

### Introduction:

For the UK NEQAS for Microbiology General Bacteriology scheme, twelve distributions are prepared and dispatched each year to UK and non-UK clinical diagnostic laboratories. Each month three simulated clinical specimens are prepared and distributed to participants, who examine the specimens in their laboratories and report their findings. Positive specimens contain well characterised organisms and correspond to those likely to be found in clinical practice. Negative samples are also included. Occasionally, more challenging specimens are distributed for educational purposes, or where recognition of an unusual pathogen may be of clinical importance. With each distribution there are two non-enteric specimens and one enteric specimen.

### Methods:

- Distribution reports were reviewed for the period April 2014 to March 2018 (144 specimens)
- The methods used by participants to identify the organisms that had been distributed were recorded and trends noted.
- Specimens which resulted in a poor overall performance were reviewed in order to identify the areas of difficulty experienced by participants

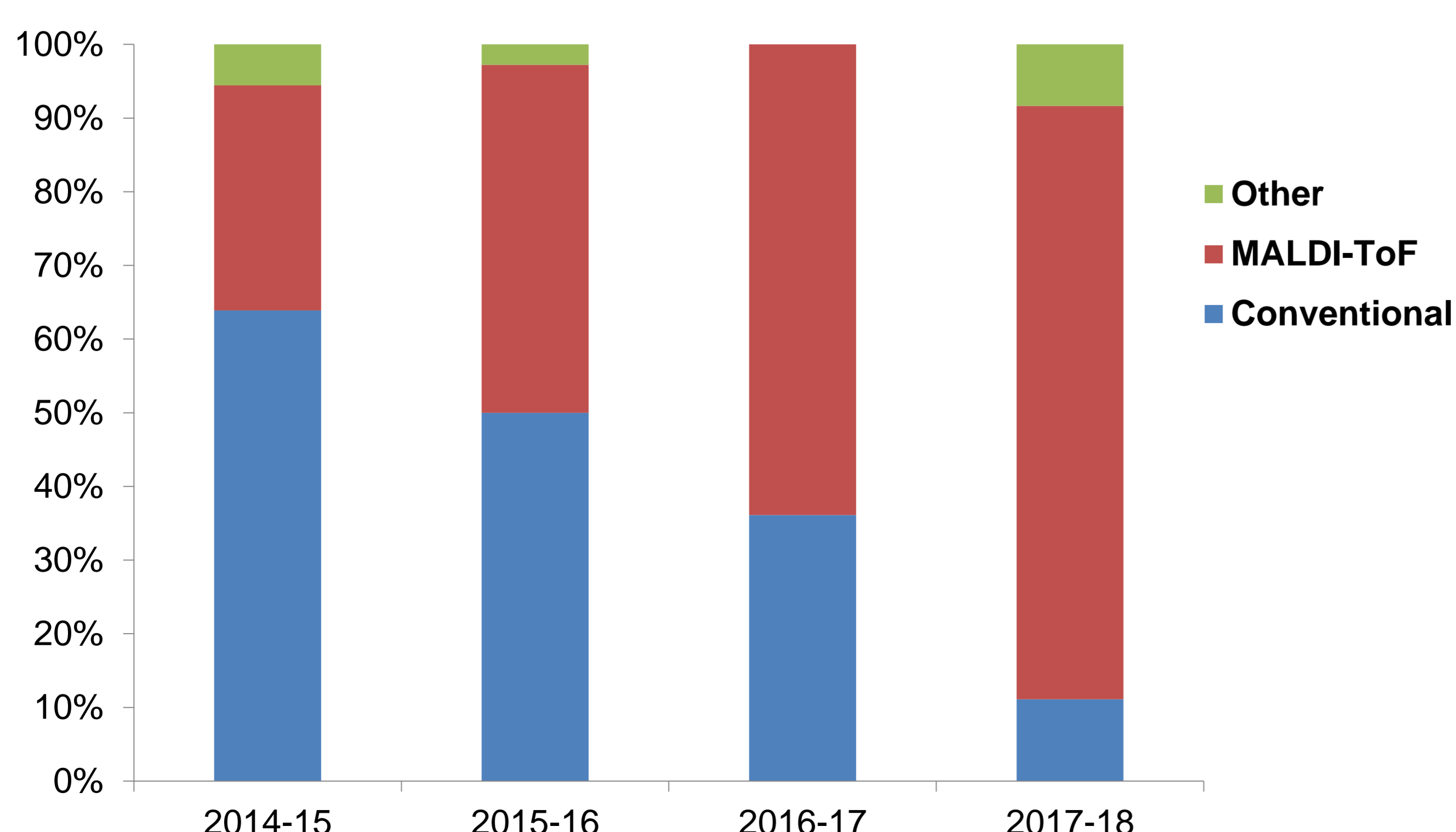
### Results:

During this period the maximum participation each year was 612, 598, 589 and 594 laboratories in 2014-15, 2015-16, 2016-17 and 2018-19 respectively.

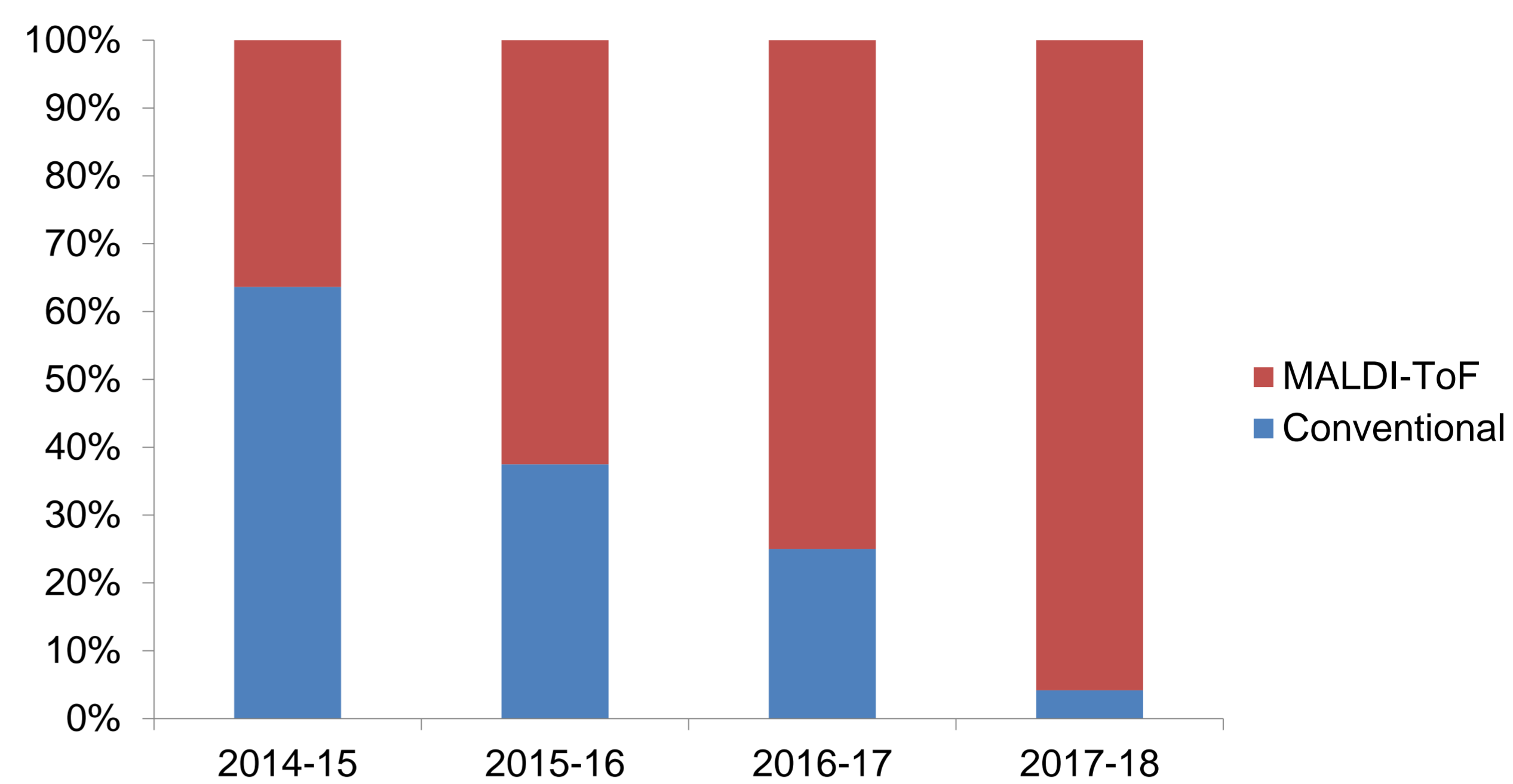
Identification methods included semi-automated systems, for example MALDI-ToF, VITEK®, molecular and conventional (non-automated) diagnostic tests. The most common methods for specimen identification were conventional (23/36) and MALDI-ToF (11/36) in 2014-15 and MALDI-ToF (29/36) and conventional (4/36) in 2017-18. Trends in methods used by year are shown in figure 1 (all specimens) and figure 2 (non-enteric specimens). There was an increase in use of MALDI-ToF each year and a decrease in use of conventional methods. This change was greatest for non-enteric specimens.

Poor performance occurred for 13 specimens (9%), where a consensus of 80% participants with the intended result was not achieved (table). These included advanced (4) and educational (2) specimens. The most common reasons for poor performance were a failure to isolate the pathogen in the specimen (9), and the misidentification of organisms using particular methods (3). However, the number of specimens that achieved poor performance reduced each year, with 4, 5, 2 and 2 in 2014-15, 2015-16, 2016-17 and 2018-19 respectively.

**Figure 1. Trends in methodology by year (all specimens)**



**Figure 2. Trends in methodology by year (non-enteric specimens)**



**Table. Organisms where there was poor performance**

Date	Distribution number	Organism(s)	Category of Organism	Specimen Type	Consensus (%)	Comments
Aug-14	3501	Group A β haemolytic streptococcus + <i>Staphylococcus aureus</i>	Core	Wound	78.9	Mixed organisms. Most common issue only <i>S. aureus</i> isolated
Aug-14	3501	Toxigenic <i>Clostridium difficile</i>	Core	Faeces	31.4	Most likely <i>C. difficile</i> not tested for in nursing home diarrhoea outbreak
Oct-14	3528	<i>Bergeyella zoohelcum</i>	Educational	Wound bite	64.5	Common misdiagnosis was <i>Myroides</i> using non MALDI-ToF methods
Mar-15	3596	<i>Bordetella parapertussis</i>	Advanced	Pernasal swab	70.8	Negative results were common
Aug-15	3713	<i>Legionella pneumophila</i>	Advanced	Sputum	54.6	Negative results were common
Nov-15	3755	<i>Bordetella parapertussis</i>	Advanced	Pernasal swab	77.4	Improved performance compared to Nov 2015
Dec-15	3768	<i>Corynebacterium macginleyi</i>	Educational	Eye	41.0	Negative, probably not looked for
Dec-15	3768	<i>Streptococcus milleri</i> group	Core	Wound hand	72.8	Most VITEK2 users misidentified this as <i>Streptococcus sanguinis</i>
Feb-16	3799	<i>Yersinia pseudotuberculosis</i>	Core	Faeces	74.2	Negative results were common
Jul-16	3926	<i>Enterococcus gallinarum</i>	Core	Blood	79.3	Common misdiagnosis was <i>Enterococcus casseliflavus</i> using non MALDI-ToF methods
Mar-17	4038	<i>Clostridium novyi</i>	Advanced	Blood	67.3	Both negative results and misidentification at species level were common
Dec-17	4182	<i>Rothia mucilaginosa</i>	Core	Sputum	54.3	Negative results were common
Feb-18	4213	<i>Yersinia pseudotuberculosis</i>	Core	Faeces	67.6	Negative results were common

### Conclusion:

- Between 2014 and 2018, laboratories have invested in new technologies.
- The change from conventional to MALDI-ToF identification methods has been greatest for the non-enteric specimens.
- Review of performance over time is useful to identify areas where participants have experienced difficulties with the distributions.
- The most common reason for overall poor performance was a failure to isolate the target organism.
- There has been a reduction in overall poor performance in recent years.