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# Laboratory surveillance of uncommon pathogens causing bacteraemia in England, Wales and Northern Ireland: 2017

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The analysis presented in this report is based on data extracted from the Public Heath England (PHE) voluntary surveillance database (Second Generation Surveillance System) on 21 November 2018 for the period between 1 January 2013 and 31 December 2017. Data from Wales and Northern Ireland were extracted separately from DataStore (on 10 April 2018) and CoSurv (on 6 November 2018), respectively. This report describes uncommon pathogens (bacterial genera with fewer than 50 reports in 2017) 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 4,043 cases of bacteraemia caused by uncommon genera reported between 2013 and 2017. From these cases 136 uncommon genera were identified, 56.6% of which were Gram-negative. These uncommon genera represent 60% of the 226 bacteraemia-associated genera recorded for 2013 to 2017.

Of the 1,026 episodes of bacteraemia caused by uncommon bacteria in 2017, 59.1% (n=606) were due to Gram-negative bacteria (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 2013 and 2017 in reports of the Gram-negative genera *Kluyvera, Leclercia, Ochrobactrum, Shigella* and *Sphingobacterium*. In contrast, an increase was noted for the following Gram-positive genera: *Actinotignum, Arcanobacterium, Arthrobacter, Dermacoccus, Globicatella, Gordonia,* and the following Gram-negatives: *Aggregatibacter, Anaerobiospirillum, Dialister, Elizabethkingia, Gardnerella* and *Parabacteroides* species.

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### Discussion

This report describes the frequency of bacteraemia caused by bacterial genera not routinely included in PHE Health Protection Reports. Monitoring trends in these uncommon pathogens allows emerging or re-emerging infections to be identified [1], providing an alert to allow opportunities for 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 in the last year these may appear as new organisms due to increased ascertainment rather than being novel or emerging bacteria causing disease e.g. *Actinobaculum massiliense* (new species) or *Lelliottia amnigena* and *Wautersiella falsenii* (further reference entry). Also, there are concerns that MALDI-TOF cannot currently be used for accurate speciation of *Elizabethkingia* and that accurate speciation within this genus requires sequence-based methods [2].

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 [3].

Bacteraemia caused by organisms normally found in the oral cavity such as *Aggregatibacter actinomycetemcomitans* have been associated with the pathogenesis of atherosclerosis [4]. *Capnocytophaga canimorsus* is also part of the normal oral microflora of humans and dogs and bloodstream infections have been described following close contact with wounds or bites from dogs [5].

*Globicatella sanguinis* bacteraemia has been identified predominantly in older females [6] whereas *Kingella kingae* bacteraemia has been reported more frequently in children than

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in adults [7]. Bacteraemia caused by *Gordonia* spp. has been noted in immunocompromised patients [8] while other uncommon genera causing bacteraemia have been associated with the use of catheters in patients with underlying morbidity e.g. *Delftia acidovorans* [9], *Dermacoccus* [10], and *Gordonia sputi* [11].

*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 [12-15].

Although rarely diagnosed in this country, infections imported from endemic regions, such as *Brucella* spp. [16], can cause severe illness in those affected.

A number of genera were reported in 2017 that were not seen in the previous four years including the Gram-positive genera *Isoptericola, Macrococcus, Propionimicrobium, Sporosarcina* and the Gram-negative genera *Acidaminococcus, Butyricimonas, Lelliottia, Obesumbacterium, Pseudochrobactrum, Thauera, Wautersiella.* 

Although bloodstream infections reported to 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 [17].

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

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