This article quantifies the relationship between parasitism and social network centrality and dominance in Japanese macaques. Overall, the paper is well written and interesting. I do have some comments on the structure of the introduction and the statistical analysis that will hopefully help improve the paper for publication.

Please note, there are no line numbers – so in some cases the line numbers I provide are approximate.

Major comments

Introduction: I think the introduction is overall well written, but I think a bit more detail and precision earlier on in the introduction would benefit the paper and provide the paper with more of a focus (specific comments below). I also think the last paragraph of the introduction could be a bit more explicit about the hypotheses being tested and the associated predictions. Currently, there is no hypothesis – so I would suggest starting there and then introducing the predictions in the context of the hypotheses.

Page 3, line 1: this is the same sentence as the first sentence in the abstract. Perhaps change up the language a little bit between these sections.

Page 3, lines ~4-7: this sentence is kind of long and unwieldly – is there any way it can be separated into fewer sentences that provide more specifics about each of the factors (i.e. density, more social partners etc) that might influence increase transmission?

Page 3, lines ~14-18: the sentences about how social interactions are structed by kinship, dominance etc as well as the subsequent sentence suggesting that social structure should influence exposure to parasites should both have a references.

Page 3, lines ~19: does "accounting for social structure" help make sense of parasite transmission? I would argue that we don't use social networks to account for social structure, we use social networks as the tool to directly test the relationship between social processes and other ecological processes (in this case parasitism). I would suggest revising this sentence accordingly.

Page 3, lines ~20-21: what can provide more information and what type of information? I would suggest this last sentence on page 3 needs to be more precise and answer the question of "why" the relationship between social behaviour and parasitism is important in the evolution of animal behaviour.

Page 4, lines ~21-22; Page 5 lines 6, 13, 15, and 16: at all of these liens the authors discuss immune responses. This is clearly a very important aspect of parasitism, however, the present study does not quantify immune responses and so I found the repeated mention of immune response and systems to be somewhat misleading. I would suggest limiting the introduction of

immune responses in the introduction and focussing instead of the variables that are actually measured in the paper (i.e. dominance, centrality, age, and sex).

Statistical analysis: overall, I think the authors did the right things, I just have some clarifying comments and some suggestions to ensure the analyses are as robust as possible. See below for specific comments on the stats.

Page 13-14: I think the description of the model set up is confusing given the number of fecal samples and number of parasite species differs per individual. It is unclear to me if for each fecal sample per individual there is a new row with the same information for all other variables? If so, why not average the parasite numbers across samples – especially given that the social network represents the sum of social encounters over the full study period, presumably the average number of parasites per fecal sample should correspond? My concern specifically is that if the same information is included multiple times in the model, there is non-independence and the coefficients will be inflated. For example, if the dataset were to look like this:

Animal ID	Parasite score	Degree	Age	Sex
1	0.5	10	2	M
1	0.7	10	2	M
2	0.1	6	4	F
2	0.3	6	4	F

My concern with this type of data structure is that the data for degree, age, and sex is replicated for each individual and included in the models multiple times. As I understand it, even accounting for ID as a random effect will still inflate coefficients because the only data that are changing is the response variable (i.e. parasitism). The alternative option is to have shorter time frames to build social networks so that if a fecal sample was collected on day 10 of the study, the degree of that individual in the days around the time of that sample would be different from the degree around day 50 (or something like that). I think this would be an elegant solution to the problem, but would require making many mini-focal networks for each individual around the time a fecal sample was collected. A good example of a study that does something like this is Turner et al. 2021 (https://doi.org/10.1111/1365-2656.13282). I would say that it isn't necessarily easy, but I would argue that perhaps it is the right way to do it.

Page 14, lines 10-17: this is an interesting interpretation of the Webber et al. (2020) paper discussing the use of multiple social network metrics. As one of the authors of this paper, I would argue that the authors missed the point a little bit and the spirit of the "less is more" approach is really about *a priori* selecting a single network metric. I would also point out that model averaging has been highly criticized and may not be appropriate (see Cade 2015 https://doi.org/10.1890/14-1639.1). My recommendation would be to remove the model averaging and select a single metric and run a single model.

Page 15, line 16: I have never used, or heard of, the rewire function. Perhaps some more detail is required here? I also would suggest the authors consider explaining the randomizations in a little more detail. Does the rewire function randomly re-assign interactions between individuals throughout the dataset? What if animals A and B didn't interact until day 50 of the study – do the authors account for temporal (or spatial) heterogeneity in interactions? Typically, network randomizations hold everything constant (i.e. space, time, group size) and shuffle the identities of individuals interacting/associating within a given sampling period. The recent review by Hobson et al. 2021 (https://doi.org/10.1111/brv.12775) is a great over-view of the theory and application of network randomizations, which I would suggest the authors read and adopt the terminology used in this paper.

Figure 2: I would suggest the panel with sex should be a boxplot with the points jittered behind the boxes. I would also suggest indicating in the caption that the values on the x-axis are scaled (as opposed to having "scaled value" written next to the top left panel). Also, the panels are missing y-axis labels and units. I assume it's EPG, but this should be included.