CULTURE-INDEPENDENT MULTILOCUS SEQUENCE TYPING OF *PSEUDOMONAS AERUGINOSA* FOR CROSS-INFECTION SCREENING

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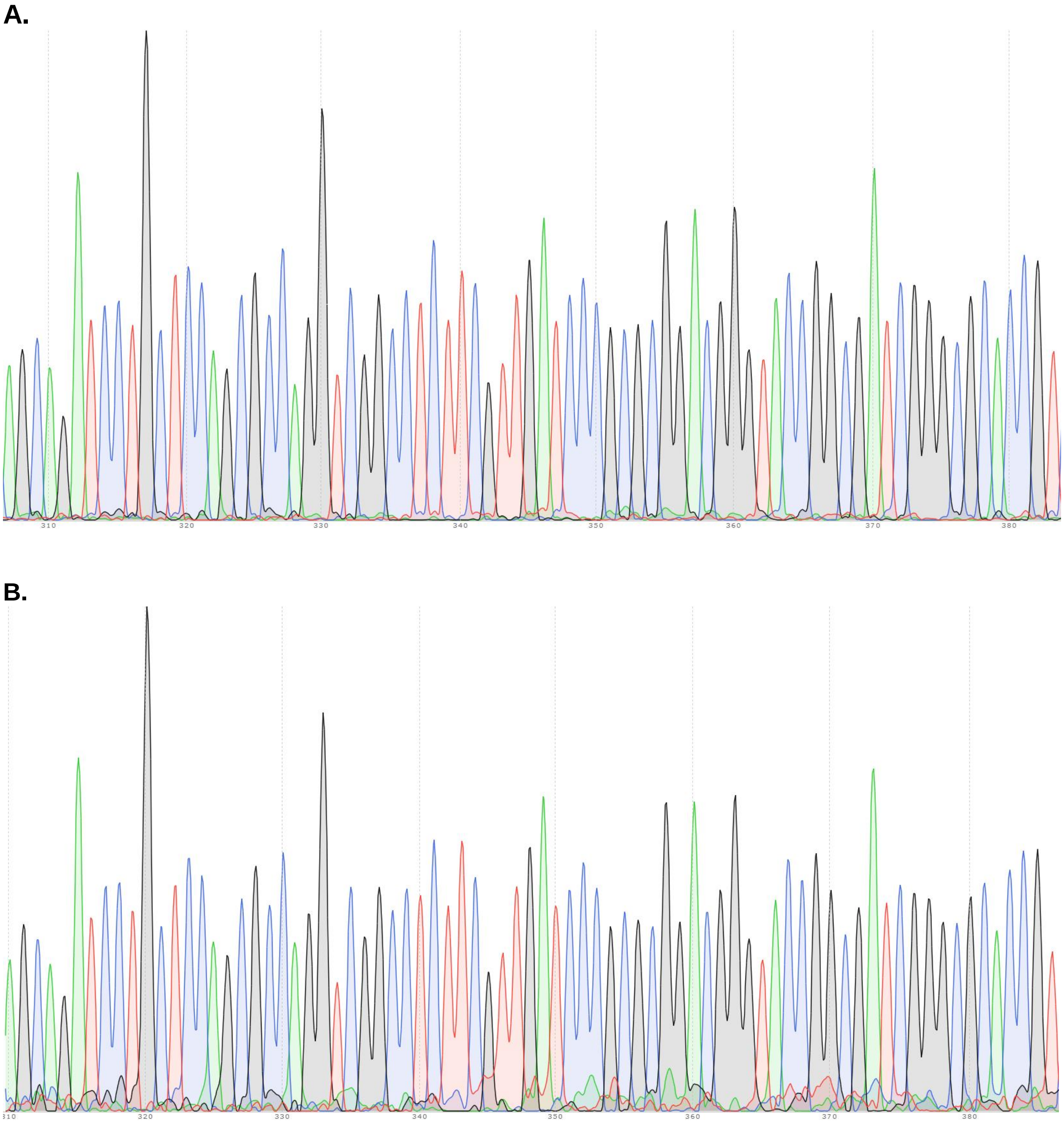
APPENDIX. SUPPLEMENTARY MATERIAL

	MLST allele							
Patient	***acsA***	***aroE***	***guaA***	***mutL***	***nuoD***	***ppsA***	***trpE***	**ST**
PIC01	6	5	1	1	1	12	1	395
PIC02	16	5	11	11	4	42	7	3323[a]
PIC06	11	5	1	7	131	4	7	3333[a]
PIC07	38	11	3	13	1	2	4	235
PIC09	6	5	6	7	4	6	7	27
PIC10	41	187	91	231	4	4	1	3334[a]
PIC12	16	22	5	3	2	15	10	1094
PIC13	28	5	11	18	4	13	271	3324[a]
PIC15	11	5	5	29	4	4	26	1228
PIC17	39	5	11	28	4	4	63	379
PIC18	23	5	11	7	1	12	7	274
PIC19	6	5	6	7	4	6	7	27
PIC20	6	5	11	3	4	23	1	146
PIC21	6	5	11	3	4	23	1	146
PIC22	6	5	6	7	4	6	7	27
PIC23	6	300	1	3	4	4	2	3335[a]
PIC24	5	3	57	6	1	33	47	312
PIC25	6	24	91	5	4	4	14	3325[a]
PIC28	6	301	11	4	3	23	272	3336[a]
PIC30	6	28	4	3	3	4	7	252
PIC31	6	10	1	29	27	4	7	3326[a]
PIC32	89	30	64	26	48	24	32	195

Supplementary Table 2. MLST profiles and sequence types (ST) determined by culture-dependent MLST. [a] Denotes novel sequence types identified in the present study (based on those documented within the MLST database; https://pubmlst.org/paeruginosa).



Supplementary Figure 1. Representative sequence chromatograms (depicting a matching region of the *trpE* locus) derived from culture-dependent MLST (A) and culture-independent MLST (B). A greater degree of noise is observed in the baseline of chromatograms derived from culture-independent MLST.