# Polymicrobial bacteraemias, England, Wales, and Northern Ireland: 2003

## Key points:

- In 2003, from 82,852 records, 12,514 bacteraemia reports were matched to at least one other report extracted from the voluntary reporting system
- Of the 76,188 patient episodes, 5850 (8%) were polymicrobial bacteraemia episodes; the remaining 70,338 were identified as monomicrobial bacteraemias
- *Enterococcus* spp, *Klebsiella* spp, *Enterobacter* spp, *Proteus* spp, and *Acinetobacter* spp were the predominant genera associated with polymicrobial bacteraemias.

## Introduction

This report covers all data on routine laboratory reporting of polymicrobial bacteraemias in England, Wales, and Northern Ireland in 2003. Polymicrobial bacteraemia is defined as the isolation of multiple organisms from the same blood culture.

## Methods

Data from the voluntary reporting scheme were extracted from LabBase2*. Multiple isolates from one blood culture are not linked on the database system, and were established by identifying records that matched on the fields: 'specimen date', 'laboratory', 'date of birth', 'gender', and 'soundex'†. A total of 83,301 bacteraemia records were extracted from the database. Fungi were not included for this analysis. Duplicates (449), with the same bacterial species were removed from the database, although we allowed inclusion of both cases where one indicated, *eg*, *Acinetobacter* spp and the other *Acinetobacter baumannii*, due to lack of speciation (15% of polymicrobial bacteraemias were not speciated past the genus level). A final dataset of 82,852 records were used in this report.

Bacteraemia rates were calculated using 2003 resident population denominators for England, Wales, and Northern Ireland. Regional analysis was performed with reference to the English boundaries introduced in April 2002. Confidence intervals were calculated using commercial software‡.

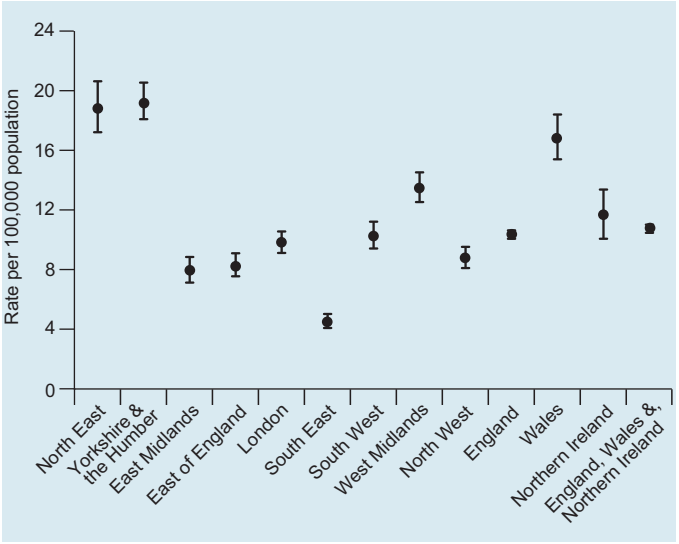
## Results

Of 82,852 records, there were 12,514 bacteraemia reports (15%) that were identified as matching at least one other report. These were grouped further to obtain the number of patient episodes of bacteraemias. Of the 76,188 patient episodes, 5850 were polymicrobial (PMB) and the remaining 70,338 were held as monomicrobial (MMB).

There was variation of PMB reports among the different English regions, Wales and Northern Ireland (figure 1). The highest rate of PMB reported in England was in Yorkshire and the Humber (19.3 per 100,000 population), followed closely by the North East region (18.9/100,000). The lowest reporting rate of PMB was in the South East region (4.5/100,000). The rate of PMB in Wales and Northern Ireland was 16.9 and 11.6/100,000 respectively. The overall rate of PMB for England, Wales, and Northern Ireland was 10.7/100,000.

Two microorganisms were isolated in 5139 polymicrobial episodes (88%), three microorganisms were isolated in 618 episodes (11%), four microorganisms were isolated in 84 episodes (1%), five

**Figure 1 Regional distribution of episodes of polymicrobial bacteraemia rates, England, Wales, and Northern Ireland: 2003***




* Rates calculated using 2003 mid-year resident population estimates

*Labbase2 is the database that collects laboratory reports of all microorganisms isolated at nearly 400 NHS and other laboratories throughout England, Wales, and Northern Ireland. The database is managed and accessedat the Health Protection Agecny's Centre for Infections.

†Soundex is a non-unique alphanumeric coding of the patients surname. When this is combined with date of birth and gender, this allows for duplicate reports of the same individual to be identified without the use of patient names.

‡Stata Statistical software: release 8.2. College Station, Texas, Stata Corporation, 2001.

**Table 1 Organisms reported in monomicrobial and polymicrobial bacteraemias, England, Wales, and Northern Ireland: 2003**

| | Monomicrobial bacteraemias | | | Polymicrobial bacteraemias | | | | Monomicrobial bacteraemias | | | Polymicrobial bacteraemias | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Organism | Number of reports | (%) | Rank* | Number of reports | (%) | Rank* | Organism | Number of reports | (%) | Rank* | Number of reports | (%) | Rank* |
| *Abiotrophia* | 7 | 0.01 | 66 | 4 | 0.03 | 50 | *Lactobacillus* | 37 | 0.05 | 42 | 8 | 0.06 | 42 |
| *Achromobacter* | 6 | 0.01 | 67 | 2 | 0.02 | 56 | *Lactococcus* | 21 | 0.03 | 49 | 8 | 0.06 | 42 |
| *Acinetobacter* | 813 | 1.16 | 11 | 273 | 2.18 | 10 | *Leclercia* | 1 | – | 87 | 1 | 0.01 | 63 |
| *Actinobacillus* | – | – | – | 1 | 0.01 | 63 | *Legionella* | 2 | – | 79 | – | – | – |
| *Actinomyces* | 4 | 0.01 | 72 | 1 | 0.01 | 63 | *Leptospira* | 9 | 0.01 | 60 | – | – | – |
| *Aerococcus* | 57 | 0.08 | 34 | 20 | 0.16 | 32 | *Leuconostoc* | 16 | 0.02 | 53 | 11 | 0.09 | 35 |
| *Aeromonas* | 85 | 0.12 | 27 | 26 | 0.21 | 25 | *Listeria* | 168 | 0.24 | 24 | 16 | 0.13 | 33 |
| *Agrobacterium* | 37 | 0.05 | 42 | 11 | 0.09 | 35 | *Micrococcus* | 217 | 0.31 | 23 | 26 | 0.21 | 25 |
| *Alcaligenes* | 82 | 0.12 | 28 | 22 | 0.18 | 30 | *Mobiluncus* | 1 | – | 87 | – | – | – |
| *Anaerobiospirillum* | 4 | 0.01 | 72 | – | – | – | *Moraxella* | 95 | 0.14 | 26 | 21 | 0.17 | 31 |
| *Arcanobacterium* | 6 | 0.01 | 67 | 1 | 0.01 | 63 | *Morganella* | 306 | 0.44 | 18 | 103 | 0.82 | 18 |
| *Bacillus* | 256 | 0.36 | 21 | 71 | 0.57 | 19 | *Mycobacterium* | 51 | 0.07 | 37 | 7 | 0.06 | 46 |
| *Bacteroides* | 886 | 1.26 | 9 | 186 | 1.49 | 11 | *Neisseria* | 46 | 0.07 | 38 | 25 | 0.20 | 27 |
| *Bifidobacterium* | 3 | – | 75 | 1 | 0.01 | 63 | *Nocardia* | 2 | – | 79 | – | – | – |
| *Bordetella* | 9 | 0.01 | 60 | – | – | – | *Ochrobactrum* | 39 | 0.06 | 41 | 11 | 0.09 | 35 |
| *Borrelia* | 46 | 0.07 | 38 | – | – | – | *Oligella* | – | – | – | 1 | 0.01 | 63 |
| *Branhamella* | 6 | 0.01 | 67 | – | – | – | *Pantoea* | 80 | 0.11 | 29 | 34 | 0.27 | 22 |
| *Brevibacterium* | 13 | 0.02 | 56 | 2 | 0.02 | 56 | *Pasteurella* | 61 | 0.09 | 31 | 5 | 0.04 | 48 |
| *Brevundimonas* | 18 | 0.03 | 52 | 2 | 0.02 | 56 | *Pediococcus* | 3 | – | 75 | 1 | 0.01 | 63 |
| *Brucella* | 15 | 0.02 | 54 | – | – | – | *Peptococcus* | 10 | 0.01 | 58 | 7 | 0.01 | 46 |
| *Burkholderia* | 45 | 0.06 | 40 | 8 | 0.06 | 42 | *Peptostreptococcus* | 112 | 0.16 | 25 | 35 | 0.28 | 21 |
| *Campylobacter* | 61 | 0.09 | 31 | 3 | 0.02 | 52 | *Porphyromonas* | 3 | – | 75 | – | – | – |
| *Capnocytophaga* | 10 | 0.01 | 58 | 1 | 0.01 | 63 | *Prevotella* | 52 | 0.07 | 35 | 9 | 0.07 | 39 |
| *Cardiobacterium* | 1 | – | 87 | – | – | – | *Propionibacterium* | 293 | 0.42 | 19 | 40 | 0.32 | 20 |
| *Cedecea* | – | – | – | 1 | 0.01 | 63 | *Proteus* spp | 277 | 0.39 | 8 | 121 | 0.97 | 8 |
| *Chromobacterium* | 2 | – | 79 | 1 | 0.01 | 63 | *Proteus mirabilis* | 1268 | 1.80 | – | 332 | 2.65 | – |
| *Chryseobacterium* | 22 | 0.03 | 48 | 9 | 0.07 | 39 | *Providencia* | 60 | 0.09 | 33 | 28 | 0.22 | 24 |
| *Chryseomonas* | 30 | 0.04 | 45 | 11 | 0.09 | 35 | *Pseudomonas* spp | 552 | 0.78 | 6 | 162 | 1.29 | 6 |
| *Citrobacter* | 450 | 0.64 | 14 | 185 | 1.48 | 12 | *Pseudomonas aeruginosa* | 1957 | 2.78 | – | 402 | 3.21 | – |
| *Clostridium* | 442 | 0.63 | 15 | 165 | 1.32 | 13 | | | | | | | |
| Coliform | 285 | 0.41 | 20 | 356 | 2.84 | 9 | *Rahnella* | 1 | – | 87 | – | – | – |
| *Comamonas* | 21 | 0.03 | 49 | 8 | 0.06 | 42 | *Ralstonia* | 9 | 0.01 | 60 | 1 | 0.01 | 63 |
| *Corynebacterium* | 381 | 0.54 | 17 | 116 | 0.93 | 16 | *Rhodococcus* | 9 | 0.01 | 60 | – | – | – |
| *Dermabacter* | 2 | – | 79 | – | – | – | *Roseomonas* | 1 | – | 87 | – | – | – |
| Diphtheroids | 239 | 0.34 | 22 | 111 | 0.89 | 17 | *Rothia* | 1 | – | 87 | – | – | – |
| *Edwardsiella* | 2 | – | 79 | – | – | – | *Salmonella* | 431 | 0.61 | 16 | 3 | 0.02 | 52 |
| *Eikenella* | 6 | 0.01 | 67 | 2 | 0.02 | 56 | *Serratia* | 836 | 1.19 | 10 | 156 | 1.25 | 14 |
| *Empedobacter* | 1 | – | 87 | 1 | 0.01 | 63 | *Shewanella* | 2 | – | 79 | 4 | 0.03 | 50 |
| *Enterobacter* | 462 | 0.66 | 7 | 129 | 1.03 | 7 | *Shigella* | 1 | – | 87 | – | – | – |
| *Enterobacter* cloacae | 1389 | 1.97 | – | 377 | 3.01 | – | *Sphingobacterium* | 2 | – | 79 | 1 | 0.01 | 63 |
| *Enterococcus* spp | 1569 | 2.23 | 4 | 802 | 6.41 | 2 | *Sphingomonas* | 35 | 0.05 | 44 | 2 | 0.02 | 56 |
| *Enterococcus faecalis* | 1870 | 2.66 | – | 766 | 6.12 | – | *Staphylococcus* spp | 144 | 0.20 | 1 | 54 | 0.43 | 1 |
| *Enterococcus faecium* | 731 | 1.04 | – | 277 | 2.21 | – | *Staphylococcus aureus* | 14,058 | 19.99 | – | 1322 | 10.56 | – |
| *Erysipelothrix* | 1 | – | 87 | 1 | 0.01 | 63 | | | | | | | |
| *Escherichia* spp | 22 | 0.03 | 2 | 4 | 0.03 | 4 | Coagulase-negative | 6196 | 8.81 | – | 1244 | 9.94 | – |
| *Escherichia coli* | 14,945 | 21.25 | – | 1415 | 11.31 | – | *Staphylococcus* | | | | | | |
| *Eubacterium* | 8 | 0.01 | 64 | 3 | 0.02 | 52 | *Staphylococcus epidermidis* | 1479 | 2.10 | – | 197 | 1.57 | – |
| *Flavimonas* | 26 | 0.04 | 46 | 15 | 0.12 | 34 | | | | | | | |
| *Flavobacterium* | 8 | 0.01 | 64 | 5 | 0.04 | 48 | Stenotrophomonas | 527 | 0.75 | 13 | 125 | 1.00 | 15 |
| *Francisella* | 1 | – | 87 | 1 | 0.01 | 63 | Stomatococcus | 6 | 0.01 | 67 | 2 | 0.02 | 56 |
| *Fusobacterium* | 65 | 0.09 | 30 | 25 | 0.20 | 27 | Streptobacillus | 1 | – | 87 | – | – | – |
| *Gardnerella* | 2 | – | 79 | 1 | 0.01 | 63 | Streptococcus spp | 3730 | 5.30 | 3 | 1170 | 9.35 | 3 |
| *Gemella* | 52 | 0.07 | 35 | 23 | 0.18 | 29 | Strep Group A | 1219 | 1.73 | – | 172 | 1.37 | – |
| *Haemophilus* | 563 | 0.80 | 12 | 29 | 0.23 | 23 | Strep Group B | 936 | 1.33 | – | 136 | 1.09 | – |
| *Hafnia* | 25 | 0.04 | 47 | 9 | 0.07 | 39 | *Streptococcus pneumoniae* | 5307 | 7.54 | – | 141 | 1.13 | – |
| *Kingella* | 4 | 0.01 | 72 | 1 | 0.01 | 63 | | | | | | | |
| *Klebsiella* spp | 1416 | 2.01 | 5 | 403 | 3.22 | 5 | *Veillonella* spp | 13 | 0.02 | 56 | 1 | 0.01 | 63 |
| *Klebsiella pneumoniae* | 2106 | 2.99 | – | 475 | 3.80 | – | *Vibrio* | 3 | – | 75 | 2 | 0.02 | 56 |
| Kluyvera | 19 | 0.03 | 51 | 3 | 0.02 | 52 | *Weeksella* | 1 | – | 87 | 1 | 0.01 | 63 |
| | | | | | | | *Yersinia* | 14 | 0.02 | 55 | 1 | 0.01 | 63 |
| **Total =** | **70,338** | **100** | | **12,514** | **100** | | | | | | | | |

* Does not correspond to patient episodes, as each organism isolation constitutes a separate report. Ranking of organisms are at the genus level.

**Figure 2 Number of organisms involved in polymicrobial bacteraemia episodes**

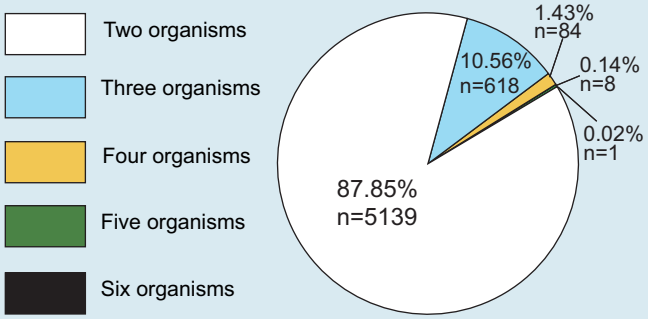
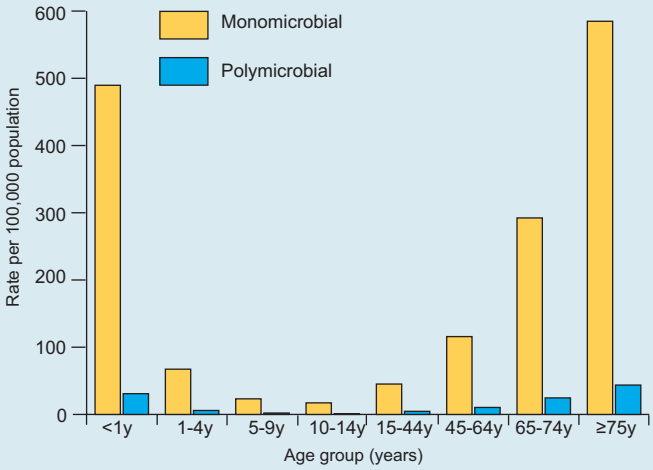



**Figure 3 Age-specific rates of mono and polymicrobial bacteraemia episodes, England, Wales, and Northern Ireland: 2003**




microorganisms were isolated in eight episodes (0.1%) and there were six microorganisms isolated in one episode (0.02%) (figure 2). The episode with six microorganisms cultured consisted of two *Acinetobacter* species, a *Pantoea* species, a coagulase-negative staphylococcus (CNS), a *Stenotrophomonas* spp and a *Streptococcus* spp isolate. Of the patient episodes where five isolates were cultured, seven of the eight episodes had two organisms of the same genus, namely, either *Clostridium*, *Enterococcus*, *Pseudomonas*, *Staphylococcus*, *Acinetobacter*, or *Klebsiella* species.

There were 99 different organisms at the genus level and 341 different organisms at the species level identified. Unspecified organisms (coliforms and diptheroids) comprised 1.2% of all bacteraemias reported in 2003. Table 1 describes the organisms at the genus level, with major organism groups which had more than 1000 reports listed at the species level. Overall, *Staphylococcus* as a group constituted the leading pathogen responsible for 30% of bacteraemias in 2003. This was followed by *Enterococcus* spp for PMB and *Escherichia* spp for MMB. At the species level, *Escherichia coli* constituted the leading pathogen responsible for 21% of all MMB and 11% of all PMB. *S. aureus* (20.0% MMB and 10.6% PMB) and CNS (8.8% MMB and 9.9% PMB) followed as the second and third most common pathogen to cause both MMB and PMB respectively.

The percentage of *Enterococcus* spp and *Enterobacter* spp organisms in PMB were higher than those in MMB. This was reflected at the species level, where there were higher proportions of *Enterobacter cloacae* (3%), *Enterococcus faecalis* (6.1%), *and Enterococcus faecium* (2.2%). Approximately 40% of bacteraemia organisms reported in 2003 were found more commonly in polymicrobial than momomicrobial bacteraemias. Some genera that featured more strongly in polymicrobials were the *Enterococcus* spp (14% PMB, 6% MMB), *Klebsiella* spp (7% PMB, 5% MMB), *Enterobacter* spp (4% PMB, 3% MMB), *Proteus* spp (4% PMB, 2% MMB), and *Acinetobacter* spp (2% PMB, 1% MMB). The rates in these polymicrobial and monomicrobials bacteraemias were significantly different.

Patients with bacteraemias (both poly- and monomicrobial bacteraemias) were predominantly in the older age groups, with the highest number of episodes and proportion in the 74 years and over age group (24,201 patient episodes, 584/100000 with MMB and 1807 patient episodes, 44/100,000 with PMB episodes) (figure 3). The median age for MMB was 68 years and for PMB 65 years, with the older age groups with higher rates of bacteraemias. The proportion of patients in each age-group was similar for poly- and momomicrobial bacteraemias with the ages ranging from under 1 year to 103 years (mean = 60 ±25).

## Discussion

Previous studies have found that polymicrobial bacteraemias have been associated with poorer outcome for the patient than those with monomicrobial bacteraemias (1,2). Polymicrobial bacteraemias have been reported to be associated with higher mortality rates than monomicrobial infections (2). In 2001 polymicrobials accounted for 14% of bacteraemias with 4212 patient episodes in England and Wales (4). In 2002, this was 12.6% with 4365 patient episodes (3). The percentage of polymicrobials in England, Wales, and Northern Ireland was 15% with 5850 patient episodes in 2003. There appears to be an increase in polymicrobial bacteraemias. Caution should be taken in comparing as data from Northern Ireland was not collected in 2001 and the two previous years included the presence of *Candida* (1.6% of total infections per year for both years), which is a fungal infection. This increase may also be as the result of increased ascertainment of reports by laboratories over the three years.

This report highlights some major organisms that are found in polymicrobial bloodstream infections for example, *E. coli*, *S. aureus*, and *Enterococcus faecalis*. *Enterobacteriaceae*, *Pseudomonas* species, streptococci other than group A and pneumococci have been detected in

polymicrobial bacteraemia in a previous study (5). In this report, *S. pneumoniae* featured strongly in MMB (8%) and poorly in PMB (1%). The high proportion of *E. coli* bacteraemia may be from an excess of urinary tract infection (where it was likely to be the sole pathogen) or an excess of intra-abdominal sepsis (where if was likely to be mixed, often with *Enterococcus* spp) (6) .

Previous studies (1) have reported higher rates of polymicrobials in geriatric populations (*ie*, aged 65 years and over), as well as in infants (*ie*, those aged under 1 year). This was observed in this patient group.

An increase in the detection of polymicrobial bacteraemia may have important therapeutic as well as patient management implications.

## Acknowledgements

These reports would not be possible without the enduring weekly contributions from microbiology colleagues in laboratories across England, Wales, and Northern Ireland, without which there would be no surveillance data. Please send any comments/feedback to Andrew Pearson <email:Andrew.pearson@hpa.org.uk> or Amy Glasswell<email:amy.glasswell@hpa.org.uk>. In addition, the support from colleagues within the Health Protection Agency, Specialist and Reference Microbiology Division in particular, is valued in the preparation of the reports. These contributions are greatly appreciated.

## References

1. Pittet D, Li N and Wenzel RP. Association of secondary and polymicrobial nosocomial bloodstream infections with higher mortality. *Eur J Clin Microbiol Infect Dis* 1993; **12**: 813-9.
2. Pittet D, Li N, Woolson RF, and Wenzel RP. Microbiological factors influencing the outcome of nosocomial bloodstream infections: A 6-year validated, population-based model. *Clin Infect Dis* 1997; **24**:1068-78.
3. Health Protection Agency. Candidaemia and polymicrobial bacteraemias: England, Wales, and Northern Ireland: 2002. *Commun Dis Rep CDR Wkly* [serial online] 2003; **13**(42): Bacteraemia. Available at <http://www.hpa.org.uk/cdr/PDFfiles/2003/cdr4203.pdf>
4. PHLS. Polymicrobial bacteraemias and candidaemia, England and Wales, 2001. *Commun Dis Rep CDR Wkly* [serial online] 2002; **12**(42): Bacteraemia. Available at <http://www.hpa.org.uk/cdr/PDFfiles/2002/cdr4202.pdf>.
5. Weinstein MP, Reller LB, and Murphy JR. Clinical importance of polymicrobial bacteraemia. *Diag Microbiol Infect Dis* 1986; **5**:185-96.
6. Siegman-Igra Y, Kulka T, Schwartz D and Konforti N. Polymicrobial and monomicrobial bacteraemic urinary tract infection. J Hosp Infect 1994; 28: 49-56.