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Egyptian Mongoose Gut Microbiota: Taxonomical and Functional Differences across Sex and Age Classes

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Abstract: Egyptian mongoose (*Herpestes ichneumon*) is a medium-size carnivore that in Europe is restricted to Iberia. The bio-ecology of this species remains to be elucidated in several dimensions, including gut microbiota that is nowadays recognized as a fundamental component of mammals. In this work, we investigated the gut microbiota of this herpestid by single-molecule real-time sequencing of twenty paired male (n=10) and female (n=10) intestinal samples. This culture-independent approach enabled microbial profiling based on 16S rDNA and investigation of taxonomical and functional features. The core gut microbiome of the adult subpopulation was dominated by Firmicutes, Fusobacteria, Actinobacteria, and Proteobacteria. Eight genera were uniquely found in adults and five in non-adults. When comparing gut bacterial communities across sex, four genera were exclusive of females and six uniquely found in males. Despite these compositional distinctions, alpha- and beta-diversity analyses showed no statistically significant differences across sex or between adult and non-adult specimens. However, males presented a significantly higher abundance of amino acid and citrate cycle metabolic pathways, compared to the significant overrepresentation in females of galactose' metabolic pathways. Adults exhibited a significantly higher abundance of cationic antimicrobial peptide resistance pathways, while non-adults bared a significant overrepresentation of two-component systems associated with antibiotic synthesis, flagellin and biofilm production and chemotaxis control. This study adds new insights into mongoose bio-ecology palette, highlighting taxonomical and functional microbiome dissimilarities across sex and age classes, possibly related to primary production resources and life-history traits that impact on behavior and diet.

Keywords: Egyptian mongoose; Gut microbiota; Microbial profiling; Bio-ecology; Mediterranean Wild Carnivores

1. Introduction

The bioecology of each mammal species is a conjugation of different domains, such as geographic range and habitat, diet, genetics, morpho-physiology, social behavior and, also, gut microbiota, which has been progressively acknowledged as a fundamental component of mammals' biology [1]. Egyptian mongoose [*Herpestes ichneumon* (Linnaeus, 1758)] is a carnivore species from the Herpestidae family, with opportunistic feeding behavior and whose diet in the Mediterranean includes wild rabbit, other small mammals like rodents, reptiles, amphibians, birds, crayfish, eggs,

and even carrion [2]. This species is mostly present in the African continent, but also on the Mediterranean Middle East, Turkey, and the Iberian Peninsula (Portugal and Spain) [3]. The historical process underlying Egyptian mongoose colonization of Iberia is an issue under debate. While Gaubert et al. (2011) supported that mongooses reached Iberia through the Strait of Gibraltar during the Middle to Late Pleistocene sea-level fluctuations [4], more recently Detry et al. (2018) suggested that this species might have been introduced by the Romans, during their establishment in Hispania [5]. In Portugal, the species distribution in the early 20th century was restricted to the south of the Tagus River [6] but it has gradually, and remarkably, expanded into central and north-eastern regions [7]. The drivers for this geographic expansion are subject to speculation but land-use changes in shrub-dominated ecosystems, deforestation, the transformation of agricultural practices, and climate change [8] seem to have jointly contributed to this phenomenon. Egyptian mongoose has a home-range of about 3 km², inhabiting locals with scrub vegetation in coastal, lacustrine, and riparian habitats, avoiding humid forests and extreme deserts. In the Iberian Peninsula, it is found in Mediterranean maqui. Listed as Least Concern, the species is widespread, common, and present in many protected areas. There are no major threats to this species across its range. Mongoose ecological features such as morpho- and stress physiology, diet, body condition, or reproduction, have been unraveled in recent years [2], driven by the opportunity to explore a large array of specimen samples in Portugal, where it is a game species under the Portuguese hunting law [9] and specific actions for predator density control are legally foreseen.

In Portugal, both sexual and regional dimorphism in body size has been reported, attributed to different feeding behaviors across sex and regions, resulting in larger and heavier male adults in the south [10]. *H. ichneumon* exhibit variability in social organization, ranging from solitary individuals to groups, which show cooperative tendencies, particularly in areas with abundant food resources. The exclusive home-range use of males in high-density populations suggests the existence of a polygynous mating system, which is accomplished by the spatial distribution of females, in combination with the absence of paternal care behavior [6,11-14]. This species microbiota has been investigated through culture-dependent methods in two separate approaches [15,16], a first preliminary study based on the limited bacteriological screening of 53 specimens and the latter focused on the microbial characterization of the gut of 20 males and females using a broad range, systematic culturomics-like strategy. This study enabled the isolation and characterization of a large array of aerobic and anaerobic bacterial microbiota, sporobiota, and mycobiota [15]. However, a deeper insight into comprehensive gut communities can only be accomplished by a culture-independent approach that complementarily allows the characterization of non-viable or viable but non-culturable bacteria.

In this work, we thus set out to explore the gut microbiota of Egyptian mongoose sampled in South Portugal, using a phylogenetic marker gene sequencing approach based on the 16S rRNA gene. The aims of this study were to: (1) characterize the gut bacterial microbiota of Egyptian mongoose population; (2) investigate sex- and age class-related taxonomic and functional differences; (3) discuss the contribution of culture-dependent and culture-independent approaches to fully characterize microbial gut ecosystems in mammals; (4) discuss of our findings in the context of mongoose bioecology and expansion patterns.

2. Materials and Methods

2.1. Egyptian mongoose specimens

Egyptian mongoose carcasses (ten male and ten female) obtained from legal predator density control actions were opportunistically used for this work. These carcasses were donated by hunters for scientific purposes and, after death, were frozen at -20°C until necropsy. No animals were sacrificed for this study. The twenty animals under analysis were selected from a wider array of available mongooses, based on several biological factors, namely sex, age class, geographic location, land-use and stomach content at the time of death. They were harvested at Baixo Alentejo region, south of Tagus River, from a landscape predominated by agroforestry and agriculture. The selected

animals had the same stomach content at death, mostly composed of mammal and egg items [2, 10]. Age class distribution was 16 adults and four non-adults (two subadults and two juveniles).

Mongooses were subjected to necropsy and specimen collection by pathologists at the necropsy facilities of INIAV, the National Reference Laboratory for Animal Health. No signs of putrefaction or disease were detected. The abdominal cavity of each specimen was opened and the intestines isolated. Solid intestinal content (colon) was collected from each animal, using a sterile feces collection tube, and immediately processed for further analysis.

2.2. DNA extraction, quantification, sequencing and reads processing

DNA was extracted from 500 mg of feces of each mongoose using the NZY Soil gDNA isolation kit (NZYTech) following the manufacturer's instructions. DNA was quantified using a Qubit fluorometer (Qiagen), following the manufacturer's instructions. Full-length 16S rRNA gene was amplified from 2.5 ng/ul of total DNA from each intestinal sample and commercially sequenced on the Pacific Biosciences RS-II platform [PacBio Single-Molecule Real-Time – SMRT (Eurofins Genomics)]. The universal primers 27F (5'-AGAGTTGATCCTGGCTCAG-3') and BS-R1407 (5'-GACGGCGGTGWGTRC-3') were used to amplify Variable Regions (V) V1 to V8, originating an expected size amplicon of 1381 bp [17]. Additionally, the more recent PacBio P6-C4 chemistry was used.

Data were preprocessed using the PacBio SMRT Analysis Portal (Pacific Biosciences, EUA), generating single-molecule circular consensus sequences (CCS). The resulting CCS were analyzed using the EzBioCloud platform [18] (January of 2019). The PKSSU4.0 taxonomy database of prokaryotic 16S rRNA gene sequences was used. The uploaded CCS were trimmed of primers and quality filter under several criteria, namely, sequence length out of the expected range (<80 bp or >2,000 bp), sequences with an average Q value lower than 25, sequences not predicted as 16S rRNA gene by the Hidden Markov Model, and sequences found to be singletons when clustering using a cutoff of 97% similarity by the UCLUST method [19]. After, the pool of CCS reads was denoised using the DUDE-Seq software [20] and non-redundant reads were extracted. Next, the resulting reads were taxonomically assigned using USEARCH [19]. The following similarity cutoff values were used for taxonomical identification: species ($\geq 97\%$), genus (between 96.9% and 94.5%), family (between 94.4% and 86.5%), order (between 86.4% and 82%), class (between 81.9% and 78.5%), and phylum (between 78.4% and 75%) [21]. Following, the non-assigned sequences were subjected to the UCHIME program [22] for the detection of chimerical sequences.

The valid reads (all reads that passed the previous filters) were then used to Operational Taxonomic Unit (OTU) picking, using an "open-reference" method with the following steps: (1) species-level identification clustering using the taxonomic assigned data; (2) OTU clustering using the UCLUST tool; and (3) a conjugation of the clusters obtained by the two previous steps. Singletons were omitted from further analysis. Also, the Good's coverage of library was calculated to assess the representativity of the obtained reads when compared with the actual population [23].

2.3. Estimation of alpha-diversity indices

Using OTU information, several diversity indices were estimated to measure bacterial species richness (ACE, Chao1, Jackknife, and number of OTU) and evenness (Shannon, Simpson, and NPShannon), using the EzBioCloud platform [24-28]. Besides these estimators, rarefaction and rank abundance curves were also plotted [29,30].

2.4. Comparison between subpopulations using beta-diversity indices

The microbial communities at the genus level of each individual host were grouped according to host biological features, namely host sex (male and female) and age (adult and non-adult). Next, the subpopulations were compared using both ordination analysis and hierarchical clustering. First, a distance matrix was calculated using four possible metrics: UniFrac, Generalized UniFrac, Bray-Curtis, and Jensen-Shannon [31-34]. Then, the resulting matrix was used to compute a principal

coordinate analysis (PCoA) or cluster using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) algorithm originating a dendrogram. The beta-diversity analysis was also performed using the EzBioCloud platform [18].

2.5. Taxonomic and functional biomarker discovery

To assess the taxonomic biomarkers of each host subpopulation, multiple comparisons between the different taxonomic taxa were performed using a Kruskal-Wallis H test ($\alpha=0.05$). To predict the differential functional profile of the host subpopulations, a linear discriminant analysis effect size (LEfSe) was performed ($\alpha=0.05$) [35]. Both analyses were performed using the EzBioCloud platform [18].

2.6. Abiotic and biotic data integration

For microbiota and bio-environmental data integration, we performed a Principal Component Analysis (PCA) using available information for the 20 Egyptian mongoose specimens [2,10]. The abiotic variables used were related to land-use, climatic data, road net, river net, and population data. The biotic variables used were related to stomach content at the time of death and different body measurements [2,10]. Data integration was performed using the R software (Version 3.6.1).

2.7. Data analysis

Considering alpha-diversity indices, results from indices estimations were displayed as means of values of the individuals belonging to each subpopulation with respective standard deviation. When comparing two conditions, the Wilcoxon rank-sum test ($\alpha=0.05$) was performed. Considering beta-diversity, comparison of microbial communities between subpopulations of hosts were evaluated using beta set-significance analysis, namely a permutational multivariate analysis of variance (PERMANOVA) test. Both statistical analyses were performed using the EzBioCloud platform [18].

3. Results

3.1. Analysis of the sequencing data

A total of 46,508 reads across all samples were generated through SMRT sequencing. The trimming based on quality detected 1091 low-quality amplicons. Next, the clustering and taxonomic assignment detected seven non-target amplicons. Also, the chimera search detected 4187 chimerical amplicons. So, the total number of valid reads was 41,223 (88.6%). The average length of these reads was approximately 1416.6 (± 10.8) nucleotides, with an average minimum length of 1320 (± 10.53) nucleotides and an average maximum length of 1478 (± 26.86) nucleotides. A total of 37,565 (91.1%) sequences were identified at a species level. Together, this work accomplished a Good's coverage of library of 99.18% (± 0.46). For more information regarding individual sample data see Supplementary Table 1.

3.2. Bacterial composition of Egyptian mongoose' gut on a population and individual level

The assignment of consensus taxonomy resulted in the identification of 11 phyla being represented across the intestinal samples of the Egyptian mongoose population. On a populational level, all intestinal samples were dominated by Firmicutes (86%), followed by the Actinobacteria (6%), Fusobacteria (3%), Proteobacteria (3%), and Bacteroidetes (1%) (Fig. 1a). Besides these phyla, some rare phyla were also detected (0.04%), namely Chloroflexi, Cyanobacteria, Planctomycetes, Saccharibacteria, TM6, and Verrucomicrobia.

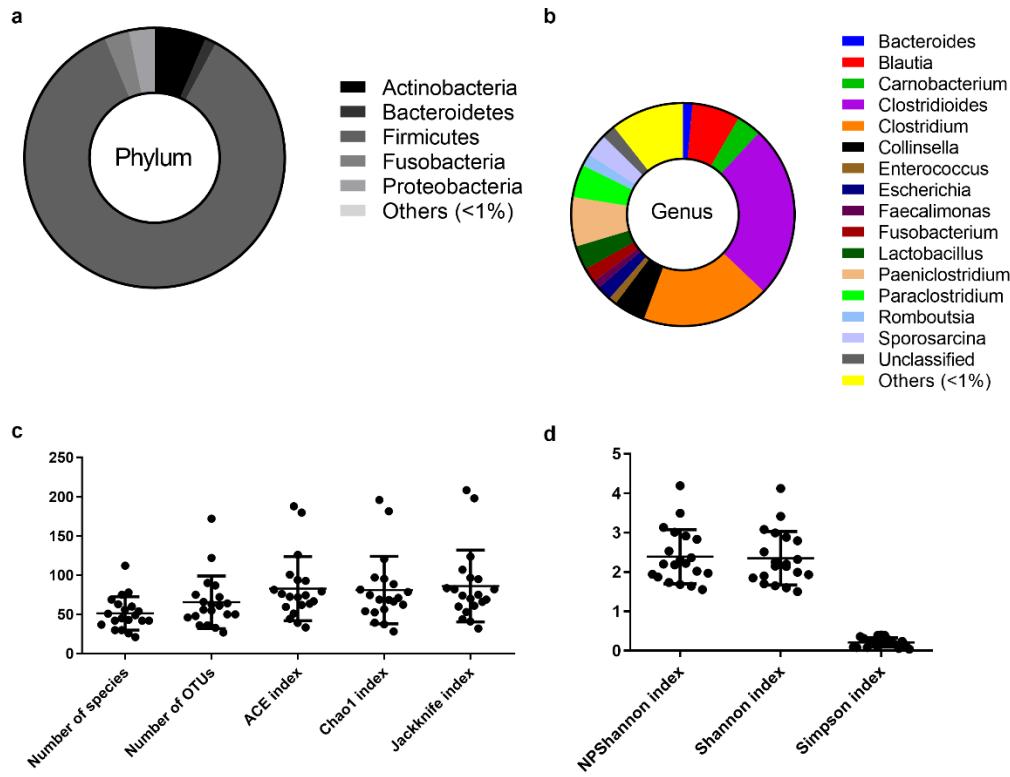


Figure 1. The core intestinal bacterial microbiota of the Egyptian mongoose population. (a) Relative abundance on a phylum and (b) genus level. (c) Species richness (number of species, number of OTUs, ACE, Chao1, and Jackknife indices) and (d) species evenness (NPShannon, Shannon, and Simpson indices).

The initial genus-level analysis focused on the most abundant OTUs (OTUs > 1% relative abundance). Genus level OTU classification resulted in the identification of 16 genera present in the gastrointestinal tract of Egyptian mongoose, with a relative abundance greater than 1% in any given sample (Fig. 1b). *Clostridioides* (25%) and *Clostridium* (19%) were the most abundant genera, representing almost half of the bacterial population (44%). At a lower, but yet high, abundance, *Blautia* (7%) and *Paenibacillus* (7%) genera were identified. Besides these genera, *Collinsella* (5%), *Paraclostridium* (5%), *Carnobacterium* (4%), *Lactobacillus* (3%), *Sporosarcina* (3%), *Escherichia* (2%), *Fusobacterium* (2%), *Romboutsia* (2%), *Bacteroides* (1%), *Enterococcus* (1%), and *Faecalimonas* (1%) were also detected. A total of 10% of reads were assigned to genera present in <1% relative abundance and only a total of 2% of the reads were not assigned to a genus.

On an individual level, Egyptian mongoose specimens exhibited similar microbial profiles, with Firmicutes prevailing (Fig. 2a). However, some notorious individual differences could be highlighted in relation to the overall population, namely mongoose individual HI467 that holds a higher abundance of Actinobacteria and mongoose HI509 that presents a higher abundance of Fusobacteria. Regarding genera compositions (Fig. 2b), a higher dissimilarity among individuals could be detected, with a more pronounced difference in mongoose HI674 that possesses higher abundance of *Sporosarcina* sp. (66%); HI508 with higher abundance of *Carnobacterium* sp. (61%); HI501 that holds a higher abundance of *Lactobacillus* sp. (47%); HI516 that presents higher abundance of *Romboutsia* sp. (26%); and HI466, showing a higher abundance of *Paraclostridium* sp. (25%). Mongoose HI460 shows a higher abundance of unclassified reads (28%) at the genus level.

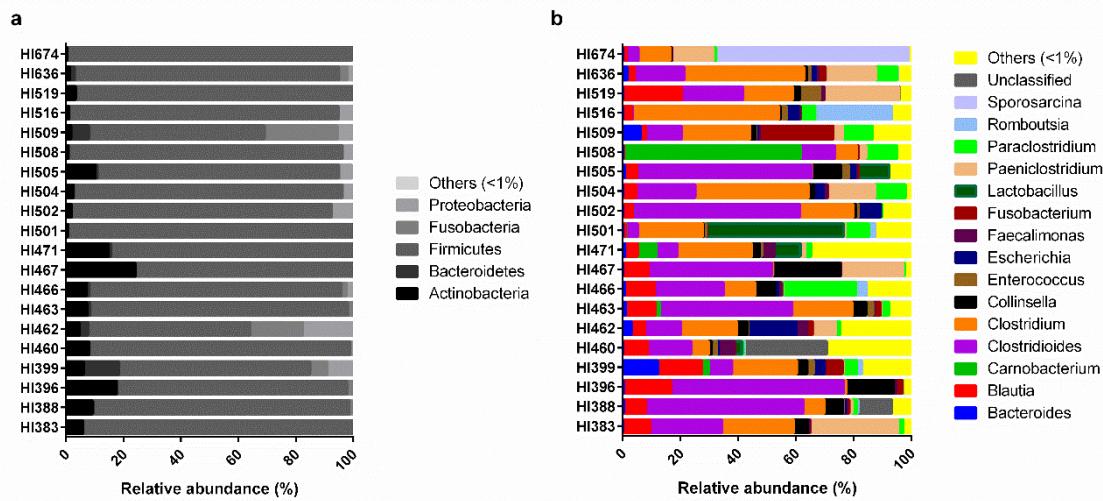


Figure 2. Relative abundance of the individual intestinal bacterial microbiota of Egyptian mongoose on a phylum (a) and genus (b) level.

Comparative analysis of OTUs across male and female intestinal samples evidenced that the majority of OTUs were shared across the individuals (Fig. 3). Of the 174 different genera identified in the gastrointestinal tract of Egyptian mongoose individuals (including OTUs with <1% relative abundance), 19 were present in >1% relative abundance in at least one subpopulation (male or female); nine were found to be shared between sexes, four were found to be unique to the female hosts (*Bacteroides*, *Carnobacterium*, *Cetobacterium*, and *Enterococcus*), and six unique to the male hosts (*Coprococcus*, *Faecalimonas*, *Romboutsia*, *Slackia*, *Sporosarcina*, and *Staphylococcus*) (Fig. 3b). Apart from these dissimilarities, similar proportions of phyla and genera were observed, with Bacteroidetes being uniquely found in the gastrointestinal tract of females (Fig. 3a).

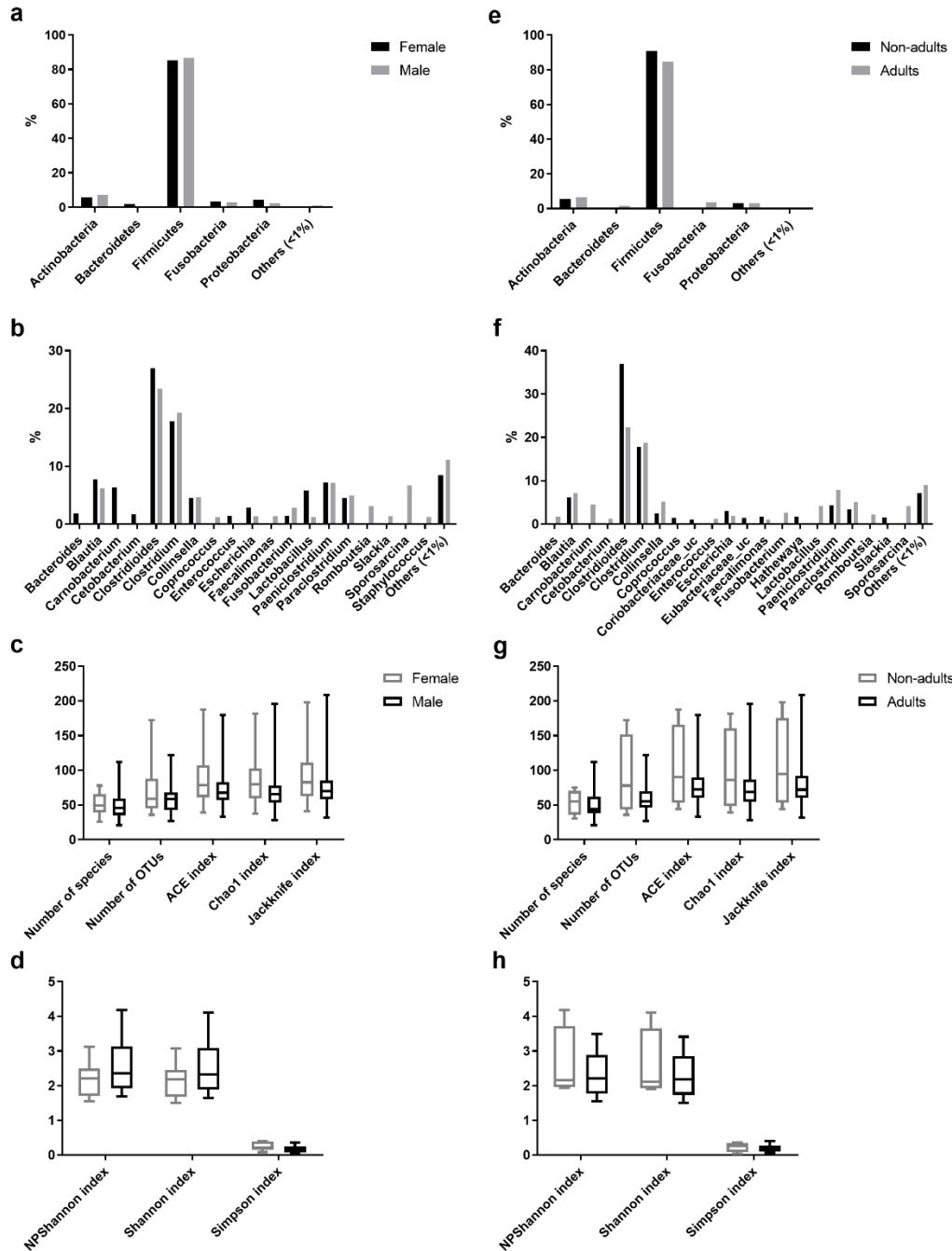


Figure 3. Comparison of the intestinal bacterial microbiota of Egyptian mongoose between sex and age class. **(a)** Relative abundance on a phylum and **(b)** genus level of female and male individuals. **(c)** Species richness (number of species, number of OTUs, ACE, Chao1, and Jackknife indices) and **(d)** species evenness (NPShannon, Shannon, and Simpson indices) of female and male individuals. **(e)** Relative abundance on a phylum and **(f)** genus level of adult and non-adult individuals. **(g)** Species richness (number of species, number of OTUs, ACE, Chao1, and Jackknife indices) and **(h)** species evenness (NPShannon, Shannon, and Simpson indices) of adult and non-adult individuals.

Comparative analysis of OTUs identified in the adult and non-adult intestinal samples found that the majority of OTUs were shared across individuals (Fig. 3). Of the 174 different genera identified in the gastrointestinal tract of Egyptian mongoose individuals (including OTUs with <1% relative abundance), 21 were present in >1% relative abundance in at least one subpopulation (adult or non-adult); eight were shared between age classes; eight were unique to the adult hosts (*Bacteroides*, *Carnobacterium*, *Cetobacterium*, *Enterococcus*, *Fusobacterium*, *Lactobacillus*, *Romboutsia*, and *Sporosarcina*),

and five unique to the non-adult hosts (*Coprococcus*, *Coriobacteriaceae*_uc, *Eubacterium*_uc, *Hathewaya*, and *Slackia*) (Fig. 3f). Besides, similar proportions of phyla and genera were observed. However, Bacteroidetes and Fusobacteria were uniquely found in the gastrointestinal tract of adults (Fig. 3e).

3.3. Estimation of alpha diversity indices

Among the species richness indices, ACE, Chao1, Jackknife, and the number of OTU were estimated. ACE and Chao1 are only sensitive indicators to rare OTUs, and Jackknife is also sensitive to abundant OTUs, with higher values indicating higher diversity [24,25,27]. Besides the difference in sensitivity, all species richness indicators showed similar values for all fecal samples (Fig. 1c) and no significant differences across sex (Fig. 3c) and age (Fig. 3g) were found, suggesting low variability across this Egyptian mongoose population sample.

Among the species evenness indices, Shannon, Simpson, and NPSHannon, were estimated. The Shannon and Simpson indicators are the most commonly used in microbial community studies, with the first displaying values higher than 0, and the maximum value corresponding to an equal distribution among all species present [28]. The second displays the probability of two randomly selected sequences belonging to the same species and uses this as a *proxy* to define even populations as the ones showing lower values [28]. NPSHanon is a non-parametric estimation of the Shannon index and takes into consideration undetectable species and species of unknown abundance in a given sample [26]. Besides individual differences in considered variables, all species evenness indicators showed similar values across all fecal samples (Fig. 1d). No significant differences across sex (Fig. 3d) and age (Fig. 3h) were found, suggesting, once again, limited variability across this Egyptian mongoose subpopulation.

Besides these estimators, rarefaction and rank abundance curves were also plotted. The rarefaction curve is the correlation between the number of reads and the number of OTUs and the steeper the slope, the higher the diversity [29]. Rarefaction curves show a good depth of sequence coverage, with curves beginning to level off after 1500 reads (Supplementary Fig. 1). The rank abundance curve is the correlation between the rank of OTUs and the relative abundance of OTUs at each rank and the steeper the slope, the lower the diversity [30]. Rank abundance curves obtained from the OTU list evidence low species evenness across all fecal samples, indicated by the relatively steep, meaning a greater abundance of high-ranking species comparing to low-ranking' (Supplementary Fig. 2).

3.4. Comparison between subpopulations using beta-diversity analysis

The beta-diversity analysis helps to assess the relationship of microbial communities of different subpopulations. This can be performed using different metrics to calculate the dissimilarity/distance matrix, such as UniFrac, Generalized UniFrac, Bray-Curtis, and Jensen-Shannon. UniFrac is a distance measure obtained from the comparison between microbial communities based on the phylogenetic analysis of their OTU [31]. Generalized UniFrac distance unifies the weighted and unweighted UniFrac, correcting their limitations by decreasing the importance given to either abundant or rare OTUs, respectively [32]. Bray-Curtis dissimilarity measure is obtained comparing the counts of each OTU in different communities [33]. Jensen-Shannon distance is the square root of the Jensen–Shannon divergence and is based on the comparison of the probability distribution of two microbial communities [34]. These dissimilarity/distance matrices can be used in an ordination analysis (such as Principal Coordination Analysis (PCoA)) or clustering in a hierarchical analysis.

Besides numerical differences in the PCoA obtained from the different metrics, samples clustered in a similar way, with samples clustering throughout the plot and with no clear differentiation between host sex (Supplementary Fig. 3) or host age-class (Supplementary Fig. 4), suggesting a comparable phylogenetic diversity across all fecal samples, on a bacterial genus level. However, the fecal samples from non-adult individuals seem to be plotted in close proximity, suggesting a similar phylogenetic diversity. The hierarchical analysis using UPGMA agglomeration metric shows similar dendrograms between UniFrac and Generalize UniFrac (Supplementary Fig. 3c, 3f and Supplementary Fig. 4c, 4f), and between Bray-Curtis and Jensen-Shannon (Supplementary Fig.

3i, 3l) and Supplementary Fig. 4i, 4l), but they were different between them. The observed clusters do not group intestinal samples according to host sex or age class, reinforcing the idea of a comparable phylogenetic diversity. PERMANOVA results show no significant difference between bacterial gut microbiota of male and female hosts and between non-adult and adult hosts (Supplementary Table 2).

3.5. Taxonomic biomarker discovery

To assess the taxonomic biomarkers of male, female, adults, and non-adults, a Kruskal-Wallis H test was performed. Regarding sex (Supplementary Table 3), only two genera and three species were significantly more abundant ($p\text{-value}=0.03$) in male mongooses when compared to female mongooses, and one species was significantly more abundant ($p\text{-value}=0.03$) in female mongooses when compared to male. Regarding age class (Supplementary Table 4), one class ($p\text{-value}=0.034$), two orders ($p\text{-value}=0.034$ and 0.048), six families ($p\text{-value}=0.003$ to 0.054), 24 genera ($p\text{-value}=0.004$ to 0.051), and 53 species ($p\text{-value}=0.004$ to 0.055) were significantly more abundant in non-adult mongoose when compared with adult.

3.6. Functional biomarker discovery

To predict the differential functional profile of female, male, adults, and non-adults, a LEfSe analysis was performed. LEfSe identifies units that are highly associated with a group in a dataset, using a non-parametric statistical test and estimating a size effect score for each differentially abundant feature, using linear discriminant analysis [35]. The functional analysis can be based in three KEGG categories: orthology, module, or pathway [36]. Regarding sex (Supplementary Table 5), 23 orthologs ($p\text{-value}=0.007$ to 0.051), two modules ($p\text{-value}=0.029$ and 0.035), and three pathways ($p\text{-value}=0.037$ to 0.054) were significantly different in abundance, with seven orthologs and one pathway being significantly more abundant in samples of female individuals, and 16 orthologs, two modules, and two pathways being significantly more abundant in samples of male individuals. Regarding age class (Supplementary Table 6), 19 orthologs ($p\text{-value}=0.006$ to 0.049), one module ($p\text{-value}=0.038$), and one pathway ($p\text{-value}=0.048$) were significantly different in abundance, with four orthologs and one module being significantly more abundant in samples of adult individuals, and 15 orthologs and one pathway being significantly more abundant in samples of non-adult individuals.

3.7. Abiotic and biotic data integration

For microbiota and bio-environmental data integration, we performed a Principal Component Analysis (PCA) integrating 35 variables, including 16 abiotic factors. Land-use, temperature, rainfall, river net, and road net, were the more influential on gut microbiota of Egyptian mongoose (Fig. 4). Additionally, several biotic factors were also tested ($n=19$), with reptiles and mammals stomach content and all biometric factors tested (body weight (BW), snout-tail length (STL), tail length (TL), head and body length (HBL), right hind leg length (RHLL), right hind foot length (RHFL), shoulder height (SH), neck perimeter (NP), head diameter (HW), head width (HW), spleen weight (SW), kidney weight (KW), solid fat index (SFI), and perivisceral fat index (PFI)) being the more influential on bacterial microbiota of Egyptian mongoose' gut (Fig. 5).

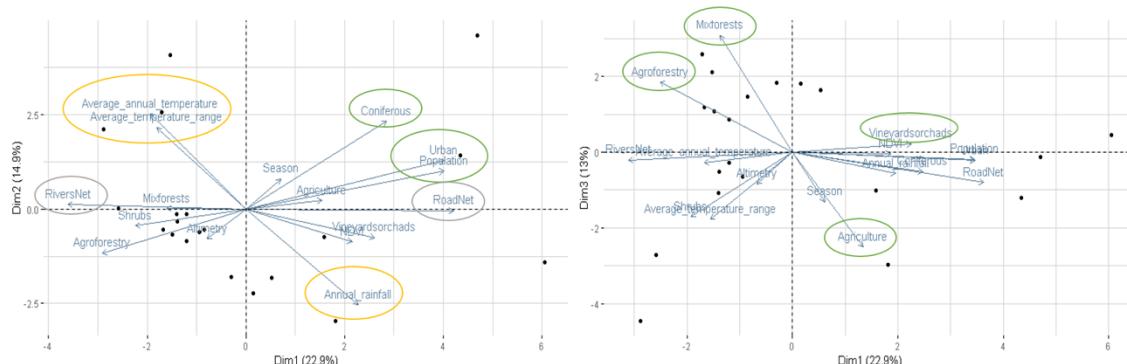


Figure 4. Interaction between bacterial gut microbiota and abiotic factors of Egyptian mongoose. Principal Component Analysis using environmental variables related to land-use, and climatic, topographic, and population data. The more influential factors are delimited using different colors: green – land-use; yellow – climatic data; grey – topographic data.

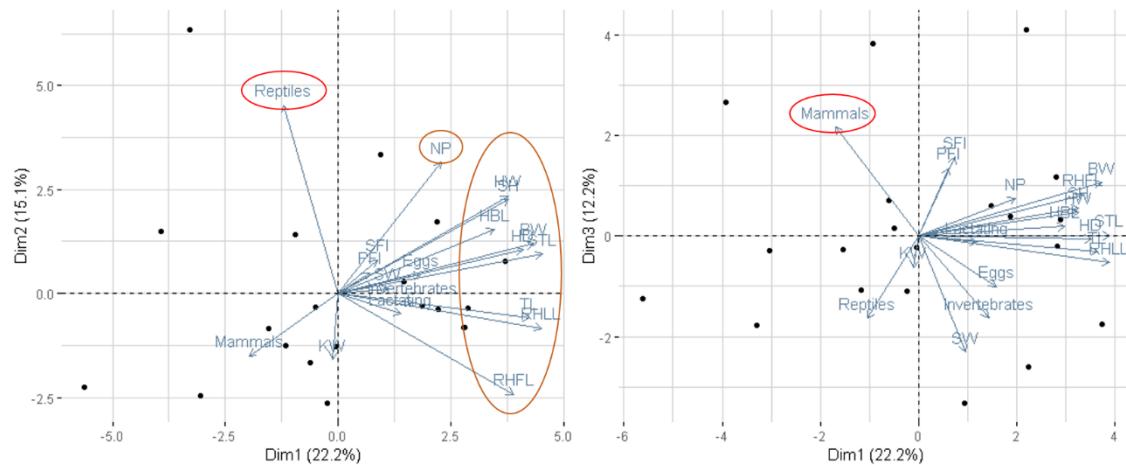


Figure 5. Interaction between bacterial gut microbiota and biotic factors of Egyptian mongoose. Principal Component Analysis using biological variables related to stomach content at the time of death and different body measurements. The more influential factors are delimited using different colors: red – stomach content; brown – biometric data.

4. Discussion

Gut microbiota is nowadays an interdisciplinary and central research topic due to its recognized importance in shaping mammal's biology. In this study, we generated an extended sequence library of the gut microbiota of Egyptian mongoose, highlighting sex- and age class-related differences on taxonomic and functional levels. To accomplish this level of information on the gut microbiome of this carnivore species, a culture-independent approach was used to complement the first insights generated by previous culturomic-based studies [15,16]. This phylogenetic marker gene strategy reinforced the notion that the gut microbiota of Egyptian mongoose adult population is remarkably dominated by Firmicutes (*Blautia*, *Clostridioides*, *Clostridium*, and *Lactobacillus*), followed, in markedly lower proportions (in decreasing order), by Actinobacteria (*Collinsella*), Fusobacteria (*Fusobacterium*), and Proteobacteria (*Escherichia*). The recovery of these taxa was not totally unexpected. Firmicutes are one of the most abundant bacterial phyla in the mammalian gastrointestinal tract, assuring protein degradation, the preservation of gut homeostasis and host immunity development [37]. Within Firmicutes, Clostridia members represented 66% of the bacterial gut microbiota of Egyptian mongoose. Their ability to breakdown carbohydrates and proteins and to promote nutrient absorption [38] place these proteolytic bacteria as central within mammal microbiota [39] under the presence of high-protein content diet [38,40]. Detection of these and other bacterial phyla in our study is consistent with the carnivorous diet of Egyptian mongoose [10,41]. Also in agreement was the detection of the Fusobacteria phylum, particularly *Fusobacterium* spp. that ferment carbohydrates and amino acids, producing a variety of organic acids, such as acetic, formic, and butyric acid [37] and short-chain fatty acids, which account for host energy sources and regulate the glucose, cholesterol, and fatty acid metabolisms [42]. The Bacilli members, like *Lactobacillus* spp., which are also reported in the vertebrates' gut [43], enclosing prebiotic and probiotic activities [44], were also disclosed in mongoose' gut. Interestingly, the Actinobacteria phylum members that are usually a minor fraction of the gut microbiota of mammals [37] were in this study the second most represented phyla. *Collinsella*, previously correlated with the human lipid metabolism [45], was the most prevalent genus within that phylum and is probably related to a high-fat diet, reinforcing, once again, the consistency of our findings with the carnivorous dietary patterns of Egyptian mongoose. Proteobacteria members,

and particularly Enterobacteriaceae such as *Escherichia* spp., were also found. These are common commensals in mammals, with extremely diverse metabolism, that include the ability to breakdown and ferment complex sugars and produce vitamins [37]. They have been reported as predominant in other Carnivora members, such as grizzly bears and giant pandas [38,46,47]. A high ratio of Proteobacteria/Bacteroidetes (calculated ratio of 3) was evident in the Egyptian mongoose samples surveyed. This finding has been previously related with a carnivorous or scavenger diet, namely in carnivores like cheetah, Tasmanian devil, spotted hyena, and polar bear [48], and also with a very efficient harvest of energy [49].

A previous study by our group using culture-dependent methods followed by 16sRNA gene sequencing of selected isolates was performed upon the same 20 Egyptian mongoose specimens surveyed in this work [15]. The detection of the phyla Firmicutes (67%), Proteobacteria (32%), and Actinobacteria (1%) was registered, enclosing twenty genera. Strikingly, *Delftia*, *Ralstonia*, *Rummelibacillus*, *Stenotrophomonas*, *Pantoea*, *Solibacillus*, and *Robinsoniella* genera were exclusively found when using a culture-dependent approach. The disparities between the data generated by both methods can be caused by the length of the 16S rRNA gene sequence used to identify the bacterial isolates in the former study, which sometimes were of shorter length, possibly leading to taxonomic misidentification. Culture-independent approaches have a minimum sequence concentration threshold, which could explain the lack of detection of poorly represented OTUs. This limitation can be overcome by culture-dependent and taxonomical enrichment approaches [50]. Discrepancies between culture-dependent and culture-independent methodologies are frequently reported by others [51-54].

Regarding sex-related differences, the male-specific bacterial groups detected here were the *Faecalimonas* genus that is usually found in the mammalian gut [55,56], the *Romboutsia* genus that is normally described in humans and rats [57,58], and the *Sporosarcina* genus typically found in birds [59]. Female-specific taxa comprised *Carnobacterium*, *Enterococcus*, and *Cetobacterium* genera, together with Bacteroidetes. The first genus was previously detected in food (fish, meat, and some dairy products) and natural environments (sediments and water) [60], however, to our knowledge, *Carnobacterium* spp. has only been identified in the gastrointestinal microbiota of Egyptian mongoose both by sequence-dependent and -independent methods [15,16]. Detection of enterococci is in agreement with other works on wild animals conducted in Portugal, particularly carnivores [15,61-63]. *Cetobacterium* genus is commonly found in the intestines of freshwater fish species [64-66], human [67], and dog feces [68]. This genus has the ability to ferment peptides and carbohydrates and to produce vitamin B12 that can be absorbed by the host [66,67]. Bacteroidetes are cosmopolitan bacteria, being one of the most frequently found members of mammals' gastrointestinal microbiota [37]. These bacteria have the ability to degrade proteins and carbohydrates. The fermentation of these compounds releases short-chain fatty acids [37,69]. Also, they can interact with the immune system of the host activating T-cells and protecting the gastrointestinal tract from pathogenic bacteria [70], although some sporadic reports of opportunistic infections are also available [71].

In our previous culture-dependent study [15], the microbial load of intestinal samples seeded in a rich medium under anaerobiosis was higher in females than in males, as indicated by aerobic/anaerobic vegetative and sporobiota communities. Also, *Paeniclostridium* spp., *Pantoea* spp., *Sporosarcina* spp., *Solibacillus* spp., and *Stenotrophomonas* spp. isolation was restricted to female individuals, while *Paenibacillus* spp., *Propionibacterium* spp., *Robinsoniella* spp. and *Staphylococcus* spp. were only isolated from males.

Regarding the taxonomic biomarker discovery analysis, we detected a significantly higher abundance of *Kocuria* spp., *Hathewaya* spp., and *Clostridium haemolyticum* in male samples. *Kocuria* genus is a typical initial gut colonizer and normally found in the intestine but more typically present on other mucosae of mammals [72]. *Clostridium haemolyticum* is the causative agent of bacillary hemoglobinuria mostly occurring in cattle [73]. Female samples showed a significantly higher abundance of *Clostridium mediterraneense*, a recently discovered species isolated from the human gut in France [74]. Besides these compositional differences, the beta-diversity analysis showed no statistically significant differences across sex. Compositional sex-differences in gut microbiota could

be the result of dietary, behavior and/or host physiology distinctions. And, in fact, previous studies exploring biometric, diet and splenic data of Egyptian mongoose from the same biogeographic region found dietary and immune system differences across sex [2,75]. Other studies in primates have also shown sex-specific bacterial microbiota frameworks [76-78].

Regarding age-related differences, several main bacterial groups were absent from non-adults, while *Coprococcus* genus was specifically associated with this age class, as was *Slackia* spp. previously found in gut samples from porcupine, beaver, coyote, and Arctic Wolf [79]. Besides the latter, other members of Coriobacteriaceae are common mammalian symbionts, responsible for the conversion of bile salts and steroids and activation of polyphenols [80]. Moreover, *Eubacterium* and *Hathewaya* genera were also confined to non-adult specimens. The presence of these species can indicate an increased digestive and absorptive capacity, promoting an increase in weight and size, essential for the normal development of juvenile and an increase in the immune system capacity when reaching the adult period, due to an increase of vitamin production and the interaction of bacterial-epithelial cells in the gastrointestinal tract.

Reinforcing these notions, the taxonomic biomarkers discovery analysis detected a significantly higher abundance of Tissierellia and Clostridia classes, Erysipelotrichales order, Eubacteriaceae, Cellulomonadaceae, Rikenellaceae, and Peptoniphilaceae families in non-adult samples. Tissierellia members have been previously detected on the gut microbiota of Canadian mink [81] and humans [82,83]. Erysipelotrichales members were associated with lipidemic profiles of human hosts, probably associated with high-fat content diets [84], together with Rikenellaceae members [85]. Eubacteriaceae bacteria have been reported as major members of the gut microbiota of Forest Musk Deer [86]. Cellulomonadaceae are considered probiotic species that can convert cellulose into other metabolites [87]. Peptoniphilaceae was reported in the gut microbiota of children [82] and women [88]. Besides compositional differences, the beta-diversity analysis also showed no statistically significant differences across age classes of Egyptian mongoose. In contrast, results from the culture-dependent methodology [15] evidenced similarities between adults and juveniles, with sub-adults clustering separately. This common framework for adults and cubs was attributed to the social behavior of the species that rely on the protection and feeding of the cubs, scent marking and social latrines [14]. This higher proximity and interaction between adults and juveniles can increase diet similarity and fecal-oral transmission of microbiota [14]. This phenomenon was previously reported in mice, birds, and humans [56].

For the first time, the differential functional profile of the Egyptian mongoose population was evaluated. Male Egyptian mongoose shows a significantly higher abundance of catabolic pathways of valine, leucine, and isoleucine amino acids. This degradation is usually performed by members of the Clostridia class [89], such as *Coprococcus*, *Faecalimonas*, and *Romboutsia* genera, which are more abundant in male gut microbiota. Male microbiota also had a significantly higher abundance of tryptophan metabolism pathways. This metabolic route is usually conducted by *Peptostreptococcus* spp., *Lactobacillus* spp., and *Clostridium* spp. [90]. Male individuals did have an overrepresentation of closely related members of *Peptostreptococcus* (i.e. *Romboutsia*). In contrast, female microbiota shows an overrepresentation of closely related members of *Lactobacillus* (i.e. *Carnobacterium* and *Enterococcus*). Male hosts also revealed a significantly higher abundance of citrate cycle modules in their microbiota. The citrate cycle includes several amino acid metabolites, such as valine, leucine, isoleucine, and tryptophan, all of them having their synthesis differentially functioning in the bacterial community of the male gut. Female mongoose exhibited a significantly higher abundance of galactose metabolic pathways, normally performed by *Bacteroides*, in particular, *Bacteroides vulgaris* [91], which is usually overrepresented in female hosts. These findings suggest that the bacterial gut of Egyptian mongoose is modulated by sex-specific strategies to produce energy.

In adult Egyptian mongoose, cationic antimicrobial peptide (CAMP) resistance genes were significantly overrepresented, specifically the dltABCD operon of Gram-positive bacteria. CAMP are short peptides secreted by immune and epithelial cells in response to bacterial products, such as lipopolysaccharide (LPS) or other inflammatory signals [92]. The resistance to CAMP enables bacterial virulence and resistance to innate immunity mechanisms, increasing immune evasion [92].

This finding may indicate the presence of opportunistic pathogenic bacteria in the bacterial community of the adult's gut, even though no signs of disease could be perceived during necropsy. Also, no high percentage of opportunistic pathogenic Gram-positive bacteria could be found. In non-adult Egyptian mongoose, two-component systems associated with antibiotic synthesis, flagellin production, chemotaxis control, and biofilm formation genes, were significantly overrepresented. All these processes are related to bacterial virulence and pathogenesis, which may indicate an overrepresentation of opportunistic bacteria in the gut of juvenile Egyptian mongoose, possibly enabled by an immature immune system, even though signs of disease were not perceived.

Abiotic and biotic factors such as land-use, climatic and topological data, feeding, and biometric data were found to exert an influence in the bacterial gut of Egyptian mongoose. The effect exerted by abiotic factors on mammalian microbiota, such as alterations in native habitat, has been reported by others [93]. Shifts in land-use and topography that cause shifts in food availability, quality, or composition have been described to impact the gut microbiome [94–96]. Temperature and rainfall can affect bacterial microbiota by directly altering environmental microbial communities and indirectly by inducing changes in primary production and host physiology [97–99]. Biotic factors such as host biometry can modify bacterial abundance and diversity, being associated with host health [96]. Other intrinsic host-associated factors, such as diet, and extrinsic features, such as land-use and climatic changes, can both lead to gut microbiota adaptations as a result of Egyptian mongoose expanding range across environmental gradients [8].

5. Conclusions

This study represents the first description of the Egyptian mongoose gastrointestinal microbiota using culture-independent methods, improving our knowledge on the bioecology of this species. It leads to a better understanding of an until now poorly characterized carnivore, together with a sex and age class comparative analyses, that help to assess the indirect effects exerted by host behavior, diet, reproduction, and other biological characteristics on gut microbiota composition and function. Altogether, our results also reinforce the need to use a combination of both culture-dependent and culture-independent strategies when the aim is to capture the maximum biodiversity across complex samples. Finally, our efforts emphasize the value of microbiome studies to fully comprehend mammal species ecology in light of behavior, diet, and geographic features.

Supplementary Materials: The following are available online at www.mdpi.com/xxx/s1, Table S1: Data of read analysis for the 20 intestinal samples of Egyptian mongoose specimens. Table S2: PERMANOVA test results of the microbial community of Egyptian mongoose comparison between female and male and between non-adult and adult. Table S3: Taxonomic biomarkers discovery of female and male Egyptian mongoose fecal bacterial microbiota using a Kruskal-Wallis H test. Table S4: Taxonomic biomarkers discovery of non-adult and adult Egyptian mongoose fecal bacterial microbiota using a Kruskal-Wallis H test. Table S5: Functional biomarkers discovery of female and male Egyptian mongoose fecal bacterial microbiota applying a LEfSe analysis. Table S6: Functional biomarkers discovery of non-adult and adult Egyptian mongoose fecal bacterial microbiota applying a LEfSe analysis. Figure S1: Rarefaction curves for the twenty different fecal samples of Egyptian mongoose measured individuals using the observed species metric. Figure S2: Rank abundance curves for the twenty different fecal samples of Egyptian mongoose individuals using the observed species metric. Figure S3: Beta-diversity analysis to compare the fecal bacterial microbiota, on a genus level, of male and female Egyptian mongoose. Figure S4: Beta-diversity analysis to compare the fecal bacterial microbiota, on a genus level, of adult and non-adult Egyptian mongoose.

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