**Supplemental Digital Content 1.** Incidence of BSI excluding CoNS stratified by birth weight

|  |  |  |
| --- | --- | --- |
| Birth Weight Classification | Incidence rate (BSI minus CoNS)/100 person days | 95% CI |
| <1000 g | 1.5 | 1.0-2.2 |
| 1,000g - <1,500g | 0.8 | 0.6-1.0 |
| >1,500 g <2,500 | 0.9 | 0.8-1.1 |
| 2,500 g | 1.1 | 0.9-1.3 |

**Supplemental Digital Content 2.** Incidence of BSI including CoNS stratified by birth weight

|  |  |  |
| --- | --- | --- |
| Birth Weight Classification | Incidence rate (BSI plus CoNS)/100 person days | 95% CI |
| <1000 g | 2.4 | 1.8-3.3 |
| 1,000g - <1,500g | 2.1 | 1.8-2.4 |
| >1,500 g <2,500 | 2.3 | 2.0-2.6 |
| 2,500 g | 2.7 | 2.4-3.0 |

Abbreviations: CoNS-Coagulase negative Staphylococcus, BSI-Bloodstream infections

**Supplemental Digital Content 3.** Pathogen profile from KBTH by day of life excluding Coagulase negative Staphylococci

**Supplemental Digital Content 4.** Pathogen profile from 37MH by day of life excluding Coagulase negative Staphylococci

Others-(Burkhoderia spp, Candida sp, Stenotrophomonas maltophilia,Aeromonas spp)

**Supplemental Digital Content 5.** Total number of organisms isolated from blood cultures from 37MH and KBTH

|  |  |  |
| --- | --- | --- |
| Organism | KBTH | 37MH |
| *Acetobacter cerevisae* | 1 | - |
| *Achromobacter xyloxidans* | 1 | - |
| *Acinetobacter baumannii* | 17 | 2 |
| *Acinetobacter junii* | 2 | 1 |
| *Acinetobacter nosocomialis* | 1 | - |
| *Acinetobacter schindleri* | 2 | - |
| *Aeromonal hydrophila* | - | 1 |
| *Aeromonas jandaei* | 1 | - |
| *Athrobacter cumminsii* | 1 | - |
| *Athrobacter stackebrandtii* | 1 | - |
| *Bacillus cereus* | - | 1 |
| *Bacillus sononrengis* | - | 1 |
| *Bacillus pumilis* | 1 | 1 |
| *Bacillus pseudomycoides* | 1 | - |
| *Bacillus sp* | 20 | - |
| *Brevibacterium luteolum* | 1 | 1 |
| *Brevundimonas aurantiaca* | 1 | - |
| *Burkholderia cenocepacia* | 1 | 2 |
| *Burkholderia vietnamensis* | 1 | - |
| *Candida sp* | 1 | 1 |
| *Candida orthopsolopsis* | 1 | - |
| *Candida tropicalis* | - | 1 |
| *Clostridium tertium* | 1 | - |
| *Coagulase negative staphylococcus* | 137 | - |
| *Corynebacterium amycolatum* | 4 | 1 |
| *Corynebacterium aurimucosum* | - | 1 |
| *Corynebacterium riegelli* | 1 | - |
| *Corynebacterium urealyticum* | - | 1 |
| *Dichelobacter nodosus* | 1 | 1 |
| *Diptheroids* | 12 | - |
| *Elizabethkingia menigoseptica* | 1 | - |
| *Enterobacter asburiae* | 1 | - |
| *Enterobacter cloacae* | 3 | 1 |
| *Enterobacter xianfangensis* | 1 | - |
| *Enterococcus casseliflavus* | 2 | - |
| *Enterococcus faecalis* | 16 | 4 |
| *Enterococcus faecium* | 9 | 1 |
| *Enterococcus raffinosus* | 1 | - |
| *Escherichia coli* | 15 | 1 |
| *Gemella mobillorum* | - | 1 |
| *Klebsiella pneumoniae* | 53 | 130 |
| *Lactobacillus fuchuensis* | 1 | - |
| *Lactobacillus sakei* | 1 | - |
| *Lysibacillus fusiformes* | - | 2 |
| *Microbacterium paraoxydans* | 1 |  |
| *Micrococcus luteus* | 32 | 10 |
| *Micrococcus lylae* | - | 1 |
| *Neisseria macacae* | 1 | - |
| *Neisseria mucosa* | 1 | - |
| *Neisseria subflava* | 3 | - |
| *Paracoccus versutus* | 1 | - |
| *Proteus mirabilis* | 1 | - |
| *Pseudoclavibacter sp* | 1 | 1 |
| *Pseudoglutamicrobacter cummnsii* | 2 | - |
| *Pseudomonas aeruginosa* | 5 | - |
| *Pseudomonas libanensis* | - | 1 |
| *Pseudomonas jinjii* | 1 | - |
| *Pseudomonas oryzhihabitans* | - | 1 |
| *Pseudomonas stutzeri* | 10 | 1 |
| *Rhizobium radiobacter* | 1 | 1 |
| *Salmonella sp* | 1 | - |
| *Serratia marcescens* | 8 | - |
| *Sphingobacterium spinfivorum* | 1 | - |
| *Staphylococcus aureus* | 17 | 6 |
| *Staphylococcus haemolyticus* | 136 | 20 |
| *Staphylococcus capitis* | 8 | 6 |
| *Staphylococcus caprae* | 1 | - |
| *Staphylococcus cohnii* | 1 | 3 |
| *Staphylococcus epidermidis* | 82 | 37 |
| *Staphylococcus equorum* | 1 | - |
| *Staphylococcus felis* | - | 1 |
| *Staphylococcus gallinarum* | - | 2 |
| *Staphylococcus hominis* | 30 | 19 |
| *Staphylococcus lentus* | - | 4 |
| *Staphylococcus lugdunensis* | 1 | - |
| *Staphylococcus pasteuri* | 1 | - |
| *Staphylococcus saprophyticus* | 2 | 4 |
| *Staphylococcus sciuri* | 3 | - |
| *Staphylococcus schleiferi* | - | 2 |
| *Staphylococcus warneri* | 2 | 6 |
| *Staphylococcus xylosus* | - | 2 |
| *Stenotrophomonas maltophilia* | 2 | 2 |
| *Streptococcus agalactiae* | 9 | 4 |
| *Streptococcus angionosus* | - | 1 |
| *Streptococcus cristatus* | 1 | - |
| *Streptococcus downei* | 1 | - |
| *Streptococcus dysagalactiae* | 1 | - |
| *Streptococcus gallolyticus* | - | 2 |
| *Streptococcus mitis* | 2 | 2 |
| *Streptococcus oralis* | 2 | 1 |
| *Streptococcus parasanguinis* | 1 | - |
| *Streptococcus pseudopneumoniae* | 1 | - |
| *Streptococcus sanguinis* | 3 | - |
| *Viridans streptococcus* | 7 | - |
| *Weisella confusa* | - | 1 |
| *Total* | 700 | 297 |

Abbreviations: BSI-Bloodstream infection, C/S-Cesarean section, SVD-Spontaneous vaginal delivery, CoNS-Coagulase negative

Staphylococcus, negative BSI includes neonates with CoNS and contaminants, statistical level of significance is set at P<0.05

**Supplemental Digital Content 6.** Pathogen profile from KBTH by day of life

CoNS-Coagulase negative Staphylococcus, Others-(Burkhoderia spp, Candida sp, Stenotrophomonas maltophilia,Aeromonas spp, Salmonella spp)

**Supplemental Digital Content 7.** Pathogen profile from 37MH by day of life

CoNS-Coagulase negative Staphylococcus, Others-(Burkhoderia spp, Candida sp, Stenotrophomonas maltophilia,Aeromonas spp

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Organism | AMP | AMC | CXM | CTX | CAZ | MEM | TZP | CIP | CN | AN | FOX | CC | E | TET | LZD | SXT | VA | P |
| Gram negatives(143) |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *Klebsiella pneumoniae(130)* | - | 130(100.0) | 130(100.0) | 129(99.2) | 129(99.2) | 0(0.0) | 9(6.9) | 118(90.8) | 126(96.9) | 0(0.0) | - | - | - | - |  | 130(100.0) |  |  |
| *Acinetobacter spp(3)* | ­- | - | - | - | - | 0(0.0) | - | 0(0.0) | 0(0.0) | 0(0.0) | - | - | - | - |  | 0(0.0) |  |  |
| *Pseudomonas spp(3)* | - | - | - | - | 0(0.0) | 0(0.0) | 0(0.0) | 0(0.0) | 0(0.0) | 0(0.0) | - | - | - | - |  | - |  |  |
| *E.coli(1)* | 1(100.0) | 1(100.0) | 1(100.0) | 1(100.0) | 1(100.0) | 0(0.0) | 1(100.0) | 0(0.0) | 1(100.0) | 1(100.0) |  |  |  |  |  | 1(100.0) |  |  |
| *Enterobacter spp(1)* | 1(100.0) | 1(100.0) | 1(100.0) | 1(100.00 | 1(100.0) | 0(0.0) | 0(0.0) | 0(0.0) | 0(0.0) | 0(0.0) |  |  |  |  |  | 1(100.0) |  |  |
| *\*Burkholderia cenocepacia(2)* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *Stenotrophomonas maltophilia(2)* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 0(0.0) |  |  |
| *Aeromonas hydrophilla(1)* |  |  |  |  | 0(0.0) |  |  | 0(0.0) |  |  |  |  |  |  |  | 0(0) |  |  |
| *Candida spp(2)* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Gram positives(128) |  | | | | | | | | | | | | | | | | | | |
| *Coagulase negative Staphylococci(107)* | - | - | - | - | - | - | - | 31(28.97) | 34(31.8) | - | 65(60.7) | 34(31.8) | 56(52.3) | 57(53.3) | 0(0.0) | 60(56.1) |  |  |
| *Streptococcus spp(10)* | 0(0.0) | - | - | - | - | - | - | - | - | - | - | - | 2(20.0) | 9(90.0) | 0(0.0) |  | 0(0.0) | 0(0.0) |
| *Enterococcus spp(5)* | 0(0.0) | - | - | - | - | - | - | - | - | - | - | - | - | - | 0(0.0) | - | 0(0.0) | - |
| *Staphylococcus aureus(6)* | - | - | - | - | - | - | - | 1(16.7) | 1(16.7) | - | 0(0.0) | 1(16.7) | 2(33.3) | 2(33.3) | 0(0.0) | 5(83.3) | - | - |
| Total |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

**Supplemental Digital Content 8.** Antibiotic susceptibility patterns of organisms isolated from 37MH

Data is presented as N (%), Abbreviations-amp-ampicillin, AMC-amoxicillin-clavulanic acid, CXM-cefuroxime, CTX-cefotaxime, CAZ-ceftazidime, MEM-meropenem, TZP-tazobactam-piperacillin, CIP-ciprofloxacin, CN-gentamicin, AN-amikacin, FOX-cefoxitin, CC-clindamycin, ERY-erythromycin, TET-tetracycline, LZD-linezolid, SXT-sulphamethoxazole-trimethoprim, VA-vancomycin, P-penicillin

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Organism | AMP | AMC | CXM | CTX | CAZ | MEM | TZP | CIP | CN | AN | FOX | CC | ERY | TET | LZD | SXT | VA | P |
| Gram negatives (125) | |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *Klebsiella pneumoniae (53)* | - | 51(96.2) | 0(100.0) | 49(92.5) | 49(92.5) | 8(15.1) | 38(71.7) | 30(56.6) | 42(79.2) | 30(56.6) | - | - | - | - | - | 47(88.7) | - | - |
| *Acinetobacter spp(22)* | - | - | - | - | - | 9(40.9) | - | 12(54.5) | 13(59.1) | 12(54.5) | - | - | - | - | - | 13(59.1) | - | - |
| *Pseudomonas spp(16)* | - | - | - | - | 3(18.75 | 4(25.0) | 6(37.5) | 4(25.0) | 3(18.75) | 2(12.5) | - | - | - | - | - | - | - | - |
| *E.coli(15)* | 14(93.3) | 10(66.7) | 9(60.0) | 8(53.3) | 8(53.3) | 0(0.0) | 4(26.7) | 6(40.0) | 6(40.0) | 0(0.0) | - | - | - | - | - | 12(80.0) | - | - |
| *Serratia marcescens(8)* | 8(100.) | 8(100.0) | 6(75.0) | 4(50.0) | 2(25.0) | 1(12.5) | 1(12.5) | 0(0.0) | 1(12.5) | 1(12.5) | - | - | - | - | - | 1(12.5) | - | - |
| *Enterobacter spp(5)* | 5(100.0) | 5(100.0) | 5(100.0) | 3(60.0) | 3(60.0) | 0(0.0) | 1(20.0) | 3(60.0) | 2(40.0) | 1(20.0) | - | - | - | - | - | 4(80.0) | - | - |
| *\*Burkholderia spp(2)* | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| *Stenotrophomonas maltophilia(2)* | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 0(0.0) | - | - |
| *Salmonella spp(1)* | - | - | - | 0(0.0) | 0(0.0) | 0(0.0) | - | 0(0.0) | - | - | - | - | - | - | - | 0(0.0) | - | - |
| *Proteus mirabilis(1)* | 0(0.0) | 0(0.0) | 0(0.0) | 0(0.0) | 0(0.0) | 0(0.0) | 0(0.0) | 0(0.0) | 0(0.0)0 | 0(0.0) | - | - | - | - | - | 0(0.0) | - | - |
| *Aeromonas spp* |  |  |  |  | 0(0.0) |  |  | 0(.0) |  |  |  |  |  |  |  | 0(0.0) |  |  |
| *Candida(2)* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Gram positives (479) | | | | | | | | | | | | | | | | | | |
| *Coagulase negative Staphylococci(405)* |  |  |  |  |  |  |  | 269(66.4) | 267(65.9) | NE | 321(79.3) | 236(58.3) | 270(66.7) | 211(52.1) | 0(0.0) | 241(59.5) |  |  |
| *Streptococcus spp(29)* | 0(0.0) |  |  |  |  |  |  |  |  |  |  |  | 11(37.9) | 19(65.6) | 0(0.0) |  | 0(0.0) | 0(0.0) |
| *Enterococcus spp(28)* | 9(32.1) |  |  |  |  |  |  |  |  |  |  |  |  |  | 0(0.0) |  | 1(3.6) |  |
| *Staphylococcus aureus(17)* |  |  |  |  |  |  |  | 3(17.6) | 1(5.9) |  | 3(17.6) | 2(11.8) | 5(29.4) | 4(23.5) | 0(0.0) |  | 2(11.8) |  |

**Supplemental Digital Content 9.** Antibiotic susceptibility patterns of organisms isolated from KBTH

Data is presented as N (%), Abbreviations-amp-ampicillin, AMC-amoxicillin-clavulanic acid, CXM-cefuroxime, CTX-cefotaxime, CAZ-ceftazidime, MEM-meropenem, TZP-tazobactam-piperacillin, CIP-ciprofloxacin, CN-gentamicin, AN-amikacin, FOX-cefoxitin, CC-clindamycin, ERY-erythromycin, TET-tetracycline, LZD-linezolid, SXT-sulphamethoxazole-trimethoprim, VA-vancomycin, P-penicillin

**Supplemental Digital Content 10.** Impact of BSI (including CoNS) on in hospital mortality

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Characteristic | Total | Dead (n, %) | Crude Hazard Ratio  [95% CI] | p-value | Adjusted Hazard Ratio  [95% CI] | p-value |
| Sex  Male  Female | 1,906  1,584 | 327 (17.2)  288 (18.2) | 0.99 (0.84-1.16) | 0.869 | 1.13 (0.96-1.34) | 0.142 |
| Birth weight  <1000 g ≥1000g -1499 g ≥1500g - ≤2499 g ≥2500 g | 163  497  1,125  1,695 | 117 (71.8)  155 (31.2)  168 (14.9)  171 (10.1) | 7.32 (5.73-9.34)  2.28 (1.81-2.87)  1.29 (1.03-1.61)  1.00 | 0.000  0.000  0.025 | 7.5 (5.84-9.65)  2.37 (1.88-2.99)  1.31 (1.04-1.64) | 0.000  0.000  0.018 |
| Mode of delivery  C/S  SVD | 1,862  1,596 | 302 (16.2)  307 (19.2) | 1.00  1.19 (1.01-1.40) | 0.036 | 1.06 (0.90-1.25) | 0.495 |
| BSI  Positive  Negative | 759  2,744 | 154(20.3)  465 (17.0) | 0.92 (0.76-1.12) | 0.439 | 0.85 (0.70-1.03) | 0.114 |

Abbreviations: BSI-Bloodstream infection, C/S-Cesarean section, SVD-Spontaneous vaginal delivery, CoNS-Coagulase negative

Staphylococcus, negative BSI includes neonates with CoNS and contaminants, statistical level of significance is set at P<0.05