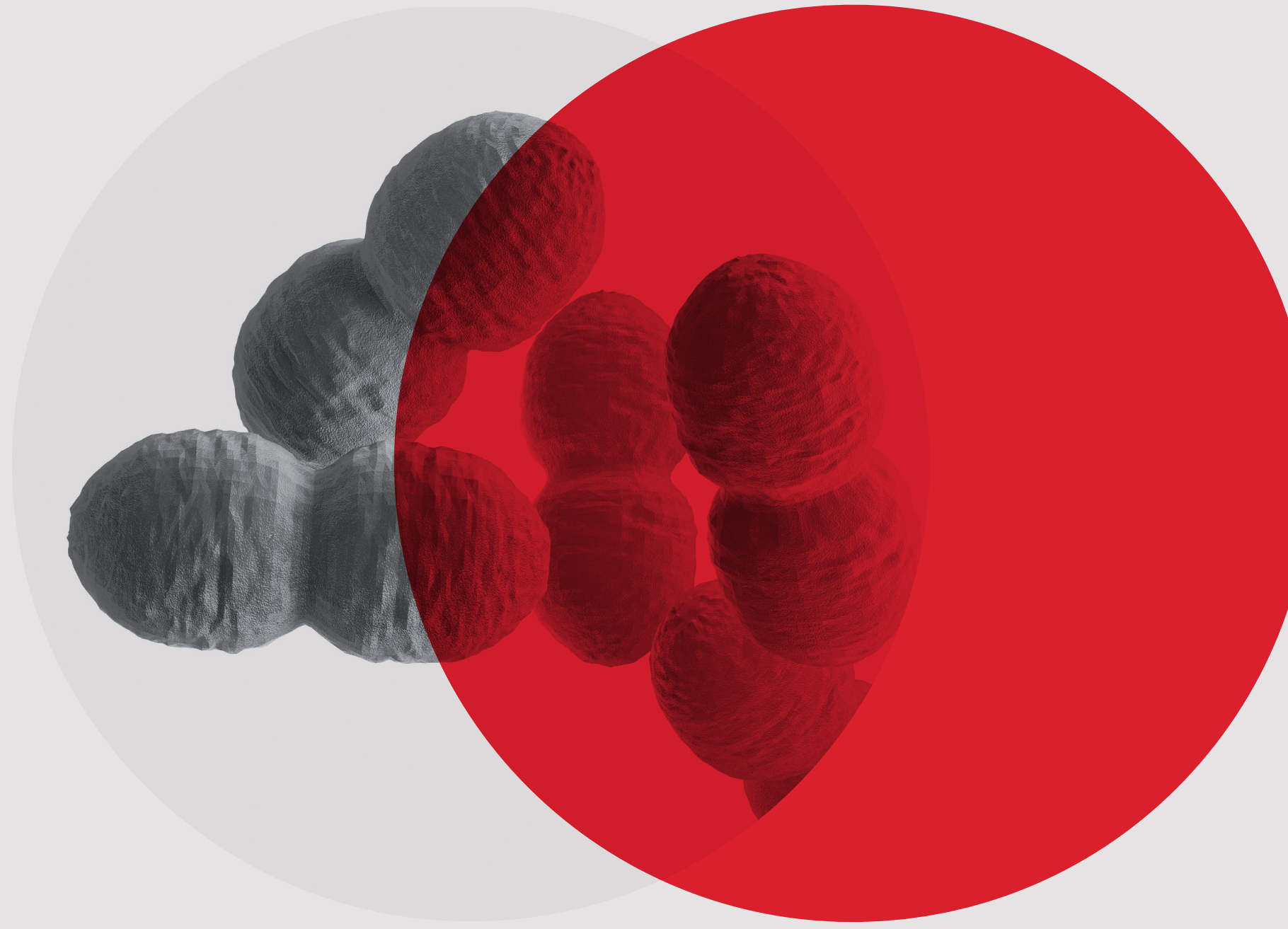


Vancomycin Resistant *Enterococci* (VRE) screening quality assurance program: a five-year review of methods and performance

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Background

VRE are strains of *Enterococci* that have developed resistance to vancomycin, a glycopeptide antibiotic used to treat serious enterococcal infections.

Vancomycin-resistant *Enterococcus* was first described in England in 1988¹. Since then, it has increasingly become a major nosocomial pathogen worldwide. In Australia, it was reported that the percentage of *E. faecium* bacteraemia isolates resistant to vancomycin is now much higher than in all European countries².

Given the importance of accurately reporting VRE, the RCPAQAP Microbiology introduced the program “*Enterococci* for identification, antimicrobial susceptibility and *van* gene detection” in 2011. It was renamed in 2013 to become the “Vancomycin Resistant *Enterococcus* (VRE) Screening” program to be more aligned with the relevant guidelines³. Participants enrolled in this program are currently from Australia, New Zealand, Asia (Hong Kong, Thailand, Malaysia, China, Singapore) and Europe (Sweden, Spain and France). Enrolments grew from 52 participants in 2011 to 96 in 2018.

Material/methods

Four lyophilised simulated samples representing rectal swabs are sent twice a year. Once reconstituted, samples are suitable for enterococcal culture and/or molecular testing. Participants are asked to perform “VRE screen” testing as per their laboratory protocol.

The RCPAQAP direct data entry is used to capture methods, results and overall comments. From 2014 to 2018, methods and algorithms used by participating laboratories to test for VRE were analysed and participant performance was assessed.

Results

From 2014 to 2018:

- Majority of participants used culture-based methods
- 25% to 31% of laboratories employed molecular methods and/or with culture/other methods
- Greater than 90% reported correct responses

Figure 1. 2014–2018 enrolled participants, methods

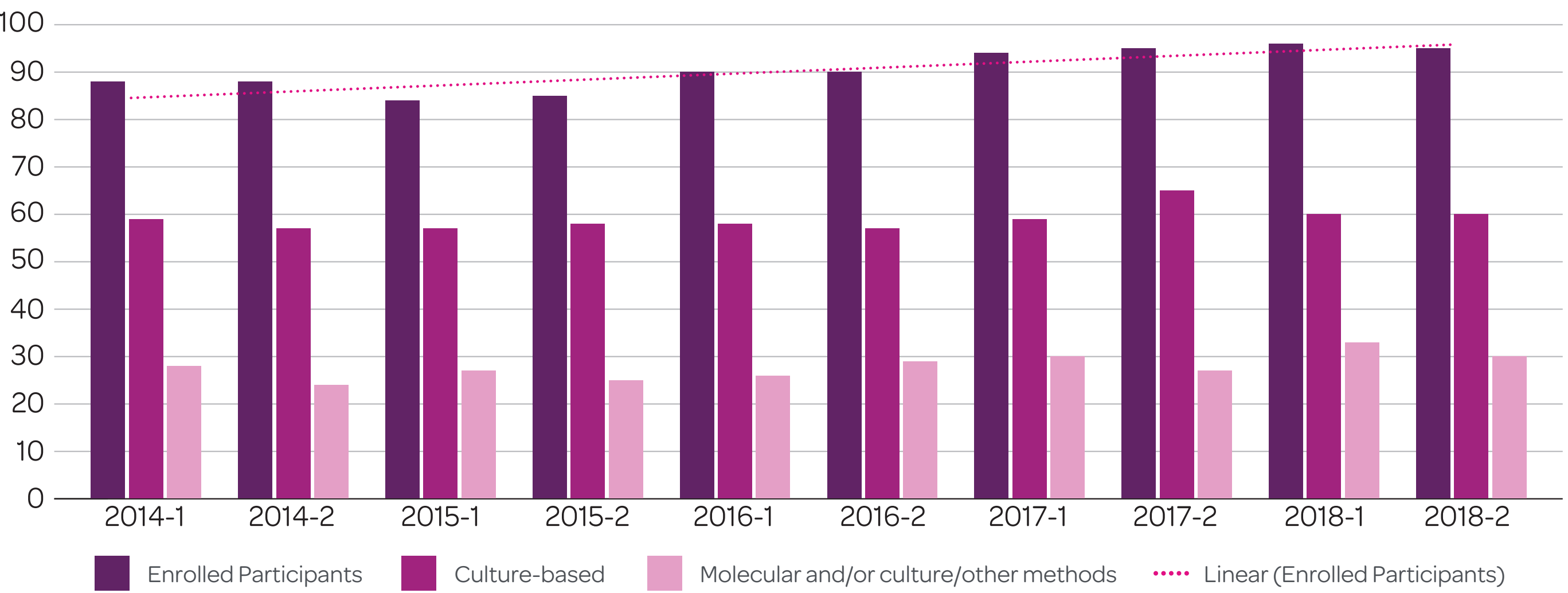


Table 1. Media used 2018 Survey 2

Media	Number of user/s
Bile esculin agar + vancomycin	1
Blood Agar	1
Blood Agar,Chromogenic agar	4
Blood Agar,Chromogenic agar,MAC,VRE broth	1
Blood Agar,Chromogenic agar,VRE broth	2
Blood Agar,Mueller Hinton	2
Blood Agar,VRE agar	1
Blood Agar,VRE broth	1
Chromogenic agar	41
Chromogenic agar,CNA	3
Chromogenic agar,GrpB broth	1
Chromogenic agar,Mueller Hinton	2
Chromogenic agar,VRE broth	18
Mueller Hinton,VRE agar	1
NEGRAM AGAR,MAC	1
VRE agar	3
VRE agar,VRE broth	3
VRE broth	1
VRE broth,Azt plate with Vanc disc	1

Table 2. Molecular detection methods used 2018 Survey 2

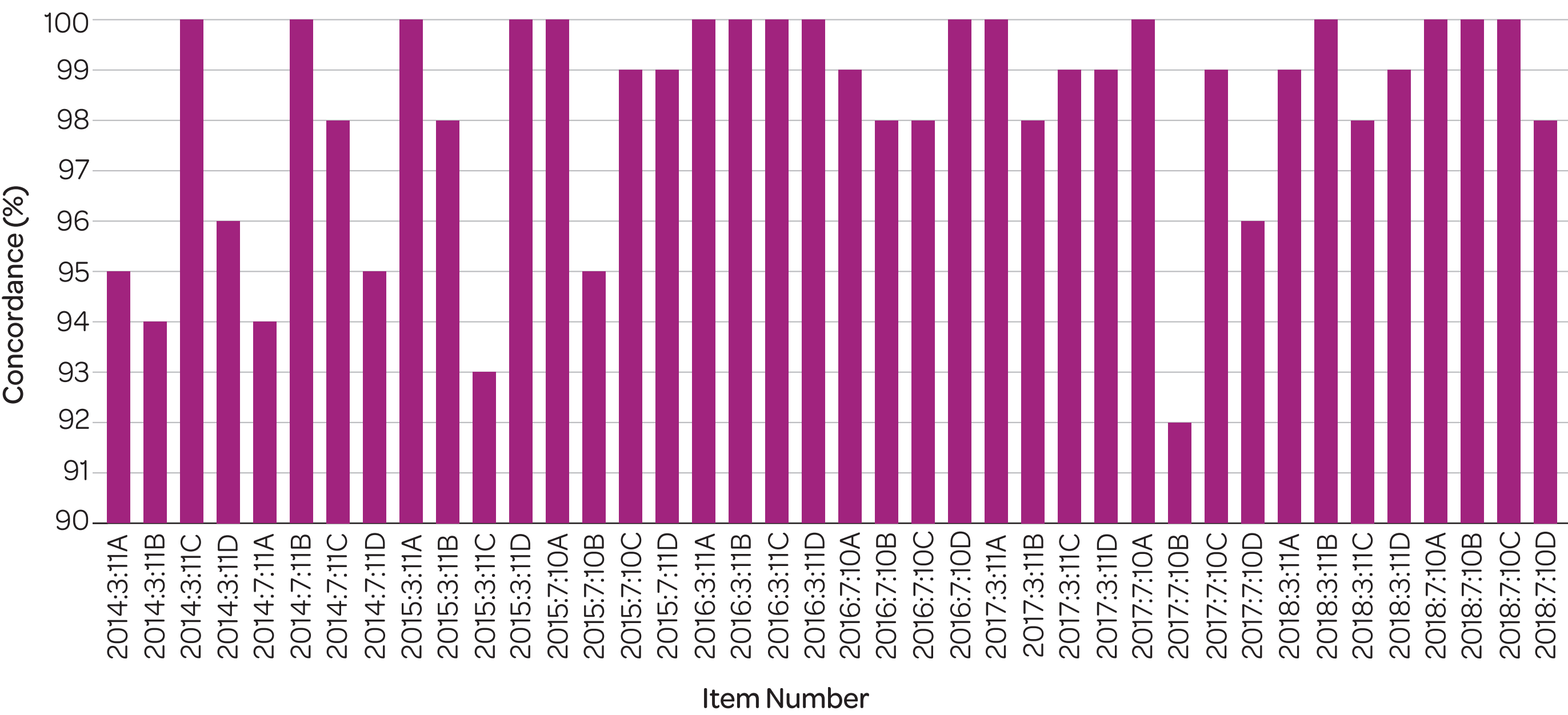
Method	Number of user/s
AMR direct flow chip kit	1
Ausdiagnostics: Staphylococcus + VRE (8 well)	1
BDMAX ExK DNA-3 and BioGX	1
GeneXpert VanA/VanB	12
Inhouse (no details)	2
Inhouse (Syto 9 Fluorescence)	1
Inhouse PCR (gel detection)	2
Inhouse Real time PCR	5
Roche LC VRE detection	3

Table 3. Items sent 2014–2018

Item number	Sample* content/s	Characteristic/s
2014:3:11A	<i>E. faecium</i>	VRE, vanB
2014:3:11B	<i>E. faecium</i>	VRE, vanA
2014:3:11C	<i>E. faecalis</i>	Non-VRE
2014:3:11D	<i>E. faecium</i> (duplicate of 11B)	VRE, vanA
2014:7:11A	<i>E. faecium</i>	VRE, vanB
2014:7:11B	<i>E. faecium</i>	VRE, vanA
2014:7:11C	<i>E. faecalis</i>	VRE, vanA
2014:7:11D	<i>E. faecium</i>	VRE, vanB
2015:3:11A	<i>E. faecium</i>	VRE, vanB
2015:3:11B	<i>E. faecalis</i>	Non-VRE
2015:3:11C	<i>E. faecium</i>	VRE, vanA
2015:3:11D	<i>E. faecalis</i>	VRE, vanB
2015:7:10A	<i>E. faecalis</i>	Non-VRE
2015:7:10B	<i>E. faecium</i>	VRE, vanB
2015:7:10C	<i>Leuconostoc lactis</i>	Vancomycin resistant gram-positive coccus, No VRE
2015:7:11D	<i>E. faecium</i>	VRE, vanA
2016:3:11A	<i>Pediococcus pentosaceus</i>	Vancomycin resistant gram-positive coccus, No VRE
2016:3:11B	<i>E. faecium</i>	VRE, vanA
2016:3:11C	<i>E. faecalis</i>	VRE, vanA
2016:3:11D	<i>E. faecium</i> and <i>E. faecalis</i>	VRE, <i>E. faecalis</i> (vanB); <i>E. faecium</i> (vanA)
2016:7:10A	<i>E. faecium</i>	Non-VRE
2016:7:10B	<i>E. faecium</i>	VRE, vanB
2016:7:10C	<i>E. faecalis</i>	VRE, vanB
2016:7:10D	<i>E. coli</i> , <i>C. freundii</i> and <i>K. pneumoniae</i>	No VRE
2017:3:11A	<i>E. faecium</i>	VRE, vanA; Teicoplanin R (MIC 24mg/L); Vancomycin R (MIC >256 mg/L)
2017:3:11B	<i>E. faecalis</i>	Non-VRE
2017:3:11C	<i>E. faecalis</i> (duplicate of 11B)	Non-VRE
2017:3:11D	<i>E. faecium</i>	VRE, vanB; Teicoplanin and vancomycin R (MIC >256 mg/L)
2017:7:10A	<i>E. faecalis</i>	Non-VRE
2017:7:10B	<i>E. faecium</i>	VRE, vanB
2017:7:10C	<i>E. faecalis</i> (duplicate of 10A)	Non-VRE
2017:7:10D	<i>E. faecium</i> (duplicate of 10B)	VRE, vanB
2018:3:11A	<i>E. faecalis</i>	Non-VRE
2018:3:11B	<i>E. faecalis</i>	Non-VRE
2018:3:11C	<i>E. faecalis</i>	VRE, vanA
2018:3:11D	<i>E. faecalis</i>	VRE, vanB
2018:7:10A	<i>E. faecium</i>	Non-VRE
2018:7:10B	<i>E. faecium</i>	VRE, vanB
2018:7:10C	<i>E. faecalis</i>	VRE, vanB

*Sample/s would have normal flora included.

Figure 2. 2014–2018 VRE screening QAP performance



Conclusions

- The choice of methods used, culture-based and/or molecular/other, still vary as per consideration of laboratories’ relevant guidelines, test sensitivity, complexity, turnaround time and cost⁴.
- Over the course of five years, whilst false positive and false negative results remain an issue for some participants, there was a high level of concordance.

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