**Social complexity as a driving force of gut microbiota exchange among conspecific hosts in nonhuman primates**

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**Supplementary Information**

Methods

As search methods and inclusion criteria we used Google Scholar to identify any primatological study that, first, related the gut microbiota with different traits of social components and, secondly, reported any measure of the gut microbiota composition: such as total, average, minimum and maximum number of observed features (operational taxonomic units, OTUs, or amplicon sequence variants, ASVs). We found a total of 36 studies of 20 primate species, including humans, published between 2010 and 2021. Most of these were cross-sectional studies (29 papers), with a few longitudinal (5 studies), and only 2 studies including both cross-sectional and longitudinal data. Moreover, thirty studies were conducted with wild primates, 3 with captive subjects, and only 2 studies included both wild and captive individuals.

Of this sample, at least 17 studies concerned the interplay between gut microbiota and host sociality, including 12 primate species. Regarding the association between gut microbiota and social complexity, we employed microbial data from 17 studies conducted in 36 wild groups of 15 primate species (see Table S1). Data of neocortex ratio were obtained from Stephan et al. (1981), Dunbar (1992), and Kudo and Dunbar (2001). Neocortex size of *Piliocolobus tephrosceles* was found in Lehmann et al. (2007). Information of body weight and average group size were obtained from (DeCasien et al. 2017). Lastly, average group size for humans was determined as described by Aiello and Dunbar (1993).

Based on these data, we used multiple linear regressions to test for (i) a quantitative influence of social group size, as a simple measure of social complexity, upon the gut microbiota, and (ii) a possible quantitative influence of neocortex ratio upon the gut microbiota. The particular method chosen was a stepwise, backward multiple linear regression, considering it preferable to the forward method due to suppressor effects and lower risks of making a Type II error (Field 2013). In this method, all predictors are first included in the model and are then excluded based on the significance of their contribution. For each predictor the significance value of a t-test is compared against a removal criterion (here set to P ≤ 0.050). When the predictor does not make a significant contribution, it is removed and the model is re-calculated, testing the contribution of each remaining predictor (Field 2013). Additionally, case-wise diagnostics were used, considering data as outliers beyond Mean ± 2SD. All statistical analyses were carried out using SPSS 21.0.

Table A1 - Excluded variables for the best-fit final stepwise linear regression (backward) model with Maximum observed features (OTUs or ASVs) as the dependent variable.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | Beta in | t | P |  | Partial  correlation | Tolerance | VIF |
| Body weight (g) | 0.079 | 0.546 | 0.590 |  | 0.103 | 0.991 | 1.009 |
| Neocortex ratio | 0.259 | 1.346 | 0.189 |  | 0.246 | 0.530 | 1.885 |

Table A2 – Casewise diagnostics for the best-fit final stepwise linear regression (backward) model with Maximum observed features (OTUs or ASVs) as the dependent variable.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Case number | Species | Std residual | Maximum observed features | Predicted value | Residual |
| 16 | *Homo sapiens* | 4.054 | 10079 | 4257.51 | 5821.493 |

Table A3 – Residual statistics for the best-fit final stepwise linear regression (backward) model with Maximum observed features (OTUs or ASVs) as the dependent variable.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Minimum | Maximum | Mean | Std. Deviation | N |
| Predicted value | 544.58 | 4343.75 | 1373.97 | 1192.752 | 31 |
| Residual | -2613.751 | 5821.493 | 0.0 | 1411.863 | 31 |
| Std. Predicted value | -0.695 | 2.490 | 0.0 | 1.0 | 31 |
| Std. Residual | -1.820 | 4.054 | 0.0 | 0.983 | 31 |

Gráfico, Histograma

Descripción generada automáticamente

Gráfico

Descripción generada automáticamente

Gráfico, Gráfico de dispersión

Descripción generada automáticamente

Table S1. Social group size, neocortex ratio and gut microbial diversity for 36 social primate groups.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Species | Neocortex ratio | Body weight (g) | Average group size | Observed Features | | | | | Reference |
|  | **Total** | **Average** | **Standard deviation** | **Minimum** | **Maximum** |
| *Alouatta pigra* | 2.15 | 8940 | 5.93 |  | 262 | 48 | 182 | 329 | Amato et al. (2017) |
| *Alouatta pigra* | 2.15 | 8940 | 5.93 |  | 247 | 15 | 231 | 264 | Amato et al. (2017) |
| *Alouatta pigra* | 2.15 | 8940 | 5.93 |  | 244 | 47 | 181 | 291 | Amato et al. (2017) |
| *Alouatta pigra* | 2.15 | 8940 | 5.93 |  | 289 | 21 | 255 | 310 | Amato et al. (2017) |
| *Alouatta pigra* | 2.15 | 8940 | 5.93 |  | 223 | 28 | 181 | 250 | Amato et al. (2017) |
| *Cercopithecus ascanius* | 2.27 | 4157 | 26.29 |  | 1666 |  | 1306 | 1867 | Yildirim et al. (2010) |
| *Colobus guereza* | 2.32 | 10052 | 8.6 |  | 1295 |  | 1072 | 1442 | Yildirim et al. (2010) |
| *Gorilla gorilla* | 2.65 | 121327 | 10.05 | 2644 | 617 | 103 | 495 | 823 | Gomez et al. (2015) |
| *Gorilla gorilla* | 2.65 | 121327 | 10.05 | 2312 | 576 | 78 | 476 | 773 | Gomez et al. (2015) |
| *Gorilla gorilla* | 2.65 | 121327 | 10.05 | 1433 | 530 | 42 | 450 | 586 | Gomez et al. (2015) |
| *Gorilla gorilla* | 2.65 | 121327 | 10.05 | 1784 | 533 | 66 | 443 | 603 | Gomez et al. (2015) |
| *Gorilla gorilla* | 2.65 | 121327 | 10.05 |  | 753 | 212 | 542 | 1361 | Narat et al. (2020) |
| *Homo sapiens* | 4.1 | 65078 | 148 | 1235 | 186 | 51 |  |  | Yang et al. (2020) |
| *Homo sapiens* | 4.1 | 65078 | 148 |  | 1427 | 847 | 51 | 3347 | Das et al. (2018) |
| *Homo sapiens* | 4.1 | 65078 | 148 |  | 1212 | 265 | 771 | 1876 | Das et al. (2018) |
| *Homo sapiens* | 4.1 | 65078 | 148 |  | 1770 | 1831 | 532 | 10079 | Das et al. (2018) |
| *Lemur catta* | 1.18 | 2380 | 15.75 | 1821 |  |  |  |  | Fogel (2015) |
| *Lemur catta* | 1.18 | 2380 | 15.75 | 501 | 293 | 22 | 263 | 311 | Bennett et al. (2016) |
| *Lemur catta* | 1.18 | 2380 | 15.75 | 854 | 280 | 49 | 201 | 372 | Bennett et al. (2016) |
| *Lemur catta* | 1.18 | 2380 | 15.75 | 765 | 288 | 31 | 255 | 335 | Bennett et al. (2016) |
| *Lemur catta* | 1.18 | 2380 | 15.75 | 610 | 273 | 39 | 208 | 316 | Bennett et al. (2016) |
| *Macaca mulatta* | 2.6 | 6472 | 36.36 | 1770 | 637 | 134 | 153 | 850 | Li et al. (2021) |
| *Macaca thibetana* | 2.6 | 7190 | 25.46 |  | 1241 | 408 | 754 | 3213 | Sun et al. (2016) |
| *Pan troglodytes* | 3.22 | 48328 | 42.71 |  | 949 | 265 | 518 | 1683 | Degnan et al. (2012) |
| *Pan troglodytes* | 3.22 | 48328 | 42.71 |  | 872 | 199 | 582 | 1225 | Degnan et al. (2012) |
| *Pan troglodytes* | 3.22 | 48328 | 42.71 |  | 497 | 60 | 381 | 663 | Moeller et al. (2016) |
| *Pan troglodytes* | 3.22 | 48328 | 42.71 |  | 792 | 136 | 585 | 932 | Narat et al. (2020) |
| *Papio cynocephalus* | 2.68 | 14291 | 48.21 | 11547 | 1440 | 226 | 958 | 1876 | Grieneisen et al. (2017) |
| *Papio cynocephalus* | 2.68 | 14291 | 48.21 | 14850 | 1638 | 307 | 704 | 2203 | Grieneisen et al. (2017) |
| *Piliocolobus tephrosceles* | 2.22 | 8105 | 29.18 |  | 2003 |  | 1697 | 2522 | Yildirim et al. (2010) |
| *Propithecus verreauxi* | 1.1 | 3389 | 5.92 | 1721 |  |  |  |  | Fogel (2015) |
| *Pygathrix nemaeus* | 2.05 | 9250 | 21.45 |  | 4231 | 584 |  |  | Clayton et al. (2018) |
| *Sapajus nigritus* | 2.25 | 2662 | 18.14 | 84 | 75 | 9 | 59 | 81 | Grassotti et al. (2021) |
| *Sapajus nigritus* | 2.25 | 2662 | 18.14 | 83 | 74 | 11 | 54 | 80 | Grassotti et al. (2021) |
| *Theropithecus gelada* | 2.55 | 14778 | 151.3 | 1624 |  |  |  |  | Trosvik et al. (2018) |
| *Theropithecus gelada* | 2.55 | 14778 | 151.3 | 3295 | 813 | 243 | 92 | 1730 | Baniel et al. (2021) |

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