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Research Article

Gastrointestinal Parasitism and Co-infection Patterns in Quarantined Olive Baboons at the Kenya Institute of Primate Research – Retrospective Analysis (2012–2013)

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ABSTRACT

Gastrointestinal (GI) parasitism remains a major health and welfare concern among captive and quarantined non-human primates (NHPs). This retrospective study assessed the prevalence and patterns of GI parasites among quarantined olive baboons (*Papio anubis*) received between 2012 and 2013 at the Kenya Institute of Primate Research (KIPRE), Nairobi, Kenya. Faecal examination records from both cohorts were reviewed to determine infection prevalence, parasite diversity, co-infection patterns, and associations with host factors (sex, age, and body weight). Results revealed an overall infection prevalence of 98% in the 2012 cohort and 99% in 2013, with protozoan infections predominating (96.0% and 97.2%, respectively). The most frequently detected protozoa were *Entamoeba* spp. and *Balantidium coli*, while strongyles were the dominant helminths. Co-infections were common, affecting over 97% of infected baboons, with triple and quadruple infections accounting for 40% and 25–30% of cases, respectively. No significant associations were found between infection status and sex, age, or weight, suggesting uniform exposure across host groups. The 2013 cohort exhibited a lower helminth prevalence compared to 2012, possibly indicating improvements in quarantine management practices. These findings highlight the persistent challenge of GI parasitism, particularly protozoan infections, in quarantined baboons and underscore the need for targeted parasite control strategies, improved environmental hygiene, and comprehensive health monitoring to enhance animal welfare and reduce zoonotic risks.

Keywords: Co-infection; Gastrointestinal parasites; *Papio anubis;* Protozoa; Quarantine

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INTRODUCTION

Non-human primates (NHPs), particularly olive baboons (*Papio anubis*), are indispensable to biomedical research owing to their close physiological, genetic, and behavioural similarities to humans (Wolfe *et al*., 1998; VandeBerg *et al*., 2009). Their use spans diverse scientific fields including infectious disease modeling, reproductive biology, and neuroscience. However, the health status of these primates, especially with respect to gastrointestinal (GI) parasitism, directly influences animal welfare, the validity of research outcomes, and zoonotic safety (Goldberg *et al*., 2007). Gastrointestinal parasites—comprising nematodes, cestodes, trematodes, and protozoa—are among the most frequently reported pathogens in both wild and captive baboon populations (Tamekloe *et al*., 2004; Larbi *et al*., 2020). Although infections may be subclinical, chronic parasitism can impair nutritional status, immune competence, and physiological performance, ultimately compromising biomedical data integrity (Benavides *et al*., 2012).

Transmission of GI parasites among captive primates typically occurs through the faecal–oral route, with environmental contamination and high population density acting as key perpetuating factors (Ryan *et al*., 2010). At the Kenya Institute of Primate Research (KIPRE), quarantine serves as a critical biosecurity phase during which newly captured or relocated baboons are screened and treated for parasitic infections prior to colony integration (Muchina *et al*., 2020). Despite these preventive measures, persistent and mixed infections remain a challenge (Gunasekera *et al*., 2012). Such persistence raises concerns about the adequacy of current control protocols, potential reinfection from contaminated enclosures, and implications for both animal and human health in the research environment.

Although KIPRE is a major primate biomedical research centre in Africa, few published studies have characterized the baseline patterns of gastrointestinal parasitism among its quarantined olive baboon populations. Understanding infection dynamics at this stage is important, as high parasite burdens and co-infections can alter physiological parameters such as body weight and haematological indices, and may pose zoonotic risks to handlers (Chapman *et al*., 2005). Retrospective analysis of diagnostic records offers a valuable opportunity to identify trends in parasite prevalence and co-infection, while assessing the effectiveness of existing management strategies (Ryan *et al*., 2010; Benavides *et al*., 2012).

This paper represents the first phase of a two-part investigation on gastrointestinal parasitism in olive baboons (*Papio anubis*) at the Kenya Institute of Primate Research. The present retrospective cohort analysis (2012–2013) characterizes the baseline prevalence, species composition, and co-infection patterns of gastrointestinal helminths and protozoa among quarantined baboons, and examines how these vary with host factors such as sex, age, and body weight. The findings aim to establish a foundational dataset for the subsequent prospective phase, which will assess parasite–host interactions under captive colony conditions. By elucidating cohort-specific infection dynamics, this study contributes to the optimization of quarantine health management, enhances data quality in primate-based research, and strengthens One Health strategies addressing pathogen persistence at the wildlife–research interface (Karesh *et al*., 2012).

MATERIALS AND METHODS

Study Design

This study employed a retrospective cohort design, analyzing diagnostic parasitological records of quarantined olive baboons (*Papio anubis*) received at the Kenya Institute of Primate Research (KIPRE), Nairobi, Kenya, in two distinct arrival years — 2012 (n = 101) and 2013 (n = 36). Both cohorts consisted of wild-caught baboons quarantined for health screening and stabilization before potential inclusion in the institute's research colonies.

Study Site

The Kenya Institute of Primate Research (KIPRE) is a biomedical research facility located within Oloolua Forest, Karen, in Nairobi County, Kenya. Oloolua Forest, situated on the outskirts of Nairobi, is a natural tropical forest reserve covering approximately 400 acres of indigenous woodland (Tchouassi *et al*., 2019). The forest provides a relatively undisturbed ecological environment that supports diverse wildlife species, including vervet (*Chlorocebus pygerythrus*) and colobus monkeys (*Colobus guereza*), olive baboons (*Papio anubis*), duikers, bush pigs, waterbucks, hyenas, and various small mammals such as rodents and bats (Meroka *et al*., 2018; Tchouassi *et al*., 2019). It creates a locally moderated microclimate—generally cooler and retaining more moisture than surrounding urban areas—which helps sustain forest fauna and small mammals and buffers temperature extremes associated with built environments (Meroka *et al*., 2018; Ndolo, 2018; Development Corridors Project ESIA, 2023; Dialogue/Earth, 2023). This relatively mild climatic range offers favourable conditions for maintaining non-human primate colonies under semi-natural environments.

Within this forested landscape, KIPRE maintains captive colonies of *Papio anubis* and other non-human primates under controlled conditions for biomedical research (D'Hooghe *et al*., 2008). Quarantine housing facilities consist of individual and group cages with concrete floors, controlled feeding regimens, and structured husbandry protocols designed to minimize stress and disease transmission. Routine veterinary examinations and faecal screening are conducted upon arrival and periodically throughout the quarantine period to monitor and manage parasitic and other infectious diseases (D'Hooghe *et al*., 2008).

Parasitological Examination

Archived parasitology reports for each animal were reviewed. Faecal samples had originally been collected either via rectal swabs or directly from cages and examined using standard parasitological techniques. These included the direct smear and sedimentation techniques for detecting protozoa (Cheesbrough, 2005), and the flotation technique using saturated salt solution for identifying helminth eggs (Zajac and Conboy, 2012). Microscopic examination was conducted to identify parasite ova, cysts, and trophozoites based on morphological features, following established taxonomic keys (Soulsby, 1982).

Data Analysis

Data were organized and analyzed to evaluate patterns of gastrointestinal parasitism among quarantined olive baboons. Records were stratified according to cohort year (2012 vs. 2013), parasite type (helminths vs. protozoa), infection pattern (mono-, dual-, triple-, or multiple infections involving four or more parasite species), and host factors such as sex, age category, and body weight. The compiled dataset was first entered and cleaned using Microsoft Excel before being exported for statistical analysis in GraphPad Instat version 3.05 (32-bit for Windows 95/NT; GraphPad Software Inc., San Diego, CA, USA; copyright 1992–2000). Descriptive statistics were applied to calculate prevalence (%) and frequency distributions of parasite species. Comparative analyses between cohorts and infection categories were conducted using Fisher's Exact Test, which is appropriate for categorical variables with small sample sizes. Odds ratios (OR) and corresponding 95% confidence intervals (CI) were computed to evaluate associations between host factors (sex and age group) and infection status. Variations in body weight across different infection intensity categories were summarized as means ± standard deviation (SD). For all analyses, statistical significance was established at $p \leq 0.05$.

Ethical Considerations

This study utilized archived diagnostic data with no direct animal handling. Data access and retrospective use were authorized by the Animal Science Department, Kenya Institute of Primate Research (KIPRE).

RESULTS

Overall Prevalence of Gastrointestinal Parasites

A total of 137 quarantined olive baboons (*Papio anubis*) were examined across the two cohorts — 101 in 2012 and 36 in 2013. The overall prevalence of gastrointestinal (GI) parasites was high in both cohorts, with infection rates of 98% (99/101) in 2012 and 97.2% (35/36) in 2013. Protozoan infections were more prevalent than helminthic infections across both years.

Among the protozoa, *Entamoeba* spp. was the most prevalent parasite overall, detected in 96.0% of the 2012 cohort and 97.2% of the 2013 cohort. *Balantidium coli* was also common, occurring in 63.4% and 52.8% of baboons in 2012 and 2013, respectively. *Blastocystis* spp. was found exclusively in the 2012 cohort (6.9%), while *Iodamoeba* spp. occurred sporadically in both years, with prevalence rates of 4.0% in 2012 and 2.8% in 2013 (Table 1).

Among the helminths, strongyles were the most prevalent, detected in 85.1% of baboons in 2012 and 47.2% in 2013, indicating a substantial decline in occurrence between the cohorts. *Strongyloides* spp. were identified in 37.6% (2012) and 16.7% (2013), whereas *Trichuris trichiura* appeared infrequently at 4.0% and 5.6%, respectively. Overall, protozoa dominated the parasite spectrum in both cohorts, though helminths remained consistently represented (Table 1).

Co-Infection Patterns

Co-infections were common and represented the dominant infection profile among quarantined baboons in both cohorts. In 2012, 99 out of 101 baboons were infected, with only 2 (2.0%) showing mono-infection. Similarly, in 2013, 35 out of 36 animals were infected, and only 1 (2.8%) had a single parasite species (Table 2). Dual infections occurred in 32.3% of infected baboons in 2012 and 25.7% in 2013, whereas triple infections were the most frequent co-infection type, recorded in 41.4% (2012) and 40.0% (2013). Multiple infections involving four or more parasite species were observed in 24.2% and 31.5% of baboons in 2012 and 2013, respectively, demonstrating a substantial parasitic burden across both cohorts (Table 2).

The most prevalent co-infection pair in both years was *Entamoeba* + strongyles, affecting 80.8% (80/99) of infected animals in 2012 and 62.9% (22/35) in 2013. The next most frequent pairing was *Entamoeba* + *Balantidium coli*, present in 62.6% and 57.1% of infected individuals in 2012 and 2013, respectively. Occasional combinations included *Strongyloides* + strongyles (39.4% in 2012; 22.9% in 2013) and *Balantidium* + *Strongyloides* (28.3% in 2012; 17.1% in 2013). Rare co-infections, such as *Trichuris* + strongyles and *Iodamoeba* + *Entamoeba*, occurred at low frequencies (≤10%) in both cohorts (Table 2).

The maximum co-infection load was comparable between cohorts, with the highest level of mixed infections observed in 2012. Overall, both cohorts exhibited a high degree of parasite diversity per individual, with protozoa forming the central component of most co-infection patterns.

Table 1. Overall Prevalence of Gastrointestinal Parasites in Quarantined Olive Baboons (*Papio anubis*) by Cohort at the Kenya Institute of Primate Research

Parasite Type	Parasite Species	2012 Cohort (n = 101)	2013 Cohort (n = 36)	Overall Observation
Helminths	Strongyles	86 (85.1%)	17 (47.2%)	Most prevalent helminth in both cohorts, though higher in 2012
	Strongyloides spp.	38 (37.6%)	6 (16.7%)	Common co-infection, reduced occurrence in 2013
	Trichuris trichiura	4 (4.0%)	2 (5.6%)	Least frequent helminth, rare in both cohorts
Protozoa	*Entamoeba* spp.	97 (96.0%)	35 (97.2%)	Most prevalent parasite overall across both cohorts
	Balantidium coli	64 (63.4%)	19 (52.8%)	Common intestinal protozoan, frequent co-infection
	Blastocystis spp.	7 (6.9%)	–	Detected only in 2012; occasional infection
	Iodamoeba butschlii / *Iodamoeba* spp.	4 (4.0%)	1 (2.8%)	Rare protozoan; low prevalence in both cohorts

Table 2. Co-infection Patterns among Quarantined Olive Baboons (*Papio anubis*) by Cohort at the Kenya Institute of Primate Research

Parasite Combination	2012 Cohort (n = 101; 99 infected)	2013 Cohort (n = 36; 35 infected)	Observation / Remarks
Single infection (mono-infection)	2 (2.0%)	1 (2.8%)	Rare; majority of baboons had ≥2 parasites
Dual infections	32 (32.3%)	9 (25.7%)	Common; usually *Entamoeba* + strongyles or *Entamoeba* + *Balantidium*
Triple infections	41 (41.4%)	14 (40.0%)	Most frequent pattern in both cohorts
≥ Four infections	24 (24.2%)	11 (31.5%)	High multiple-infection burden, especially with protozoa
Most frequent co-infection pair	*Entamoeba* + strongyles (80/99; 80.8%)	*Entamoeba* + strongyles (22/35; 62.9%)	Consistent dominant pairing
Next most common pair	*Entamoeba* + *Balantidium* (62/99; 62.6%)	*Entamoeba* + *Balantidium* (20/35; 57.1%)	Frequent protozoan association
Occasional combinations	*Strongyloides* + strongyles (39/99; 39.4%), *Balantidium* + *Strongyloides* (28/99; 28.3%), *Entamoeba* + *Blastocystis* (13/99; 13.1%)	Strongyles + *Strongyloides* (8/35; 22.9%), *Balantidium* + *Strongyloides* (6/35; 17.1%)	Variable but recurring mixed infections

Rare co-infections	*Trichuris* + strongyles (5/99; 5.1%), *Iodamoeba* + *Entamoeba* (10/99; 10.1%)	*Trichuris* + *Balantidium* (3/35; 8.6%), *Iodamoeba* + *Entamoeba* (1/35; 2.9%)	Sporadic occurrences
Highest co-infection load	Up to 5 parasite species per host	Up to 5 parasite species per host	Heavy mixed infections more frequent in 2012

Association between Host Factors and Infection Status

Sex

In both cohorts, infection was evenly distributed between males and females. In 2012, 55 males (54%) and 44 females (44%) were infected, with only one non-infected individual in each sex category. Similarly, in 2013, 26 males (72%) and 9 females (25%) were infected, while one male (3%) was non-infected. Statistical analysis using Fisher's Exact Test indicated no significant association between sex and infection status in either cohort ($p = 1.0000$). The calculated Odds ratios (2012: 1.25, 95% CI 0.076–20.57; 2013: 0.93, 95% CI 0.035–24.86) further confirmed the lack of sex predisposition to parasitic infection (Table 3).

Age

Across both cohorts, infection prevalence approached 100% in all age groups, including adults, sub-adults, and juveniles. In 2012, infection rates were 98.3% in adults, 100% in juveniles, and 85.7% in sub-adults. In 2013, infection was 95.7% in adults and 100% in both juveniles and sub-adults. Statistical comparisons revealed no significant differences in infection status across age categories (all $p > 0.05$). Although adults and juveniles in 2012 displayed slightly higher infection rates than sub-adults, these differences were not statistically meaningful (Table 3).

Body Weight

In the 2012 cohort, body weight ranged from 3.2 to 27.2 kg, with an overall mean of 13.2 ± 5.7 kg. Non-infected baboons (n = 2) had a mean body weight of 12.0 ± 1.4 kg, while animals with single to triple infections averaged between 13.5 and 13.7 kg. Those with four or more infections had slightly lower body weight (12.1–10.5 kg), suggesting a possible negative association between heavy polyparasitism and body weight. In 2013, mean body weight varied by infection type: non-infected (16.1 kg), protozoan-only infections (13.08 ± 5.43 kg), and mixed infections (16.97 ± 6.14 kg). Although animals with mixed infections showed somewhat higher mean weights, the differences were not statistically significant (Table 3).

Overall Associations

Across both cohorts, no significant associations were detected between infection status and sex, age, or body weight. Fisher's Exact tests consistently yielded $p > 0.05$, and all Odds ratios had wide confidence intervals overlapping 1.0. Thus, infection appeared to be ubiquitous across host categories, reflecting broad environmental exposure and uniform transmission pressure within the quarantine setting.

Table 3. Association Between Host Factors and Infection Status in Two Cohorts of Quarantined Olive Baboons (Papio anubis) at the Kenya Institute of Primate Research

Host Factor	Category / Comparison	Cohort	Infected (%)	Non-infected (%)	p-value	Odds Ratio (95% CI)	Significance / Remarks
Sex	Male vs. Female	2012	55 (54%) vs. 44 (44%)	1 (1%) vs. 1 (1%)	1.0000	1.25 (0.076–20.57)	NS — infection equally distributed between sexes
	Male vs. Female	2013	26 (72%) vs. 9 (25%)	1 (3%) vs. 0 (0%)	1.0000	0.93 (0.035–24.86)	NS — no sex predisposition observed
Age	Adult vs. Juvenile	2012	57/58 (98.3%) vs. 36/36 (100%)	1 vs. 0	1.0000	0.53 (0.021–13.25)	NS — all age groups highly infected
	Adult vs. Sub-adult	2012	57/58 (98.3%) vs.	1 vs. 1	0.2053	9.50 (0.524–172.2)	NS — slight trend toward

Host Factor	Category / Comparison	Cohort	Infected (%)	Non-infected (%)	p-value	Odds Ratio (95% CI)	Significance / Remarks
			6/7 (85.7%)				higher infection in adults
	Juvenile vs. Sub-adult	2012	36/36 (100%) vs. 6/7 (85.7%)	0 vs. 1	0.1628	16.85 (0.616–460.6)	NS — juveniles fully infected, not statistically significant
	Adult vs. Juvenile	2013	22/23 (95.7%) vs. 5/5 (100%)	1 vs. 0	1.0000	1.36 (0.049–38.27)	NS — similar infection across ages
	Adult vs. Sub-adult	2013	22/23 (95.7%) vs. 8/8 (100%)	1 vs. 0	1.0000	0.88 (0.033–23.86)	NS — infection ubiquitous
	Juvenile vs. Sub-adult	2013	5/5 (100%) vs. 8/8 (100%)	0 vs. 0	–	–	Not testable — complete infection in both groups
Body Weight (kg)	—	2012	3.2–27.2	—	—	—	Mean = 13.2 ± 5.7; weight decreased with increasing parasite load
	Non-infected	2012	n = 2	—	—	—	Mean = 12.0 ± 1.4 kg; relatively higher than heavily infected groups
	Single to triple infection	2012	n = 64	—	—	—	Mean = 13.7–13.5 kg; moderate infection associated with average weight
	≥ 4 infections	2012	n = 35	—	—	—	Mean = 12.1–10.5 kg; heavy polyparasitism linked to lower body weight
	Infection category	2013	Non-infected = 1; Protozoan-only = 13; Mixed = 22	—	—	—	Mean weights = 16.1 kg; 13.08 ± 5.43 kg; 16.97 ± 6.14 kg respectively; no significant difference, though mixed infections tended toward higher mean body weight

DISCUSSION

The present retrospective analysis revealed an extremely high prevalence of gastrointestinal (GI) parasite infection in quarantined olive baboons (*Papio anubis*) at the Kenya Institute of Primate Research (KIPRE), with infection rates exceeding 97% in both the 2012 and 2013 cohorts. This finding is consistent with previous studies in non-human primates (NHPs) in captive or semi-wild settings, which have reported prevalences often >90% (Houmsou *et al*., 2019; Vonfeld *et al*. 2022).

The dominance of protozoan parasites (notably *Entamoeba* spp.) across both cohorts (96.0% in 2012, 97.2% in 2013) underscores the pervasiveness of faecal-oral transmission in the quarantine environment. The observation that protozoa out-numbered helminths echo report in other captive primate collections showing relatively low helminth burdens but widespread protist infections (Marchiori *et al*. 2024). The higher prevalence of helminths in the 2012 cohort compared to 2013 (85.1% vs 47.2% for strongyles) may reflect improved control or environmental changes between years.

Co-infection was the rule rather than the exception: over 97% of infected animals had at least two parasite taxa, with triple infections accounting for ~40% and ≥4 infections 24–31%. Such high multiparasite burdens are consistent with ecological studies showing that primates often harbour multiple GI parasites simultaneously (Kouassi *et al*., 2015; Friant *et al*., 2016). Complex co-infection patterns — most notably the pairing of *Entamoeba* + strongyles and *Entamoeba* + *Balantidium coli* — likely reflect overlapping transmission pathways (faecal contamination, group-living dynamics) and perhaps compromises in host gut ecology or immunity under quarantine stress. Indeed, co-infection may amplify pathology or alter host responses, a point well-documented in the literature (Klaus *et al*., 2017, Obanda *et al*., 2019 and Sirima *et al*., 2021).

No statistically significant associations were found between infection status and sex, age or weight in either cohort. That nearly all age groups and both sexes had similarly high prevalences suggests a uniform exposure risk in the quarantine environment, and aligns with findings in wild baboons where infection was widespread across host categories (Mason *et al*. 2022). The body weight trend in 2012 (lower weights in ≥4 parasite groups) suggests a possible impact of heavy polyparasitism on host condition, although the lack of statistical significance limits conclusions.

The findings have several important implications for primate quarantine programmes and biomedical research. Firstly, the extremely high parasite burden and multi-species co-infection highlight the need for robust screening, treatment, and environmental sanitation during quarantine. Since many protozoa (e.g., *Entamoeba* spp*., Balantidium coli*) and helminths have zoonotic potential, the captive context raises occupational health concerns (Patouillat *et al*. 2024). Secondly, persistent protozoan dominance suggests that standard deworming programmes targeted at helminths may leave protozoan infections unchecked; targeted protocols including protozoa may be warranted. Thirdly, the consequence of high infection and co-infection may compromise animal welfare and research validity: infected animals may experience altered physiology, immune responses, or gut microbial interactions, which can confound biomedical work.

This study is retrospective and relies on archived diagnostic records; thus, parasite intensity (egg/cyst counts), seasonal variation, and environmental contamination data were not available. The cohort reduction in helminth prevalence from 2012 to 2013 hints at improvements but cannot be causally attributed. Future work should include longitudinal monitoring, molecular characterisation of the parasites (including zoonotic genotypes), and assessment of risk factors such as housing density, hygiene protocols, diet, and stress. Also, investigations of how parasite burden influences specific physiological or immunological endpoints in quarantined baboons would strengthen the translational relevance.

CONCLUSION

In summary, the 2012 and 2013 arrival cohorts of olive baboons at KIPRE showed extremely high GI parasite prevalence, heavy multiparasite burdens, dominance of protozoa, and minimal variation by host demographic factors. These results underscore the challenge of intestinal parasitism in captive primate settings and call for enhanced quarantine health management to safeguard animal welfare, research quality, and zoonotic safety.

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