**Supplemental Material and Methods**

**Culture analysis of the samples and bacterial identification**

Adequate dilutions of human milk, infant formula, meconium and stool samples were spread onto different culture media as previously described [1]. Microbial counts were recorded as the colony forming units (CFU)/ml or g and transformed to log10 values before statistical analysis. At least one representative of each colony morphology type was isolated from each plate and genotyped and identified as previously described [1].

**Random Amplification of Polymorphic DNA (RAPD) and Pulse Field Gel Electrophoresis.**

Genetic relatedness among selected bacteria from milk and infants feces was investigated by RAPD to avoid duplication of isolates from the same host sample and to determine if a given genotype was shared. RAPD profiles were obtained using primer OPL5 (5’-ACGCAGGCAC-3’) [2]. This primer was originally designed for lactobacilli but it has been shown to be useful also for typing other species [3].

Those isolates with the same RAPD profile were subjected to pulsed field gel electrophoresis (PFGE) in a CHEF DR II apparatus (Bio-Rad, Birmingham, UK) with different protocols. To separate *Sma*I fragments of enterococci and staphylococci species a pulse time was applied from 2 to 28 s for 24 h for the former and from 5 to 15 s for 10 h and then another from 15 to 60 s for 13 h, for the latter. The chromosomal DNA of *K. pneumoniae* isolates were digested with *Xba*I enzyme and the restriction fragments separated by electrophoresis with a pulse time from 1 to 40 s for 20 h. Computer-assisted analysis was performed with InfoQuest FP software (Bio-Rad Laboratories, Inc., Hercules, CA, USA). Cluster analysis of RAPD and PFGE pattern profiles was performed using the UPGMA method based on the Dice correlation similarity coefficient.

**Scanning electron microscopy (SEM) analysis**

The 6 feeding devices were fixed in 4% (v/v) paraformaldehyde and 2.5% (v/v) glutaraldehyde in PBS pH 7.2 for 4 h at 4 ºC and, then, washed with cold PBS every 20 min for, at least, 4 times. The tubes were cut into 1 cm long pieces and dissected to expose the internal surface longitudinally. The tube pieces were stained with 1% (v/v) osmium tetroxide (EM grade) solution for 90 min at room temperature. This was followed by washing with deionized water and a complete dehydration of the samples in a series of increasing ethanol concentrations (50% to 100%). Subsequently, the samples were dried without introducing surface tension artifacts by using a critical point drier. The air-dried biopsies were then mounted on aluminum stubs, sputter-coated with a very thin film of gold and examined using a scanning electron microscope (JEOL 6400 JSM) at the Centro Nacional de Microscopía Electrónica (Madrid).

**Statistical Analysis**

Quantitative data were expressed as the mean and 95% confidence interval (CI) of the mean or, when they were not normally distributed, as the median and interquartile range (IQR). The bacterial richness and diversity of the collected samples were determined by calculating the Shannon-Weaver diversity index, which takes into account the number and evenness of the bacterial species. Chi-square statistics, including the Fisher’s exact test and the Freeman-Halton extension of the Fisher exact probability test for 2×4 contingency tables, were used to compare proportions. Friedman’s non-parametric repeated measures comparisons and paired samples *t*-tests were applied to determine differences between the bacterial counts of each identified microbial group across time. Differences were considered significant at P < 0.05. Statgraphics Centurion XVI version 16.1.15 (Statpoint Technologies Inc., Virginia, USA) and R 2.13.2 (R project, Statistical Software) software were used to carry out the analyses cited above.

**References**

1. Moles L, Gómez M, Heilig H, et al. Bacterial diversity in meconium of preterm neonates and evolution of their fecal microbiota during the first month of life. PLoS ONE. 2013;8:e66986.

2. Veyrat A, Miralles MC, Pérez-Martínez G. A fast method for monitoring the colonization rate of lactobacilli in a meat model system. J Appl Microbiol. 1999;87:49-61.

3. Jimenez E, Delgado S, Maldonado A, et al. *Staphylococcus epidermidis*: a differential trait of the fecal microbiota of breast-fed infants. BMC Microbiol. 2008;8:143-2180-8-143.