

Review on PCI Ecology revised ms by A Sevchik, C Rowney, CJ Logan, A Blackwell & D Lukas

This revised version of the manuscript takes into account all comments made on the first round, and I find that the new outline of the main and alternative hypotheses is much clearer and faithful to what the authors have explored and tested. I do have a some remaining comments however, and overall, I felt that important statements should be supported by literature, while the reference list is presently very thin.

In the introduction, the very simplified version of hypotheses outline avoids several confusing predictions that were present in the initial manuscript. I do find it very dry now, with even less biological insight on the species allowing one to formulate reasonable predictions, yet I understand that perhaps the knowledge is lacking preventing clear elaborate predictions. Related to this comment on natural history insight, is the fact that the focal population is urban, and it might well be that dispersal patterns in such environments are not similar to what happens in wild areas. This is a comment I made earlier (R1.4) on which the authors chose not to include a mention in the ms. I do feel that it may be an important feature to mention since results could have been very different in a wetland or mangrove.

Also, I am somewhat uncomfortable with the use of the term 'predict'. Usually predictions are tested and following the results, they are confirmed or invalidated. Here, some of the 'predictions' are rather assumptions that are essential to make further predictions, but they are not themselves predictions. For ex., take this prediction from line 88 "We predict that the movement of individuals will influence the spatial distribution of genetic relatives", testing this prediction would require to compare the distribution of genetic relatives between groups of individuals that move or do not move, in order to show that movement is related to genetic relatedness. This is not what the authors have done, and in fact they probably don't need to do that as this relationship is already well described for many species. So in this sentence, I would not use the term 'predict', but rather 'we assume', or simply 'Our study is based on the fact/assumption that..', ideally supported by a few references. I am not including this comment in the minor details section below as I do not think it is 'just' one word to change in the text, I think the authors need to rethink what they consider a prediction.

Finally, I was struck by the mention line 234 that the authors consider they have a "large number of SNP loci": although 635 SNPs might have been a common genomic sample size 10 years ago, it is now in the low end of sample sizes used, so I wouldn't call it a large number of SNPs. In fact, I am surprised that this low SNP number and the potentially low power to assess relatedness is not discussed, and that generally the ms contains very few insight and references on genetic/genomic approaches to estimate relatedness since this is an important topic for the authors' aims. See for example:

- A comparison of 16 microsats vs 4800 RADseq SNPs :
<https://onlinelibrary.wiley.com/doi/full/10.1002/ece3.4905>
- Santure 2010: <https://pubmed.ncbi.nlm.nih.gov/20149098/>, see in particular their conclusion that "Our data suggest that using marker information to reconstruct the pedigree, and then calculating relatedness from the pedigree, is likely to give more accurate relatedness estimates than using marker-based estimators directly"
- Smouse 2010 - how many SNPs are enough (summarising Santure):
<https://pubmed.ncbi.nlm.nih.gov/20456228/>
- There are probably more recent papers on this topic!

Minor details

- Line 79: I don't understand why there is a 'Hypothesis' term at the start of this line, isn't it the same main hypothesis as in the previous paragraph?
- Line 96: individuals is misspelled.
- I do not see the difference between the 'first' prediction outlined lines 93-94 ("higher levels of average relatedness are expected among all individuals of the philopatric sex than among all individuals of the sex that disperses") and the 'second' prediction in lines 96-97 ("finding close genetic relatives in short distances from each other indicates that these individuals have remained philopatric"). I think this might be because of the formulation of the second prediction, which could be rephrased, but they also might be redundant predictions.
- Line 101: Will this preregistration mention appear in the final ms? Are details in this preregistration essential for the good understanding of this ms? If so I feel that it would be better to have them included in the present ms rather than for the reader to have to download also the preregistration document. Reading the methods section, it feels like in fact it has been updated, hence I think it would be clearer to simply remove the preregistration mention, but I will let the Editor decide on this.
- Line 158: I would remove "the" in front of "individuals"
- Results are presented alternatively in past tense (e.g. line 157 and onwards) and present tense (e.g. lines 170 and onwards). Please homogenize.
- Lines 174-181: what is the criterion to decide that distances are shorter or not different to what is "expected by chance"? This criterion is particularly elusive in the case of males since you have only one closely related male dyad.
- Table 1's title requires more detail to explain what are the corrected probabilities.
- Line 224: "to where they hatched" is in fact, if I'm not mistaken, a speculation, since you do not have data on where any of the birds have hatched, right? I think this point should be clarified.