



## Infection report

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### Bacteraemia

#### Uncommon pathogens involved in bacteraemia: England, Wales and Northern Ireland, 2009-2013

The analysis presented in this report is based on data extracted from the Public Health England (PHE) voluntary surveillance database, LabBase2, on 24 September 2014 for the period between 1 January 2009 to 31 December 2013 in England, Wales, and Northern Ireland. The reports made to PHE provide data on both community and hospital-acquired bacteraemia. This report describes uncommon pathogens (genera with fewer than 50 reports in 2013) identified from blood cultures or blood specimens where the diagnostic method was not stated. Data in this report may differ slightly from data in earlier publications due to inclusion of late reports.

A total of 104,879 bacterial isolates from blood samples were reported by laboratories in England, Wales, and Northern Ireland in 2013. One hundred and four uncommon genera causing bacteraemia were reported in 2013, comprising a total of 734 bacteraemic episodes. Gram-negative organisms accounted for 58.3% of these episodes. By definition of inclusion in this analysis, small numbers of reports preclude robust or meaningful analysis of trends, but of note are the general decreases in *Anaerococcus*, *Delftia*, *Alcaligenes*, *Bordetella* and *Eikenella*, and increases in *Bifidobacterium*, *Brevibacterium*, *Dermabacter*, *Eggerthella*, *Kocuria*, *Cardiobacterium*, *Gardnerella*, *Kingella* and *Kluyvera*.

### Discussion

The purpose of this review is to describe the unusual bacterial genera not included in the monthly bacteraemia reports published in the Health Protection Report. Examining trends in these unusual pathogens can also provide a means of identifying emerging or re-emerging infections [1], providing opportunities for preventive measures or education of frontline clinical staff.

There has been a general improvement in the identification of cultured organisms to the species level 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 permits robust trend analysis of hitherto difficult to identify species causing significant disease, such as identification of *Kocuria* spp that were previously identified as coagulase-negative staphylococci or micrococci. It should be borne in mind that findings by MALDI-TOF reflect organisms that are present in the database, therefore non-identification or identification at the genus level is expected to be improved with expansion of the database.

Although these bacteria only account for a very low proportion of total bacteraemia reports, they can be associated with important clinical consequences, such as endocarditis [2]. Infections imported from endemic regions, such as *Brucella* species [4] or *Vibrio cholerae* although rarely diagnosed in this country can cause severe illness in those affected. Others

represent opportunistic pathogens causing infection in specific subpopulations, such as *Granulicatella* [4] in immunocompromised patients or *Yersinia* in elderly, or are associated with specific exposures, such as catheter-related bacteraemia due to *Brevibacterium* [5], or infections due to *Erysipelothrix rhusiopathiae* in workers in contact with animals or handling animal products [6].

There has been an increase in reports of bacteraemia caused by *Bifidobacterium* genus in the 5 year period, notably in 2013 (table 1). Reports of bacteraemia caused by members of *Dermabacter* genus have increased sharply in 2013 comparing to previous years (table 1). While *Dermabacter hominis* is commonly found on human skin, it has been isolated from a range of clinical specimens, such as blood cultures, abscesses, and wound and eye infections [7]. Marked increase in *Kocuria* reports have been observed during last two years, mostly accounted for by increase in *Kocuria kristinae* and other *Kocuria* species. Similar trends have been observed in other countries [8]. Reports in *Cardiobacterium* have also increased during the five year period, predominantly due to a rise in *Cardiobacterium hominis*, a well-documented cause of endocarditis [9].

Reports of bacteraemia due to *Peptoniphilus* and *Psychrobacter* were noted for the first time in 2012 during the five year period [10]. The number of reports increased since then. Both of these have been reported to cause blood stream infections in patients with underlying morbidities [11,12].

A number of new genera featured in this report, namely *Alistipes*, *Atopobium*, *Helcococcus*, *Slackia*, *Janthinobacterium*, and *Paracoccus*. All of these have been previously recorded to cause bacteraemia in patients with comorbidities or intravenous drug users [13,14,15,16,17, 18].

*Rothia* and *Burkholderia* were sufficiently common in 2013 to warrant removal from this report. A total of 75 laboratory reports of *Rothia* spp were made in 2013, doubling of episodes compared to 2012. *Burkholderia* exceeded the inclusion criteria by 1 bacteraemia report.

Bacteraemias caused by *Shigella* are rare, and tend to be associated with foreign travel. The slight increase over this 5 year period may be explained by the ongoing outbreak of *Shigella flexneri* in men who have sex with men (this includes invasive infections in the immunosuppressed host) [19].

Whilst the bacteraemia reported to this voluntary surveillance system should, according to national reporting guidelines, reflect clinically significant disease, it should be borne in mind that some of these reports may reflect skin colonisers or contaminants due to difficulties in blood culture sampling or contamination in laboratory processing [20,21]. Inclusion of reports with diagnostic method recorded in the database as unknown should be taken into account in interpreting these data, as some of these reports may not represent bloodstream infections. Improvements in laboratory reporting of diagnostic methods when entering the data into the database would allow the exclusion of these reports without artificially decreasing the number of genuine bacteraemia infections.

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

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