

# Comparison of virulence factor-encoding genes and genotypes distribution amongst clinical *Pseudomonas aeruginosa* strains

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**Table S1.** Distribution of the genes and genotypes with respect to antimicrobial susceptibility profiles of the multidrug-sensitive *P. aeruginosa* strains included in the study ( $n = 74$ ).

Strain number ( $n = 74$ )	<i>lasB</i>	<i>pLC N</i>	<i>pLC H</i>	<i>exoU</i>	<i>nan1</i>	<i>pilA</i>	<i>pilB</i>	Genotype	<i>n</i>	%
11	+	+	+	+	+	-	+	I-S	1	1.4
8	+	+	+	+	+	-	-	II-S	10	13.5
14	+	+	+	+	+	-	-			
32	+	+	+	+	+	-	-			
38	+	+	+	+	+	-	-			
59	+	+	+	+	+	-	-			
62	+	+	+	+	+	-	-			
64	+	+	+	+	+	-	-			
66	+	+	+	+	+	-	-			
72	+	+	+	+	+	-	-			
73	+	+	+	+	+	-	-			
12	+	+	+	+	-	-	-	III-S	15	20.3
23	+	+	+	+	-	-	-			
26	+	+	+	+	-	-	-			
27	+	+	+	+	-	-	-			
29	+	+	+	+	-	-	-			
36	+	+	+	+	-	-	-			
47	+	+	+	+	-	-	-			
49	+	+	+	+	-	-	-			
50	+	+	+	+	-	-	-			
55	+	+	+	+	-	-	-			
57	+	+	+	+	-	-	-			
58	+	+	+	+	-	-	-			
70	+	+	+	+	-	-	-			
80	+	+	+	+	-	-	-			
83	+	+	+	+	-	-	-			
63	+	+	+	-	+	+	-	IV-S	1	1.4
42	+	+	+	-	+	-	-	V-S	6	8.1
75	+	+	+	-	+	-	-			
44	+	+	+	-	+	-	-			
52	+	+	+	-	+	-	-			
60	+	+	+	-	+	-	-			
65	+	+	+	-	+	-	-			
25	+	+	+	-	-	+	-	VI-S	2	2.7
31	+	+	+	-	-	+	-			
3	+	+	+	-	-	-	-	VII-S	22	29.7
13	+	+	+	-	-	-	-			
16	+	+	+	-	-	-	-			
18	+	+	+	-	-	-	-			
19	+	+	+	-	-	-	-			
24	+	+	+	-	-	-	-			
28	+	+	+	-	-	-	-			
30	+	+	+	-	-	-	-			
33	+	+	+	-	-	-	-			
34	+	+	+	-	-	-	-			
37	+	+	+	-	-	-	-			
40	+	+	+	-	-	-	-			

41	+	+	+	-	-	-	-				
48	+	+	+	-	-	-	-				
51	+	+	+	-	-	-	-				
53	+	+	+	-	-	-	-				
61	+	+	+	-	-	-	-				
67	+	+	+	-	-	-	-				
71	+	+	+	-	-	-	-				
76	+	+	+	-	-	-	-				
79	+	+	+	-	-	-	-				
81	+	+	+	-	-	-	-				
20	+	+	-	+	+	-	-	VIII-S	1	1.4	
43	+	+	-	+	-	-	-	IX-S	2	2.7	
85	+	+	-	+	-	-	-				
46	+	-	+	+	+	-	-	X-S	2	2.7	
78	+	-	+	+	+	-	-				
84	+	-	+	+	-	-	-	XI-S	1	1.4	
77	+	-	+	-	+	+	-	XII-S	1	1.4	
5	+	-	+	-	+	-	-	XIII-S	1	1.4	
15	+	-	-	+	-	-	-	XIV-S	2	2.7	
74	+	-	-	+	-	-	-				
45	+	-	-	-	-	-	-	XV-S	1	1.4	
21	-	+	-	+	-	-	-	XVI-S	2	2.7	
22	-	+	-	+	-	-	-				
7	-	+	-	-	-	-	-	XVII-S	3	4.1	
17	-	+	-	-	-	-	-				
39	-	+	-	-	-	-	-				
68	-	-	-	-	-	-	-	XVIII-S	1	1.4	
<i>n</i>	68	65	62	36	23	4	1				
%	91.9	87.8	83.8	48.6	31.1	5.4	1.4				
<i>lasB</i> <i>plcN</i> <i>plcH</i> <i>exoU</i> <i>nan1</i> <i>pilA</i> <i>pilB</i>											

(+) – presence of a particular gene; shaded boxes, (-) – absence of a particular gene.

**Table S2.** Origin and detailed distribution of the genes and genotypes with respect to antimicrobial susceptibility profiles of the multidrug-resistant *P. aeruginosa* strains included in the study ( $n = 57$ ).

Strain number ( $n = 57$ )	<i>lasB</i>	<i>plC N</i>	<i>plC H</i>	<i>exoU</i>	<i>nan1</i>	<i>pilA</i>	<i>pilB</i>	Genotype	<i>n</i>	%
12	+	+	+	+	+	+	-	I-R	1	1.8
10	+	+	+	+	+	-	-	II-R	8	14.0
58	+	+	+	+	+	-	-			
59	+	+	+	+	+	-	-			
61	+	+	+	+	+	-	-			
71	+	+	+	+	+	-	-			
74	+	+	+	+	+	-	-			
78	+	+	+	+	+	-	-			
82	+	+	+	+	+	-	-			
1	+	+	+	+	-	-	-	III-R	20	35.1
7	+	+	+	+	-	-	-			
13	+	+	+	+	-	-	-			
14	+	+	+	+	-	-	-			
15	+	+	+	+	-	-	-			
18	+	+	+	+	-	-	-			
20	+	+	+	+	-	-	-			
27	+	+	+	+	-	-	-			
29	+	+	+	+	-	-	-			
34	+	+	+	+	-	-	-			
51	+	+	+	+	-	-	-			
63	+	+	+	+	-	-	-			
64	+	+	+	+	-	-	-			
65	+	+	+	+	-	-	-			
66	+	+	+	+	-	-	-			
68	+	+	+	+	-	-	-			
79	+	+	+	+	-	-	-			
81	+	+	+	+	-	-	-			
84	+	+	+	+	-	-	-			
85	+	+	+	+	-	-	-			
6	+	+	+	-	+	+	+	IV-R	1	1.8
35	+	+	+	-	+	-	-	V-R	5	8.8
37	+	+	+	-	+	-	-			
41	+	+	+	-	+	-	-			
50	+	+	+	-	+	-	-			
70	+	+	+	-	+	-	-			
21	+	+	+	-	-	+	-	VI-R	1	1.8
3	+	+	+	-	-	-	-	VII-R	19	33.3
4	+	+	+	-	-	-	-			
5	+	+	+	-	-	-	-			
9	+	+	+	-	-	-	-			
16	+	+	+	-	-	-	-			
17	+	+	+	-	-	-	-			
24	+	+	+	-	-	-	-			
26	+	+	+	-	-	-	-			
28	+	+	+	-	-	-	-			
30	+	+	+	-	-	-	-			

31	+	+	+	-	-	-	-				
32	+	+	+	-	-	-	-				
46	+	+	+	-	-	-	-				
47	+	+	+	-	-	-	-				
53	+	+	+	-	-	-	-				
54	+	+	+	-	-	-	-				
56	+	+	+	-	-	-	-				
60	+	+	+	-	-	-	-				
77	+	+	+	-	-	-	-				
2	+	+	-	+	+	-	-	VIII-R	1	1.8	
52	+	+	-	-	-	-	-	IX-R	1	1.8	
<i>n</i>	57	57	55	30	16	3	1				
%	100.0	100.0	96.5	52.6	28.1	5.3	1.8				
	<i>lasB</i>	<i>plC N</i>	<i>plC H</i>	<i>exoU</i>	<i>nan1</i>	<i>pilA</i>	<i>pilB</i>				

(+) – presence of a particular gene; shaded boxes, (-) – absence of a particular gene

**Table S3.** The Spearman's rank correlation coefficient for the particular genes pair with respect to antimicrobial susceptibility profiles of *P. aeruginosa* strains included into the study

(types of correlation:  $r > 0$  positive correlation,  $r = 0$  lack of correlation,  $r < 0$  negative correlation; the strength of relation:  $< 0.2$  – lack of relation,  $0.2-0.4$  – weak,  $0.4-0.7$  – moderate,  $0.7-0.9$  – quite strong  $> 0.9$  – very strong; the statistically significant differences are marked in red)

MDR (n = 57)	<i>plC H</i>	<i>exoU</i>	<i>nan1</i>	<i>pilA</i>	<i>pilB</i>
<i>plC H</i>	1.000000	0.010050	-0.093066	0.044947	0.025482
<i>exoU</i>	0.010050	1.000000	0.123466	-0.091099	-0.140859
<i>nan1</i>	-0.093066	0.123466	1.000000	0.202458	0.213913
<i>pilA</i>	0.044947	-0.091099	0.202458	1.000000	<b>0.566947</b>
<i>pilB</i>	0.025482	-0.140859	0.213913	<b>0.566947</b>	1.000000

MDS (n = 74)	<i>lasB</i>	<i>plC N</i>	<i>plC H</i>	<i>exoU</i>	<i>nan1</i>	<i>pilA</i>	<i>pilB</i>
<i>lasB</i>	1.000000	0.040938	<b>0.675191</b>	0.091020	0.199480	0.071007	0.034766
<i>plC N</i>	0.040938	1.000000	<b>0.284966</b>	-0.051421	-0.107439	-0.093892	0.043552
<i>plC H</i>	<b>0.675191</b>	<b>0.284966</b>	1.000000	-0.085245	0.216230	0.105166	0.051491
<i>exoU</i>	0.091020	-0.051421	-0.085245	1.000000	0.164199	<b>-0.232670</b>	0.120248
<i>nan1</i>	0.199480	-0.107439	0.216230	0.164199	1.000000	0.097715	0.174285
<i>pilA</i>	0.071007	-0.093892	0.105166	<b>-0.232670</b>	0.097715	1.000000	-0.027978
<i>pilB</i>	0.034766	0.043552	0.051491	0.120248	0.174285	-0.027978	1.000000

MDS+MDR (n = 131)	<i>lasB</i>	<i>plC N</i>	<i>plC H</i>	<i>exoU</i>	<i>nan1</i>	<i>pilA</i>	<i>pilB</i>
<i>lasB</i>	1.000000	0.084851	<b>0.633358</b>	0.074704	0.142646	0.052055	0.027280
<i>plC N</i>	0.084851	1.000000	<b>0.296773</b>	-0.028106	-0.087160	-0.069654	0.033819
<i>plC H</i>	<b>0.633358</b>	<b>0.296773</b>	1.000000	-0.046777	0.117148	0.082188	0.043072
<i>exoU</i>	0.074704	-0.028106	-0.046777	1.000000	0.145285	-0.171530	-0.000951
<i>nan1</i>	0.142646	-0.087160	0.117148	0.145285	1.000000	0.142229	<b>0.191241</b>
<i>pilA</i>	0.052055	-0.069654	0.082188	-0.171530	0.142229	1.000000	<b>0.247239</b>
<i>pilB</i>	0.027280	0.033819	0.043072	-0.000951	<b>0.191241</b>	<b>0.247239</b>	1.000000

**Figures S1-S7.** Pictures of the electrophoretic gels showing the amplicons of PCR for the corresponding genes investigated in the present study

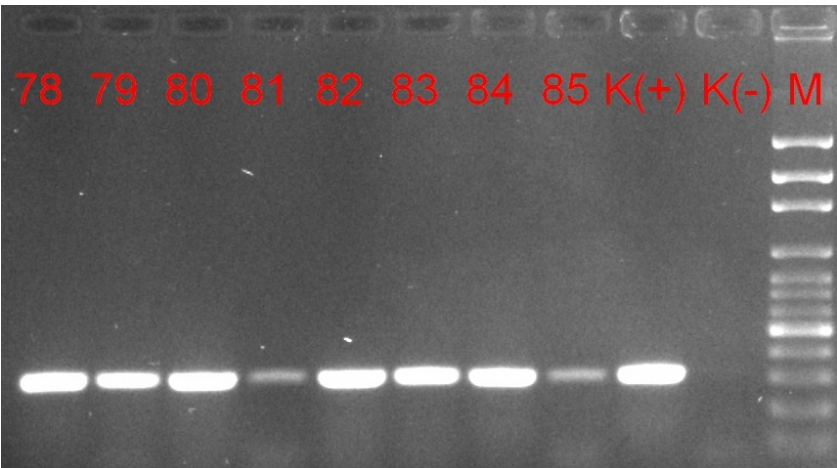


Figure S1 – *lasB* gene (300 bp); M – DNA size marker of 100-3000 bp; numbers – names assigned to a particular strain; K(+) – positive PCR control; K(-) – negative PCR control

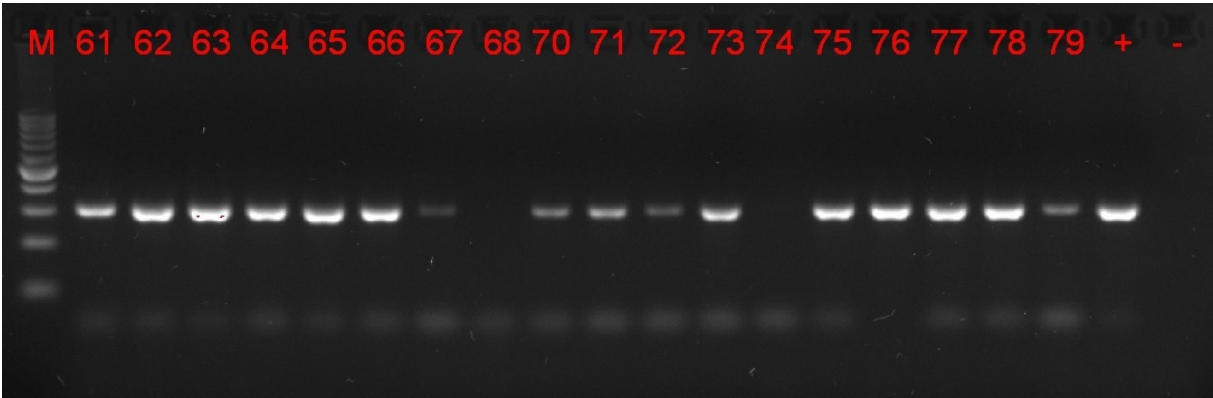


Figure S2 – *plC H* gene (307 bp); M – DNA size marker of 100-1000 bp; numbers – names assigned to a particular strain; (+) – positive PCR control; (-) – negative PCR control

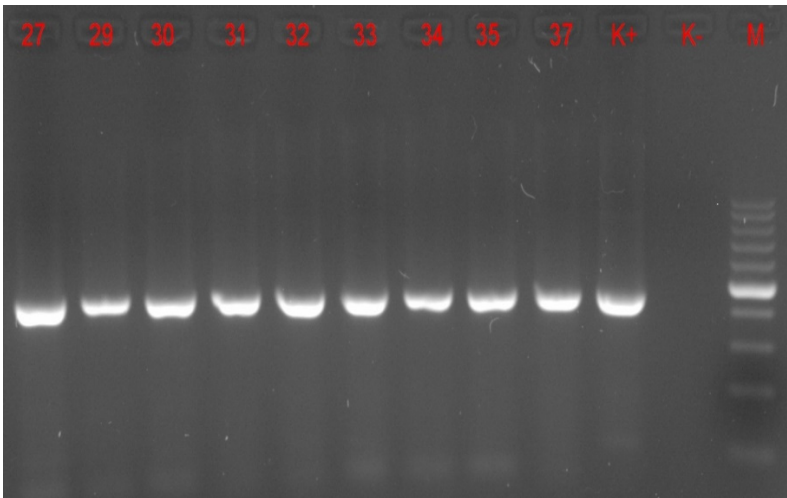


Figure S3 – *plC N* gene (466 bp); M – DNA size marker of 100-1000 bp; numbers – names assigned to a particular strain; K(+) – positive PCR control; K(-) – negative PCR control

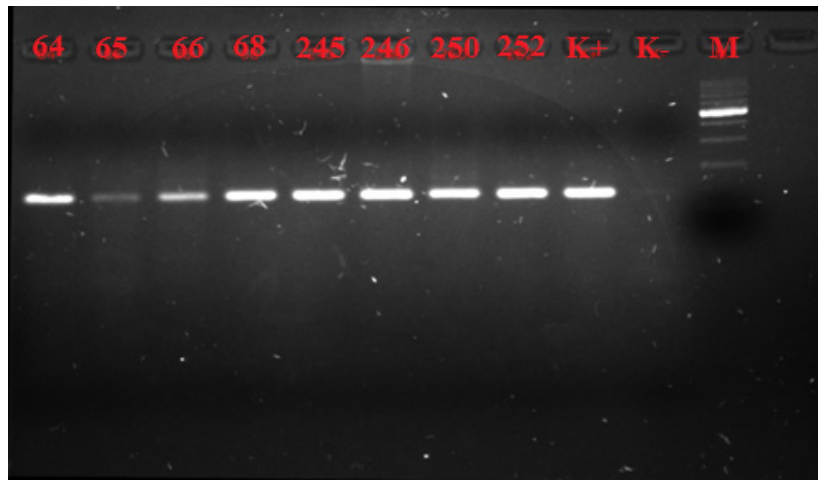


Figure S4 – *exoU* gene (134 bp); M – DNA size marker of 100-1000 bp; numbers – names assigned to a particular strain; K(+) – positive PCR control; K(-) – negative PCR control

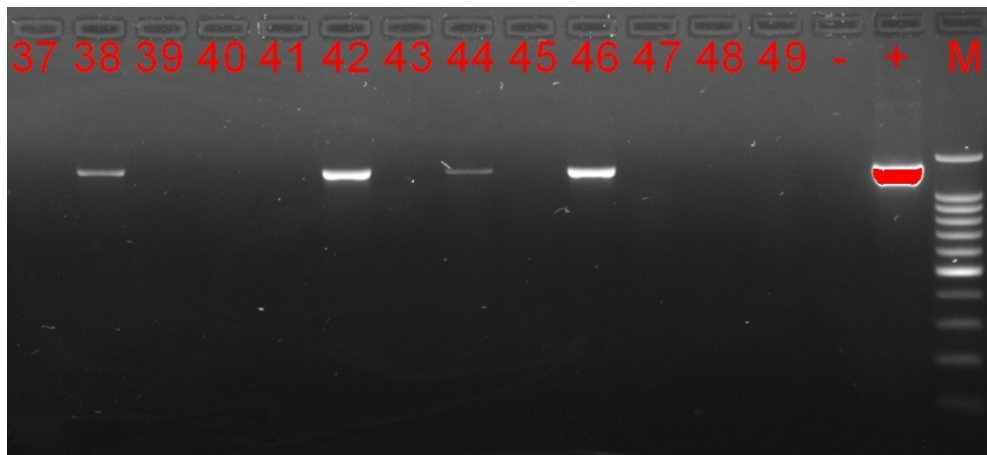


Figure S5 – *nan1* gene (1316 bp); M – DNA size marker of 100-1500 bp; numbers – names assigned to a particular strain; (+) – positive PCR control; (-) – negative PCR control

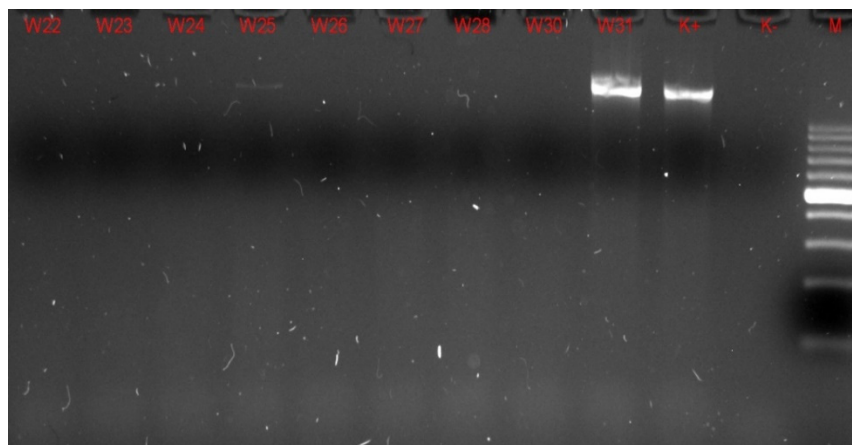


Figure S6 – *pilA* gene (1675 bp); M – DNA size marker of 100-1000 bp; “W”+numbers – names assigned to a particular strain; K(+) – positive PCR control; K(-) – negative PCR control



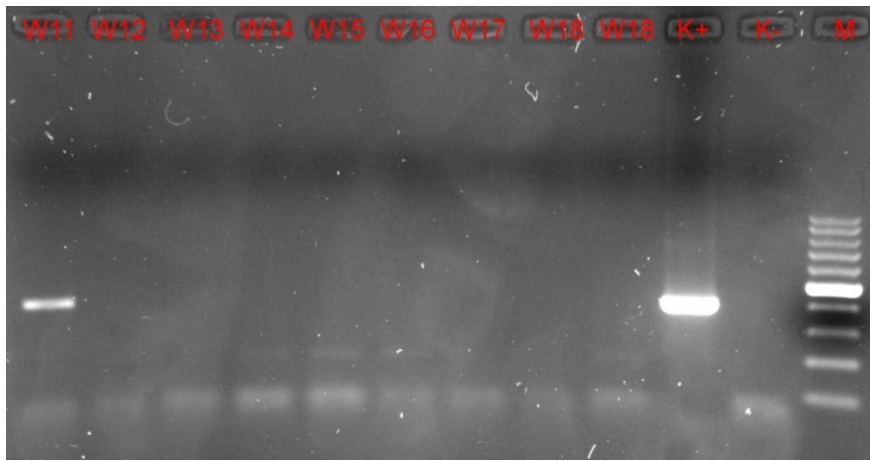


Figure S7 – *pilB* gene (408 bp); M – DNA size marker of 100-1000 bp; “W”+numbers – names assigned to a particular strain; K(+) – positive PCR control; K(-) – negative PCR control