

Progress Report

Commonwealth Contract – Services

Reference ID: E21-52135

Supplier: Australian Society for Antimicrobials

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Project 1:

AESOP – Molecular Characterisation of the *van* operon in vancomycin variable *Enterococcus faecium* isolated in the Australian *Enterococcus* Septicaemia Outcome Program (AESOP)

We have examined the 2013 to 2020 AESOP databases and have determined of the 3,467 *Enterococcus faecium* referred to the AESOP reference laboratory (the Antimicrobial Resistance and Infectious Diseases Research at Murdoch University), 632 (18.3%) harboured *vanA*, 983 (28.4%) *vanB*, and 15 (0.4%) *vanA* and *vanB* (Table 1).

TABLE 1: AESOP 2013 to 2020: *Enterococcus faecium* referred to the AESOP reference laboratory

	2013	2014	2015	2016	2017	2018	2019	2020	Total
<i>E. faecium</i> Reported									
	325	380	400	413	481	490	596	488	3,573
<i>E. faecium</i> Referred									
<i>vanA</i>	8	35	78	85	112	122	128	64	632
<i>vanB</i>	128	154	134	110	119	108	127	103	983
<i>vanA+vanB</i>	0	0	6	3	2	2	1	1	15
Non <i>vanA</i> or <i>vanB</i>	171	181	175	202	235	243	320	310	1,837
Total	307	370	393	400	468	475	576	478	3,467

Using the Vitek[®] 2 (bioMérieux, France) or BD Phoenix[™] (Becton Dickinson, USA) automated microbiology systems, 52 *vanA*- and 66 *vanB*-positive *E. faecium* were reported as vancomycin susceptible and therefore classified as vancomycin variable *E. faecium* (VVEfm) (Table 2).

TABLE 2: AESOP 2013 to 2020: Vancomycin variable *Enterococcus faecium* referred to the AESOP reference laboratory

	2013	2014	2015	2016	2017	2018	2019	2020	Total
<i>vanA</i>	0	4	7	3	7	10	12	9	52
<i>vanB</i>	8	14	14	3	11	8	5	3	66
<i>vanA+vanB</i>	0	0	0	0	0	0	0	0	0
Total	8	18	21	6	18	18	17	12	118

We have retrieved the 118 isolates from the -80°C freezer and have commenced:

- Determining the vancomycin minimum inhibitory concentration (MIC) by microdilution according to CLSI criteria
- Performing bioinformatics analysis of the VVEfm genomes previously sequenced by Illumina sequencing to determine the genetic factors responsible for vancomycin susceptibility in *vanA*- and *vanB*-positive VVEfm

We anticipate the following objectives will be completed by 31 March 2023

- Confirming the molecular mechanism responsible for VVEfm
- Determining if VVEfm exposed to increasing concentrations of vancomycin can revert to a vancomycin-resistant phenotype
- Performing long read sequencing on a representative set of VVEfm isolates

Project 2:

ASSOP – Investigating the genetic factor(s) responsible for daptomycin resistance in *Staphylococcus aureus* reported in the Australian *Staphylococcus aureus* Septicaemia Outcome Program (ASSOP)

We have examined the 2013 to 2020 ASSOP databases and have determined of the 19,848 *Staphylococcus aureus* referred to the ASSOP reference laboratory (the Antimicrobial Resistance and Infectious Diseases Research at Murdoch University), 16,204 (81.6%) were methicillin-sensitive *S. aureus* (MSSA) and 3,644 (18.4%) were methicillin-resistant *S. aureus* (MRSA) (Table 1).

TABLE 1: ASSOP 2013 to 2020: *Staphylococcus aureus* referred to the ASSOP reference laboratory

	2013	2014	2015	2016	2017	2018	2019	2020	Total
<i>S. aureus</i> Reported									
	2,114	2,206	2,399	2,540	2,515	2,673	3,157	2,734	20,338
<i>S. aureus</i> Referred									
MSSA	1,688	1,754	1,931	1,975	1,992	2,153	2,510	2,201	16,204
MRSA	375	405	428	481	466	453	568	468	3,644
Total	2,063	2,159	2,359	2,456	2,458	2,606	3,078	2,669	19,848

Using the Vitek[®] 2 (bioMérieux, France) or BD Phoenix[™] (Becton Dickinson, USA) automated microbiology systems, 43 MSSA and 32 MRSA were reported daptomycin resistant (Table 2).

TABLE 2: ASSOP 2013 to 2020: Daptomycin resistant *Staphylococcus aureus* referred to the ASSOP reference laboratory

	2013	2014	2015	2016	2017	2018	2019	2020	Total
MSSA	5	4	2	4	7	6	5	10	43
MRSA	4	6	3	4	3	8	0	4	32
Total	9	10	5	8	10	14	5	14	75

We have retrieved the 75 isolates from the -80°C freezer and have commenced:

- Determining the daptomycin minimum inhibitory concentration (MIC) by broth microdilution according to CLSI criteria
- Evaluating the performance of the daptomycin Etest[®] susceptibility strip with broth microdilution

We anticipate the following objectives will be completed by 31 March 2023:

- Identifying single nucleotide polymorphisms (SNPs) in *S. aureus* associated with daptomycin resistance on isolates determined daptomycin resistant by broth microdilution
- Elucidating the role of identified SNPs in daptomycin-resistant *S. aureus*
- Performing long read sequencing on representative isolates harbouring SNPs associated with daptomycin resistance.