Temporal dynamics of microbial community composition and antimicrobial resistance in a mass gathering setting using culturomics and metagenomic approaches

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SUPPLEMENTARY DATA

Suppl. Table I. Details of strains isolated from the Prayagraj test sample

S. No	Strain ID	*Taxonomic affiliation*	Gene accession ID
1	VRL_PW2.3	*Priestia aryabhattai*	PP085228
2	VRL_PW2.4	*Bacillus cereus*	PP085229
3	VRL_PW2.7	*Mesobacillus boroniphilus*	PP085230
4	VRL_PW2.8	*Priestia megaterium*	PP085231
5	VRL_PW1.8	*Aeromonas sanarellii*	PP085232
6	VRL_PW3.1	*Pseudomonas tianjinensis*	PP085233
7	VRL_PW3.3	*Aeromonas rivipollensis*	PP085234
8	VRL_PW3.5	*Acidovorax temperans*	PP085235
9	VRL_PW3.7	*Mesobacillus maritimus*	PP085236
10	VRL_PW3.11	*Shewanella xiamenensis*	PP085237
11	VRL_PW4.1	*Priestia flexa*	PP085238
12	VRL_PW4.2	*Metabacillus indicus*	PP085239
13	VRL_PW4.3	*Bacillus cabrialesii*	PP085240
14	VRL_PW4.4	*Pseudomonas otitidis*	PP085241
15	VRL_PW4.5b	*Pseudomonas guangdongensis*	PP085242
16	VRL_PW4.7	*Bacillus licheniformis*	PP085243
17	VRL_PW4.8	*Priestia aryabhattai*	PP085244
18	VRL_PW4.10a	*Lelliottia jeotgali*	PP085245
19	VRL_PW4.11	*Mesobacillus thioparans*	PP085246
20	VRL_PW4.12	*Aeromonas enteropelogenes*	PP085247
21	VRL_PW4.13	*Aeromonas sanarellii*	PP085248
22	VRL_PW4.14	*Cytobacillus oceanisediminis*	PP085249
23	VRL_PW4.15	*Exiguobacterium mexicanum*	PP085250
24	VRL_PW4.20	*Bacillus zhangzhouensis*	PP085251
25	VRL_PS4.1_1	*Metabacillus indicus*	PP085252
26	VRL_PS4.1_2	*Fictibacillus phosphorivorans*	PP085253
27	VRL_PS4.1_4	*Peribacillus simplex*	PP085254
28	VRL_PS4.1_8	*Robertmurraya beringensis*	PP085255
29	VRL_PS4.1_9	*Mesobacillus subterraneus*	PP085256
30	VRL_PS4.1_10	*Bacillus tequilensis*	PP085257
31	VRL_PS4.1_12	*Kaistella anthropi*	PP085258
32	VRL_PS4.1_14.2	*Bacillus aryabhattai*	PP085259
33	VRL_PS4.1_15	*Lysinibacillus composti*	PP085260
34	VRL_PS4.1_16	*Mesobacillus subterraneus*	PP085261
35	VRL_PS4.1_17	*Cytobacillus firmus*	PP085262
36	VRL_PS4.1_18	*Exiguobacterium mexicanum*	PP085263
37	VRL_PS4.1_19	*Bacillus tequilensis*	PP085264
38	VRL_PS4.1_23	*Exiguobacterium aurantiacum*	PP085265

39	VRL_PS4.1_24	*Sutcliffiella horikoshii*	PP085266
40	VRL_PS4.1_25	*Lysinibacillus composti*	PP085267
41	VRL_PS4.1_27	*Mesobacillus thioparans*	PP085268
42	VRL_PS4.1_28	*Thauera phenylacetica*	PP085269
43	VRL_PS4.1_29	*Mesobacillus subterraneus*	PP085270
44	VRL_PS4.1_30	*Mesobacillus thioparans*	PP085271
45	VRL_PS4.1_33	*Neomicrococcus lactis*	PP085272
46	VRL_PS4.2_2	*Glutamicibacter nicotianae*	PP085273
47	VRL_PS4.2_3	*Bacillus fengqiuensis*	PP085274
48	VRL_PS4.2_4	*Pseudarthrobacter phenanthrenivorans*	PP085275
49	VRL_PS4.2_6	*Cytobacillus firmus*	PP085276
50	VRL_PS4.2_7	*Metabacillus indicus*	PP085277
51	VRL_PS4.2_8	*Pseudomonas chlororaphis subsp. chlororaphis*	PP085278
52	VRL_PS4.2_11	*Bacillus stercoris*	PP085279
53	VRL_PS4.2_12	*Glutamicibacter mysorens*	PP085280
54	VRL_PS4.2_15	*Bacillus australimaris*	PP085281
55	VRL_PS4.2_17	*Pseudomonas hibiscicola*	PP085282
56	VRL_PS4.2_18	*Pseudomonas straminea*	PP085283
57	VRL_PS4.2_21	*Bacillus altitudinis*	PP085284
58	VRL_PS4.2_22	*Glutamicibacter mysorens*	PP085285
59	VRL_PS4.2_24	*Glutamicibacter mysorens*	PP085286
60	VRL_PS4.2_25	*Priestia flexa*	PP085287
61	VRL_PS4.2_29	*Cupriavidus alkaliphilus*	PP085288
62	VRL_PS4.2_36	*Pseudomonas chlororaphis subsp. chlororaphis*	PP085289
63	VRL_PS4.2_37	*Bacillus australimaris*	PP085290
64	VRL_PS4.2_41	*Brachybacterium phenoliresistens*	PP085291
65	VRL_PS4.2_43	*Neobacillus drentensis*	PP085292
66	VRL_PS4.2_45	*Exiguobacterium mexicanum*	PP085293
67	VRL_PS4.2_48	*Janibacter anophelis*	PP085294
68	VRL_PS4.2_53	*Planococcus citreus*	PP085295
69	VRL_PS4.2_56	*Mesobacillus boroniphilus*	PP085296
70	VRL_PW3.9	*Aeromonas hydrophila*	-
71	VRL_PW3.12	*Exiguobacterium sp*	-
72	VRL_PW4.17	*Bacillus vietnamensis*	-
73	VRL_PS4.1_5	*Bacillus cereus*	-
74	VRL_PS4.1_13	*Bacillus cereus*	-
75	VRL_PS4.1_14.2	*Bacillus aryabhattai*	-
76	VRL_PS4.1_20	*Bacillus licheniformis*	-
77	VRL_PS4.1_22	*Pseudomonas tianjinensis*	-
78	VRL_PS4.1_31	*Bacillus cereus*	-
79	VRL_PS4.1_31.1	*Exiguobacterium aurantiacum*	-

80	VRL_PS4.2_10	*Pantoea agglomerans*	-
81	VRL_PS4.2_16	*Pseudomonas koreensis*	-
82	VRL_PS4.2_23	*Bacillus niacini*	-
83	VRL_PS4.2_33	*Bacillus arsenicus*	-
84	VRL_PS4.2_42	*Bacillus arsenicus*	-
85	VRL_PS4.2_44	*Exiguobacterium aurantiacum*	-
86	VRL_PS4.2_50	*Bacillus arsenicus*	-
87	VRL_PS4.2_54	*Mesobacillus boroniphilus*	-
88	VRL_PS4.2_46	*Enterococus faecium*	-
89	VRL_PS4.2_49	*Enterococus faecium*	-
90	VRL_PS4.2_14	*Pseudomonas koreensis*	-
91	VRL_PS4.2_19	*Pseudomonas strutzeri*	-
92	VRL_PS4.2_51	*Pseudomonas straminea*	-
93	VRL_PS4.2_57	*Pseudomonas strutzeri*	-

-, MALDI based identification

Suppl. Table II. Details of strains isolated from the Prayagraj control sample

S. No.	**Lab strain ID**	**Taxonomic affiliation**	**Gene accession ID**
1	VRL_PW1.1	*Mammaliicoccus sciuri*	PP085297
2	VRL_PW1.2	*Pseudomonas alcaligenes*	PP085298
4	VRL_PW1.3	*Acinetobacter johnsonii*	PP085299
5	VRL_PW1.6	*Rheinheimera chironomi*	PP085300
6	VRL_PW1.9	*Rheinheimera mesophila*	PP085301
7	VRL_PW5.1	*Bacillus cereus*	PP085302
8	VRL_PW5.2	*Cytobacillus firmus*	PP085303
9	VRL_PW5.3	*Chryseomicrobium aureus*	PP085304
10	VRL_PW5.7	*Bacillus paralicheniformis*	PP085305
11	VRL_PW5.12	*Pseudomonas kunmingensis*	PP085306
12	VRL_PW5.23a	*Jonesia quinghaiensis*	PP085307
23	VRL_PW5.25	*Cytobacillus oceanisediminis*	PP085308
24	VRL_PW5.27	*Bacillus megaterium*	PP085309
25	VRL_PW6.1	*Fictibacillus phosphonivorans*	PP085310
26	VRL_PW6.3	*Acinetobacter lwoffii*	PP085311
27	VRL_PW6.5	*Acinetobacter junii*	PP085312
28	VRL_PW6.7	*Pseudomonas chengduensis*	PP085313
29	VRL_PW6.9	*Pseudomonas titanjinesis*	PP085314
30	VRL_PW6.10	*Pseudomonas alcaliphila*	PP085315
31	VRL_PW6.11	*Bacillus paralicheniformis*	PP085316
32	VRL_PW6.12	*Pseudommonas alcaligenes*	PP085317
33	VRL_PW6.14	*Cellvibrio mixtus subsp. mixtus*	PP085318
34	VRL_PW6.16_1	*Acinetobacter junii*	PP085319

35	VRL_PW6.16_2	*Bacillus altitudinis*	PP085320
36	VRL_PS6.2_1	*Metabacillus indicus*	PP085321
37	VRL_PS6.2_2	*Exiguobacterium mexicanum*	PP085322
38	VRL_PS6.2_4	*Cytobacillus oceanisediminis*	PP085323
39	VRL_PS6.2_5	*Exiguobacterium mexicanum*	PP085324
40	VRL_PS6.2_6	*Bacillus firmus*	PP085325
41	VRL_PS6.2_9a	*Mesobacillus boroniphilus*	PP085326
42	VRL_PS6.2_10a	*Bacillus onubensis*	PP085327
43	VRL_PS6.2_12.1	*Bacillus fengqiuensis*	PP085328
44	VRL_PS6.2_14.1	*Sutcliffiella horikoshii*	PP085329
45	VRL_PS6.2_14.3	*Agromyces indicus*	PP085330
46	VRL_PS6.2_15	*Cytobacillus firmus*	PP085331
47	VRL_PS6.2_18	*Bacillus cereus*	PP085332
48	VRL_PS6.2_20	*Exiguobacterium mexicanum*	PP085333
49	VRL_PS6.2_3	*Aeromonas sanarellii*	PP085334
50	VRL_PS6.2_17	*Priestia flexa*	PP085335
51	VRL_PS6.2_21	*Pseudoxanthomonas mexicana*	PP085336
52	VRL_PW1.4	*Bacillus megatarium*	-
53	VRL_PW5.13	*Bacillus megaterium*	-
54	VRL_PW5.19	*Bacillus arsenicus*	-
55	VRL_PW5.24	*Staphylococcus equorum*	-
56	VRL_PW5.23b	*Cytobacillus oceanisediminis*	-
57	VRL_PW6.4	*Bacillus megaterium*	-
58	VRL_PW6.15	*Bacillus vietnamensis*	-
59	VRL_PW6.16	*Acinetobacter junii*	-
60	VRL_PS6.2_16	*Bacillus arsenicus*	-

-, MALDI based identification

Suppl. Table SIII. Relative abundance of genera isolated from Prayagraj samples

S. No.	Genera	Test (%)	Control (%)	Human origin*
1	*Bacillus*	15	10	Yes
2	*Pseudomonas*	8	5	Yes
3	*Aeromonas*	4	1	Yes
4	*Mesobacillus*	4	1	Yes
5	*Priestia*	3	2	Yes
6	*Cytobacillus*	2	2	Yes
7	*Exiguobacterium*	2	1	Yes
8	*Fictibacillus*	2	1	-
9	*Metabacillus*	1	1	Yes
10	*Peribacillus*	1	0	Yes
11	*Brachybacterium*	2	0	Yes
12	*Cupriavidus*	1	0	Yes
13	*Janibacter*	1	0	Yes
14	*Kaistella*	1	0	Yes
15	*Lelliottia*	1	0	Yes
16	*Lysinibacillus*	1	0	Yes
17	*Neobacillus*	1	0	Yes
18	*Neomicrococcus*	1	0	-
19	*Pantoea*	1	0	Yes
20	*Planococcus*	1	0	Yes
21	*Robertmurraya*	1	0	Yes
22	*Shewanella*	1	0	Yes
23	*Sutcliffiella*	1	0	-
24	*Thauera*	1	0	-
25	*Glutamicibacter*	2	0	Yes
26	*Pseudarthrobacter*	1	0	Yes
27	*Enterococcus*	1	0	Yes
28	*Acidovorax*	1	0	Yes
29	*Acinetobacter*	0	3	Yes
30	*Rheinheimera*	0	2	-
31	*Agromyces*	0	1	Yes
32	*Cellvibrio*	0	1	-
33	*Chryseomicrobium*	0	1	-
34	*Jonesia*	0	1	-
35	*Staphylococcus*	0	1	Yes
36	*Sutcliffiella*	0	1	-
37	*Pseudoxanthomonas*	0	1	Yes
38	*Fredinandcohnia*	0	1	Yes
39	*Mammaliicoccus*	0	1	Yes

*Data obtained from literature; -, Not known

Suppl. Table IV. Common and unique genera in both Test and Control samples

Common	Test sample	Control sample
Bacillus	*Peribacillus*	*Acinetobacter*
Pseudomonas	*Brachybacterium*	*Rheinheimera*
Aeromonas	*Cupriavidus*	*Agromyces*
Mesobacillus	*Janibacter*	*Cellvibrio*
Priestia	*Kaistella*	*Chryseomicrobium*
Exiguobacterium	*Lelliottia*	*Jonesia*
Fictibacillus	*Lysinibacillus*	*Staphylococcus*
Metabacillus	*Neobacillus*	*Psueudoxanthomonas*
Sutcliffiella	*Neomicrococcus*	*Fredinandcohnia*
	Pantoea	*Mammaliicoccus*
	Planococcus	
	Robertmurraya	
	Shewanella	
	Thauera	
	Glutamicibacter	
	Pseudarthrobacter	
	Enterococus	
	Acidovorax	

Suppl. Table V. Bacterial genera from test and control samples which are known to be associated with human microflora

Test sample	Control sample
Bacillus	*Acinetobacter*
Aeromonas	*Staphylococcus*
Enterococcus	
Staphylococcus	
Shewanella	
Janibacter	
Cupriavidus	
Glutamicibacter	
Acinetobacter	
Brachybacterium	
Cupriavidus	
Pantoea	

Suppl. Table VI. Different classes of ARG family and their variants associated with clinical strains

Gene family	Variants	Associated clinical strains
Oxacillinases (OXA)	*bla*OXA-23	*Acinetobacter baumannii* *Klebsiella pneumoniae* *Pseudomonas aeruginosa* *Salmonella Typhimurium*
	*bla*OXA-235	
	*bla*OXA-236	
Cephalosporinases (CMY)	*bla*CMY-1	*Klebsiella pneumoniae*
	*bla*CMY-8	
	*bla*CMY-9	
	*bla*CMY-10	
	*bla*CMY-11	
	*bla*CMY-19	
Moxalactam (MOX)	*bla*MOX-2	*Klebsiella pneumoniae* *Aeromonas caviae* *Citrobacter freundii*
	*bla*MOX-4	
	*bla*MOX-6	
	*bla*MOX-7	
	*bla*MOX-8	
	*bla*MOX-9	
IMP-type metallo-beta-lactamases (MBL)	IMP−1	*Achromobacter xylosoxidans*
		Comamonas thiooxydans
		Pseudomonas aeruginosa
		Pseudomonas putida
		Pseudomonas fluorescens
	IMP−1	*Serratia marcescens*
		Klebsiella pneumoniae
		Acinetobacter spp.
		Acinetobacter bereziniae
		Acinetobacter calcoaceticus
		Acinetobacter baumannii
		Acinetobacter pittii
		Acinetobacter nosocomialis
		Citrobacter freundii
		Citrobacter youngae
		Enterobacter aerogenes
		Enterobacter cloacae
		Enterobacter hormaechei
		Escherichia coli
		Proteus mirabilis
		Proteus vulgaris
		Providencia rettgeri
		Leclercia adecarboxylata
	IMP−2	*Acinetobacter baumannii*
		Serratia marcescens

Gene family	Variants	Associated clinical strains
IMP-type metallo-beta-lactamases (MBL)	IMP−2	*Pseudomonas aeruginosa*
	IMP−3	*Shigella flexneri*
	IMP−4	*Acinetobacter baumannii*
		Acinetobacter calcoaceticus
		Citrobacter freundii
		Escherichia coli
		Enterobacter cloacae
		Enterobacter aerogenes
		Klebsiella pneumoniae
		Klebsiella oxytoca
		Pseudomonas aeruginosa
	IMP−5	*Acinetobacter baumannii*
	IMP−6	*Escherichia coli*
		Serratia marcescens
		Providencia rettgeri
		Pseudomonas aeruginosa
	IMP−7	*Pseudomonas aeruginosa*
	IMP−8	*Acinetobacter baumannii*
		Escherichia coli
		Enterobacter cloacae
		Klebsiella pneumoniae
		Klebsiella oxytoca
		Serratia marcescens
	IMP−9	*Pseudomonas aeruginosa*
	IMP−10	*Achromobacter xylosoxidans*
		Pseudomonas aeruginosa
		Pseudomonas putida
		Klebsiella pneumoniae
	IMP−11	*Pseudomonas aeruginosa*
		Acinetobacter baumannii
		Enterobacter cloacae
	IMP−12	*Pseudomonas putida*
	IMP−13	*Pseudomonas aeruginosa*
		Pseudomonas monteilii
		Klebsiella pneumoniae
	IMP−14	*Achromobacter xylosoxidans*
		Pseudomonas aeruginosa

Gene family	Variants	Associated clinical strains
IMP-type metallo-beta-lactamases (MBL)	IMP−15	*Pseudomonas aeruginosa*
	IMP−16	
	IMP−17	
	IMP−18	
	IMP−19	*Acinetobacter baumannii*
		Achromobacter xylosoxidans
		Enterobacter cloacae
		Aeromonas caviae
		Klebsiella pneumoniae
		Pseudomonas aeruginosa
		Pseudomonas putida
		Serratia marcescens
	IMP−20	*Pseudomonas aeruginosa*
	IMP−21	
	IMP−22	*Providencia rettgeri*
		Pseudomonas aeruginosa
		Pseudomonas fluorescens
	IMP−23	*Citrobacter freundii*
	IMP−24	*Serratia marcescens*
	IMP−25	*Pseudomonas aeruginosa*
		Stenotrophomonas maltophilia
	IMP−26	*Enterobacter cloacae*
		Pseudomonas aeruginosa
	IMP−27	*Morganella morganii*
		Proteus mirabilis
		Providencia rettgeri
	IMP−28	*Klebsiella oxytoca*
	IMP−29	*Pseudomonas aeruginosa*
	IMP−30	*Escherichia coli*
		Pseudomonas aeruginosa
	IMP−31	*Pseudomonas aeruginosa*
	IMP−32	*Klebsiella pneumoniae*
	IMP−33	*Pseudomonas aeruginosa*
	IMP−34	*Klebsiella oxytoca*
		Acinetobacter colistiniresistens
	IMP−35	*Pseudomonas aeruginosa*
	IMP−37	
	IMP−38	*Klebsiella pneumoniae*
	IMP−39	*Pseudomonas aeruginosa*
	IMP−40	
	IMP−41	
	IMP−43	
	IMP−44	

Gene family	Variants	Associated clinical strains
IMP-type metallo-beta-lactamases (MBL)	IMP−45	*Pseudomonas aeruginosa*
	IMP−42	*Acinetobacter soli*
	IMP−46	*Pseudomonas putida*
	IMP−47	*Serratia marcescens*
	IMP−48	*Pseudomonas aeruginosa*
	IMP−49	
	IMP−51	
	IMP−52	*Escherichia coli*
	IMP−53	*Pseudomonas aeruginosa*
	IMP−54	
	IMP−55	*Acinetobacter baumannii*
	IMP−56	*Pseudomonas aeruginosa*
	IMP−58	*Pseudomonas putida*
	IMP−59	*Escherichia coli*
	IMP−60	*Enterobacter cloacae*
	IMP−61	*Acinetobacter baumannii*
	IMP−62	*Pseudomonas aeruginosa*
	IMP−63	
	IMP−64	*Proteus mirabilis*
	IMP−65	*Pseudomonas aeruginosa*
	IMP−66	*Escherichia coli*
	IMP−67	*Providencia rettgeri*
	IMP−68	*Klebsiella pneumoniae*
	IMP−69	*Providencia* spp.
	IMP−70	*Pseudomonas aeruginosa*
		Providencia rettgeri
	IMP−71	*Pseudomonas aeruginosa*
	IMP−72	
	IMP−73	
	IMP−74	
	IMP−75	
	IMP−76	
	IMP−77	
	IMP−78	
	IMP−79	
	IMP−80	
	IMP−81	
	IMP−82	
IMP-type metallo-beta-lactamases (MBL)	IMP−88	*Pseudomonas aeruginosa*
	IMP−90	
	IMP−91	
	IMP−89	*Pseudomonas putida*