

The feeding of human milk to infants reduces the risk of diarrheal diseases. Components in milk that are mitigating this effect are still not clearly defined. Milk is a complex fluid that contains myriad factors including a diverse bacterial community. The influence of the milk bacterial community on the structure of the infant's bacterial community is unknown but we hypothesize that bacterial populations in milk affect the presence and relative abundances of bacteria in the infant's gastrointestinal tract. To examine this, we collected milk samples and infant fecal samples from mother/infant dyads at 9 time points from day 2 to 6 mo pp. DNA was extracted and the bacterial DNA amplified using universal primers targeting the V1-V3 region of the 16S rRNA gene. Amplicons were sequenced using the Illumina MiSeq v3 2 x 300 bp protocol. Sequencing reads were filtered for quality, then joined and classified using a custom python pipeline (dbcAmplicons; <https://github.com/msettles/dbcAmplicons>). We utilized multivariate poisson prediction models with cross-validation using the 'glmnet' package in R to capture the complex interactions of the milk bacterial populations on the infant fecal bacterial populations. These models provide an efficient framework that can handle the sparse and high dimensional input matrix of microbiome data. Several bacteria (e.g. *Veillonellaceae*, *Bifidobacteriaceae*, and *Pasteurellaceae*) in milk were positive predictors (effect of 0.019, 0.004, and 0.003, respectively) of the relative abundance of *Bacteroides* in infant feces. *Staphylococcaceae* in milk was a negative predictor of the relative abundances of *Bifidobacteriaceae* and *Coriobacteriaceae* (-0.051 and -0.240, respectively) and positive predictor of the relative abundances of *Staphylococcus* and *Weissella* (0.184 and 0.312, respectively) in infant feces. Individual mothers were found to have an effect on the relative abundances of several bacteria in their infant feces suggesting that the environment (e.g. diet), genetics of the mother, and/or other components unique to the milk from that mother predict the variation observed for those bacteria. These results suggest that members of the milk bacterial community impact the structure of the infant's bacterial fecal community. More research is needed to confirm this in a larger and/or different population. This project was funded by the Bill and Melinda Gates Foundation, the Idaho Agricultural Experiment Station, the Bioinformatics and Computational Program at the University of Idaho in partnership with the Institute for Bioinformatics and Evolutionary Studies (IBEST), and guided by the Center for Modeling Complex Interactions.