**Supplementary Table 1**. Polymicrobial Pathogenic organisms isolated from 52 patients with bloodstream infections at Cipto Mangunkusumo National Hospital, Indonesia, between 2019 and 2020

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Pathogens** | **Total\*(N=52)** | **Year 2019****(N=29)** | **Year 2020****(N=23)** | **Community-origin BSI****(N=14)** | **Hospital-origin BSI****(N=38)** |
| *Acinetobacter* spp.+ *Klebsiella pneumoniae* | 7 | 2 | 5 | 1 | 6 |
| *Acinetobacter* spp. + *Pseudomonas aeruginosa* | 2 | 1 | 1 | 0 | 2 |
| *Acinetobacter* spp. + *Staphylococcus aureus* | 1 | 0 | 1 | 0 | 1 |
| *Citrobacter* spp. + *Escherichia coli* | 1 | 0 | 1 | 1 | 0 |
| *Escherichia coli + Klebsiella pneumoniae* | 10 | 7 | 3 | 4 | 6 |
| *Escherichia coli* + *Klebsiella* spp. | 2 | 2  | 0 | 2 | 0 |
| *Escherichia coli* + *Proteus* spp. | 2 | 1 | 1 | 2 | 0 |
| *Escherichia coli* + *Pseudomonas aeruginosa* | 1 | 1 | 0 | 0 | 1 |
| *Escherichia coli* + *Salmonella* spp. | 1 | 1 | 0 | 1 | 0 |
| *Escherichia coli* + Other Gram-negative bacteria | 2 | 2 | 0 | 0 | 2 |
| *Enterococcus faecium* + *Klebsiella pneumoniae* | 1 | 1 | 0 | 0 | 1 |
| *Enterococcus faecalis* + *Staphylococcus aureus* | 2 | 0 | 2 | 0 | 2 |
| *Enterococcus faecalis* + Other Gram-negative bacteria | 1 | 1 | 0 | 0 | 1 |
| *Klebsiella pneumoniae* + *Pseudomonas aeruginosa* | 2 | 2 | 0 | 0 | 2 |
| *Klebsiella pneumoniae* + *Proteus* spp. | 2 | 1 | 1 | 1 | 1 |
| *Klebsiella pneumoniae* + *Serratia* spp. | 1 | 1 | 0 | 0 | 1 |
| *Klebsiella pneumoniae* + Non-albicans *Candida* | 1 | 1 | 0 | 0 | 1 |
| *Klebsiella pneumoniae* + Other Gram-negative bacteria | 10 | 2 | 8 | 2 | 8 |
| *Klebsiella* spp. + *Salmonella enterica* | 1 | 1 | 0 | 0 | 1 |
| *Klebsiella* spp. + Other Gram-negative bacteria | 1 | 1 | 0 | 0 | 1 |
| *Pseudomonas aeruginosa* + Other Gram-negative bacteria | 1 | 1 | 0 | 0 | 1 |

BSI = bloodstream infections **\*** All patients with BSI caused by polymicrobial pathogenic organism were non-COVID-19 cases. Community-origin and hospital-origin BSI are defined as proposed by WHO GLASS.

**Supplementary Table 2**. Pathogenic organisms isolated from 1,895 patients with bloodstream infections at Cipto Mangunkusumo National Hospital, Indonesia, between 2019 and 2020 \*

|  |  |  |  |
| --- | --- | --- | --- |
| **Pathogens** | **Community-origin BSI****(N=515)** | **Hospital-origin BSI****(N=1380)** | **P value** |
| **Gram negative bacteria** |  |  |  |
| *Escherichia coli* | 103 (20%) | 127 (9.2%) | <0.001 |
| *Klebsiella pneumonia* | 57 (11.1%) | 351 (25.4%) | <0.001 |
| *Klebsiella* spp. | 10 (1.9%) | 24 (1.7%) | 0.76 |
| *Proteus* spp. | 5 (1%) | 14 (1%) | 0.93 |
| *Salmonella* spp. | 18 (3.5%) | 15 (1.1%) | <0.001 |
| *Salmonella enterica* | 2 (0.4%) | 2 (0.1%) | 0.29 |
| *S. enterica serotype typhi* | 6 (1.2%) | 0 (0%) | <0.001 |
| *Shigella* spp. | 1 (0.2%) | 0 (0%) | 0.27 |
| *Pseudomonas aeruginosa* | 62 (12%) | 95 (6.9%) | <0.001 |
| *Pseudomonas* spp. | 1 (0.2%) | 3 (0.2%) | >0.99 |
| *Acinetobacter* spp. | 60 (11.7%) | 193 (14%) | 0.18 |
| *Aeromonas* spp. | 3 (0.6%) | 7 (0.5%) | 0.73 |
| *Burkholderia cepacian* | 4 (0.8%) | 9 (0.7%) | 0.75 |
| *Citrobacter* spp. | 0 (0%) | 7 (0.5%) | 0.20 |
| *Serratia* spp. | 2 (0.4%) | 15 (1.1%) | 0.39 |
| Other Gram-negative bacteria | 39 (7.6%) | 107 (7.8%) | 0.89 |
| **Gram positive bacteria** |  |  |  |
| *Staphylococcus aureus* | 87 (16.9%) | 129 (9.4%) | <0.001 |
| *Streptococcus pneumoniae* | 3 (0.6%) | 0 (0%) | 0.02 |
| *Streptococcus pyogenes* | 4 (0.8%) | 0 (0%) | 0.01 |
| *Enterococcus faecium* | 1 (0.2%) | 10 (0.7%) | 0.30 |
| *Enterococcus faecalis* | 15 (2.9%) | 46 (3.3%) | 0.64 |
| *Lactococcus garvieae*  | 0 (0%) | 1 (0.1%) | >0.99 |
| **Fungi** |  |  |  |
| *Candida* *albicans* | 2 (0.4%) | 35 (2.5%) | 0.01 |
| Non-albicans *Candida* | 16 (3.1%) | 147 (10.7%) | <0.001 |
| *Cryptococcus* spp. | 0 (0%) | 2 (0.1%) | >0.99 |
| Other fungi  | 0 (0%) | 3 (0.2%) | 0.56 |
| **Polymicrobial infections\*\*** | 14 (2.7%) | 38 (2.8%) | 0.96 |

BSI = bloodstream infections \* Only the first pathogenic isolate per patient during the study period was included.\*\* Three most common polymicrobial infections were *Escherichia coli + Klebsiella pneumoniae* (10 patients), *Klebsiella pneumoniae* + Other Gram-negative bacteria (10 patients), *Acinetobacter* sp+ *Klebsiella pneumoniae* (7 patients). Polymicrobial infections was described in Supplementary Table 1.

**Supplementary Table 3.** Prevalence of WHO global priority AMR pathogens causing bloodstream infections stratified by infection origin

|  |  |  |  |
| --- | --- | --- | --- |
| **Priority AMR pathogens \*** | **Community-origin** | **Hospital-origin** | **P value** |
| Carbapenem resistant *Acinetobacter* spp.  | 16.4% (10/61) | 56.9% (115/202) | <0.001 |
| Carbapenem resistant *P. aeruginosa* | 11.3% (7/62) | 33.7% (34/101) | <0.001 |
| Carbapenem resistant \*\*\* *K.* *pneumoniae*  | 21.5% (14/65) | 38.7% (146/377) |  0.01 |
| 3rd Cephalosporin resistant \*\*\**K.* *pneumoniae* | 61.5% (40/65) | 87.8% (331/377) | <0.001 |
| Carbapenem resistant \*\*\**E*. *coli* | 11.6% (13/112) | 15.3% (21/137) |  0.40 |
| 3rd Cephalosporin resistant \*\*\**E*. *coli*  | 67.8% (76/112) | 77.6% (111/137) |  0.02 |
| Vancomycin resistant *E*. *faecium*  | 0% (0/1) | 9.1% (1/11) | >0.99 |
| Methicillin resistant *S*. *aureus* | 5.8% (5/87) | 7.6% (10/132) |  0.60 |
| Fluoroquinolone resistant *Salmonella* spp.  | 11.1% (3/27) | 16.7% (3/18) |  0.67 |
| Fluoroquinolone resistant *Shigella* spp.  | 100% (1/1) | 0% (0/0) |  |
| Penicillin resistant S. *pneumoniae*  | 33.3%(1/3) | 0% (0/0) |  |
| Overall\*\*\*\*  | 34.1%(143/419) | 61.8%(605/978) | <0.001 |

CO = community-origin. HO = hospital-origin. CO and HO are defined as proposed by WHO GLASS.(WHO, 2020) \* Only the first pathogenic isolate per patient during the study period was included. **\*\*** All COVID-19 cases were in 2020. \*\*\* All carbapenem-resistant *E. coli* and *K. pneumoniae* were also resistant to 3rd cephalosporin. \*\*\*\* Among patients with blood culture positive for *Acinetobacter* spp., *P. aeruginosa*, *K.* *pneumoniae, E*. *coli, E*. *faecium, S*. *aureus, Salmonella* spp, *Shigella* spp or S. *pneumoniae*

**Supplementary Table 4.** Proportion of WHO global priority AMR pathogens causing bloodstream infections stratified by infection origin and COVID-19 status

|  |  |  |
| --- | --- | --- |
| **Priority AMR pathogens \*** | **Community-origin** | **Hospital-origin** |
|  | **Non-COVID-19 cases** | **COVID-19 cases** | **P values** | **Non-COVID-19 cases** | **COVID-19 cases** | **P values** |
| Carbapenem resistant *Acinetobacter* spp.  | 17%(10/59) | 0%(0/2) | >0.99 | 57.6%(113/196) | 33.3%(2/6) | 0.41 |
| Carbapenem resistant *P. aeruginosa* | 12%(7/58) | 0%(0/4) | >0.99 | 43%(43/100) | 0%(0/1) | >0.99 |
| Carbapenem resistant \*\*\* *K.* *pneumoniae*  | 21,8%(14/64) | 0%(0/1) | >0.99 | 38%(141/372) | 55.5%(5/9) | 0.23 |
| 3rd Cephalosporin resistant \*\*\**K.* *pneumoniae* | 62.5%(40/64) | 0%(0/1) | 0.38 | 86.5%(322/372) | 100%(9/9) | 0.61 |
| Carbapenem resistant \*\*\**E*. *coli* | 10,4%(11/106) | 33.3%(2/6) | 0.14 | 15%(20/134) | 33.3%(1/3) | 0.4 |
| 3rd Cephalosporin resistant \*\*\**E*. *coli*  | 67%(71/106) | 83.3%(5/6) | 0.66 | 81.3%(109/134) | 66.6%(2/3) | 0.45 |
| Vancomycin resistant *E*. *faecium*  | 0%(0/1) | -(0/0) | - | 9%(1/11) | -(0/0) | - |
| Methicillin resistant *S*. *aureus* | 5.8%(5/86) | 0%(0/1) | >0.99 | 7.7%(10/130) | 0%(0/2) | >0.99 |
| Fluoroquinolone resistant *Salmonella* spp  | 11.1%(3/27) | 0%(0/1) | >0.99 | 16.6%(3/18) | -(0/0) | - |
| Fluoroquinolone resistant *Shigella* spp  | 100%(1/1) | -(0/0) | - | -(0/0)  | -(0/0) | - |
| Penicillin resistant S. *pneumoniae*  | 50%(1/2) | 0%(0/1) | >0.99 | -(0/0) | -(0/0) | - |
| Overall\*\*\*\*  | 35% (138/404) | 33.3% (5/15) | 0.95 | 61.8% (592/957) | 62%(13/21) | 0.99 |

CO = community-origin. HO = hospital-origin. CO and HO are defined as proposed by WHO GLASS.(WHO, 2020) \* Only the first pathogenic isolate per patient during the study period was included. **\*\*** All COVID-19 cases were in 2020. \*\*\* All carbapenem-resistant *E. coli* and *K. pneumoniae* were also resistant to 3rd cephalosporin. \*\*\*\* Among patients with blood culture positive for *Acinetobacter* spp., *P. aeruginosa*, *K.* *pneumoniae, E*. *coli, E*. *faecium, S*. *aureus, Salmonella* spp, *Shigella* spp or *S.* *pneumoniae*