Laboratory surveillance of uncommon pathogens causing bacteraemia in England, Wales and Northern Ireland: 2018

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The analysis presented in this report is based on data extracted from the Public Health England (PHE) voluntary surveillance database (Second Generation Surveillance System) on 6 September 2019 for the period between 1 January 2014 and 31 December 2018. Data from Wales and Northern Ireland were extracted separately from DataStore (on 23 July 2019) and CoSurv (on 18 June 2019), respectively. This report describes uncommon pathogens (bacterial genera with fewer than 50 reports in 2018) causing infections identified from blood cultures. Reports for England and Northern Ireland represent clinically significant isolates, whereas reports for Wales include isolates that may not be of clinical significance. Data in this report may differ slightly from data in earlier publications due to inclusion of late reports and reclassification of organisms.

There were 5,918 cases of bacteraemia caused by uncommon genera reported between 2014 and 2018. A total of 172 uncommon genera were identified, 54.1% of which were Gram-negative, representing 69% of the 249 genera associated with bacteraemia during this period [1].

Of the 1,299 episodes of bacteraemia caused by uncommon genera in 2018 specifically, 56.7% (n=737) were due to Gram-negative pathogens (see web appendix). By definition of inclusion in this analysis, small numbers of reports preclude robust or meaningful analysis of trends, but of note are continuing decreases between 2014 and 2018 in reports of the Gram-positive genera Atopobium and Erysipelothrix and the addition of Abiotrophia, Lactococcus and Leuconostoc whose numbers fell below 50 reports in 2018. Decreases in reported cases were also seen in the Gram-negative genera Eikenella, Ochrobactrum, and Sphingobacterium together with the addition of Agrobacterium, Burkholderia and Hafnia, in 2018 compared to 2017. In contrast, an increase was noted for the following Gram-positive genera: Actinotignum, Arcanobacterium, Dolosigranulum, Facklamia, Globicatella, and the following Gram-negatives: Aggregatibacter, Anaerobiospirillum and Legionella species, in 2018 compared to 2017.

A number of genera were reported in 2018 that were not seen in the previous four years including the Gram-positive genera Bhargavaea, Carnobacterium, Catabacter, Coprobacillus, Kurthia,
Lachnoanaerobaculum, Olsenella, Pseudarthrobacter, Robinsoniella, Thermoanaerobacterium, and the Gram-negative genera, Francisella, Gabonibacter, Mannheimia, Pluralibacter and Variovorax.

**Age distribution**

The highest rates of bacteraemia due to these uncommon pathogens in England were observed in infants aged under one year, 4.1 and 3.6 Gram-positive and Gram-negative per 100,000 population respectively, and those aged 75 years and older (3.7 for Gram-positive and Gram-negatives).

**Figure 1. Age-specific rates of uncommon pathogens associated with bacteraemia (England only): 2018**

![Graph showing age-specific rates of uncommon pathogens](image)

**Antimicrobial resistance**

Antimicrobial resistance was explored for genera with >30 episodes in 2018 (England data only), however relatively little data on antimicrobial susceptibility testing was available for several of these genera. Of the Gram-positive genera, penicillin susceptibility was reported for >50% of Abiotrophia, Arcanobacterium and Lactococcus episodes, with 24%, 5% and 8% resistant respectively. Equivalent analysis for Gram-negative genera identified third-generation cephalosporins resistance in 65% of Brevundimonas, aminoglycoside resistance in 11% and quinolones resistance in 62% of episodes. For Burkholderia, 36% were reported as resistant to
third-generation cephalosporins, 48% to carbapenems and 68% to aminoglycosides and for *Hafnia* 27% were resistant to third-generation cephalosporins, and 93% resistant to ampicillin/amoxicillin.

**Discussion**

This report describes the frequency of bacteraemia caused by bacterial genera many of which are not routinely included in PHE Health Protection Reports (with the exception of *Brucella* bacteraemia). Monitoring trends in these uncommon pathogens allows emerging or re-emerging infections to be identified [2], providing an alert to facilitate preventative measures or education of frontline clinical staff.

There has been a general improvement in the identification of cultured organisms through increased use of automated biochemical identification systems, molecular techniques such as 16S ribosomal RNA, and the introduction of MALDI-TOF mass spectrometry in some laboratories. This has increased the accuracy of species identification, and improved our understanding of the relative importance of these hitherto difficult to identify species in causing disease. It should be noted that isolates identified by MALDI-TOF reflect organisms that are present in its reference database and therefore identification is expected to improve with expansion of the database. Where new species have been added or reference entries amended in the database, these may appear as new organisms due to increased ascertainment rather than being novel or emerging bacteria causing disease e.g. *Bhargavaea, Kurthia Robinsoniella peoriensis, Weissella confuse, Alistipes putredinis* (new genus/species), *Carnobacterium maltaromaticum, Thermoanaerobacterium thermosaccharolyticum, Flavobacterium lindanitolerans, Pluralibacter* (further reference entry). In addition, there are concerns that MALDI-TOF could not be used for accurate speciation of *Elizabethkingia* [3] until the recent addition of *Elizabethkingia anopheles* to the database in 2019.

Although uncommon bacteria only account for a very low proportion of total bloodstream infections, they can be associated with important clinical consequences, such as endocarditis [4]. Amongst other causes, endocarditis may arise through bacteraemia following occupational exposure to farm livestock (e.g. *Brucella* and *Erysipelothrix*) or from heart surgery (*Nocardia*). A *Facklamia hominis* bacteraemia has also been associated with infectious endocarditis [5], as have bacteraemia caused by organisms normally found in the oral cavity such as *Aggregatibacter actinomycetemcomitans* [6]. Please note that the *Brucella* spp. reported here are not all necessarily confirmed by the national reference laboratory. (For brucellosis, please refer to the common animal associated infections quarterly reports for England and Wales in 2018 based on
culture positive results confirmed at the OIE/FAO Reference Laboratory for brucellosis at the Animal and Plant Health Agency (APHA) [7].)

Although *Burkholderia* are an important cause of infections in patients with cystic fibrosis, these infections are predominantly isolated from sputum rather than blood [8]. However, *Burkholderia* bacteraemia, including *Burkholderia cepacian*, can cause healthcare associated infections in non-cystic fibrosis patients and outbreaks due to *Burkholderia* species have been reported in Intensive Care Units [8,9]. These infections are complicated by intrinsic resistance to key antibiotics via a number of mechanisms [10,11], and in this dataset, where more than 50% of isolates have been tested, resistance to cephalosporins, carbapenems and aminoglycosides was noted. Antimicrobial resistance to penicillin was noted for *Abiotrophia* (24%), similar to published findings [12].

Three of the *Burkholderia* bacteraemia reports in 2018 were *Burkholderia pseudomallei*, an imported pathogen which is the causative agent of meliodosis. *Burkholderia pseudomallei* is found mainly in Southeast Asia and Northern Australia and is acquired by exposure to contaminated soil or water droplets via wounded skin or inhalation [13]. Another imported pathogen is *Francisella tularensis*, the causative agent for the zoonotic disease tularemia, which is distributed throughout the northern hemisphere including Europe but is not found in the UK [14,15]. *Francisella tularensis* is mainly transmitted through contact with infected animals or via bites from infected insects and ticks [16].

Bacteraemia caused by *Gordonia* spp. and *Anaerobiospirillum succiniciproducens* have been noted in immunocompromised patients [17,18], whilst other uncommon genera causing bacteraemia have been associated with the use of catheters in patients with underlying morbidity eg *Delftia acidovorans* [19], *Dermacoccus* [20], and *Gordonia sputi* [21]. *Actinotignum* bacteraemia have been found to affect elderly patients with underlying conditions, a majority having the urinary tract as a focus of the bacteraemia [22]. *Globicatella sanguinis* bacteraemia have been identified predominantly in older females [23] whereas *Kingella kingae* bacteraemia has been reported more frequently in children than in adults [24].

*Gardnerella vaginalis* is found in the genitourinary tract of women and bacteraemia has been associated with gynaecology, obstetric, and neonatal patients, and very rarely adult male patients [25-28].

For all the uncommon zoonotic pathogens, please also refer to the common animal associated infections quarterly reports (England and Wales) that can be found on the PHE gov.uk website.
Please note the numbers may differ slightly between these two reports as the common animal associated infections quarterly reports for England and Wales use data that are not limited to blood samples only.

Although bloodstream infections reported to the voluntary surveillance system for England and Northern Ireland should reflect only clinically significant disease, difficulties in blood culture sampling or contamination in laboratory processing may lead to inclusion of skin colonisers or contaminants [29].

If confirmation of unusual bacterial pathogens is required, isolates can be sent to the relevant laboratory within the **Bacteriology Reference Department, National Infection Service, Colindale, Public Health England**.

For confirmation of *Brucella* spp., isolates can be sent to the OIE/FAO Reference Laboratory for Brucellosis at APHA for culture confirmation and to the Brucella Reference Unit (BRU) in Liverpool for serology testing and molecular diagnostic service.

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References


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Health Protection Report is a national public health bulletin for England and Wales, published by Public Health England. It is PHE’s principal channel for the dissemination of laboratory data relating to pathogens and infections/communicable diseases of public health significance and of reports on outbreaks, incidents and ongoing investigations.

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