

Second review of the preregistration “Investigating sex differences in genetic relatedness in great-tailed grackles in Tempe, Arizona to infer potential sex biases in dispersal” by Sevchik et al., submitted to PCI Ecology

The authors have done a great job responding to both reviewers. They addressed each comment with care, which lead to clarify several aspects. In particular, I am very happy with the new way the authors present their alternatives and the corresponding predictions, this is much clearer and easier to visualize! The Mantel correlogram analysis is better described. I have one remaining major comment about alternatives (plus very few minor comments).

Alternatives 1 and 5: Globally, I am confused with the new alternatives 1 and 5 which involve both dispersal rates and dispersal distances. This makes the predictions a bit hard to follow, and raises the question of why you did not include the other possible alternatives (eg dispersal rate males > females and dispersal distance males < females). Alt 1 and 5 may rather be seen as limitations of the study; ie the negative relationship you expect to observe between relatedness and distance in males under your main hypothesis may be weakened by the strong dispersal of few males (alt1) or the weak dispersal of all males (alt5).

Moreover, I am unsure about the predictions for alt 1 and 5. Maybe this reflects the difficulty to make accurate predictions when introducing more variables (rate and distance).

Alternative 1:

- analysis i: if only very few males disperse, I do not expect mean relatedness in males to decrease to the point of being similar to females, because there would still be many male relatives in the sampled area.
- analysis iii: I do not expect a U-shaped relationship for males. In high distance classes, a majority of philopatric males would still be associated to unrelated males. Moreover, the few males that disperse would be associated to some related males at high distance, but mostly to many unrelated males, thus positive autocorrelation should not be expected for high distance classes.

Alternative 5:

- analysis iii: I do not expected an inverted U-shaped relationship for males. Males are not expected to be very unrelated at short distance if they do not move very far, so I don't think there will be a negative autocorrelation at short distance classes. Moreover, you will not find only relatives at intermediate distances, but also unrelated individuals, so there will be no positive autocorrelation for intermediate distance classes.

To conclude, in my opinion, it would be better to keep things simple. It may be clearer to remove alternatives 1 and 5, and maybe include more information on signal weakness in the limitations of the study.

Minor comments

Reply 11 from the response to reviewers: I did not mean to suggest a new alternative; rather I was trying to understand the sentence I quoted. I think there has been a misunderstanding, because on the

previous version of the manuscript the sample area was described as within a 500m circle (contrary to a 1000m radius circle in the present version). I was referring to the possibility that males move outside the campus area, but I was just trying to describe how I understood the sentence of the authors. Sorry for any confusion.

B. Hypothesis “the third [analysis] aims to determine separately for each sex whether individuals are likely to have dispersed or not”: autocorrelation analysis does not provide the likelihood of dispersal for individuals, but describes the genetic structure in the population in regards with relatedness. Please reformulate.

Figure 1: please remove the box on the top left corner mentioning genetic diversity, or adapt its content in regards to relatedness. In the legend, change “higher levels of genetic relatedness than *males*” to “higher levels of genetic relatedness than *females*”

Ability to detect actual effects: “the signal might be too inclusive in either or both sexes” I don’t understand what you mean with “inclusive”... Weak?

Analysis Plan. Analysis iii: Given the modification of the sample area size from the first version of the manuscript, the authors have modified the bin size from 50 to 200m. I suggest being careful with this change: a too big bin size may lead to group both related and unrelated males in the smallest class, which will prevent detection of the expected positive autocorrelation. This is especially relevant here as males are expected to move around 50m because of the distance between trees if I understand correctly. Maybe a way to resolve this issue is to try several bin sizes as suggested in Peakall et al 2003: “Sampling at intervals greater than the scale of genetic structure will fail to detect the genetic structure at all, whereas sampling at intervals well below the scale of genetic structure may be associated with unnecessarily small sample sets, and therefore limited statistical power. Because there is no a priori way to predict the extent of genetic structure from a single autocorrelation analysis, we have calculated r (along with associated errors about r and the null hypothesis), for increasing distance class sizes that span the minimum distance between samples to the maximum distance of sampling (10–800 m). »