

# External Quality Assessment Scheme for MRSA Screening

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## Introduction

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a well-known cause of healthcare-associated infection and is a major problem in hospitals. MRSA infections can range from asymptomatic colonisation to fatal septicaemia and is therefore a significant contributor to prolonged hospital stays, poor clinical outcomes and increased healthcare costs amongst surgical patients (Gordon & Lowy, 2008). Screening for MRSA and subsequent control measures helps to reduce the incidence of MRSA infections (Fagan *et al.*, 2010).

The United Kingdom National External Quality Assessment Service (UK NEQAS) for Microbiology distributes clinically relevant and educational specimens for external quality assessment (EQA). The MRSA screening scheme enables participants to assess the quality of the culture and molecular screening techniques employed for the detection of MRSA. Twelve distributions were dispatched between April 2009 and March 2011, each comprising of two simulated nasal swabs. A total of 302 laboratories, representing 19 countries (Table 1), participated in the scheme by March 2011.

Table 1. Countries participating in MRSA screening scheme (March 2011)

Participating countries			
Austria	France	Netherlands	Sweden
Belgium	Hong Kong	Norway	Switzerland
Croatia	Ireland	Saudi Arabia	United Arab Emirates
Denmark	Italy	Slovenia	United Kingdom
Finland	Kuwait	South Africa	

## Purpose

To evaluate the results from clinical diagnostic microbiology laboratories taking part in the UK NEQAS for Microbiology MRSA screening scheme between 2009 and 2011.

## Methods

- Quality assessment of MRSA screening was performed on twenty-four simulated nasal swab specimens.
- Specimens sent included 16 positive and eight negative for MRSA.
- Results reported by participants for these specimens were analysed to determine their performance with these specimens.

## Results

### Culture Results

- Analysis of the results showed that with the exception of one specimen (specimen 9281) performance by culture was good with over 93% of participants reporting correctly on the detection of MRSA (Tables 2a, 2b).
  - Specimen 9281 contained a MRSA and a coagulase negative staphylococcus; only 86.4% of participants reported correctly (Table 2b).
- The overall false positive rate for the MRSA negative specimens was 1.7% (30/1732).
- Whilst the overall false negative rate for the MRSA positive specimens was 2.25% (84/3737).
- One specimen contained a ciprofloxacin susceptible community acquired MRSA: 12 laboratories incorrectly reported as negative for MRSA (Table 2b).
- The most commonly used culture method was Oxoid *Brilliance*™ MRSA chromogenic agar plates (Figure 1).
  - The number of participants using this agar increased from 64 to 118 over the 24 month period (Table 3).
  - In the final distribution a further 12 participants used the Oxoid *Brilliance*™ MRSA 2.

Table 2a. Participant performance with specimens that did not contain MRSA

Specimen number	Percentage of participants fully correct:	
	Culture	Molecular
9358	98.3 (177/180)	95.5 (21/22)
9440	98.3 (178/181)	92.9 (26/28)
9603	98.4 (182/185)	100 (34/34)
9604	100 (186/186)	100 (34/34)
9693	99.5 (183/184)	94.4 (34/36)
9872	98.1 (256/261)	44.0 (22/50)
0024	98.3 (281/286)	98.4 (60/61)
0116	96.3 (259/269)	92.2 (47/51)

Table 2b. Participant performance with specimens containing MRSA

Specimen number	Percentage of participants fully correct:	
	Culture	Molecular
9281	86.4 (153/177)	92.9 (26/28)
9282	93.1 (161/173)	92.6 (25/27)
9359	97.8 (176/180)	84.0 (21/25)
9439	98.9 (179/181)	93.1 (27/29)
9507	95.2 (179/188)	81.1 (30/37)
9508	98.9 (186/188)	100 (37/37)
9694	97.3 (180/185)	94.9 (37/39)
9776	98.9 (266/269)	96.5 (55/57)
9777	99.3 (267/269)	100 (55/55)
9871	98.5 (256/260)	98.2 (55/56)
9945	98.9 (272/275)	94.0 (63/67)
9946	99.3 (274/276)	94.0 (63/67)
0023	99.7 (285/286)	97.0 (65/67)
0115	99.6 (269/270)	98.3 (58/59)
0213	99.3 (278/280)	94.5 (69/73)
0214	96.8 (271/280)	94.6 (70/74)

Figure 1: UK NEQAS for Microbiology scheme for MRSA screening (2009/2011): culture method breakdown by distribution

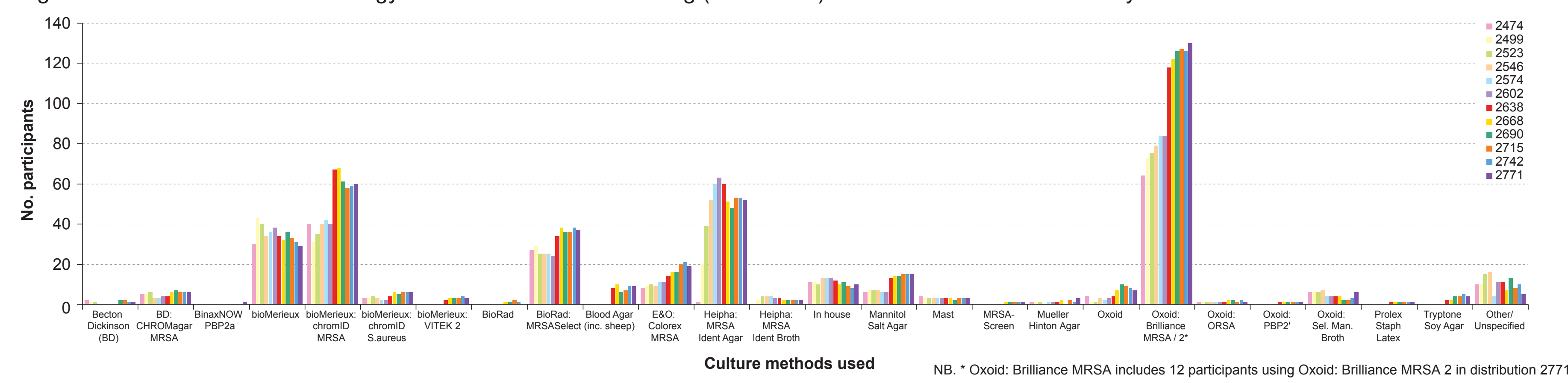


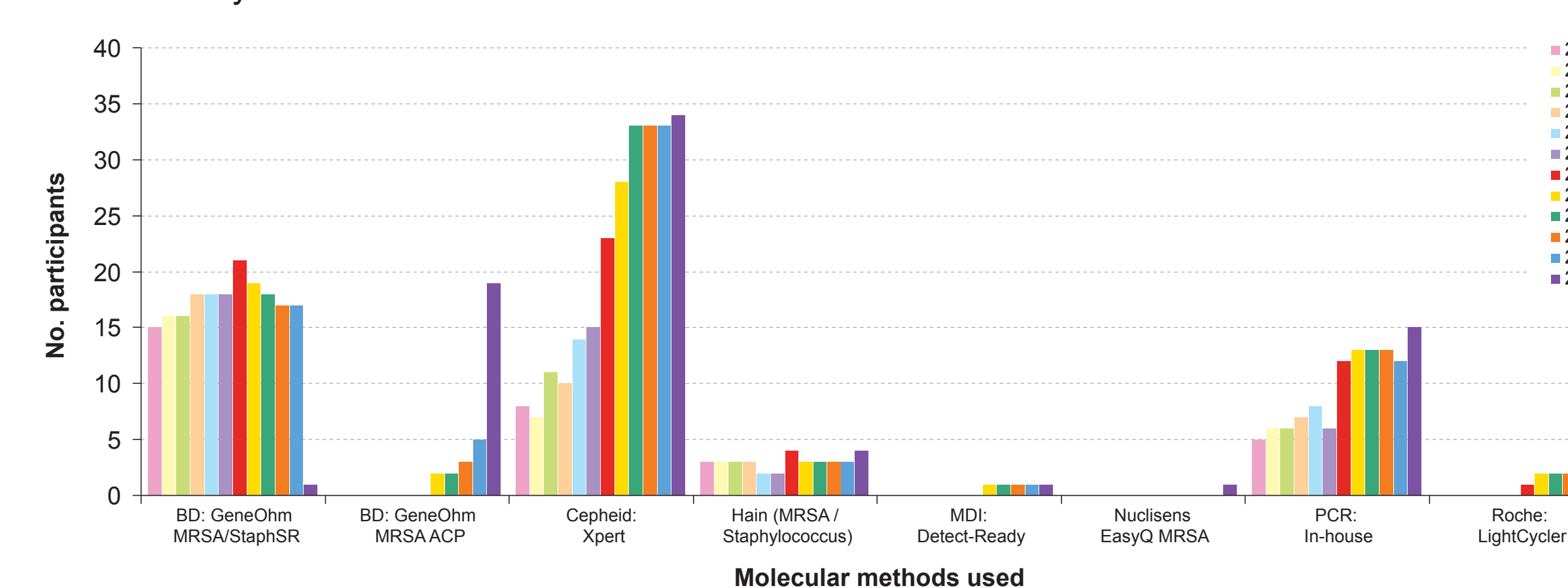
Table 3. Methods used by participants over the first two years of the scheme

Methods	Distribution 2474 (May 2009)	Distribution 2771 (Feb 2011)
Becton Dickinson	2	1
BD: CHROMagar MRSA	5	6
BinaxNOW PBP2a	0	1
bioMerieux	30	1
bioMerieux: chromID MRSA	40	29
bioMerieux: chromID S.aureus	3	3
bioMerieux: VITEK 2	0	3
BioRad	0	0
BioRad: MRSASelect	27	37
Blood Agar	0	9
E&O: Colorex MRSA	8	19
E&O: Salt Broth	0	0
Heipha: MRSA Ident Agar	1	52
Heipha: MRSA Ident Broth	0	2
In house	11	10
Mannitol Salt Agar	6	15
Mast	4	3
MRSA-Screen	0	1
Mueller Hinton Agar	1	3
Nutrient Agar	0	0
Oxoid	4	7
Oxoid: Brilliance MRSA	64	118
Oxoid: Brilliance MRSA 2	0	12
Oxoid: ORSA	1	1
Oxoid: PBP2'	0	1
Oxoid: Sel. Man. Broth	6	6
Prolex Staph Latex	0	1
Tryptone Soy Agar	0	4
Other	10	5
BD: GeneOhm MRSA	15	0
BD: GeneOhm MRSA ACP	0	19
BD: GeneOhm StaphSR	0	1
Cepheid: Xpert	8	34
Hain	3	1
Hain: MRSA	0	2
Hain: Staphylococcus	0	1
MDI: Detect-Ready	0	1
Nuclisens EasyQ MRSA	0	1
PCR: In-house	5	15
Roche: LightCycler	0	2

### Molecular Results

- Overall performance by molecular methods was good with 93% (1034/1113) of participants reporting correctly on the detection of MRSA.
- The overall false positive rate for molecular methods with the MRSA negative specimens was 11.07% (35/316).
- The overall false negative rate for molecular methods with the MRSA positive specimens was 4.9% (39/797).
- Specimen 9872 contained a multi-resistant methicillin-sensitive *S. aureus* (MSSA) that was oxacillin susceptible and negative by PCR for the *mecA* gene.
  - 57.1% (28/49) reported a false positive result with the following assays: BD GeneOhm MRSA (8), BD GeneOhm MRSA ACP (1), Cepheid Xpert (17), Roche LightCycler MRSA Advanced (1) and one participant did not specify the molecular assay used.
- The most commonly used molecular method was Cepheid Xpert MRSA (Table 3, Figure 2).
  - The number of Cepheid Xpert users increased from eight to 34 over the first two years of the scheme (Table 3).

Figure 2: UK NEQAS for Microbiology scheme for MRSA screening (2009/2011): molecular method breakdown by distribution



## Conclusions

- The UK NEQAS for Microbiology MRSA screening scheme has been operating for 24 months and results from the scheme help participants monitor the performance of their methods.
- The most commonly used culture method over the 24 months was Oxoid *Brilliance*™ MRSA chromogenic agar (Figure 1).
- The most commonly used molecular method for all participants was the BD GeneOhm MRSA assay during the first year of the scheme, this changed to Cepheid Xpert by the end of the second year (Figure 2).
- The results from participating laboratories demonstrated a good performance.
- The scheme has highlighted problems with identifying ciprofloxacin susceptible community MRSA (specimen 9282):
  - There is an increasing number of ciprofloxacin susceptible MRSA being reported in the UK and in other countries. These organisms can be found in both community and healthcare settings and have been identified in nosocomial outbreaks.
- Some molecular techniques give false positive results when confronted with a *mecA* knockout gene (specimen 9872):
  - The partial (or complete) excision of staphylococcal cassette chromosome *mec* (SCC*mec*) from MRSA resulting in loss of the *mecA* gene ± other fragments of the cassette is known to occur. Whilst the frequency or factors involved in driving such events are unclear, the potential for some molecular assays to amplify residual elements of SCC*mec* resulting from such partial excision event(s) giving rise to false positives is well recognised (Donnio *et al.*, 2007, Farley *et al.*, 2008).
- During the 24 months the scheme has been running, the number of laboratories reporting molecular screening results has risen from 22 to 74, which was an increase of >200%.
- The scheme has been well received and participation increased from 194 laboratories (13 countries), when the scheme was introduced in 2009, to 312 laboratories (19 countries) by April 2011.

## Acknowledgements

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## References

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