

Supplementary Material

Temporal Dynamics of Air Bacterial Communities in a University Health Centre using Illumina MiSeq Sequencing

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Figure S1: Map of JNU Health Centre (28.54 N, 77.16 E).

Figure S2: Rarefaction analysis of bacterial communities in air samples collected from indoor and outdoor area of JNU Health Centre in each season: Monsoon Indoor (MI), Monsoon Outdoor (MO), Spring Indoor (SPI), Spring Outdoor (SPO), Summer Indoor (SUI), Summer Outdoor (SUO), Winter Indoor (WI), and Winter Outdoor (WO).

Table S1: Meteorological conditions, PM_{2.5} and PM₁₀ concentration during air sampling at JNU Health Centre in each season: Spring Indoor (SPI), Spring Outdoor (SPO), Monsoon Indoor (MI), Monsoon Outdoor (MO), Winter Indoor (WI), Winter Outdoor (WO), Summer Indoor (SUI), Summer Outdoor (SUO).

Table S2: SRCCs between dominant phyla of bacterial community and Temperature (T), Relative Humidity (RH), PM_{2.5} and PM₁₀.

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Table S4: Numbers of taxa classified at different taxonomic levels in air samples collected from indoor and outdoor area of JNU Health Centre in each season: Spring Indoor (SPI), Spring Outdoor (SPO), Monsoon Indoor (MI), Monsoon Outdoor (MO), Winter Indoor (WI), Winter Outdoor (WO), Summer Indoor (SUI), Summer Outdoor (SUO).

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Table S6: Raw data of ESKAPE pathogens determined in the total sequences acquired in each season: Monsoon Indoor (MI), Monsoon Outdoor (MO), Spring Indoor (SPI), Spring Outdoor (SPO), Summer Indoor (SUI), Summer Outdoor (SUO), Winter Indoor (WI), Winter Outdoor (WO).

Table S7: Inter-phyla correlations using Spearman's Rank Correlation Coefficient (SRCC)

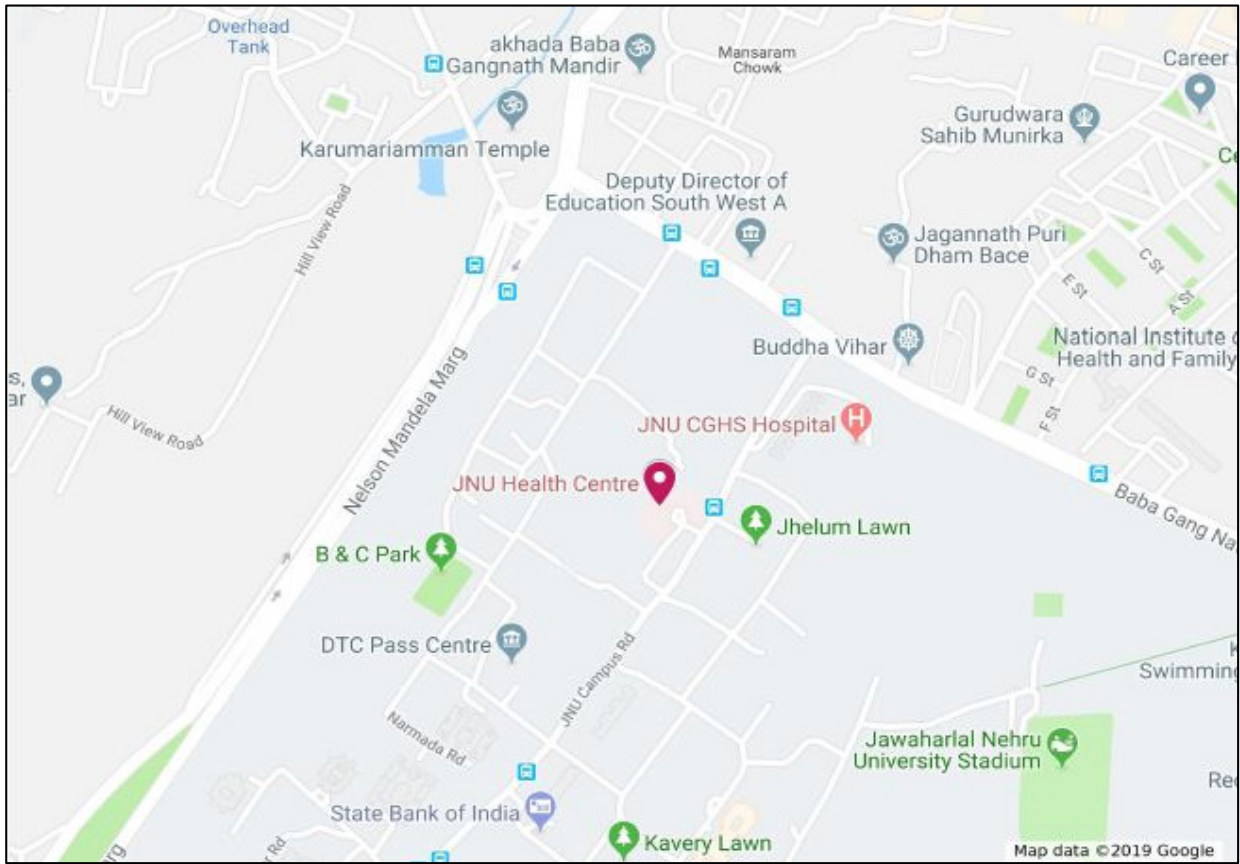


Figure S1: Map of JNU Health Centre (28.54 N, 77.16 E).

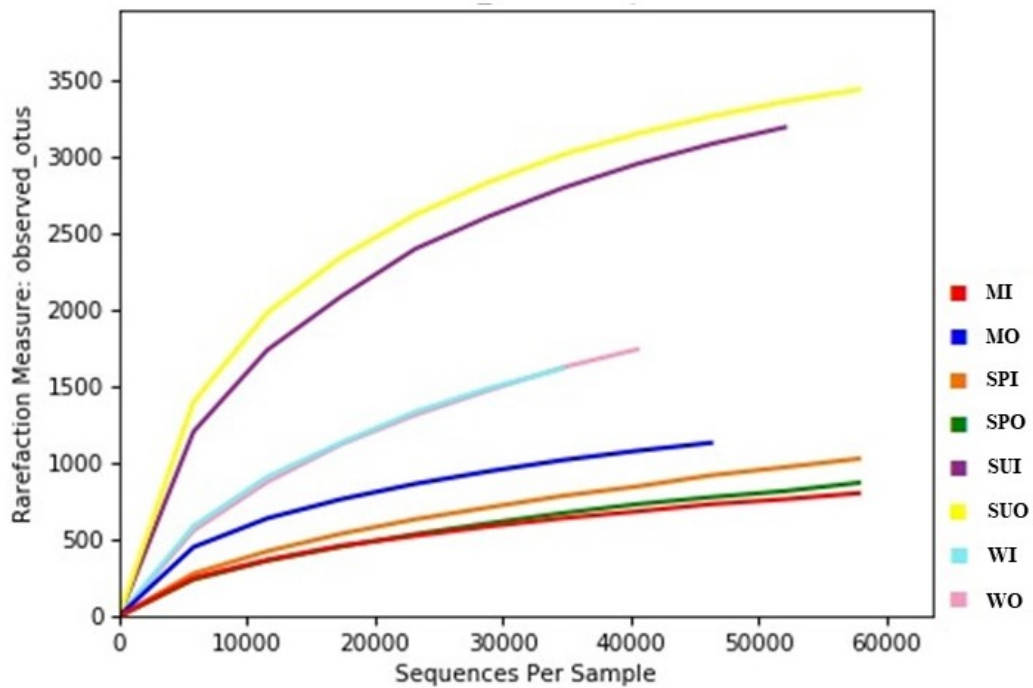


Figure S2: Rarefaction analysis of bacterial communities in air samples collected from indoor and outdoor area of JNU Health Centre in each season: Monsoon Indoor (MI), Monsoon Outdoor (MO), Spring Indoor (SPI), Spring Outdoor (SPO), Summer Indoor (SUI), Summer Outdoor (SUO), Winter Indoor (WI), and Winter Outdoor (WO).

Table S1: Meteorological conditions, PM_{2.5} and PM₁₀ concentration during air sampling at JNU Health Centre in each season: Spring Indoor (SPI), Spring Outdoor (SPO), Monsoon Indoor (MI), Monsoon Outdoor (MO), Winter Indoor (WI), Winter Outdoor (WO), Summer Indoor (SUI), Summer Outdoor (SUO).

Sample ID	Date of Sampling	Temperature (°C)	Relative Humidity (%)	PM_{2.5} (µg m⁻³)	PM₁₀ (µg m⁻³)
SPI	23/Feb/2018	25.1	51.8	156.76	560.10
SPO	23/Feb/2018	27.9	39.7	NA*	NA*
MI	12/Sept/2018	29.8	67.5	13.53	80.17
MO	12/Sept/2018	30.5	70.0	46.82	201.06
WI	03/Jan/2019	17.6	58.7	477.6	739.02
WO	03/Jan/2019	17.2	54.8	326.38	604.30
SUI	08/Jun/2019	35.4	33.6	46.32	254.92
SUO	08/Jun/2019	40.9	19.9	43.99	377.15

*NA= Not Available

Table S2: SRCCs between dominant phyla of bacterial community and Temperature (T), Relative Humidity (RH), PM_{2.5} and PM₁₀.

Variables		Proteobacteria	Actinobacteria	Firmicutes	Bacteroidetes	Planctomycetes	Verrucomicrobia	Thermi	Acidobacteria	TM7	Others
T	SRCC	-0.548	.762*	0.643	-0.143	0.571	0.571	0.619	0.214	0.571	0.357
	p values	0.160	0.028	0.086	0.736	0.139	0.139	0.102	0.610	0.139	0.385
RH	SRCC	0.000	0.143	0.024	0.000	-0.238	-0.238	-0.286	-0.619	-0.310	-0.548
	p values	1.000	0.736	0.955	1.000	0.570	0.570	0.493	0.102	0.456	0.160
PM_{2.5}	SRCC	.857*	-.893**	-.893**	0.357	-0.250	-0.250	-0.286	0.107	-0.107	0.071
	p values	0.014	0.007	0.007	0.432	0.589	0.589	0.535	0.819	0.819	0.879
PM₁₀	SRCC	0.714	-.964**	-0.750	0.143	-0.179	-0.179	-0.143	0.393	0.036	0.357
	p values	0.071	0.000	0.052	0.760	0.702	0.702	0.760	0.383	0.939	0.432

*. Correlation is significant at the 0.05 level (2-tailed).

**.. Correlation is significant at the 0.01 level (2-tailed).

Table S3: Diversity and richness estimation of 16S rRNA gene libraries of air samples collected from indoor and outdoor area of JNU Health Centre in each season: Spring Indoor (SPI), Spring Outdoor (SPO), Monsoon Indoor (MI), Monsoon Outdoor (MO), Winter Indoor (WI), Winter Outdoor (WO), Summer Indoor (SUI), Summer Outdoor (SUO) using Illumina MiSeq PE300 sequencing.

Sample ID	OTUs	Shannon	Simpson	Chao1	Equitability
SPI	1239	4.7	0.90	1934.2	0.46
SPO	1075	3.2	0.66	1671.4	0.31
MI	822	3.7	0.83	1198.9	0.39
MO	1185	6.0	0.96	1694.0	0.58
WI	1702	5.0	0.89	2413.0	0.46
WO	1818	4.6	0.83	2643.5	0.42
SUI	3253	7.7	0.94	3835.9	0.66
SUO	3606	9.1	0.99	3879.2	0.77

Table S4: Numbers of taxa classified at different taxonomic levels in air samples collected from indoor and outdoor area of JNU Health Centre in each season: Spring Indoor (SPI), Spring Outdoor (SPO), Monsoon Indoor (MI), Monsoon Outdoor (MO), Winter Indoor (WI), Winter Outdoor (WO), Summer Indoor (SUI), Summer Outdoor (SUO).

Taxonomic level	Total	SPI	SPO	MI	MO	WI	WO	SUI	SUO
Phylum	34	17	19	16	22	21	21	26	27
Class	96	47	50	39	49	58	55	74	78
Order	182	77	82	56	85	101	106	144	146
Family	339	170	165	115	178	209	211	281	283
Genus	749	315	302	220	340	404	412	578	604

Table S5: The proportions of unclassified taxa reported in air samples collected from indoor and outdoor area of JNU Health Centre in each season: Spring Indoor (SPI), Spring Outdoor (SPO), Monsoon Indoor (MI), Monsoon Outdoor (MO), Winter Indoor (WI), Winter Outdoor (WO), Summer Indoor (SUI), Summer Outdoor (SUO) at different taxonomic levels.

Taxonomic level	Proportions of unclassified taxa* (%)							
	SPI	SPO	MI	MO	WI	WO	SUI	SUO
Phylum	0	0	0	0	0	0	0	0
Class	0.003	0.007	0.008	0.063	0.007	0.018	0.070	0.162
Order	0.055	0.045	0.047	0.598	0.247	0.237	1.269	1.559
Family	0.847	0.795	0.986	3.727	1.990	2.363	8.813	9.353
Genus	18.581	10.789	21.404	35.373	43.634	18.675	29.055	30.677
Species	79.779	35.240	96.849	77.278	61.462	52.551	65.149	90.191

*Sequences that could not be assigned to any known group were assigned as unclassified

Table S6: Raw data of ESKAPE pathogens determined in the total sequences acquired in each season: Monsoon Indoor (MI), Monsoon Outdoor (MO), Spring Indoor (SPI), Spring Outdoor (SPO), Summer Indoor (SUI), Summer Outdoor (SUO), Winter Indoor (WI), Winter Outdoor (WO).

Species	MI	MO	SPI	SPO	SUI	SUO	WI	WO
<i>Enterococcus cecorum</i>	0	0	0	0	0	3	3	0
<i>Enterococcus casseliflavus</i>	0	0	0	0	0	3	1	0
<i>Enterococcus asini</i>	0	2	0	0	0	2	5	7
<i>Enterococcus unclassified</i>	0	9	1	0	7	169	52	26
<i>Staphylococcus unclassified</i>	17	60	44	54	35	2814	88	52
<i>Staphylococcus sciuri</i>	5	49	1	0	1	212	1	1
<i>Staphylococcus epidermidis</i>	2	3	0	0	2	44	1	0
<i>Staphylococcus pettenkoferi</i>	0	0	0	0	0	7	0	0
<i>Staphylococcus equorum</i>	0	0	1	1	0	25	18	22
<i>Staphylococcus aureus</i>	0	0	1	1	0	6	1	2
<i>Staphylococcus saprophyticus</i>	0	0	0	0	0	8	0	0
<i>Klebsiella unclassified</i>	3	0	1	1	9	288	0	0
<i>Acinetobacter unclassified</i>	164	51	21	8	359	3359	18	42
<i>Acinetobacter schindleri</i>	21	1	5	0	47	581	2	0
<i>Acinetobacter johnsonii</i>	3	0	1	4	8	85	4	4
<i>Acinetobacter guillouiae</i>	2	3	0	0	0	3	0	1
<i>Acinetobacter lwoffii</i>	1	10	33	7	63	102	3	5
<i>Acinetobacter rhizosphaerae</i>	0	0	1	0	2	13	0	0
<i>Pseudomonas unclassified</i>	10065	1953	148	13	58	361	26	7
<i>Pseudomonas pseudoalcaligenes</i>	23	56	0	0	1	2	0	0
<i>Pseudomonas stutzeri</i>	9	10	3	0	1	4	0	0
<i>Pseudomonas viridiflava</i>	4	2	0	0	0	0	0	0
<i>Pseudomonas alcaligenes</i>	4	2	0	0	2	48	0	0
<i>Pseudomonas veronii</i>	0	0	0	0	0	0	0	2
<i>Pseudomonas nitroreducens</i>	0	0	0	0	4	6	0	0
<i>Pseudomonas fragi</i>	0	0	0	0	0	0	1	1
<i>Enterobacter turicensis</i>	0	0	0	0	0	4	0	0
<i>Enterobacter gergoviae</i>	0	0	0	0	2	6	0	0
<i>Enterobacter cowanii</i>	0	0	0	1	0	3	0	0
<i>Enterobacter cloacae</i>	0	0	0	0	1	5	0	0
<i>Enterobacter unclassified</i>	0	0	0	0	4	6	0	0
Total Pathogenic Sequences	10323	2211	261	90	606	8169	224	172

Table S7: Inter-phyla correlations using Spearman's Rank Correlation Coefficient (SRCC)

Variables		Proteobacteria	Actinobacteria	Firmicutes	Bacteroidetes	Planctomycetes	Verrucomicrobia	Thermi	Acidobacteria	TM7	Others
Proteobacteria	SRCC	1.000	-.762*	-0.595	0.048	-0.143	-0.143	-0.119	0.167	-0.119	0.262
	p values		0.028	0.120	0.911	0.736	0.736	0.779	0.693	0.779	0.531
Actinobacteria	SRCC	-.762*	1.000	.738*	-0.190	0.238	0.238	0.286	-0.333	0.119	-0.214
	p values	0.028		0.037	0.651	0.570	0.570	0.493	0.420	0.779	0.610
Firmicutes	SRCC	-0.595	.738*	1.000	-0.524	0.595	0.595	0.643	0.119	0.429	0.238
	p values	0.120	0.037		0.183	0.120	0.120	0.086	0.779	0.289	0.570
Bacteroidetes	SRCC	0.048	-0.190	-0.524	1.000	0.048	0.048	-0.095	0.167	0.071	-0.095
	p values	0.911	0.651	0.183		0.911	0.911	0.823	0.693	0.867	0.823
Planctomycetes	SRCC	-0.143	0.238	0.595	0.048	1.000	1.000**	.952**	.762*	.929**	.786*
	p values	0.736	0.570	0.120	0.911			0.000	0.028	0.001	0.021
Verrucomicrobia	SRCC	-0.143	0.238	0.595	0.048	1.000**	1.000	.952**	.762*	.929**	.786*
	p values	0.736	0.570	0.120	0.911			0.000	0.028	0.001	0.021
Thermi	SRCC	-0.119	0.286	0.643	-0.095	.952**	.952**	1.000	0.690	.905**	.833*
	p values	0.779	0.493	0.086	0.823	0.000	0.000		0.058	0.002	0.010
Acidobacteria	SRCC	0.167	-0.333	0.119	0.167	.762*	.762*	0.690	1.000	.786*	.881**
	p values	0.693	0.420	0.779	0.693	0.028	0.028	0.058		0.021	0.004
TM7	SRCC	-0.119	0.119	0.429	0.071	.929**	.929**	.905**	.786*	1.000	.857**
	p values	0.779	0.779	0.289	0.867	0.001	0.001	0.002	0.021		0.007
Others	SRCC	0.262	-0.214	0.238	-0.095	.786*	.786*	.833*	.881**	.857**	1.000
	p values	0.531	0.610	0.570	0.823	0.021	0.021	0.010	0.004	0.007	

*. Correlation is significant at the 0.05 level (2-tailed).

** . Correlation is significant at the 0.01 level (2-tailed).