**SUPPLEMENTAL TABLE 2**. Mean counts and frequency of microbial groups isolated from meconium and feces of preterm neonates through the hospital stay.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Meconium**  **(n = 12)** | | **1st month feces**  **(n= 76)** | | **2nd month feces**  **(n= 27)** | | **3rd month feces**  **(n= 17)** | |  | |
| **Microorganism** | **Number of**  **positive samples (%)** | **Microbial Countsa**  **Mean**  **(95% CI)** | **Number of**  **positive samples (%)** | **Microbial Countsa**  **Mean**  **(95% CI)** | **Number of**  **positive samples (%)** | **Microbial Countsa**  **Mean**  **(95% CI)** | **Number of**  **positive samples (%)** | **Microbial Countsa**  **Mean**  **(95% CI)** | ***P*b** | ***P*c** |
| *Bifidobacterium* | 0 (0) | - | 3 (4) | 9.25 (8.53- 9.70)d | 1 (4) | 10.00 | 2 (12) | 9.47 (9.31-9.63)d | 0.393 | 0.342 |
| *Enterococcus* | 3 (19) | 5.27 (2.83;7.71) | 67(88) | 8.52 (8.20-9.15)d | 25 (93) | 8.28 (7.82; 8.74) | 17 (100) | 8.75 (8.40; 9.10) | 0.000 | 0.073 |
| *Lactobacillus* | 7 (44) | 6.48 (3.95;9.01) | 11 (14) | 6.93 (5.66; 8.19) | 4 (15) | 8.37 (6.98; 9.75) | 1 (6) | 7.55 | 0.738 | 0.084 |
| *Staphylococcus* | 5 (20) | 6.15 (3.64;8.66) | 47 (62) | 7.23 (6.91; 7.56) | 9 (33) | 7.10 (6.47; 7.73) | 7 (41) | 7.35 (6.19; 8.51) | 0.047 | 0.546 |
| *Streptococcus* | 3 (19) | 4.77 (0.07;9.47) | 4 (5) | 7.88 (6.44-9.33)d | 0 (0) | - | 1 (6) | 9.26 | 0.089 | 0.212 |
| Other G+e | 2 (13) | 5.20 (4.70;5.70)d | 6 (8) | 7.73 (7.15; 8.31) | 3 (11) | 7.47 (5.70-8.74)d | 2 (12) | 5.70 | 0.902 | 0.077 |
| *E. coli* | 0 (0) | - | 36 (47) | 8.95 (8.70-9.48)d | 15 (56) | 8.72 (8.36; 9.08) | 12 (71) | 8.57 (7.87; 9.26) | 0.000 | 0.302 |
| *Klebsiella* | 1 (6) | 7.27 | 45 (59) | 8.88 (8.74-9.40)d | 18 (67) | 8.57 (8.11; 9.04) | 13 (76) | 7.93 (7.27; 8.59) | 0.000 | 0.012 |
| *Serratia* | 0 (0) | - | 34 (45) | 9.07 (8.70-9.59)d | 18 (67) | 8.51 (8.07; 8.96) | 8 (47) | 8.63 (8.07; 9.20) | 0.000 | 0.034 |
| Other G-f | 1 (6) | 6.38 | 19 (25) | 8.92 (8.33-9.69)d | 10 (37) | 8.25 (7.67; 8.83) | 5 (29) | 8.88 (7.80; 9.96) | 0.163 | 0.049 |
| Yeast | 1 (6) | 6.08 | 5 (7) | 6.33 (4.40;8.25) | 0 (0) | - | 1 (6) | 6.40 | 0.606 | 0.879 |

n, indicates total number of samples analyzed.

aBacterial and yeast counts (LOG CFU/g).

bχ2 were used to analyzed the frequency data

cANOVA or KW was used to analyzed the microbial counts data

dMedian (IQR)

eOther Gram-positive bacteria included the following genera: *Bacillus, Corynebacterium, Dermabacter, Lactococcus, Micrococcus, Pediococcus, Propionibacterium, Rathayibacter* and *Wautersiella.*

fOther Gram-negative bacteria included the following genera: *Citrobacter, Enterobacter, Erwinia, Morganella, Pantoea, Pseudomonas, Proteus, Shigella, Stenotrophomonas* and *Veionella.*