NNE	36.0	29.87
Feb. 16, 2018	5	1.41	2.0	ENE	37.1	29.89
Feb. 17, 2018	6	1.26	4.2	NNE	37.3	29.83
Feb. 18, 2018	7	1.25	4.0	NNE	39.1	29.78
Feb. 19, 2018	8	1.14	10.3	NE	38.2	29.75
Feb. 20, 2018	9	1.58	9.4	NNE	33.0	29.79

[a] Wind direction is expressed as majority wind direction, calculated by categorizing the instantaneous wind velocity into cardinal wind directions and taking the majority from each sampling day.

Table S2. Samples tested for species with known pathogenic strains using PCR.

Pathogen target	Sample Tested	Particle Size (µm)	+ / -
Bacillus cereus	D2.C.F	<0.5	+
	D3.C.F	<0.5	+
	D7.C.P1	2.5-1.0	-
Escherichia coli	D3.C.F	<0.5	+
	D3.C.P1	2.5-1.0	-
	D9.C.P0.5	1.0-0.5	+
Fusobacterium nucleatum	D6.C.P1	2.5-1.0	+
	D3.C.P0.5	1.0-0.5	-
	D9.C.F	<0.5	-
	D4.C.P2.5	10.0-2.5	+
Streptococcus pneumoniae	D3.C.P0.5	1.0-0.5	-
Staphylococcus epidermidis	D9.C.P2.5	10.0-2.5	-
	D8.C.P1	2.5-1.0	-
	D5.C.P0.5	1.0-0.5	-
	D4.C.P1	2.5-1.0	-
Pseudomonas aeruginosa	D3.C.P2.5	10.0-2.5	+

Table S3. Primer set sequences for PCR of potential pathogens.

Species	***Primer sequence***
Escherichia coli	EcoliuidA_FPrimer: CGGAAGCAACGCGTAAACTC EcoliuidA_RPrimer: TGAGCGTCGCAGAACATTACA EcoliuidA_Probe: /56-FAM/CGCGTCCGATCACCTGCGTC/3BHQ_1/
Pseudomonas aeruginosa	pseuF: ACTTTAAGTTGGGAGGAAGGG pseuR: ACACAGGAAATTCCACCACCC pseuProbe: Fam-ACAGAATAAGCACCGGCTAAC-BHQ
Streptococcus pneumoniae	Sp-lytAF: ACG CAA TCT AGC AGA TGA AGC A Sp-lytAR: TCG TGC GTT TTA ATT CCA GCT Sp-lytAP: /56-FAM/CCGAAAACGCTTGATACAGGGAG/3BHQ_1/
Staphylococcus epidermidis	StaphepiF: ACTGGTTACCCTGGTGACAAACCA StaphEpiR: ACTGGAGATCCAGAGTTTCCACCT staphepiProbe: /56-FAM/AGCCACAATGTGGGAAAGTGTAGGT/3BHQ_1/
Bacillus cereus	bacCereusF: CTGTAGCGAATCGTACGTATC bacCereusR: TACTGCTCCAGCCACATTAC bacCereusP: /56-FAM/GGAGCTGTACAACTTGCCA/3BHQ_1/
Fusobacterium nucleatum	FnucleatF-R-P: proprietary

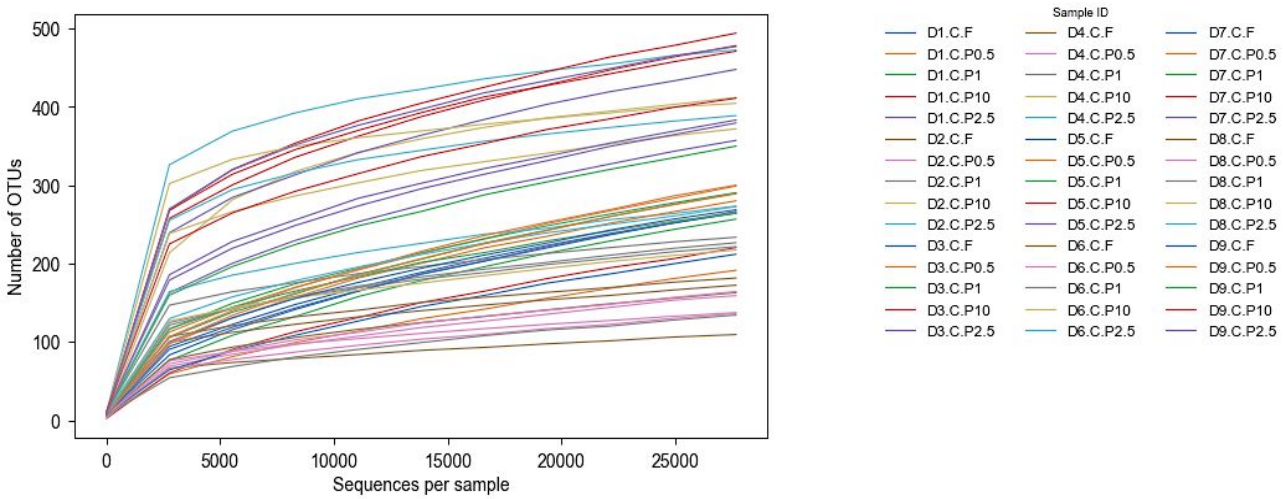

Figure S1. Rarefaction curves of operational taxonomic units (OTUs) clustered at 99% sequence identity across all samples.

Table S4. Taxonomic assignment for OTUs that differed significantly across the various particle sizes and the particle size fraction with greatest abundance.

Taxonomic Assignment	Particle size preference (µm)
p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Geodermatophilaceae; g__Geodermatophilus; s__obscurus	>10.0
p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Aerococcaceae; g__; s__	10.0-2.5
p__Firmicutes; c__Clostridia; o__Clostridiales; f__Ruminococcaceae; g__; s__	>10.0
p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Intrasporangiaceae	10.0-2.5
p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Intrasporangiaceae	10.0-2.5
p__Firmicutes; c__Clostridia; o__Clostridiales; f__Ruminococcaceae; g__; s__	>10.0
p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae	2.5-1.0
p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Corynebacteriaceae; g__Corynebacterium; s__	2.5-1.0
p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Geodermatophilaceae; g__Geodermatophilus; s__obscurus	>10.0
p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Nocardioidaceae; g__; s__	10.0-2.5
p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Corynebacteriaceae; g__Corynebacterium; s__	2.5-1.0
p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Bradyrhizobiaceae; g__Balneimonas; s__	10.0-2.5
p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Moraxellaceae; g__Psychrobacter; s__pulmonis	>10.0
p__Actinobacteria; c__Actinobacteria; o__Actinomycetales	>10.0

Additional Text: Difference in bacterial diversity across particle sizes

Additional details on genera detected and corresponding potential sources are presented in Additional Text Table 1. At the genus level, *Geodermatophilus,* a soil-associated genus, was more abundant in the largest (>10 μm) size fraction (Kruskal-Wallis test, FDR $p<0.05$). Prior work found strains of *Geodermatophilus* in 1-2 mm sand from the Saharan desert,[1] consistent with detection in this study preferentially on the largest particle sizes. The *Ruminococcaceae* family exhibited a preference for the largest particle size fraction (Kruskal-Wallis, FDR $p<0.05$). This family was previously identified as an indicator for bovine fecal contamination.[2] The family *Dermatophilaceae*, which are common on animal and human skin, were most abundant in the largest two size fractions. Our sampling location was 11 km downwind of a cattle market, which could be a source of large, locally generated particles with distinct microbial composition.

One taxonomic class (Thermomicrobia) out of the 62 classes detected statistically differed among the five atmospheric particle sizes (Kruskal-Wallis test, FDR $p<0.05$), with greatest abundance in the particle size range of 10.0-2.5 μm. This class has been found in a wide range of soil types, typically isolated from human activity.[3] Thermomicrobia were previously found in the desert soil of the Sahara[4], indicating the potential for local sources with larger particles that did not yet fall out due to gravitational settling.

Additional Text Table 1. Genera detected in the samples and corresponding potential sources.

Soil	Skin	Stool	Compost	Wastewater Treatment	Land Application Biosolids
Bradyrhizobium	*Propionbacterium*	*Bacteroides*	*Saccharopolyspora*	*Arcobacter*	*Clostridium*
Mesorhizobium	*Staphylococcus*	*Faecalibacterium*			
	Corynebacterium	*Oscillospira*			
	Streptococcus	*Roseburia*			
	Rothia	*Coprococcus*			
	Micrococcus	*Ruminococcus*			
	Anaerococcus	*Parabacteroides*			
	Brevibacterium	*Phascolarctobacterium*			
		Sutterella			
		Blautia			

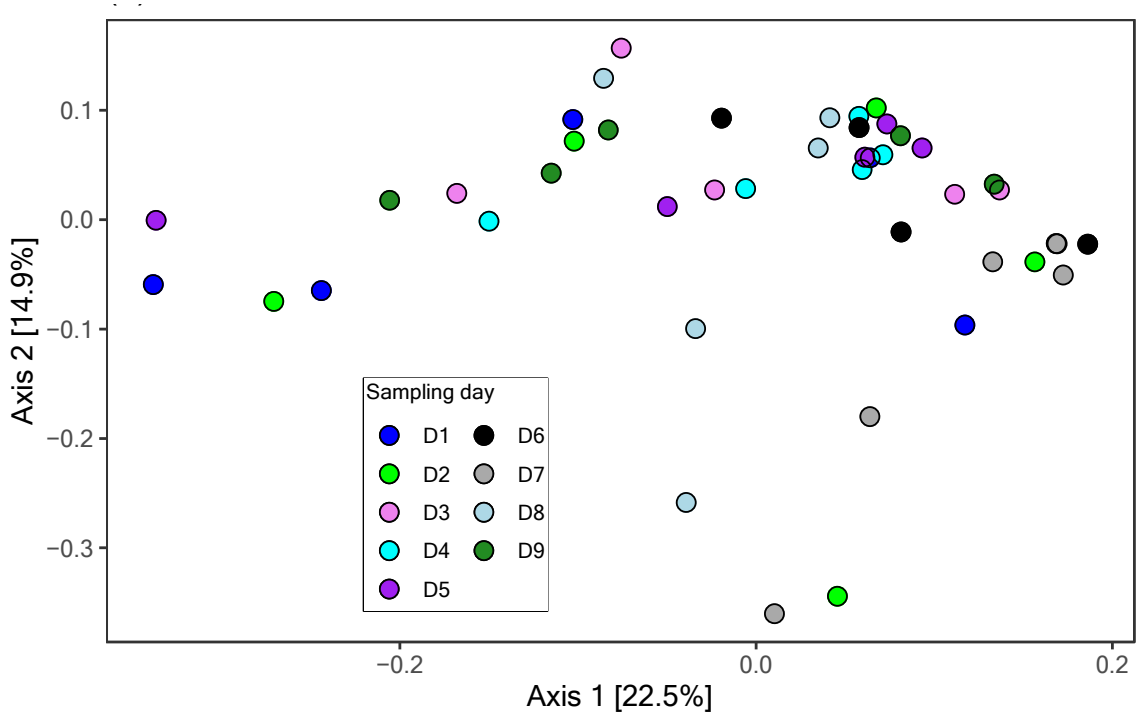

Figure S2. Community analysis using pairwise, weighted UniFrac distances visualized on a principal coordinates analysis (PCoA) plot with the percent of variation explained by each axis noted in brackets. Samples were grouped by sampling day.

Table S6. Taxa detected with features for survival in harsh atmospheric conditions.

Taxa detected in the samples	Relevant trait
Burkholderiales, Pseudomonadales, Flavobacteriales	Common in outdoor air[5]
Bacillaceae	Forms endospores
Gemmatimonadetes, Thermus, Chloroflexi, *Psychrobacter*, Myxococcales	Commonly found in extreme environments
Gemmatomonadetes, *Deinococcus*	Associated with hyper-arid environments; bioindicators for Saharan dust events[6–8]
Gemmatomonadetes	UV protection during aerial transport due to carotenoid pigmentation[9,10]
Methylobacterium, *Rubrobacter*	Possess structures to resist environmental stresses[6,11]
Arthrobacter, *Methylobacterium*	Dessication-resistant[6]
Bacillus, *Kocuria*, *Micrococcus*	Detected in culture-based air samples in Mali[12]
Bacteroidetes	Preference for desert soils
Cytophagaceae (*Hymenobacter*), *Flavobacteriaceae*	Pigmented and psychrotolerant; previously found in Saharan dust[13]
Nocardioides, Sporichthya, Beijerinckiaceae, Hyphomicrobiaceae, Acetobacteraceae, Skermanella, Rhodocyclaceae, Rhodospirillaceae, Sphingomonadaceae	Motile spores
Mesorhizobium	Motile by symbiosis with plant roots
Patulibacter, Rhodobacteraceae, Modestobacter	Psychrotolerance aids survival in Sahara at night[6]
Rubrobacteraceae, Streptosporangiaceae, Pseudonocardia, Rubellimicrobium, Streptomyces	Heat tolerant and thermophilic[6,14]
Rubrobacter, Hymenobacter, Methylobacterium	Gamma radiation-resistant[6,14]
Bacillus, Paenibacillus, Arthrobacter, Cellulomonas, Janthinobacterium, Modestobacter, Pseudomonas, Sphingomonas	UV resistant[15]
Nocardioides	Halophilic
Bacillaceae, Paenibacillaceae, Bacillus	Spore-forming
Geodermatophilaceae, Pseudonocardiaceae, Rhodocyclaceae, Rubrobacteraceae	oligotrophic
Frankia, Beijerinckiaceae, Bradyrhizobiaceae, Rhizobium, Rhizobiaceae, Mesorhizobium, Azospirillum, Rhodospirillaceae, Frankia, Oxalobacteraceae	Nitrogen-fixing
Methylobacterium	convert nitrogen gas to ammonia and feed on methanol
Hyphomicrobiaceae	phototrophic
Rhodobacteraceae, Rhodocyclaceae, Rhodospirillaceae, Sphingomonas (aerobic)	Photoheterotrophic
Cellulosimicrobium, Actinobacteria	biodegrade cellulose or lignin
Cytophagaceae	Capable of degrading plant material
Clostridiaceae, Fusobacteriaceae, Lactobacillaceae, Oxalobacteraceae, Rhodospirillaceae	Strict anaerobes
Enterobacteriaceae, Myxococcaceae, Rhodospirillaceae	Facultative anaerobes
Methanobacteriales	thermophilic anaerobic methanogens

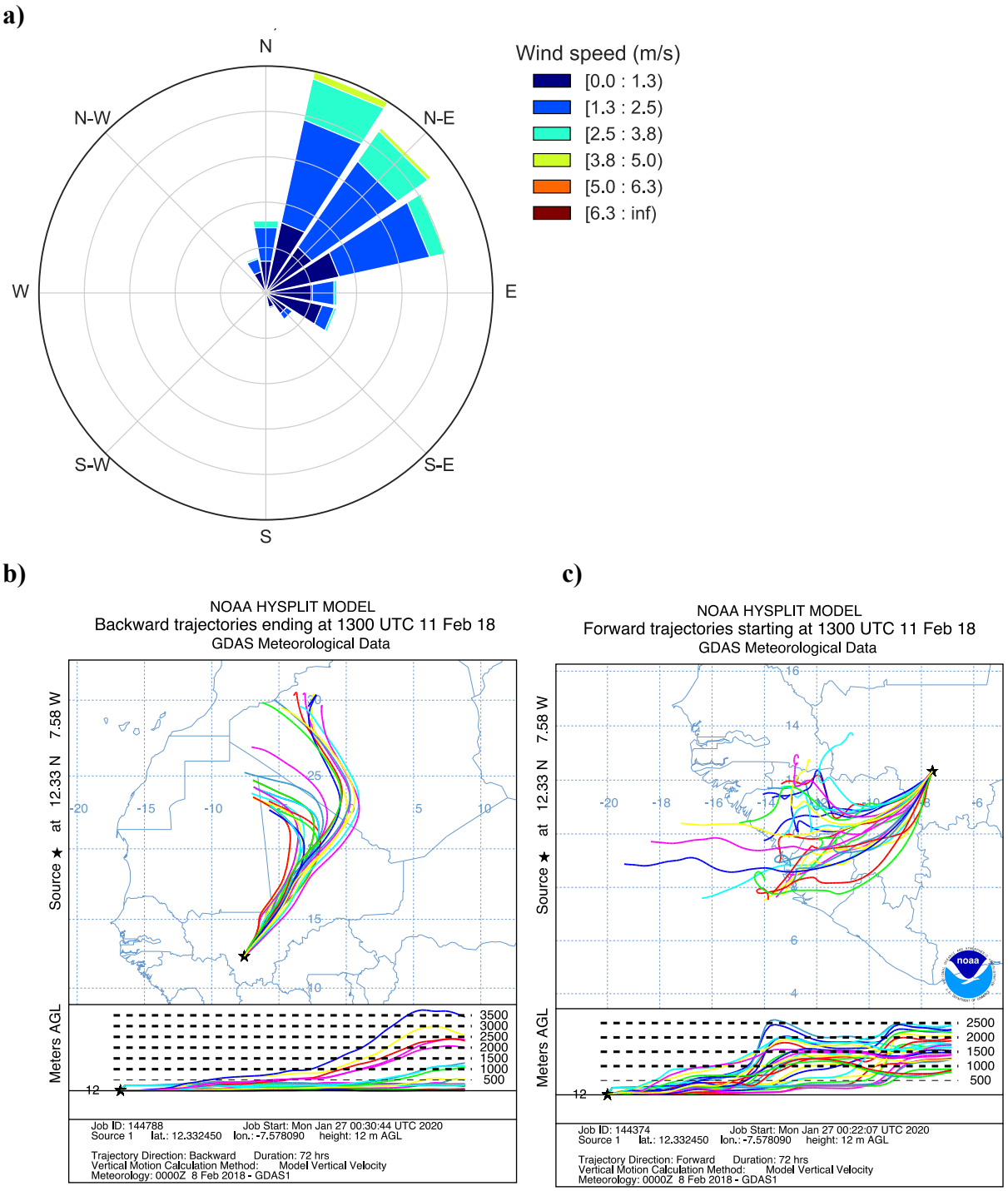

Figure S3. (a) Wind direction and wind speed for sampling day 1 (Feb. 11, 2018); (b) HYSPLIT 72-hour backward trajectories from the sampling site for sampling day 1; HYSPLIT 72-hour forward trajectories from the sampling site for sampling day 1. All other sampling days exhibited wind patterns and trajectories similar to sampling day 1 (Figure S4).

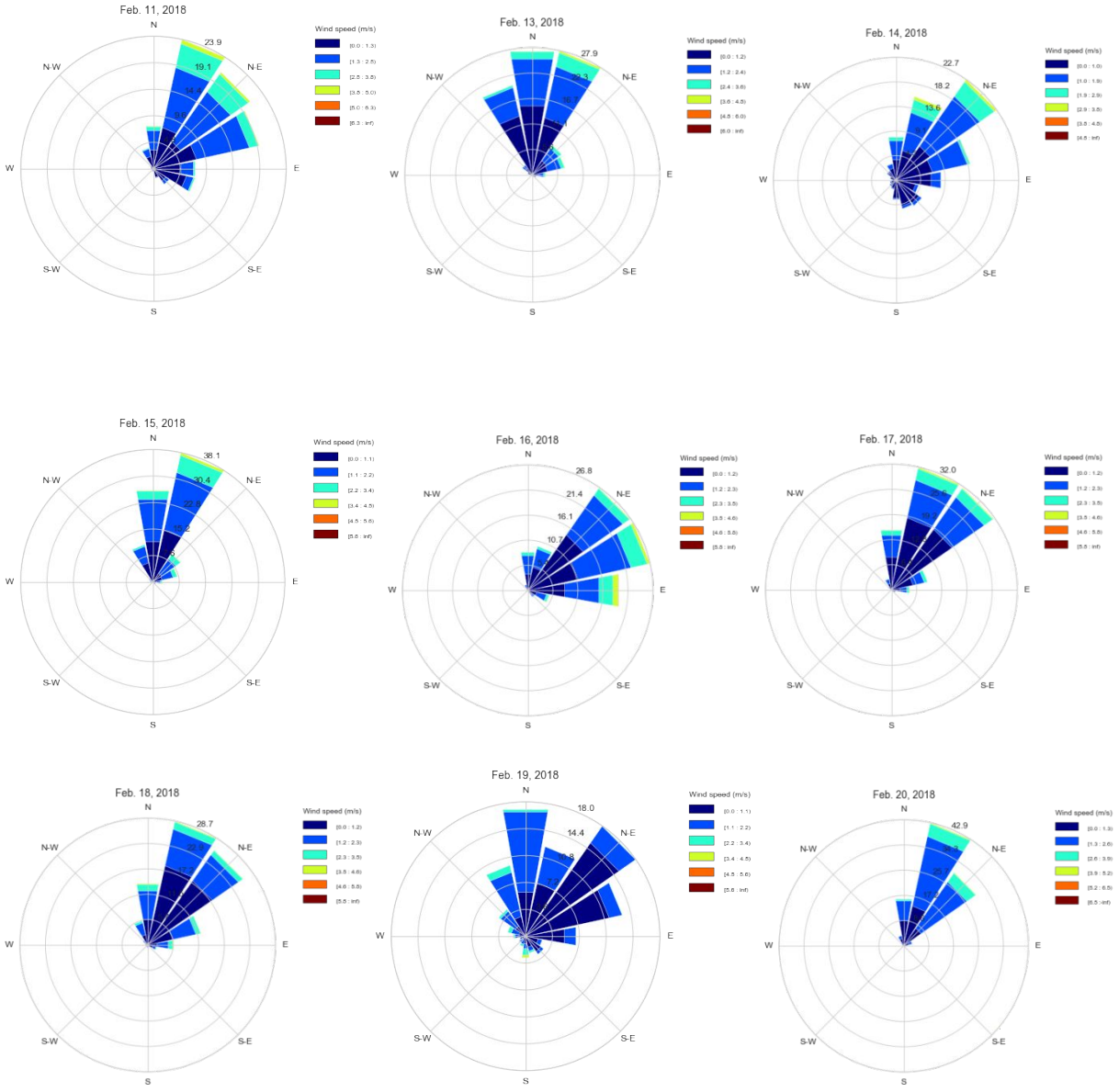

Figure S4. Wind rose plots of instantaneous wind direction and velocity (m s^{-1}) during each of the sampling days reveal the winds were predominantly from the northeast.

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