

Supporting Information

Dominguez-Bello et al. 10.1073/pnas.1002601107

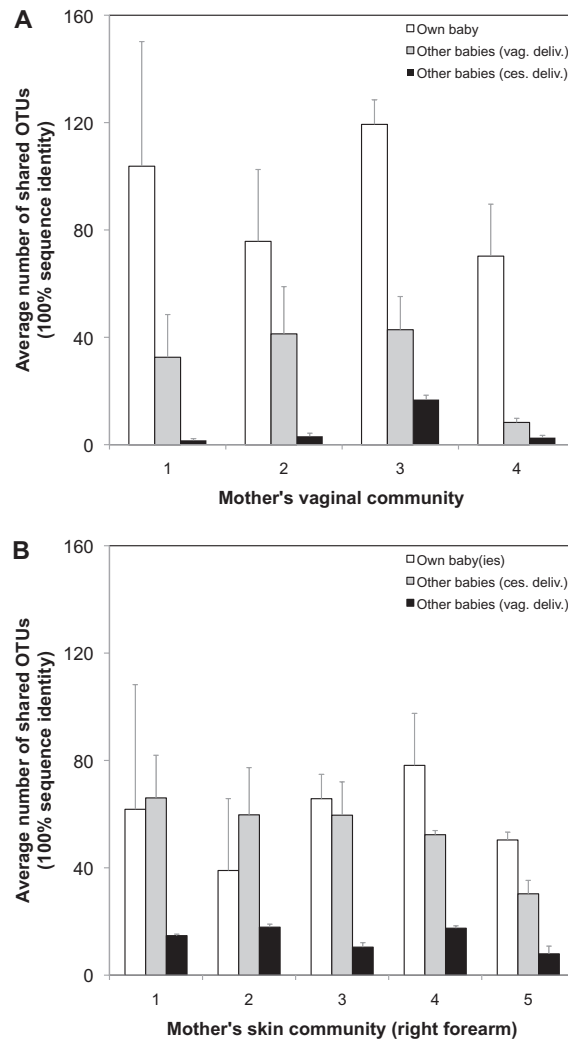


Fig. S1. Delivery mode influences the average number of nearly identical sequences shared between mothers and babies. Each baby sample was compared with (A) the vaginal community of each mother that delivered vaginally and (B) the right forearm skin community of each mother that delivered via C-section. Comparisons were made between mothers and their own babies (white bars), and other babies born by the same (gray bars) or different (black bars) delivery mode. Highly similar sequences were found by picking operational taxonomic units (OTUs) at 100% sequence identity using UCLUST. OTUs containing only one sequence, or appearing in only one sample, were removed from the analysis. Sequencing depth was standardized by randomly selecting 900 sequences from each sample. An OTU was considered shared if it contained at least one sequence from the mother sample and one sequence from the baby sample. Error bars are 1 SEM.

Table S1. Analysis of similarity results for comparisons made in this study

Comparison groups		Unweighted UniFrac Global <i>R</i>	Weighted UniFrac Global <i>R</i>
Mothers' body habitats	Skin vs. oral	0.992 (**)	1.000 (**)
	Skin vs. vagina	0.958 (**)	0.939 (**)
	Oral vs. vagina	0.965 (*)	0.928 (**)
Infants' body habitats	Cesarean (all habitats)	-0.002 (N.S.)	-0.064 (N.S.)
	Vaginal (all habitats)	0.046 (N.S.)	0.136 (N.S.)
Mothers by delivery mode	Cesarean vs. vaginal	0.008 (N.S.)	-0.016 (N.S.)
Infants by delivery mode	Cesarean vs. vaginal	0.779 (**)	0.831 (**)
Mothers' body habitats vs.	Skin vs. vaginal	0.747 (**)	0.741 (**)
Infants by delivery mode	Oral vs. vaginal	0.871 (**)	0.674 (**)
	Vagina vs. vaginal	0.493 (*)	0.198 (N.S.)
	Skin vs. cesarean	0.369 (**)	0.322 (**)
	Oral vs. cesarean	0.995 (**)	0.951 (**)
	Vagina vs. cesarean	0.963 (**)	0.968 (**)
Twins	Twin A vs. twin B	-0.177 (N.S.)	-0.219 (N.S.)

One thousand permutations were performed for each comparison. A pair of asterisks indicates significance with $P < 0.001$, a single asterisk indicates $P < 0.01$. N.S. = not significant ($P > 0.01$). Analysis of similarity is a permutation-based test of the null hypothesis that within-group distances are not significantly smaller than between-group distances. The test statistic (*R*) can range from 1 to -1, with a value of 1 indicating that all samples within groups are more similar to each other than to any other samples from different groups. *R* is ≈ 0 when the null hypothesis is true, that distances within and between groups are the same on average. In cases where only two groups were compared, they are listed below (e.g., skin vs. oral). When more than two groups were compared (e.g., all habitats), they were gut, skin, oral mucosa, and nasopharyngeal aspirate.

Table S2. Distribution of vaginal bacterial taxa among individual mothers

Mother		V1_Mom1	V2_Mom2	V3_Mom6	V4_Mom10	C1_Mom4	C2_Mom7	C4_Mom9
Delivery		Vaginal	Vaginal	Vaginal	Vaginal	C-section	C-section	C-section
Ethnicity		Mestizo	Mestizo	Amerindian	Amerindian	Mestizo	Mestizo	Mestizo
Taxa		Percentage of sequences by taxa						
Firmicutes	<i>Lactobacillus</i>	92.39	88.15	19.24	1.93	93.92	6.30	52.04
Bacteroidetes	<i>Prevotella</i>	0.21	0.32	9.54	56.14	0.03	18.57	12.96
Actinobacteria	<i>Atopobium</i>	0.00	0.00	4.87	7.80	0.00	34.11	0.00
Fusobacteria	<i>Sneathia</i>	0.00	0.00	12.89	0.00	0.00	8.71	0.00
Firmicutes	Lactobacillales	4.51	5.88	1.88	0.12	2.97	0.65	3.59
Fusobacteria	Fusobacteriaceae	0.00	0.00	13.35	0.00	0.00	5.28	0.00
Firmicutes	Veillonellaceae	0.08	0.05	0.61	12.32	0.00	2.49	0.00
Firmicutes	Megasphaera	0.05	0.09	1.12	10.06	0.00	3.44	0.04
Actinobacteria	<i>Corynebacterium</i>	0.00	0.00	2.89	0.00	0.14	0.33	10.23
Bacteroidetes	Prevotellaceae	0.00	0.00	7.36	0.16	0.00	0.04	2.61
Firmicutes	Lactobacillaceae	2.36	3.78	1.07	0.12	1.19	0.12	1.18
Firmicutes	<i>Dialister</i>	0.03	0.00	0.66	3.86	0.00	3.72	0.41
Actinobacteria	Coriobacteriaceae	0.00	0.00	2.08	0.94	0.00	4.95	0.04
Firmicutes	Ruminococcaceae	0.03	0.00	3.10	1.60	0.00	2.41	0.00
Actinobacteria	<i>Gardnerella</i>	0.08	0.00	0.30	0.74	0.10	2.86	0.00
Firmicutes	Clostridiales	0.00	0.09	1.12	0.41	0.00	1.51	0.61
Tenericutes	<i>Ureaplasma</i>	0.00	0.55	0.91	0.16	1.19	0.00	0.29
Firmicutes	<i>Streptococcus</i>	0.05	0.59	0.30	1.31	0.00	0.08	0.24
Firmicutes	Lachnospiraceae	0.00	0.00	1.78	0.00	0.00	0.00	0.53
Firmicutes	<i>Anaerococcus</i>	0.00	0.00	0.81	0.62	0.00	0.00	0.81
N sequences		3,766	2,181	1,971	2,455	2,870	2,449	2,460

Vaginal swabs were not obtained from Mestizo mother C3_Mom8 and Amerindian mother C5_Mom11 [Cesarean (C-section) deliveries].