Supplementary Material.

Table 1. The PVL encoding phages and the amount of PVL detected in culture supernatants of isolates of different lineages of PVL-MRSA.

*: SCC*mec* V (5C2&5), [a]: SCC*mec* V (5C2). [b]: SCC*mec* IV Non-typeable. Disease Presentations: Community-Associated Pneumonia (CAP), Bacteraemia (BACT), Skin and Soft Tissue Infection (SSTI), Upper Respiratory Tract Infection (URTI), Asymptomatic (AS), Not Known (NK). [F]: Fatal, five of the patients with PVL-MRSA infection subsequently died (3.5%; four with community-associated pneumonia (CC22 n=2, CC80 n=2) and one with bacteraemia (CC22)). Sex: Female (F), Male (M). NK: Not known or not available. GR: Geographic Region- Nine regions of England designated by the Health Protection Agency, including Wales (defined as a 10th region for the purposes of this study).

MLST Lineage (n)	MLST Sequence type	*spa*-type	PVL Phage (Φ)	*agr*	SCC*mec* (n)	Disease (n)	GR (n)	Sex (n)	Age Range (Yrs)					PVL Range µg/ml	Mean PVL (µg/ml)	Mean SD / isolate	Mean SD / Lineage
									0-16	17-40	41-60	60+	NK				
CC1 (11)	ST1 ST772	t127 (7) t128 (3) t657 (1)	Sa2USA (7) Sa2MW (3) Unknown (1)	3	IVa (9) IVc (1) V *(1)	SSTI (8) AS (3)	3	F (2) M (7) NK (2)	4	4	-	-	3	0.117 – 0.954	0.55	0.110	0.220
CC5 (9)	ST5	t002 (9)	Sa2USA (7) Unknown (1) Icosahedral (1)	2	IVc (7) IVh (1) IVNT (1)	SSTI (9)	7	F (5) M (4)	2	5	2	-	-	0.209 – 0.489	0.326	0.140	0.100
CC8 (17)	ST8	t008 (14) t4069 (2) t024 (1)	Sa2USA (17)	1	IVa (16) IVb (1)	AS (3) CAP (1) SSTI(12) NK (1)	9	F (5) M (12)	7	5	4	1	-	0.072 – 4.865	1.198	0.184	1.052
CC22 (48)	ST22	t005 (34) t852 (9) t1790 (2) t1516 (1) t2816 (1) t849 (1)	PVL (34) 108PVL (8) Icosahedral (6)	1	IVc (43) IVd (3) IVNT^{b} (1) V^{a} (1)	AS (20) BACT (1)^{F} NA (5) CAP (2)$^{F, F}$ SSTI (16) URTI (4)	9	F (21) M (25) NK (2)	25	8	12	2	1	0.038 – 0.881	0.359	0.097	0.167
CC30 (9)	ST30	t019 (6) t318 (2) t012 (1)	Icosahedral (5) Elongated (3) Unknown (1)	3	IVa (3) IVc (5) IVd (1)	AS (1) SSTI (8)	7	F (3) M (6)	2	4	2	1		0.074 – 1.080	0.634	0.193	0.318
CC59 (3)	ST59	t437 (3)	Sa2958like (2) Unknown (1)	1	V * (3)	SSTI (2) NA (1)	2	F (1) M (2)	1	2	-	-		0.324 – 0.560	0.438	0.157	0.118
CC80 (27)	ST80	t044 (24) t131 (1) t1759 (1) t2891 (1)	Sa2MW (27)	3	IVc (27)	AS (5) BACT(1) CAP (8)$^{F, F}$ SSTI (13)	10	F (12) M (14) NA (1)	3	10	5	7	2	0.020 – 0.955	0.239	0.062	0.241
CC88 (5)	ST88	t690 (2) t448 (2) t186 (1)	Elongated (5)	3	IVa (5)	AS (1) SSTI (4)	4	F (3) M (2)	2	1	-	-	2	0.144 – 0.296	0.190	0.110	0.061
ST93 (13)	ST93	t202 (12) t3949 (1)	Sa2USA (13)	3	IVa (13)	CAP (1) SSTI (12)	6	F (5) M (8)	4	7	2	-	-	0.582 – 1.992	0.926	0.206	0.357

Table 2. Pearson's Chi Squared test for variation examining the affects of age, sex and geographic region on disease presentation.

Significance was set at $p<0.05$. None of the variables had a significant affect.

Variables Tested by Pearson’s Chi Squared Test	**P-value**
Age on disease presentation	0.08833
Sex on disease presentation	0.8996
Geographic region on disease presentation	0.1324

Table 3. Coefficients for the Generalised Linear Model (GLM) examining the effect of MLST clonal complex on PVL production.

The intercept was set as CC8 as this was the highest PVL-producing lineage.

Significance was set at p<0.05. Std. Error: Standard Error.

Coefficients:

	Estimate	**Std. Error**	**t value**	**Pr(>|t|)**	**Significance**
(Intercept)	4.4303	0.1870	23.693	<2e-16	<0.001
CC1	-0.5319	0.2983	-1.783	0.076857	0.1
CC5	-0.9851	0.3178	-3.100	0.002366	<0.001
CC22	-0.9868	0.2176	-4.535	1.27e-05	<0.001
CC30	-0.4891	0.3178	-1.539	0.126189	1
CC59	-0.6756	0.4828	-1.399	0.164027	1
CC80	-1.8048	0.2387	-7.561	5.85e-12	<0.001
CC88	-1.5220	0.3922	-3.880	0.000163	<0.001
ST93	0.0472	0.2841	0.166	0.868286	1

(Dispersion parameter for gaussian family taken to be 0.2589196)

Residual standard error: 0.5088 on 133 degrees of freedom
Multiple R-squared: 0.447, Adjusted R-squared: 0.4137
F-statistic: 13.44 on 8 and 133 DF, p-value: 3.936e-14