Transcription shifts in gut bacteria shared between mothers and their infants: data from the NiPPeR Study

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Abstract

The infant gut microbiome contains a portion of bacteria that originate from the maternal gut. In the infant gut these bacteria encounter a new metabolic environment that differs from the adult gut, consequently requiring adjustments in their activities. We utilized community RNA sequencing data (metatranscriptomes) from ten mother-infant dyads participating in the NiPPeR Study to characterize bacterial gene expression shifts following mother-to-infant transmission. Maternally derived bacterial strains adapted by large scale gene expression shifts following the transmission to the infant gut, with 12,564 activated and 14,844 deactivated gene families, including 1,007 transferases and 85 bacteriophage genes. The implicated genes were most numerous and the magnitude shifts greatest in Bacteroides spp. This study demonstrates environment-dependent, strain-specific shifts in gut bacteria function and underscores the importance of metatranscriptomic analysis in microbiome studies.

Full Text

Due to technical limitations, full-text HTML conversion of this manuscript could not be completed. However, the manuscript can be downloaded and accessed as a PDF.

Tables

Due to technical limitations, table 1 is only available as a download in the Supplemental Files section.

Figures

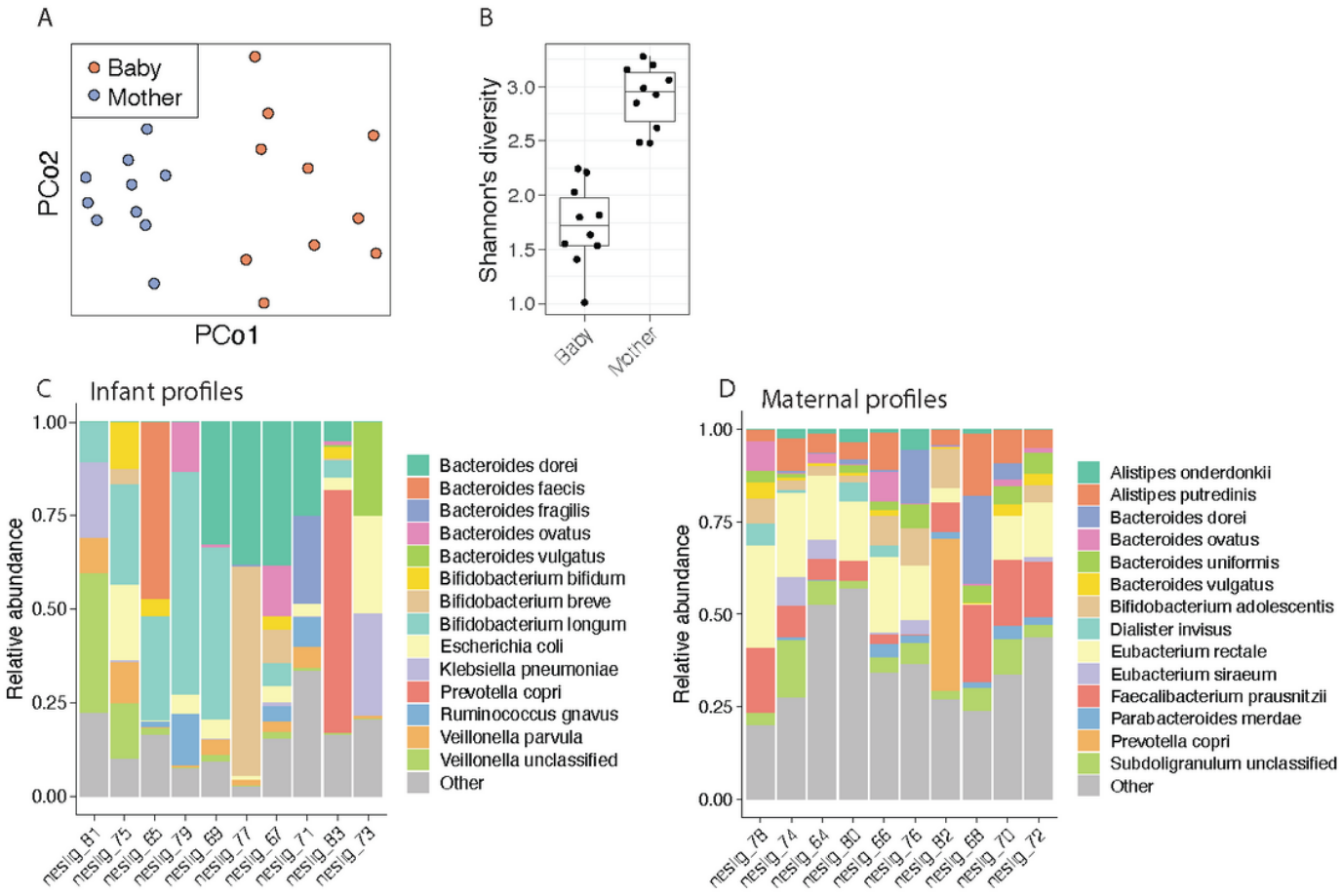

Figure 1

Distinctive microbial profiles separated infants from their mothers. A) Principal Coordinate Analysis ordination of bacterial taxonomic profiles. B) Shannon's diversity of microbial species profiles. The box of the boxplot shows the interquartile range, whiskers show the range of data and horizontal line in the box shows the median. C-D) Relative abundances of the 14 most abundant species (on average) in the infant (C) and maternal (D) stool samples.

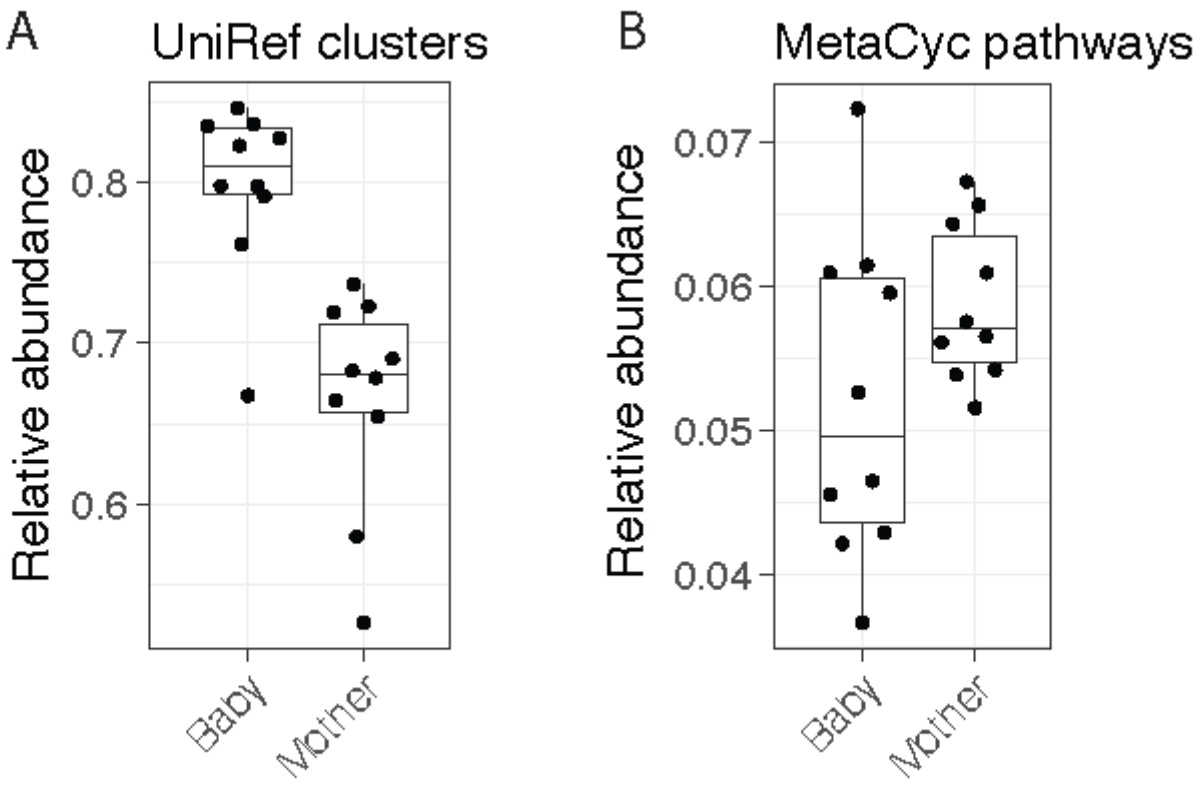

Figure 2

Mapping metagenomic DNA to protein databases and MetaCyc pathways. A) Larger proportion of DNA reads from the infant metagenomes were mapped against UniRef protein clusters compared to adult metagenomes (Wilcoxon test, p = 0.0003). B) Proportion of mapped DNA reads in A that also contributed to quantifications of MetaCyc pathways. The difference between mothers and infants was not statistically significant (Wilcoxon test, p = 0.16).

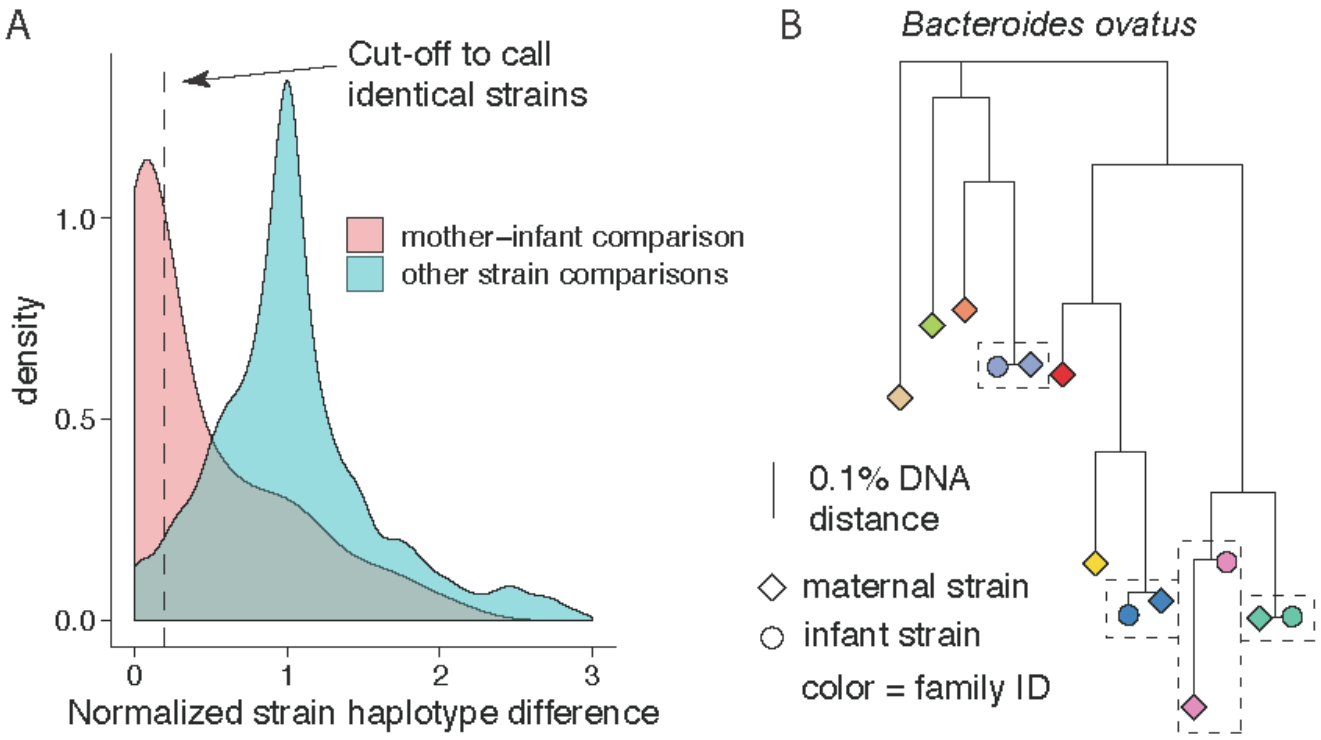

Figure 3

Bacterial strains shared between a mother and her infant. A) Density plot of within-species strain comparisons between all detected strains per species. X-axis shows median normalized SNP-haplotype DNA distance (Jukes-Cantor model) divided by the median DNA distance per species (0 = equal strain haplotypes, 1 = median SNP haplotype dissimilarity). Red area shows comparisons within mother-infant pairs (given that a strain was detected from both infant and mother), teal area shows all other strain comparisons representing strain comparisons between random gut microbiomes. B) Phylogenetic tree of Bacteroides ovatus strains detected in this cohort. Colors represent different mother-infant pairs (families) and scale shows the branch length corresponding to 0.1% DNA dissimilarity. Four family-specific strains are highlighted with dashed boxes.

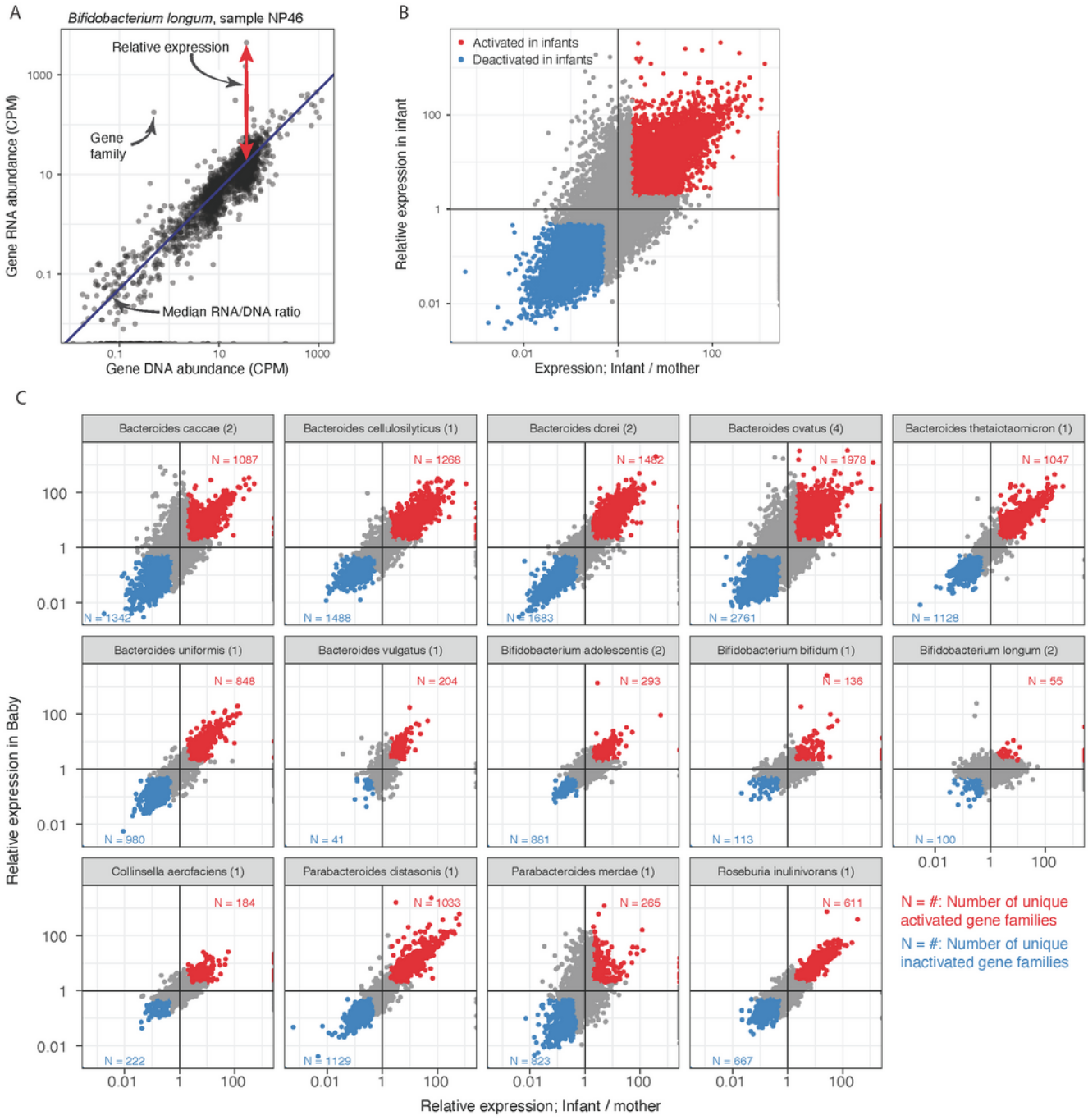

Figure 4

Gene expression changes in the strain shared within a family. A) DNA and RNA abundances in copies-per-million (CPM) in Bifidobacterium longum in an infant sample (NP46). Gene family relative expression is calculated by normalizing the RNA/DNA ratio with the species and sample specific median RNA/DNA ratio. B) A scatterplot of gene family relative expression change in infants vs. mothers (x-axis) and infant relative expression (y-axis), The gene families that were activated or inactivated after mother-to-infant transmission are highlighted in red and blue, respectively; activation denotes to infant relative expression

> 2 (y-axis) and Infant/mother relative expression > 2 (x-axis); deactivation denotes to infant relative expression < ½ and infant/mother relative expression < ½. C) Panel B stratified by species. Numbers in parentheses following the species name shows the number of families sharing a strain in the given species and panel-specific gene family frequencies (N = ...) denote the number of unique gene families that were activated or deactivated in red and blue, respectively (if the same gene family was activated in multiple infants it was counted only once).

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- VatanenMBIOTable1.xlsx
- VatanenMBIOTableS1.xlsx
- VatanenMBIOTableS2.xlsx
- VatanenMBIOTableS3.xlsx