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Laboratory surveillance of uncommon pathogens causing bacteraemia in England, Wales and Northern Ireland: 2016

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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 31 October 2017 for the period between 1 January 2012 and 31 December 2016. Data from Wales and Northern Ireland were extracted separately from DataStore (on 24 February 2017) and CoSurv (on 28 September 2017), respectively. This report describes uncommon pathogens causing clinically significant infections (bacterial genera with fewer than 50 reports in 2016) identified from blood cultures. Data in this report may differ slightly from data in earlier publications due to inclusion of late reports and reclassification of organisms.

There were 4,037 cases of bacteraemia caused by uncommon bacterial genera reported between 2012 to 2016. From these cases 153 uncommon genera were identified, 56.3% of which were Gram-negative. Of these episodes of bacteraemia in 2016 (n=1,228), 55.7% were due to Gram-negative bacteria (see the [web appendix](#) associated with this report). 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 2012 and 2016 in reports of the Gram-negative genera *Kluyvera* and *Sphingobacterium*. In contrast, an increase was noted for the following Gram-positive genera: *Abiotrophia*, *Actinotignum*, *Anaerococcus*, *Arthrobacter*, *Atopobium*, *Dermacoccus*, *Eggerthella*, *Finegoldia*, *Globicatella*, *Gordonia*, *Microbacterium*, *Solobacterium*; and Gram-negative *Aggregatibacter*, *Brucella*, *Capnocytophaga*, *Delftia*, *Dialister*, *Eikenella*, *Kingella*, *Leptotrichia*, *Myroides*, *Parabacteroides*, *Paracoccus*, and *Sphingomonas* species.

Discussion

The purpose of this review is to describe unusual bacterial genera not routinely included in the monthly bacteraemia reports published in the Health Protection Report.

Examining trends in these pathogens can provide a means of identifying emerging or re-emerging infections [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 by 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 identified, and we now have a better understanding of the relative importance of these hitherto difficult to identify species causing significant disease. However, there are concerns that MALDI-TOF cannot currently be used for accurate speciation of *Elizabethkingia* and accurate speciation within the *Elizabethkingia* genus requires sequence-based methods [2]. It should be borne in mind that findings by MALDI-TOF reflect organisms that are present in the database, therefore identification is expected to improve with expansion of the database.

Although these bacteria only account for a very low proportion of total bloodstream infections, they can be associated with important clinical consequences, such as endocarditis [3].

Abiotrophia defectiva can be isolated from the oral cavity and bacteraemia may follow dental treatment, potentially leading to endocarditis [4]. *Capnocytophaga canimorsus* are also part of the normal oral microflora of humans and dogs and bloodstream infections have been described following wounds or bites from dogs [5].

Actinotignum schaalii (previously *Actinobaculum schaalii* [6]) bacteraemia have been associated with urinary tract infection in the elderly [7] whereas *Kingella kingae* bacteraemia have been reported more frequently in children than adults [8].

Infections imported from endemic regions, such as *Brucella* species [9] although rarely diagnosed in this country can cause severe illness in those affected. Other bacteraemia

have been associated with the use of catheters in patients with underlying morbidity or who are immunocompromised e.g. *Delftia acidovorans* [10].

A number of genera were reported in 2016 that were not seen in the previous 4 years: *Actinotignum*, *Agromyces*, *Curtobacterium*, *Deinococcus*, *Dietzia*, *Erwinia*, *Geobacillus*, *Leifsonia*, *Lysinibacillus*, *Murdochiella*, *Oceanobacillus*, *Pseudoclavibacter*, *Salana*, *Weissella* (Gram-positive) and *Kosakonia*, *Megasphaera*, *Methylopila*, *Pseudoflavonifractor*, *Pseudoxanthomonas*, *Rhodobacter*, *Selenomonas*, *Suttonella*, *Xanthomonas* (Gram-negative).

Whilst the bloodstream infections reported to this voluntary surveillance system should, according to national reporting guidelines, reflect clinically significant disease, some of these reports may reflect skin colonisers or contaminants due to difficulties in blood culture sampling or contamination in laboratory processing [11].

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.

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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.

Public Health England, Wellington House, 133-155 Waterloo Road, London SE1 8UG

Tel: 020 7654 8000 www.gov.uk/phe

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Queries relating to this document should be directed to:

HCAI-AMR Department, National Infection Service,

PHE Colindale,

61 Colindale Avenue, London NW9 5EQ.

immunisation@phe.gov.uk

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