**Supplementary Materials**

**Supplementary Tables:**

**Supplementary Table 1**. Average of relative abundances of OTUs shared in saliva samples (core saliva microbiota) in all points of the time-course.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| *Genus* | 7 days | 15 days | 30 days | 90 days | 180 days |
| *Rothia* | 0.013 | 0.010 | 0.018 | 1.615 | 0.217 |
| *Staphylococcus* | 17.630 | 18.948 | 15.391 | 16.996 | 12.791 |
| *Streptococcus* | 71.308 | 77.453 | 79.661 | 75.874 | 66.999 |
| *Gemellaceae\_g* | 6.494 | 1.008 | 0.714 | 0.944 | 2.322 |
| *Veillonella* | 0.006 | 0.041 | 0.098 | 1.583 | 4.976 |

**Supplementary Table 2**. Average of elative abundances of OTUs shared in fecal samples (core gut microbiota) in all points of the time-course.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Genus** | **BIRTH** | **7 days** | **15 days** | **30 days** | **90 days** | **180 days** |
| Enterobacteriaceae\_g | 81.186 | 13.110 | 21.255 | 26.289 | 14.122 | 14.749 |
| *Erwinia* | 0.012 | 0.022 | 0.141 | 0.277 | 0.034 | 0.176 |
| *Klebsiella* | 0.024 | 0.011 | 0.035 | 0.027 | 0.023 | 0.181 |
| *Bacteroides* | 3.458 | 4.180 | 13.095 | 8.197 | 1.295 | 0.191 |
| *Parabacteroides* | 0.002 | 0.001 | 0.012 | 0.222 | 0.007 | 0.003 |
| *Bifidobacterium* | 0.142 | 0.013 | 2.271 | 6.935 | 41.467 | 13.901 |
| *Akkermansia* | 0.001 | 0.002 | 0.023 | 0.183 | 0.009 | 0.106 |
| *Staphylococcus* | 0.002 | 4.031 | 1.249 | 0.153 | 0.350 | 0.031 |
| *Enterococcus* | 0.001 | 0.038 | 0.015 | 0.121 | 0.643 | 0.607 |
| *Streptococcus* | 0.067 | 1.592 | 0.520 | 1.455 | 4.068 | 3.051 |
| Ruminococcaceae\_g | 0.105 | 0.005 | 0.012 | 1.405 | 0.788 | 0.146 |
| Lachnospiraceae\_g | 0.087 | 0.005 | 0.036 | 0.118 | 0.114 | 0.059 |
| *Clostridium* | 0.001 | 0.002 | 0.004 | 0.005 | 0.008 | 0.010 |
| *Veillonella* | 0.347 | 0.022 | 0.378 | 0.175 | 0.301 | 1.528 |

**Supplementary Table 3.** OTUs shared between gut and salivary microbiota of the cohort of infants at each point of the time-course.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Shared OTUsa** | | | | |
| **7 days** | **15 days** | **30 days** | **90 days** | **180 days** |
| ***Streptococcus*** | ***Streptococcus*** | ***Streptococcus*** | ***Streptococcus*** | ***Streptococcus*** |
| ***Staphylococcus*** | ***Staphylococcus*** | ***Staphylococcus*** | ***Staphylococcus*** | ***Staphylococcus*** |
| ***Veillonella*** | ***Veillonella*** | ***Veillonella*** | ***Veillonella*** | ***Veillonella*** |
| *Haemophilus* | Planococcaceae\_g | Enterobacteriaceae\_g | Enterobacteriaceae\_g | *Gemella* |
| *Acinetobacter* | Enterobacteriaceae\_g |  | *Corynebacterium* | Planococcaceae\_g |
| *Gemella* | Gemellaceae\_g |  | *Haemophilus* | Gemellaceae\_g |
| Planococcaceae\_g |  |  | Gemellaceae\_g | *Granulicatella* |
| *Rothia* |  |  |  | *Haemophilus* |
| Gemellaceae\_g |  |  |  | *Prevotella* |

a in bold are highlighted OTUs shared between gut and salivary microbiota in all points of the time course.

**Supplementary Table 4.** Characteristics of networks of saliva, stool and saliva versus stool samples.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | ***Saliva*** | | | | | ***Stool*** | | | | | | ***Stool vs. Saliva*** | | | | |
| ***7 days*** | ***15 days*** | ***30 days*** | ***90 days*** | ***180 days*** | ***Birth*** | ***7 days*** | ***15 days*** | ***30 days*** | ***90 days*** | ***180 days*** | ***7 days*** | ***15 days*** | ***30 days*** | ***90 days*** | ***180 days*** |
| Avg. number of neighbors | 5.48 | 5.95 | 9.13 | 9.10 | 10.81 | 14.03 | 12.11 | 11.55 | 8.82 | 12.86 | 8.06 | 5.51 | 5.40 | 8.27 | 5.53 | 6.58 |
| Network diameter | 12 | 5 | 8 | 10 | 8 | 8 | 8 | 8 | 11 | 9 | 11 | 6 | 6 | 9 | 8 | 8 |
| Characteristic path length | 3.12 | 1.96 | 3.17 | 4.13 | 3.00 | 3.50 | 3.97 | 2.79 | 4.34 | 3.26 | 4.71 | 2.08 | 2.27 | 3.96 | 3.21 | 3.45 |
| Clustering coefficient | 0.73 | 0.77 | 0.84 | 0.83 | 0.79 | 0.94 | 0.90 | 0.92 | 0.83 | 0.87 | 0.85 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Network centralization | 0.16 | 0.21 | 0.19 | 0.16 | 0.15 | 0.11 | 0.11 | 0.14 | 0.11 | 0.24 | 0.10 | 0.06 | 0.05 | 0.09 | 0.07 | 0.07 |
| Network heterogeneity | 0.67 | 0.54 | 0.48 | 0.51 | 0.61 | 0.41 | 0.51 | 0.71 | 0.43 | 0.70 | 0.46 | 0.65 | 0.40 | 0.51 | 0.57 | 0.55 |
| Network radius | 1 | 1 | 1 | 5 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| Network density | 0.11 | 0.15 | 0.14 | 0.16 | 0.14 | 0.19 | 0.10 | 0.11 | 0.08 | 0.12 | 0.08 | 0.07 | 0.09 | 0.09 | 0.07 | 0.07 |
| Connected components | 6 | 5 | 2 | 1 | 3 | 4 | 2 | 7 | 3 | 4 | 6 | 11 | 6 | 3 | 7 | 5 |
| Shortest paths | 722 | 594 | 3666 | 3306 | 4984 | 2346 | 1217 | 2660 | 9714 | 9202 | 5648 | 1230 | 996 | 8042 | 2228 | 6080 |
| Number of nodes | 50 | 41 | 64 | 58 | 77 | 75 | 124 | 102 | 105 | 112 | 107 | 78 | 60 | 98 | 76 | 96 |

**Supplementary Figures**

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**Supplementary Figure 1. Panel A. OTUs distribution of the salivary microbiota at phylum level.** The bar graphs represent the average distribution of OTUs. **Panel B. Histograms are referred to Kruskal Wallis test-based phyla distribution with a *p*FDR<0.05**.

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**Supplementary Figure 2. Panel A.** OTUs distribution of the gut microbiota at phylum level. The bar graphs represent the average distribution of OTUs. **Panel B.** Histograms above are referred to Kruskal Wallis test-based phyla distribution with a *p*FDR<0.05.

B

A

**Supplementary Figure 3.** Colonization trends of the bacterial genera shared in all points of the time course between salivary (A) and gut (B) ecosystems.