Higher body condition with infection by *Haemoproteus* parasites in Bananaquits (*Coereba flaveola*)

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Abstract

Parasite transmission is a heterogenous process in host-parasites interactions, being particularly important for vector-borne diseases where the vector adds an additional level of heterogeneity. Haemosporidian parasites, a widespread protist, cause a malaria-like disease in birds globally, but we still have much to learn about the consequences of infection to hosts' health. In the Caribbean, where malarial parasites are endemic, studying host-parasites interactions may give us important insights about energetic trade-offs involved in malarial parasites infections in birds. In this study, we tested the consequences of *Haemoproteus* infection on the Bananaquit, a resident species of Puerto Rico. We also tested for potential sources of individual heterogeneity in the consequences of infection such as host age and sex. To quantify the consequences of infection to hosts' health we compared three complementary body condition indices between infected and uninfected individuals. Our results showed that Bananaquits infected by *Haemoproteus* had higher body condition than uninfected individuals. This result was consistent among the three body condition indices. Still, we found no clear evidence that this

25 effect was mediated by host age or sex. We discuss a set of non-mutually exclusive hypotheses

26 that may explain this pattern including metabolic syndrome, immunological responses leading to

27 host tolerance or resistance to infection, and potential changes in consumption rates. Overall, our

28 results suggest that other mechanisms, may drive the consequences of avian malarial infection.

29 *KEYWORDS:* Birds, Caribbean, heterogeneity, haemosporidian, Puerto Rico, virulence.

30 **Introduction**

31   Virulence, or host fitness reduction as a consequence parasite infection, is often viewed

32 as an unavoidable cost for the parasite that reproduces at the expense of host resources (Bull

33 1994, Ewald 1994). This traditional understanding of the eco-evolutionary consequences of

34 parasite infection comes from theoretical models that make simplifying assumptions such as

35 homogeneous transmission (Anderson and May 1982, Alizon et al. 2009). Still, in nature,

36 parasite transmission is a heterogeneous process (VanderWaal and Ezenwa 2016). Variability in

37 parasite transmission strategies, individual traits (i.e., host immunity), and environmental factors

38 may interact in complex ways resulting in a wide array of host virulence patterns (Acevedo et al.

39 2019). This complexity is particularly true in vector-borne parasite systems where infected

40 vectors are the agents of transmission that interact with the host in heterogeneous environments

41 while finding competent hosts (Lachish et al. 2011, Acevedo et al. 2019).

42   Haemosporidian parasites (Order Haemosporida, genera *Plasmodium, Haemoproteus*,

43 *Parahaemoproteus*, and *Leucocytozoon*) are worldwide protists infecting birds of different

44 families, causing a malaria-like disease (Valkiunas 2014). The impacts of these parasites on bird

45 host fitness are generally not well understood with empirical research showing mixed results

46 (e.g., Moller et al. 2009, LaPointe et al. 2012, Cornet et al. 2013, Ilgunas et al. 2019, Videval et

47 al. 2020). Malarial parasites may cause detrimental effects on hosts, such as increasing mortality,

48 and decreasing overall body condition (e.g., Atkinson et al. 1995). On the other hand,

49 particularly where haemosporidian parasites are endemic, there might not be any negative

50 reported effects to the hosts (e.g., Bensch et al. 2007). Multiple mechanisms have been proposed

51 to explain this lack of negative fitness consequences including immunological strategies such as

52 tolerance and resistance (Sorci 2013). Within these strategies, strong negative fitness costs are

53 avoided because the host clears the infection (resistance) or has developed an immune response

54 that allows it to withstand infection (tolerance).

55   Haemosporidian parasites may have different effects depending on the age and sex of

56 individuals, such that juveniles tend to develop a more severe infection, and even have higher

57 mortality compared to adults (Isaksson et al. 2013). For instance, juvenile feral pigeons infected

58 with *Haemoproteus columbae* are more likely to have increased infection levels and higher

59 mortality than adults (Sol et al. 2003). The naïve immune system of juveniles can be more

60 susceptible to infection leading to higher within-host replication rates and higher virulence

61 (Padgett and Glasser 2003, Calero-Riestra & Garcia 2016, Hammers et al. 2016). In sex-

62 dependent studies, infected female Tawny pipits had reduced body condition compared to

63 infected male Tawny pipits (Calero-Riestra & Garcia 2016). This may be related to higher

64 reproductive costs for females compared to males during the breeding season. Still, this pattern

65 sex-mediated costs of infection is not necessarily generalizable. A recent meta-analysis shows no

66 clear difference in parasite virulence among males and females (Hasik and Siepielski 2022).

67   In this study, we assessed the consequences of infection by avian malarial parasites on

68 host body condition in the most abundant bird species in Puerto Rico and the Caribbean, the

69 Bananaquit (*Coereba flaveola*). Specifically, we asked: (1) do *Haemoproteus*-infected

70   individuals suffer from reduced body condition when compared to uninfected individuals? and 2)

71   are related changes in body condition dependent on age or sex? We expected, following

72   predictions from the classical theory, that infected individuals would have lower body condition

73   and that this effect would be more pronounced in juveniles and mediated by sex. If body

74   condition decreases with infection, it would provide evidence of negative consequences of

75   endemic malarial parasites as predicted by the classical theoretical models and recent syntheses

76   (Alizon et al. 2009, Hasik and Siepielski 2022). If not, it may suggest that other eco-

77   evolutionary mechanisms are at play.

Materials & Methods

79   The Caribbean has been proposed as an ideal natural laboratory to study the ecology and

80   evolution of vector-borne parasite-host interactions (Ricklefs et al. 2016). In the Caribbean,

81   malaria parasites are endemic, and host species diversity is low, but many species are generalists

82   occupying a wide variety of habitats (Acevedo and Restrepo 2008). These factors create a unique

83   set of conditions for host-parasite co-evolution. While multiple studies describe the

84   biogeographic patterns of malaria parasites of Caribbean bird hosts (e.g., Fallon et al. 2004,

85   Ricklefs et al. 2016), our understanding of the potential health consequences of malaria infection

86   to Caribbean bird hosts is limited.

87   We conducted the study from June 2018 to January 2019 in 13 urban forest patches (each

88   site was visited 1–4 times, Table SI) in the metropolitan area of Puerto Rico, an urbanized area

89   that comprises 10% of the island (Fig. S1; Table S1) (Martinuzzi et al. 2007). In Puerto Rico,

90   Bananaquits breed throughout the year with increased reproductive activity between February

91   and June (Wunderle 1982). We chose Bananaquits (*Coereba flaveola*) as our study species

92   because it is the most abundant species in urban forests in the Caribbean and previous studies

93   show that *Plasmodium* and *Haemoproteus* parasites commonly infect this species (Wolff et al.

94   2018, Antonides et al. 2019). Note that, while we use the basal genus *Haemoproteus* to describe

95   the parasites in this study, it is likely that these lineages belong to the *Parahaemoproteus*

96   subgenus (Martinsen et al. 2008). All bird handling procedures were conducted with approval of

97   the Institutional Animal Care and Use Committee (IACUC) of the University of Puerto Rico

98   protocol number 3011-02-05-2018, the USGS Federal Bird Banding Permit number 21669, and

99   the Department of Natural and Environmental Resources of Puerto Rico permit number 2018-IC-

100 066. All individuals in this study were captured using 2.5m x 6m and 2.5m x 12m mist nets. We

101 used 4 to 8 mist nets per sampling period. Nets were opened by sunrise and closed between 8:30-

102 10:00 AM depending on sunlight, weather, or presence of raptors. Upon capture, we aged and

103 sexed individuals using standard procedures such as visual inspection of cloacal protuberance,

104 brood patch, and skull pneumatization (Ralph et al. 1993). Individuals with a defined brood

105 patch were classified as female and individuals with a prominent cloacal protuberance were

106 classified as males (Ralph et al. 1993). Bananaquits are difficult to sex and/or age due to their

107 monomorphic plumage. We measured wing length and tarsus length as parameters for body

108 condition index to the nearest 0.1 mm (Wunderle 1994). Also, we measured bird body mass as

109 another parameter for body condition index to the nearest 0.1 g to estimate residual body

110 condition indices. After taking measurements and extracting a small blood sample, we released

111 all the individuals back to their habitat.

112   To diagnose infection status, we extracted 10–30 µl of blood from the brachial vein

113 which we collected on filter paper and stored at 20°C. We extracted DNA from the blood

114 samples using DNeasy Blood & Tissue Kit (Qiagen) and a nested PCR to amplify possible

115 parasite sequences present in the avian host species. We used two sets of primers, the Haem

116   primers and the MalUniv primers (S. Perkins, unpublished data) to increase the probability of

117   detection (Fallon et al. 2003, Hellgren et al. 2004). We used the diagnostic standard protocol

118   established by Hellgren (2004). For Mal Univ, we used 10 µl of TopTaq Polymerase, 1 µl of

119   MalUnivF primer, 1 µl of MalUnivR primer, 2 µl of coral load, 5 µl of nuclease-free water, and

120   1 µl of DNA template per reaction (SI Article). Positive samples were detected when a band

121   appeared in the electrophoresis gel at 500 bp and negative when no band was found (Figure 1A).

122   We purified positive samples using the Qiagen PCR purification kit. Positive samples were

123   sequenced using the Sanger Sequencing Service at the Sequencing and Genotyping Facility

124   (University of PR, Rio Piedras). We analyzed the sequence using Mega X software (Kumar et al.

125   2018) and then used the BLAST database (https://blast.ncbi.nlm.nih.gov/Blast.cgi) to determine

126   the parasite genus. Then, we extracted the results that had 97% or more identification accuracy to

127   identify the avian malaria parasite genus. All the infected were classified as *Haemoproteus*,

128   *Plasmodium*, or as unclassified positive when we could not classify them based on the base pairs

129   in the sequence. Given the limited number of *Plasmodium*-infected individuals (n=3), we

130   restricted our analysis to *Haemoproteus* infections.

131   **Statistical Analysis**

132   To test if body condition decreased with infection by *Haemoproteus*, we quantified three

133   types of body condition indices, two residual indices of body mass and a body size measurement,

134   and a Principal Components Analysis (PCA). All the statistical analyses were conducted using

135   the infection status results from molecular diagnostics. We used a residual body condition index

136   by analyzing residuals of a linear relationship between natural log body mass predicted by

137   natural log wing length, and the linear relationship between natural log body mass predicted by

138   natural log tarsus length (SI Article). Residual indices describe body condition as a function of

139   the relationship between body length and mass (Peig & Green 2010). The residual is the

140   difference between the observed and predicted values (Larsen & McCleary 1972). Individuals

141   with residuals above zero are considered to have higher body condition than average and

142   individuals with residual values below zero have poorer body condition than average. These

143   body condition indices are commonly applied in similar studies to assess the consequences of

144   malaria parasites on birds' health (e.g., Brock et al. 2013, Marzal et al. 2015).

145   We also tested for a decrease in body condition by avian malaria infection using a

146   principal component analysis (PCA) which synthesizes multiple correlated variables such as

147   mass, wing length, and tarsus length into correlated axes (Peig & Green 2010). In the PCA, the

148   data were scaled and centered. We used the PC1 loadings as an index of body condition because

149   PC1 explains most of the variance compared to other axes (see results section). This type of

150   analysis is commonly applied to assess the potential negative effects of infection on hosts' health

151   (e.g., Hatchwell et al. 2001). Still, some studies suggest caution when applying body condition

152   indices because these are highly dependent on the body measurements used to calculate the index

153   (Sánchez et al. 2018). To address this issue, we applied these three complementary types of body

154   condition indices. If the results of the indices are consistent it would suggest that the result is

155   robust. We also tested for the distributional assumption of normality of these parametric models

156   using a Shapiro-Wilk test. To determine if body condition changed with infection status and age

157   or sex, we used linear models with infection status and an interaction effect with age (hatch-year

158   or juveniles-HY or after hatch-year or adults-AHY), or sex (male or female) as a predictor for

159   body condition. Note that we conducted different models for age and sex and only on individuals

160   with known sex or age, and infection status. We tested the need to add the mist-netting site as a

161   random effect using a likelihood ratio test. We conducted the statistical analysis using R

162 statistical software v4.3.0 (R Core Team 2019). We used the following packages for data

163 organization, analyses, and visualization: "ggplot2" (Wikham 2016), "dplyr" (Wikham 2023),

164 "lme4" (Bates et al. 2015), "lmerTest" (Kuznetsova et al. 2017), "Matrix" (Bates et al. 2023),

165 "tidyverse" (Wikham et al. 2023), "devtools" (Wikham et al. 2022), "ggbiplot" (Vu 2011),

166 "sjPlot" (Ludecke 2023), "sjmisc" (Ludecke 2018), "sjlabelled" (Ludecke 2022), "snakecase"

167 (Grosser 2019), "RColorBrewer" (Neuwirth 2022), "RLRsim" (Scheipl et al. 2008), "ggpubr"

168 (Kassambara 2023), "olsrr" (Hebbali 2020) and "effects" (Fox and Weisberg 2018).

169 **Results**

170 **Body condition and infection status**

171   We captured a total of 79 Bananaquits and collected blood samples from 66 individuals.

172 Thirteen individuals were not included in the analyses either because they escaped before the

173 processing was completed, available blood after puncturing the brachial vein was insufficient, or

174 because the blood coagulated in the capillary tube. Out of these, 47 were classified as adults

175 (AHY), 13 were classified as juveniles (HY) and 2 were unidentified (U) (Table S2). From the

176 total captured, we were able to classify 19 as male and 10 as females. A total of 18 individuals

177 were detected through molecular diagnostics as infected by haemosporidian parasites for an

178 overall prevalence of 27% from the sampled population. Most infections corresponded to the

179 genus *Haemoproteus* (n=15) followed by parasites from the genus *Plasmodium* (n=3) and 3

180 unclassified positives. *Plasmodium* infected individuals were not included in the analysis.

181   As expected, the linear regression model of log(weight) as a function of log(wing length)

182 showed a clear positive relationship ($t = 6.20$, $p < 0.001$, $R^2 = 0.39$; Table S3a). Similarly, the

183 linear regression model of log(weight) as a function of log(tarsus length) also showed a strong

184   positive relationship ($t = 2.98$, $p < 0.01$, $R^2 = 0.13$; Table S3b). Tarsus and wing length were

185   moderately correlated ($r = 0.32$).

186   On average, the body condition of infected Bananaquits was higher than uninfected ones

187   (0.05 ± 0.02 SE) when comparing body weight relative to wing length ($t = 2.16$, $p = 0.04$; Fig

188   2A; Table S4a). Similarly, the body condition of infected Bananaquits was higher than

189   uninfected ones (0.07 ± 0.03 SE) when comparing body weight relative to tarsus length ($t = 2.59$,

190    $p = 0.01$; Fig 2B; Table S4b). The linear mixed-effects model for wing length showed a singular

191   fit and the likelihood ratio test comparing the tarsus-length model with and without a random

192   effect for site show no clear evidence for the need for this random effect ($LRT = 0.20$, $p = 0.21$).

193   Therefore, we made the inferences above using fixed effects models.

194   Although the distribution of wing length deviated slightly from a normal distribution, we

195   kept it in the PCA model after inspecting the histogram and quantile-quantile plot that showed

196   just small deviations from normality (Fig S2–S4). The first axis, PC1, explained 62.7% of the

197   variance, while PC2 explained 24.6%. Similar to the residual body condition index, the model

198   predicting PCA body condition index as a function of infection status showed that infected

199   Bananaquits had higher body condition ($b_1 = 0.96 \pm 0.40$ SE) than uninfected individuals ($t =$

200   2.43, $p = 0.02$; Figure 2C, Table S4c).

201   **Individual heterogeneity in body condition by infection status**

202   We did not find evidence that the effect of infection on the Bananaquit body condition

203   varied by age ($N = 60$) or sex ($N = 29$). Age did not significantly contribute to variation in the

204   body condition index either using weight relative to wing (interaction: $t = -1.01$, $p = 0.32$; Table

205   S5a) or tarsus length (interaction: $t = -0.11$, $p = 0.91$; Table S5b), or using the PCA body

206   condition index (interaction: $t = -0.31$, $p = 0.76$; Table S5c; Fig. S5). Similarly, sex did not

207   significantly contribute to variation in the body condition index using weight relative to wing

208   (interaction: $t = -0.61$, $p = 0.55$; Table S6a) or tarsus length (interaction: $t = -0.02$, $p = 0.98$; Table

209   S6b), or using the PCA body condition index either (interaction: $t = 0.51$, $p = 0.62$; Table S6c)

210   (Fig. S6).

211   **Discussion**

212   Many studies have described the negative consequences of malaria infection to naïve

213   bird populations (LaPointe et al. 2012). Still, we know less about the consequences of infection

214   in regions where the parasite is endemic and infections chronic. While a decrease in host

215   survival, fecundity or other sub-lethal measures are an expected outcome of many parasitic

216   infections (Hasik and Siepielski 2022), our results showed that infected individuals had higher

217   body condition than uninfected ones. We found no clear evidence that these effects varied with

218   sex or age. Therefore, our results suggest that there may be alternative underlying mechanisms

219   that do not necessarily result in negative consequences for body condition. Three non-mutually

220   exclusive hypotheses may explain this result: (1) metabolic syndrome that predicts higher fat

221   storage in infected individuals, (2) host tolerance or resistance to infection, and (3) changes in

222   foraging behavior.

223   Parasite infection can trigger immunological responses that often lead to inflammatory

224   reactions, a decrease in muscle performance, and increased levels of carbohydrates in the blood

225   which is commonly known as the metabolic syndrome (Schilder & Marden 2006). Excess

226   carbohydrates and lipids can explain why some individuals have better body condition (i.e.,

227   larger mass relative to the average). In birds, accumulated lipids provide extra energy storage to

228   survive long-distance travel (Guglielmo 2018) and in some species like the Blue Petrel is

229   associated with improved reproductive success (Chastel et al. 1995). Still, during our sampling

230   period, our study species showed little to no body fat accumulation (per. obs.), which is

231   consistent with Bananaquits in moist forests. Therefore, while metabolic syndrome may explain

232   fat accumulation in other species, there is no strong evidence supporting this hypothesis in our

233   host-parasite system.

234   Immunological strategies such as tolerance and resistance may also explain the body

235   condition patterns in our study (Sorci 2013). Tolerant individuals do not reduce or clear the

236   infection but have mechanisms to reduce their negative effects on their survival, reproduction or

237   other sub lethal effects (Medzhitov et al. 2012). Hence, tolerant individuals suffer small to no

238   parasite-induced mortality or changes in body condition. For instance, tree swallows and eastern

239   bluebirds' nestlings show no decrease in survival when infected by the parasitic flies

240   (*Protocalliphora sialia*) (Grab et al. 2019). In rodents, it has been shown that infection by

241   macroparasites leads to increased body condition (Jackson et al. 2014). Alternatively, resistant

242   individuals reduce or clear parasite infection by activation of innate and adaptive immunological

243   responses (Medzhitov et al. 2012). Contrary to tolerance, resistance can be costly to host fitness

244   because it often results in tissue damage through the immunological response activation to

245   eliminate the pathogen (Medzhitov et al. 2012). For instance, a study of the Seychelles warbler

246   found that individuals' infection status was related to reactive oxygen metabolites (ROMs; van

247   de Crommenacker et al. 2012). During the breeding stage, ROMs were significantly higher in

248   infected individuals compared to non-infected individuals, which may indicate an immunological

249   activation and/or the metabolic residual of the parasite infecting the individuals. Higher body

250   condition of infected individuals compared to uninfected individuals may suggest a tolerance

251   mechanism on the host because body condition parameters show no negative effects on host

252   physiology (Atkinson et al. 2013). One related plausible hypothesis is that we are more likely to

253   trap chronically infected individuals because acutely infected individuals may suffer from lower

254   mobility (Mukhin et al. 2016) and, thus, may be less likely to be trapped in our mist nets. . While

255   our data does not allow us to differentiate between tolerance, resistance, or trapping bias, these

256   remain key alternative hypotheses to test in future studies. For instance, previous studies have

257   experimentally infected individuals to track their immune responses and other physiological

258   factors through peak infection and beyond (Adelman et al. 2013).

259   As a response to offsetting the cost of infection, host species may change behavior by

260   increasing their foraging activity which can ultimately result advantageous to the host and the

261   parasite (Weinersmith & Earley 2016). While a recent meta-analysis showed that parasite-

262   infected hosts consume on average 25% less food than uninfected individuals, the study showed

263   great variability among taxa with multiple examples of the opposite pattern (Mrugala et al.

264   2023). For instance, parasite-infected rusty crayfish consume more macrophytes and

265   macroinvertebrates than uninfected ones likely due to increased feeding behavior boldness

266   induced by infection (Reisinger and Lodge 2016). Also, hosts with access to more or higher

267   quality food resources would have on average better body condition and thus experience higher

268   parasitism rates because they are optimal hosts for the parasite. Indeed, Hasik & Siepielski

269   (2022) found that hosts with access to more prey were more heavily parasitized, though they did

270   not relate this increased parasitism to the quality of the host for the parasite. The relationship

271   between cost of infection and feeding behavior is likely mediated by food availability. Our study

272   species, the Bananaquit, is a generalist highly adapted to exploit a wide variety of food resources.

273   Therefore, the availability of a wide variety of food resources combined with a potential increase

274   in foraging activity as a compensatory behavioral response to infection (Ots et al. 1998, Sorci

275   2013, Toscano et al. 2014) may also explain an increase in body condition. Natural disturbance

276   can also have a mediating role in the effects of parasite infection on hosts' health (Sousa 1984).

277   In September 2017, Puerto Rico suffered the impact of a strong category 4 hurricane that

278   devastated a large portion of the island causing high mortality in flora and fauna, including birds

279   (Wunderle 2018). Haemosporidian-infected individuals suffering strong negative consequences

280   of infection may have suffered increased mortality due to the hurricane resulting in a strong

281   selection event for tolerant individuals. Previous studies have shown variable effects on

282   individuals after natural disturbances. For instance, a study of Cerulean warblers' responses to

283   simulated natural disturbances in the Appalachian Mountains showed that males in areas of less

284   disturbance had better body condition compared to males in areas of heavy disturbance (Boves et

285   al. 2013). In contrast, amphibians showed a reduced risk of Bd (*Batrachochytrium*

286   *dendrobatidis*) infection in areas with higher canopy openings resulting from Cyclone Yasi

287   compared to undamaged areas (Roznik et al. 2015). Therefore, hurricane disturbance may have

288   been a strong selection event that had a mediator effect on the result of our study.

289   Lastly, we found no clear statistical evidence of changes in the consequences of infection

290   due to sex or age. There are strong theoretical arguments to suggest that sex and age of the

291   infection are key determinants of quantifiable virulence traits of the host (Day 2003, Frank and

292   Schmid-Hempel 2008, Lively 2010). There is also empirical support for this theoretical idea in

293   many host-parasite systems (e.g. Sorci and Faivre 2022, Izhar and Ben-Ami 2015, De Roode et

294   al. 2006). There are two potential explanations for the lack of evidence in our study. Our sample

295   size was limited when dividing the data among sex or age. Therefore, if the effect size of the

296   effect of infection by these covariates in this system is small, the analyses may not have enough

297   power to detect them. Alternatively, there may not necessarily be a strong difference between

298   these traits. For instance, a recent meta-analysis on parasitism and host fitness variation also

299   shows no clear effect by sex (Hasik and Siepielski 2022). But they found high variability and

300   some studies in avian malaria still have found differences in infection rates by sex (e.g., Calero-

301   Riestra and Garcia 2016). Thus, potential heterogeneities in virulence due to age or sex are still a

302   plausible hypothesis worth further consideration.

303   **Conclusions**

304   Our study provides insights into the consequences of malarial infections to the most

305   common bird in the Caribbean showing that infected individuals had higher body condition

306   compared to uninfected individuals. Multiple hypotheses can explain the pattern in our system

307   including tolerance in infected individuals. The tolerance hypothesis is an interesting explanation

308   for the observed patterns in our study that can be further tested by conducting controlled

309   infection experiments.

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Figure 1

Diagnostic techniques of *Haemoproteus* parasite infection in the Bananaquit

A) Sample 095 is positive for haemosporidian infection with a band at approximately 500 bp. Bands at 50 bp are primer dimers, a by-product of the PCR. B) Image shows a Giemsa-stained slide showing an infected erythrocyte of sample 095. Red arrow indicates an erythrocyte infected by an haemosporidian. Although we show a Giemsa-stained slide, all analyses were based on molecular diagnostics.
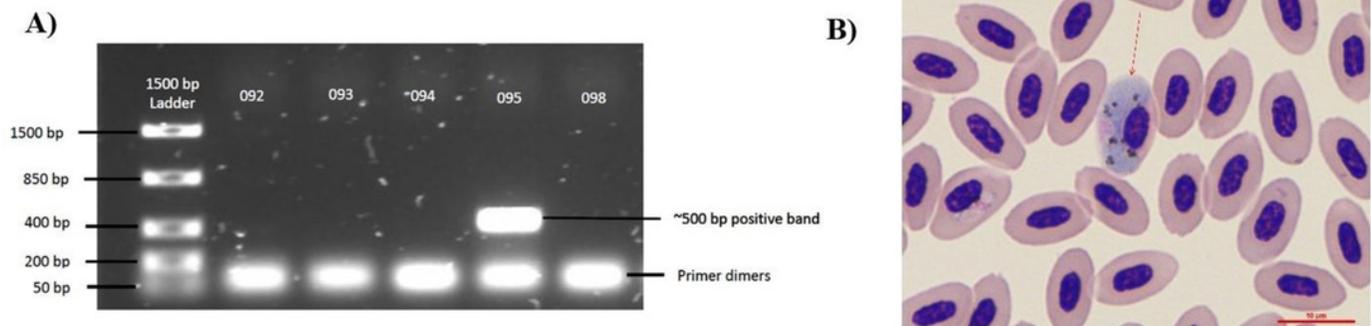
Figure 2

Comparison between body condition of uninfected and infected Bananaquits by *Haemoproteus* parasites using two residual body condition indexes and a PCA body condition index

Comparison of body condition of uninfected (n=47) and infected by *Haemoproteus* (n=15) Bananaquits using a (A) wing and weight residuals index, (B) tarsus and weight residuals index and (C) PCA body condition index. The horizontal dash line at zero represents the average body condition. Individuals above the line have higher body mass than average, while individuals below the line have lower body mass than average. Jittered dots indicate individuals included in the analysis and their classification as non-infected and infected individuals. The lines indicate the 95% confidence intervals, dot indicates the point estimate of the model of the non-infected individuals and triangle indicates the point estimate of the model of the infected individuals.

A)

B)

C)