

Table 2. Clinical characteristics of subjects infected with MRSA belonging to distinct clusters by whole genome sequencing.

Characteristic	Cluster A N = 54	Cluster B N = 14	Cluster C N = 6	<i>P</i> overall	<i>P</i> A vs B
Age, years[†] Median [IQR]	24.1 [14.8 - 32.5]	11.1 [8.5 - 17.2]	19.1 [5.2 – 29.0]	0.005 *	0.0009 #
MRSA acquisition date, Median [IQR]	3/31/11 [3/12/07 – 9/16/14]	8/11/13 [1/13/11– 7/22/15]	11/27/14 [5/17/06 – 4/17/17]	0.0547 *	0.0203 #
Female Sex	28 (51.9%)	6 (42.9%)	2 (33.3%)	0.69 ‡	0.77 ‡
Genotype				0.62 ‡	0.43 ‡
ΔF508/ΔF508	29 (53.7%)	6 (42.9%)	2 (33.3%)		
ΔF508/other	22 (40.7%)	8 (57.1%)	4 (66.7%)		
Other/other	3 (5.6%)	0	0		
CFTR related metabolic syndrome	0	1 (7.1%)	0	-	-
Lung Transplant as of 1 Jan 2017	4 (7.4%)	0	0	-	-
Outcome**	Cluster A	Cluster B	Cluster C	<i>P</i>	<i>P</i>

	N = 50	N = 13	N = 6	overall	A vs B
Sputum production N (%)	45 (90%)	11 (84.6%)	5 (83.3%)	0.5482 [‡]	0.6266 [‡]
<i>P. aeruginosa</i> N (%)	37 (74%)	7 (54.0%)	5 (83.3%)	0.3711 [‡]	0.1857 [‡]
Spirometry performed N (%)	47 (94.0%)	13 (100%)	5 (83.3%)	0.4389 [‡]	1.00 [‡]
FEV₁ % Predicted Median [IQR]	64.0 [53 – 88]	98.0 [86.0 – 116.0]	67.0 [45.0 – 78.0]	0.001 [*]	0.0003 [#]

[†] Age determined on July 1, 2017. ^{**}Outcome data from calendar year 2017, excluding measurements after lung transplant and subjects with CFTR related metabolic syndrome. *P* values determined by [‡]Fisher's exact test, ^{*}Kruskal-Wallis test, or [#]Wilcoxon rank sum test.