

ONLINE DATA SUPPLEMENT

SHARED *PSEUDOMONAS AERUGINOSA* GENOTYPES ARE COMMON IN AUSTRALIAN CYSTIC FIBROSIS CENTRES.

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Table S4 Comparison of multilocus sequence type (MLST) sequence type (ST) with enterobacterial repetitive intergenic consensus (ERIC-PCR) genotype

References

Table S1 Study population, number of patients and isolates genotyped and sampling time frame

State/CF Centre*†	Centre type‡	Patient population	Patients recruited	<i>P. aeruginosa</i> positive patients genotyped (isolates genotyped) §	Sampling timeframe (mm/yyyy)
NSW/01	P	149	75	18 (54)	11/2007 - 03/2009
NSW/02	A	237	160	113 (331)	12/2007 - 07/2009
NSW/03	P	259	233	61 (178)	11/2007 - 11/2009
NSW/04	A	57	21	20 (56)	11/2007 - 03/2009
NSW/05	P	66	19	14 (37)	10/2007 - 03/2009
VIC/01	P	294	136	64 (192)	02/2008 - 02/2010
VIC/02	A	270	130	124 (355)	06/2008 - 06/2010
VIC/03	C	172	88	50 (148)	06/2008 - 06/2010
QLD/01	P	265	207	57 (163)	09/2007 - 03/2009
QLD/02	A	211	211	171 (511)	09/2007 - 08/2009
QLD/03	P	93	28	20 (58)	12/2007 - 07/2009
QLD/04	A	56	41	38 (113)	11/2007 - 01/2009
QLD/05	A	50	16	15 (44)	10/2007 - 01/2009
QLD/06	P	25	17	5 (15)	12/2007 - 08/2009
SA/01	A	139	74	72 (213)	02/2008 - 07/2009
SA/02	P	150	42	24 (72)	02/2008 - 08/2008
WA/01	A	145	102	92 (272)	01/2008 - 04/2009
TAS/01	A	39	28	25 (75)	11/2007 - 09/2008
Total		2677	1628	983 (2887)	09/2007 - 06/2010

* Geographic location of each cystic fibrosis (CF) centre by Australian State; NSW, New South Wales;

VIC, Victoria; QLD, Queensland; SA, South Australia; WA, Western Australia; TAS, Tasmania.

† Australian CF centres not included in the study consisted of two paediatric, 1 adult, and 1 combined paediatric and adult centre.

‡ Type of CF Centre; P, Paediatric; A, Adult; C, Combined adult and paediatric.

§ As determined by *Pseudomonas aeruginosa* specific real-time PCR analysis [1].

Table S2 Comparison of microbiological data with enterobacterial repetitive intergenic consensus (ERIC)-PCR genotype.*†

	Unique	AUST-01	AUST-02	AUST-04	AUST-05	AUST-06
Number of patients	373	220	173	47	37	31
Methicillin sensitive <i>Staphylococcus aureus</i>	25.2	7.7	23.7	10.6	5.4	22.6
Methicillin resistant <i>S. aureus</i>	1.3	2.7	3.5	8.5	-	-
<i>Haemophilus influenzae</i>	0.5	0.5	2.3	-	2.7	-
<i>Burkholderia cepacia complex</i>	2.4	0.5	1.2	2.1	-	3.2
<i>Stenotrophomonas maltophilia</i>	2.9	0.9	2.3	2.1	-	3.2
<i>Achromobacter xylosoxidans</i>	1.1	-	4.6	-	-	3.2
Non-tuberculous <i>Mycobacterium spp.</i>	0.3	-	-	-	-	-
<i>Aspergillus spp.</i>	12.1	5.0	6.9	12.8	2.7	-
Nil co-pathogens detected	51.7	69.5	55.5	57.4	54.1	67.7

* Data expressed as the percentage of patients with co-pathogens reported at the time of sputum specimen collection.

† Chi-square (2 x 2) analysis was used to assess the association between ERIC-PCR genotype and other microorganisms at the time of sample collection. Bold type indicates *P*-values <0.005 for comparison with unique strains.

Table S3 Comparison of enterobacterial repetitive intergenic consensus (ERIC)-PCR genotype with multilocus sequence type (MLST) sequence type (ST)

ERIC-PCR genotype	MLST ST	No. of isolates	ERIC-PCR genotype	MLST ST	No. of isolates	ERIC-PCR genotype	MLST ST	No. of isolates
AUST-01	649	15	AUST-27	455	2	U328	845	1
AUST-02	266	1	AUST-28	241	2	U329	377	1
AUST-02	775	13	AUST-29	261	2	U330	11	1
AUST-03	242	5	AUST-30	1036	2	U332	806	1
AUST-04	788	3	AUST-31	274	2	U333	807	1
AUST-05	274	6	AUST-32	236	2	U334	569	1
AUST-05	781	1	AUST-33	12	2	U335	796	1
AUST-06	801	4	AUST-34	1038	1	U342	12	1
AUST-07	262	3	AUST-34	N/A	1	U344	798	1
AUST-08	782	3	AUST-35	553	2	U347	899	1
AUST-08	783	1	AUST-36	277	2	U348	494	1
AUST-08	784	1	AUST-37	155	2	U349	282	1
AUST-08	785	1	AUST-38	254	1	U353	273	1
AUST-09	274	4	AUST-38	1041	1	U355	779	1
AUST-09	1043	1	U027	1035	1	U356	780	1
AUST-10	155	2	U061	668	1	U358	882	1
AUST-10	179	6	U108	385	1	U359	873	1
AUST-11	803	2	U119	1040	1	U360	259	1
AUST-11	1034	1	U280	904	1	U365	147	1
AUST-11	1037	1	U281	275	1	U366	828	1
AUST-11	508	1	U284	399	1	U373	27	1
AUST-11	804	1	U289	27	1	U374	14	1
AUST-11	822	1	U290	253	1	U375	471	1
AUST-11	882	1	U293	274	1	U376	15	1
AUST-12	179	3	U294	880	1	U379	116	1
AUST-13	389	1	U296	902	1	U380	155	1
AUST-13	800	4	U299	821	1	U381	847	1
AUST-14	155	2	U300	2	1	U382	857	1
AUST-14	179	1	U301	829	1	U387	557	1
AUST-15	17	1	U302	910	1	U390	905	1
AUST-16	905	3	U303	257	1	U429	791	1
AUST-17	810	3	U304	844	1	U433	260	1
AUST-18	274	2	U310	905	1	U434	1042	1
AUST-19	155	2	U311	245	1	U439	795	1
AUST-19	786	1	U312	275	1	U440	794	1
AUST-20	655	2	U313	644	1	U444	676	1
AUST-21	808	2	U314	851	1	U445	793	1
AUST-22	809	2	U318	776	1	U449	792	1
AUST-23	833	2	U321	443	1	U484	1039	1
AUST-24	308	2	U322	862	1	U488	790	1
AUST-25	274	2	U326	270	1	U492	146	1
AUST-26	179	2	U327	797	1	U493	179	1

Table S4 Comparison of multilocus sequence type (MLST) sequence type (ST) with enterobacterial repetitive intergenic consensus (ERIC)-PCR genotype.

MLST ST	ERIC-PCR genotype(s) (No. of isolates)
2	U300 (1)
11	U330 (1)
12	AUST-33 (2), U342 (1)
14	U374 (1)
15	U376 (1)
17	AUST-15 (1)
27	U289 (1), U373 (1)
116	U379 (1)
146	U492 (1)
147	U365 (U)
155	AUST-10 (2), AUST-14 (2), AUST-19 (2), AUST-37 (2), U380 (1)
179	AUST-10 (6), AUST-12 (3), AUST-14 (1), AUST-26 (2), U493 (1)
236	AUST-32 (2)
241	AUST-28 (2)
242	AUST-03 (5)
245	U311 (1)
253	U290 (1)
254	AUST-38 (1)
257	U303 (1)
259	U360 (1)
260	U433 (1)
261	AUST-29 (2)
262	AUST-07 (3)
266	AUST-02 (1)
270	U326 (1)
273	U353 (1)
274	AUST-05 (6), AUST-09 (4), AUST-18 (2), AUST-25 (2), AUST-31 (2), U293 (1)
275	U281 (1), U312 (1)
277	AUST-36 (2)
282	U349 (1)
308	AUST-24 (2)
377	U329 (1)
385	U108 (1)
389	AUST-13 (1)
399	U284 (1)
443	U321 (1)
455	AUST-27 (2)
471	U375 (1)
494	U348 (1)
508	AUST-11 (1)
553	AUST-35 (2)
557	U387 (1)
569	U334 (1)
644	U313 (1)
649	AUST-01 (15)
655	AUST-20 (2)
668	U061 (1)
676	U444 (1)
775	AUST-02 (13)
776	U318 (1)
779	U355 (1)
780	U356 (1)
781	AUST-05 (1)

Table S4 (continued) Comparison of multilocus sequence type (MLST) sequence type (ST) with enterobacterial repetitive intergenic consensus (ERIC)-PCR genotype

MLST ST	ERIC-PCR genotype(s) (No. of isolates)
782	AUST-08 (3)
783	AUST-08 (1)
784	AUST-08 (1)
785	AUST-08 (1)
786	AUST-19 (1)
788	AUST-04 (3)
790	U488 (1)
791	U429 (1)
792	U449 (1)
793	U445 (1)
794	U440 (1)
795	U439 (1)
796	U335 (1)
797	U327 (1)
798	U344 (1)
800	AUST-13 (4)
801	AUST-05 (4)
803	AUST-11 (2)
804	AUST-11 (1)
806	U332 (1)
807	U333 (1)
808	AUST-21 (2)
809	AUST-22 (2)
810	AUST-17 (3)
821	U299 (1)
822	AUST-11 (1)
828	U366 (1)
829	U301 (1)
833	AUST-23 (1)
834	AUST-23 (1)
844	U304 (1)
845	U328 (1)
847	U381 (1)
851	U314 (1)
857	U382 (1)
862	U322 (1)
873	U359 (1)
880	U294 (1)
882	AUST-11 (1), U358 (1)
899	U347 (1)
902	U296 (1)
904	U280 (1)
905	AUST-16 (3), U310 (1), U390 (1)
910	U302 (1)
1034	AUST-11 (1)
1035	U027 (1)
1036	AUST-30 (2)
1037	AUST-11 (1)
1038	AUST-34 (1)
1039	U484 (1)
1040	U119 (1)
1041	AUST-38 (1)
1042	U434 (1)
1043	AUST-09 (1)
INDEL01	AUST-34 (1)

References

- 1 Anuj SN, Whiley DM, Kidd TJ, et al. Identification of *Pseudomonas aeruginosa* by a duplex real-time polymerase chain reaction assay targeting the *ecfX* and the *gyrB* genes. *Diagn Microbiol Infect Dis* 2009;**63**:127-31.